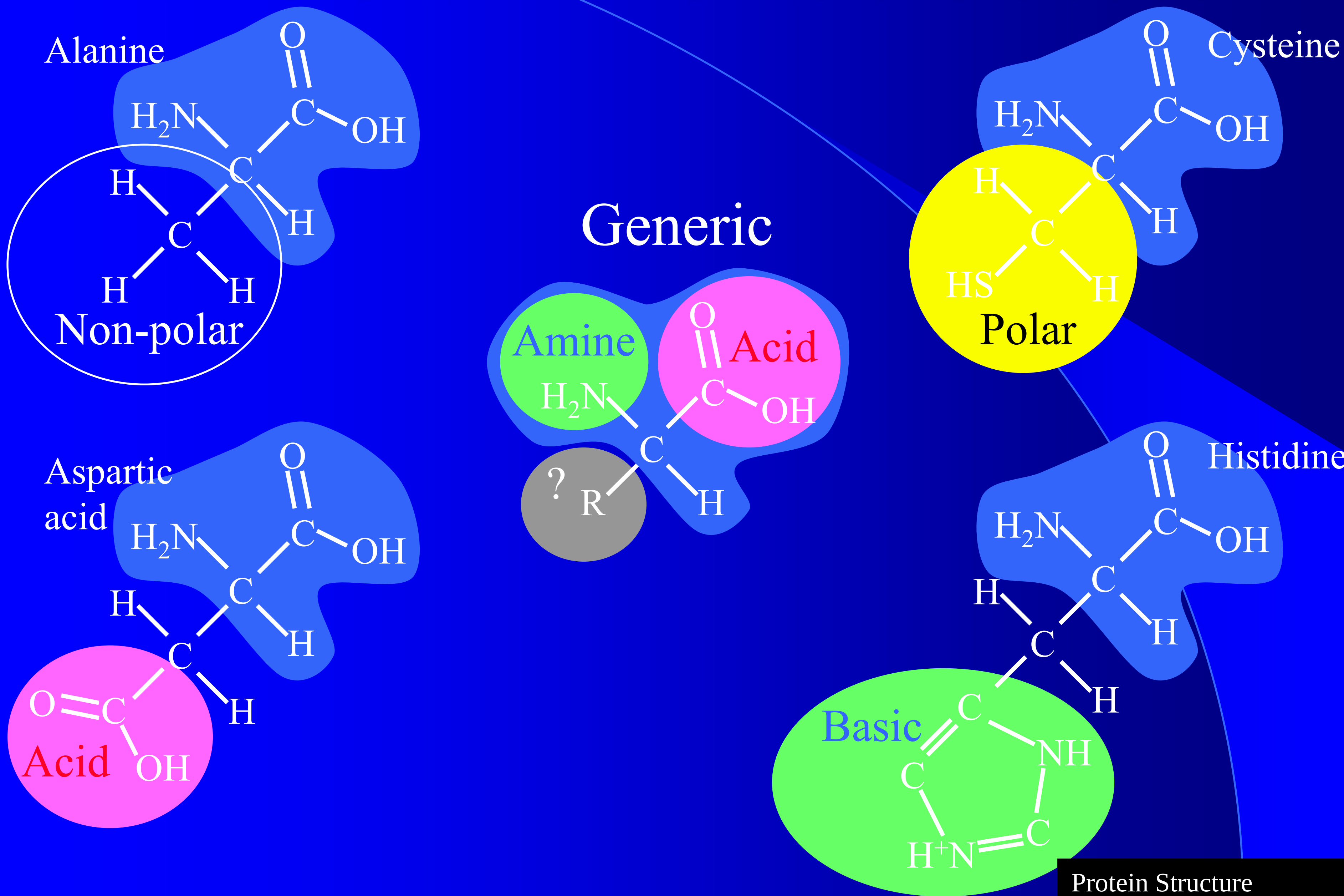
Bielkoviny, enzýmy

Július Cirák

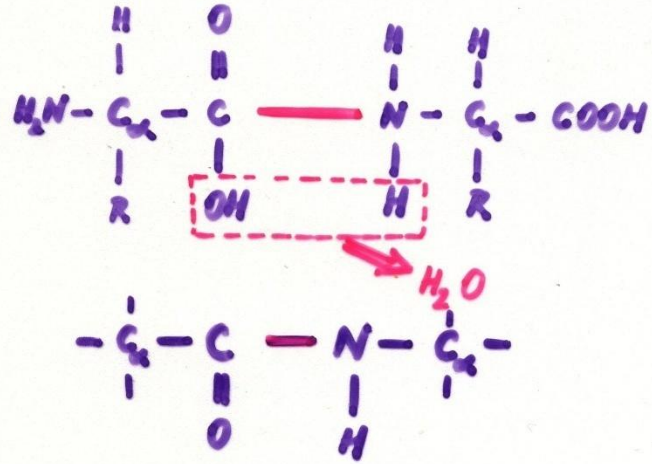
Different Amino Acid Classes

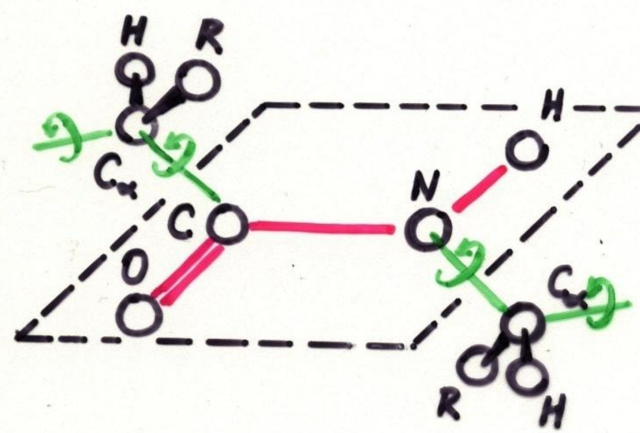


Levels Of Protein Organization

- **Primary Structure -** The sequence of amino acids in the polypeptide chain
- **Secondary Structure -** The formation of α helices and β pleated sheets due to hydrogen bonding between the peptide backbone
- **Tertiary Structure -** Folding of helices and sheets influenced by R group bonding
- **Quaternary Structure -** The association of more than one polypeptide into a protein complex influenced by R group bonding

BIELKOVINY (PROTEINY)





Levels Of Protein Organization

Primary Structure

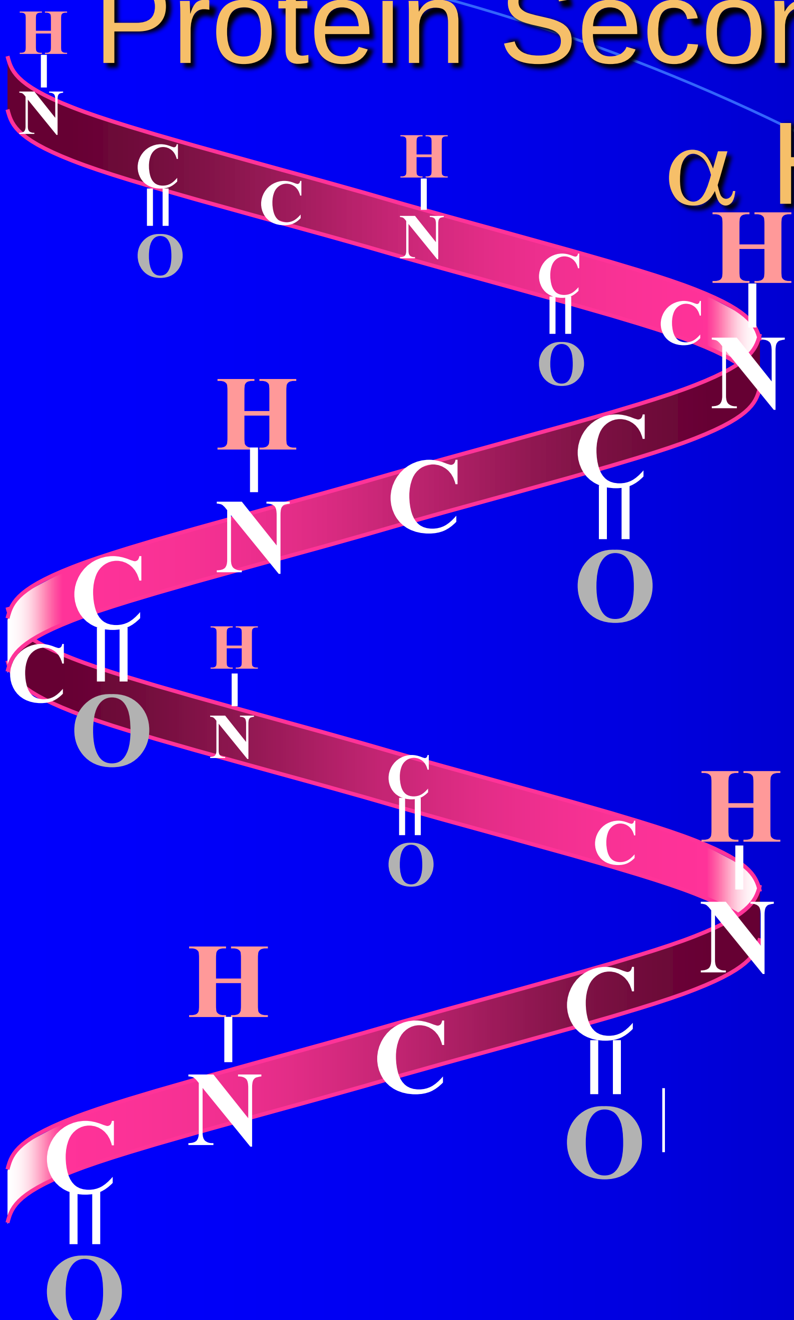
Met-Gly-Ala-Pro-His-Ile-Asp-Glu-Met-Ser-Thr-...

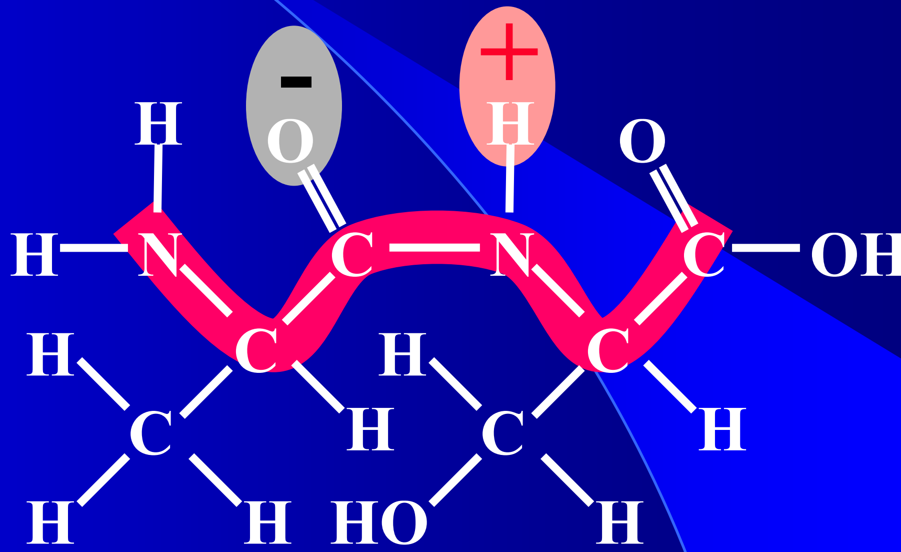
The sequence of amino acids in the primary structure determines the folding of the molecule.

Protein Secondary Structure

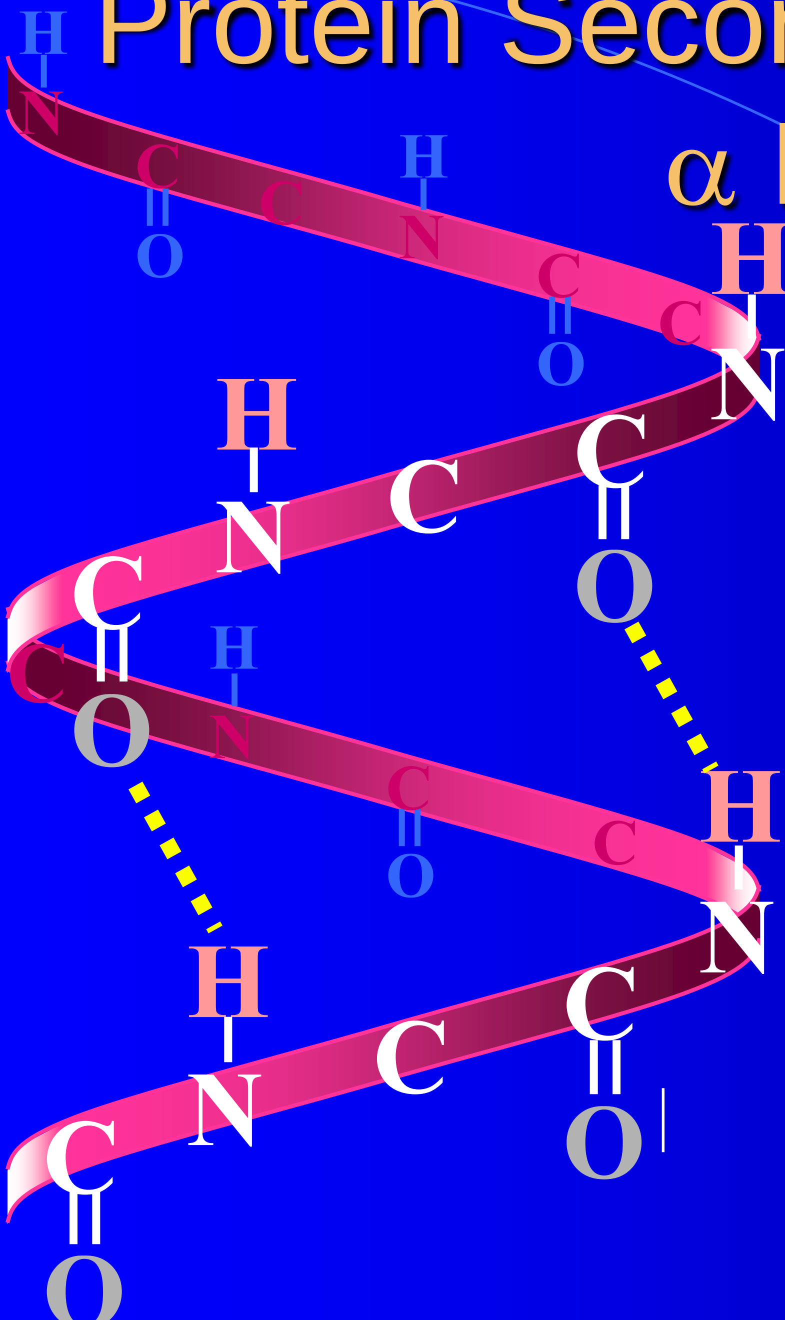
- The peptide backbone has areas of positive charge and negative charge
- These areas can interact with one another to form hydrogen bonds
- The result of these hydrogen bonds are two types of structures:
  - α helices
  - β pleated sheets

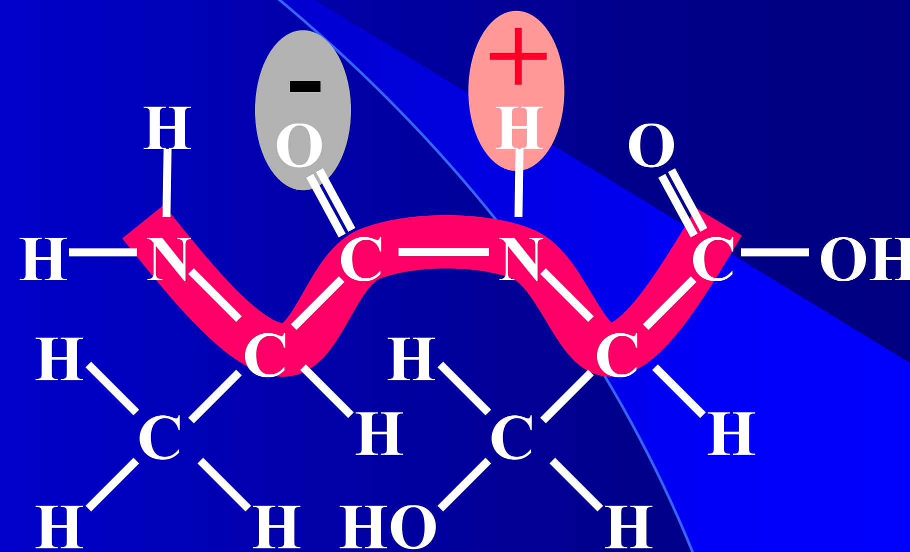
Protein Secondary Structure: α Helix





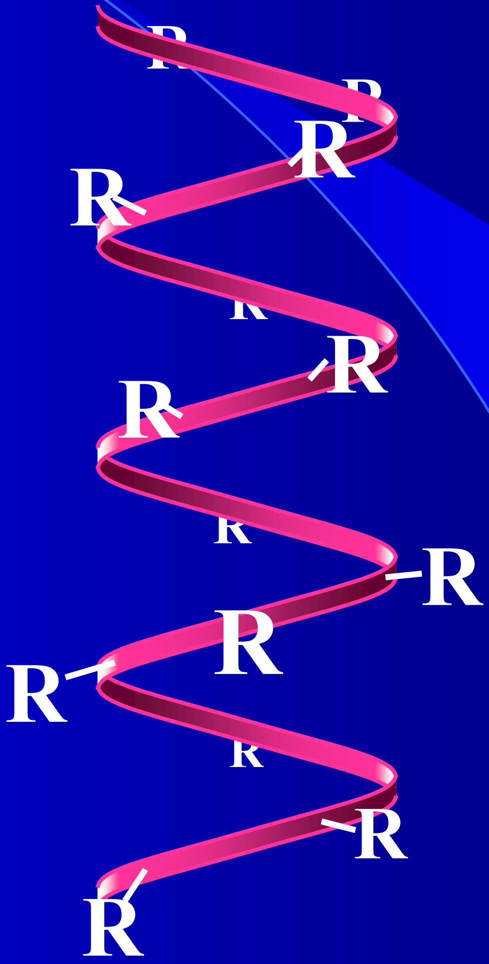
Protein Secondary Structure: α Helix



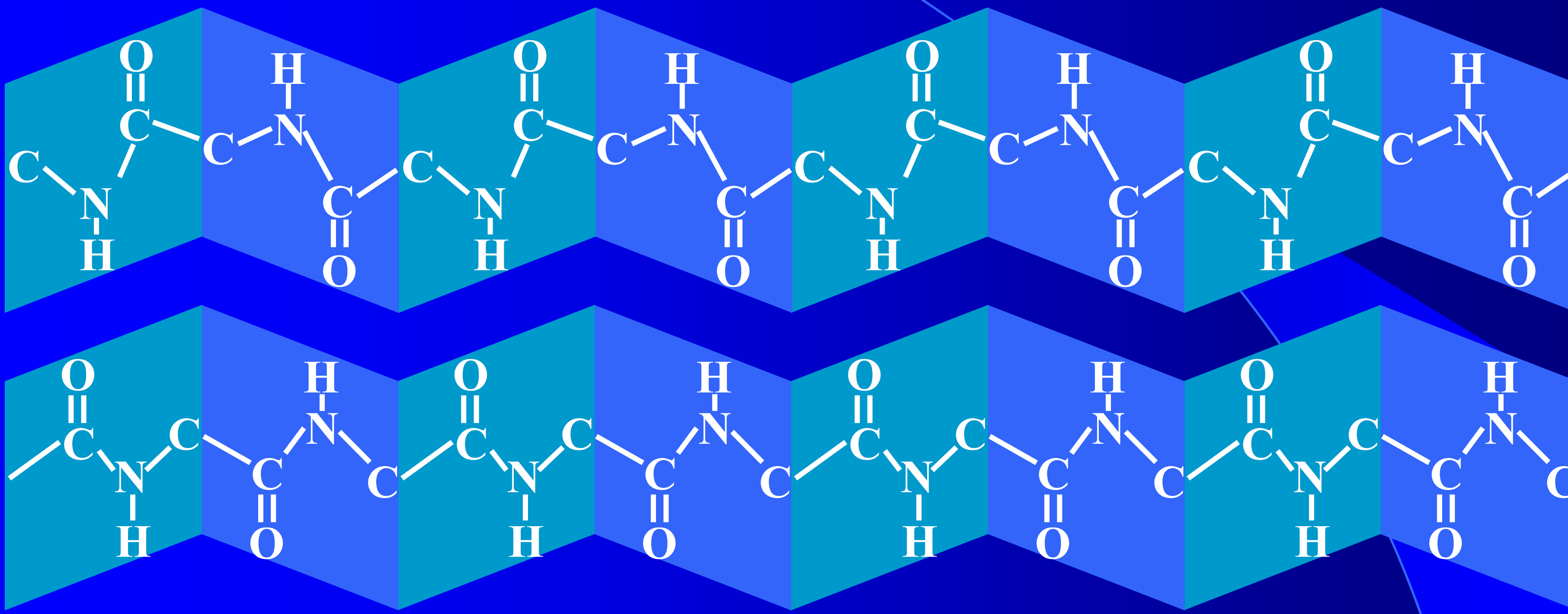


Protein Secondary Structure: α Helix

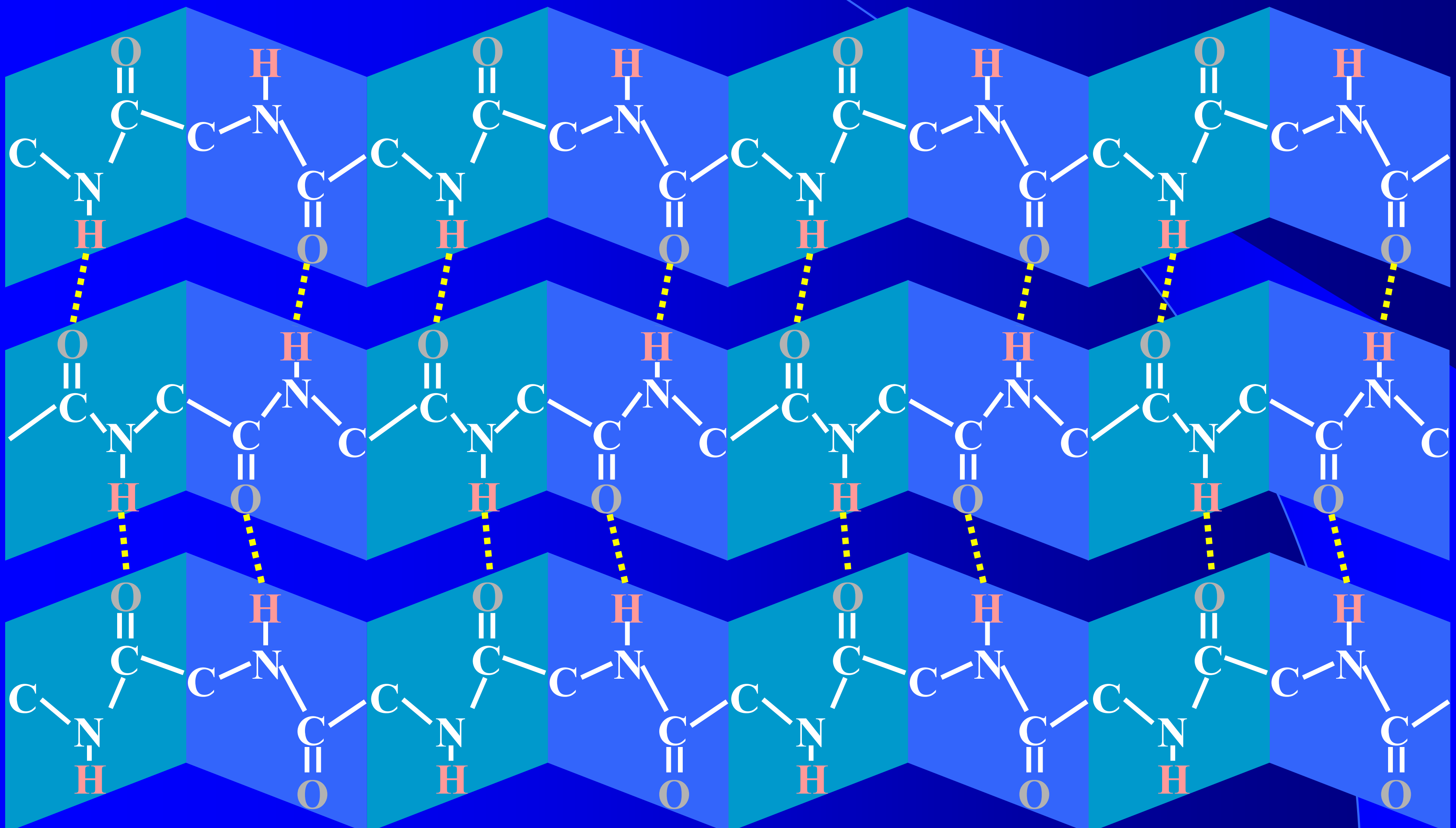
R groups stick out from the α helix influencing higher levels of protein organization



Protein Secondary Structure: β Pleated Sheet



Protein Secondary Structure: β Pleated Sheet



Levels Of Protein Organization
Tertiary Structure

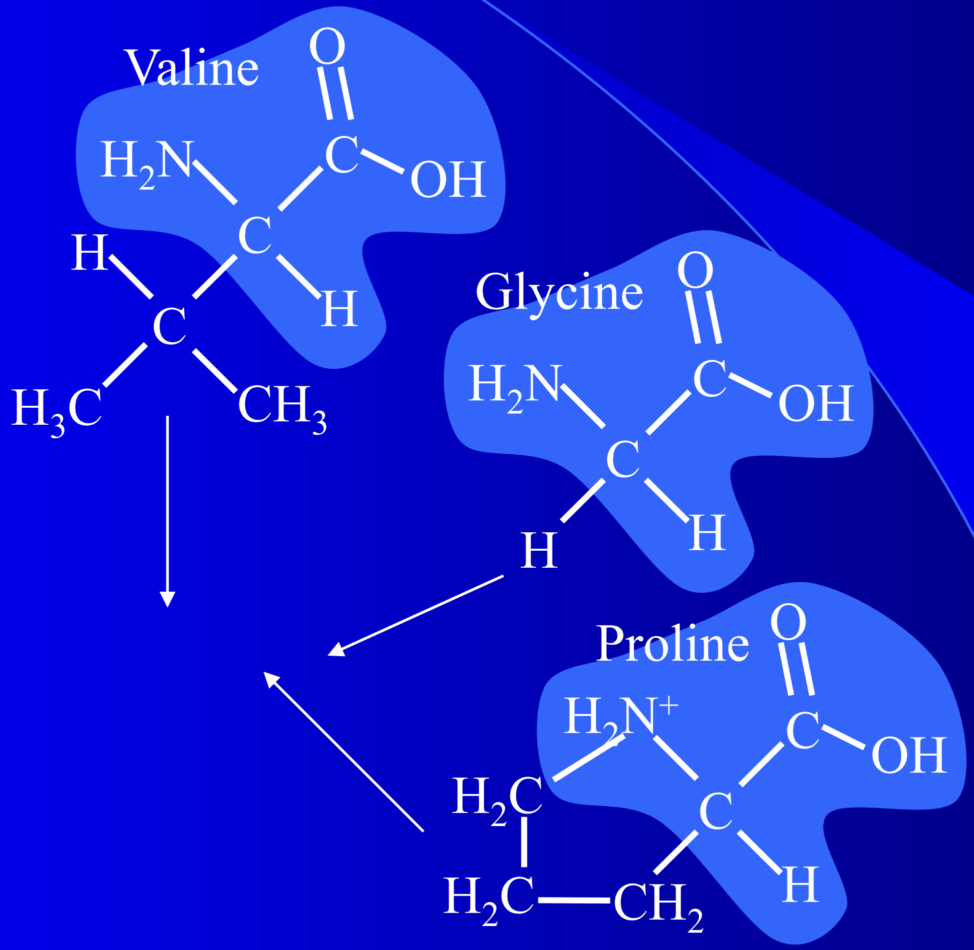
- Tertiary structure results from the folding of α helices and β pleated sheets
- Factors influencing tertiary structure include:
- Hydrophobic interactions
- Hydrogen bonding
- Disulphide bridges
- Ionic bonds

Globular and Fibrous

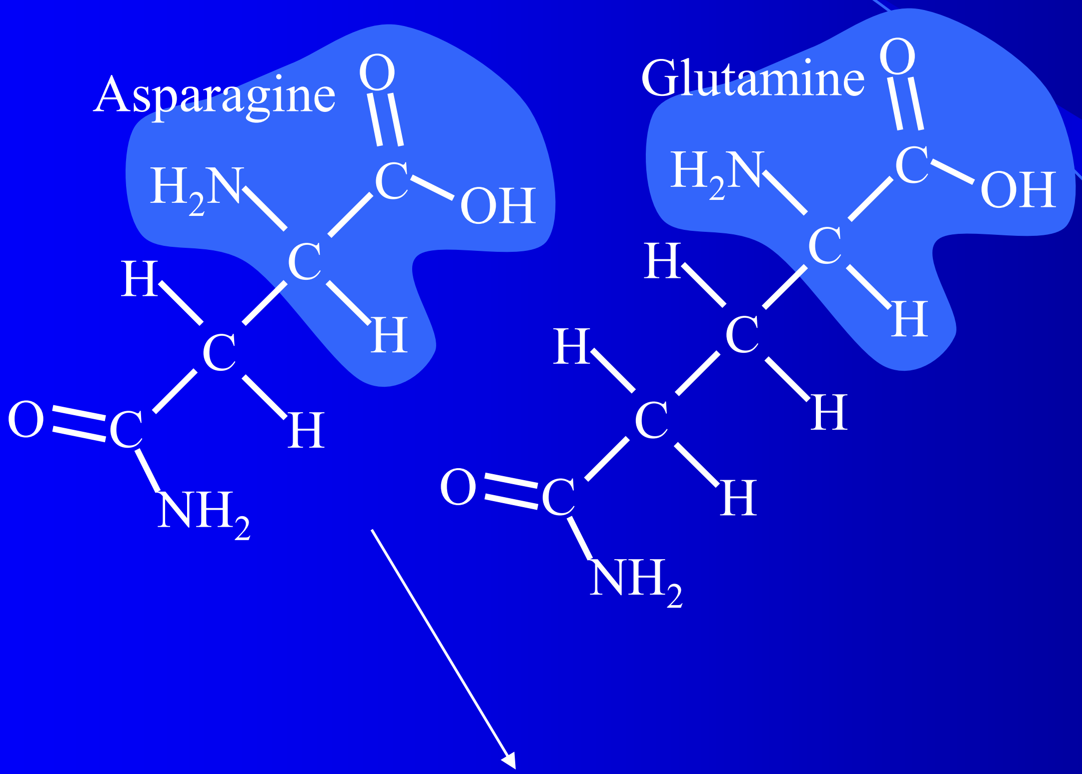
- e.g. haemoglobin
- 3^{o} structure normally folds up in a ball
- hydrophilic R groups point outwards
- Hydrophobic R groups point inwards
- soluble
- metabolic functions

- e.g. collagen
- 2^{o} structure does not fold up, form fibres
- not surrounded by hydrophilic R groups
- insoluble
- structural functions

Hydrophobic interactions



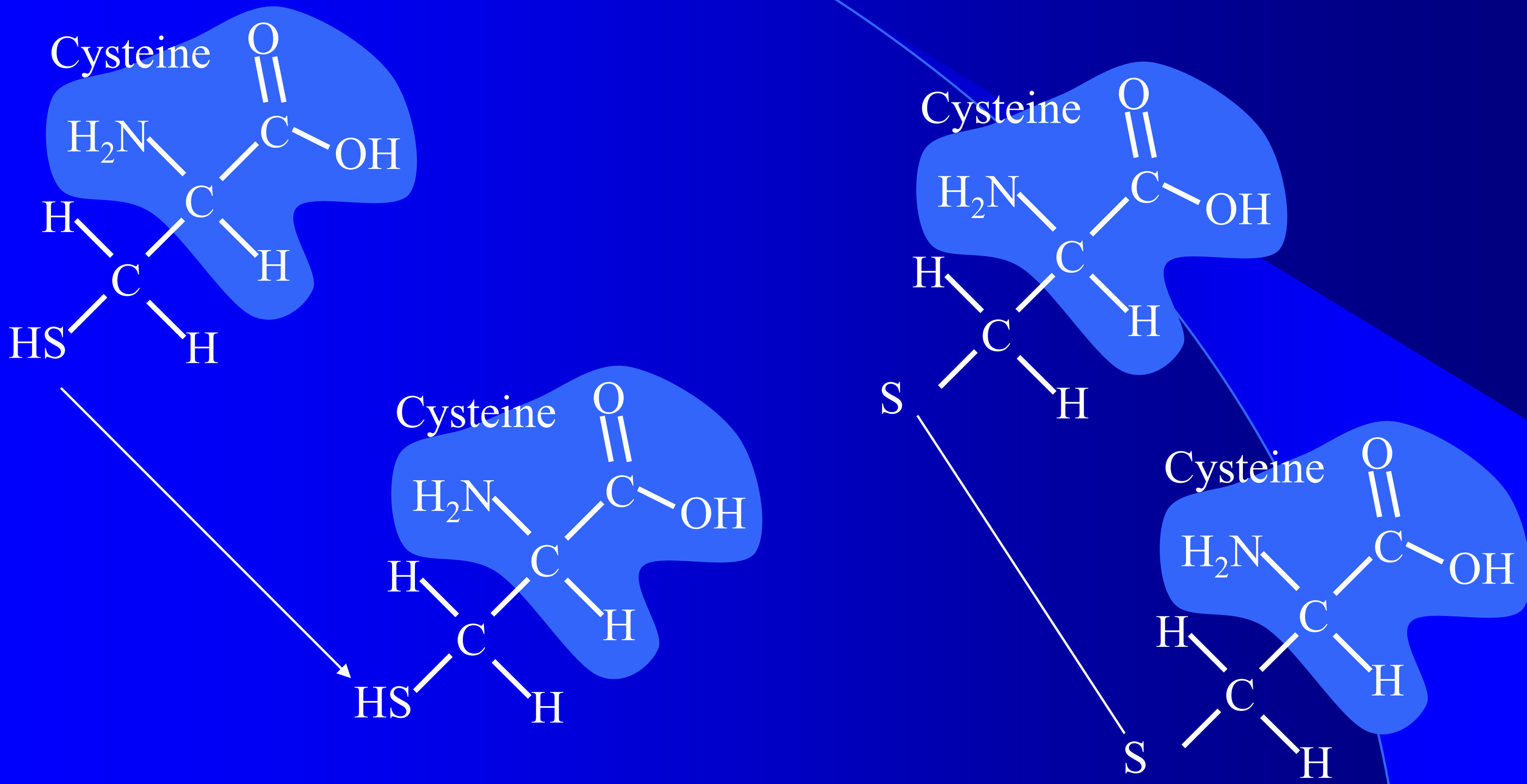
Hydrogen Bonding



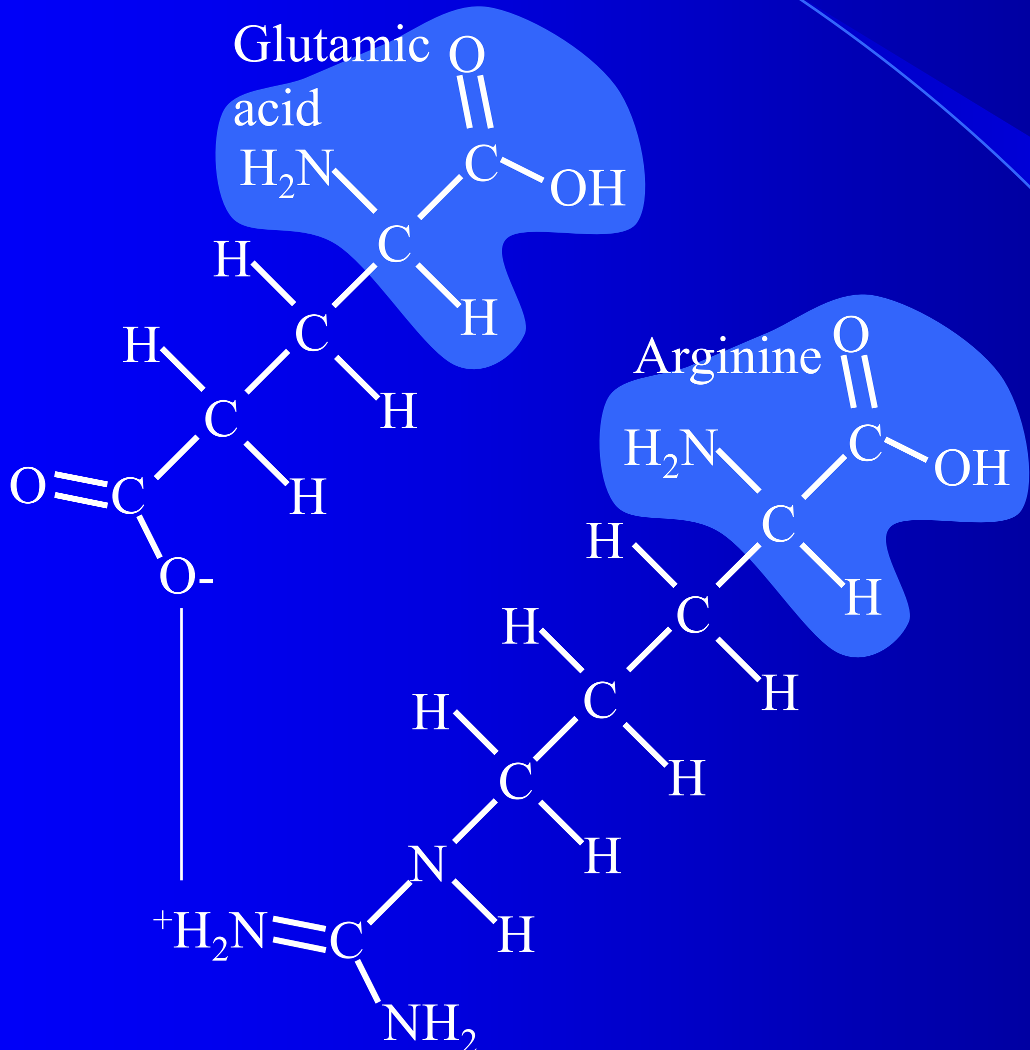
N-------H (+)
slightly

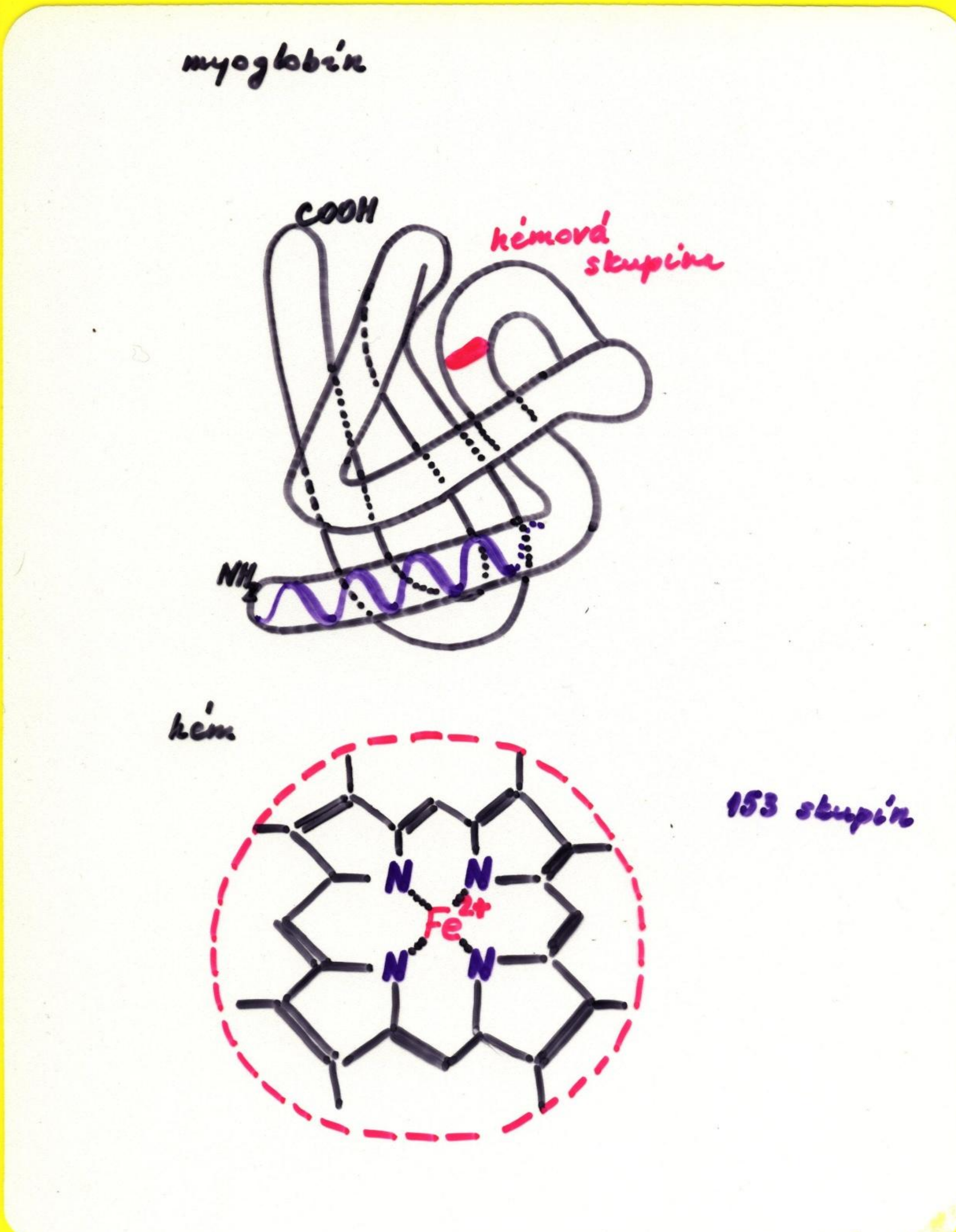
(-) O -------C
slightly

Disulphide bridges

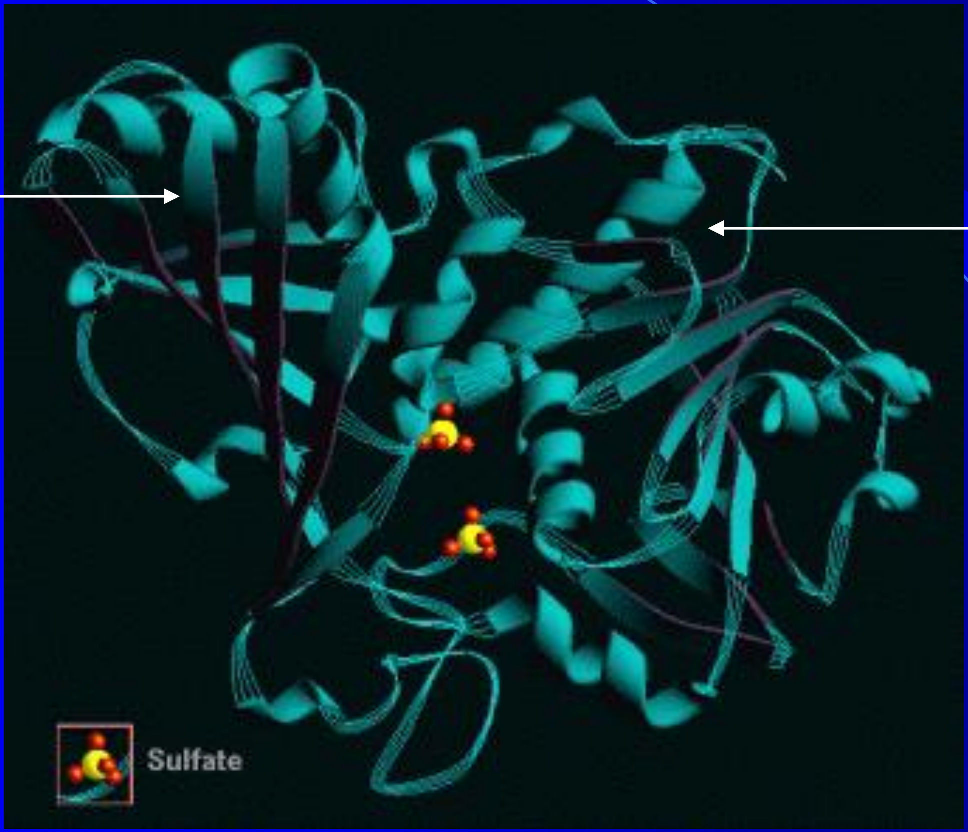


Ionic Bonds

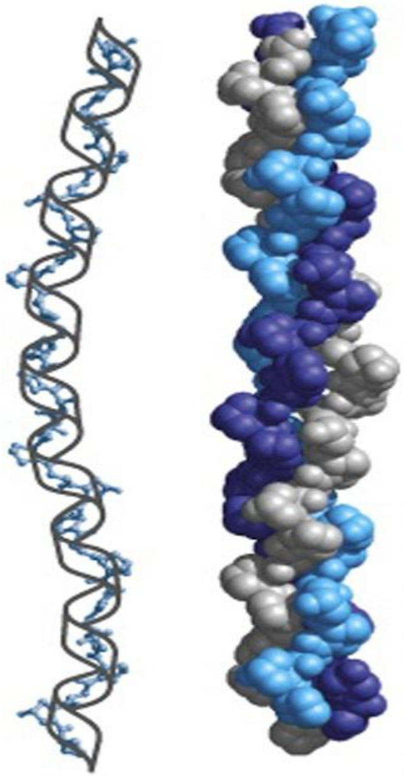

Glutamic acid
O
C
OH
H_2N
C
H
H
C
H
H
C
H
O
C
H
O-
Arginine
O
H_2N
C
OH
C
H
H
C
H
H
C
H
H
C
H
N
H
$^{+}H_2N$
C
NH_2


myoglobín
COOH
hémová skupina
NH2
hém
N
N
N
N
Fe2+
153 skupín

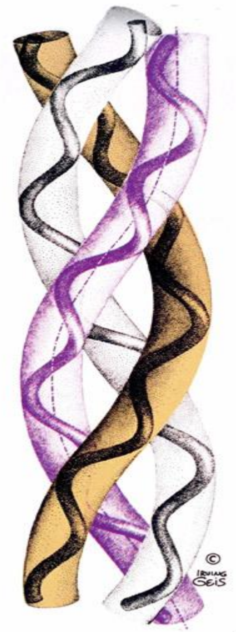
e.g.G-3-P Dehydrogenase
Tertiary Structure

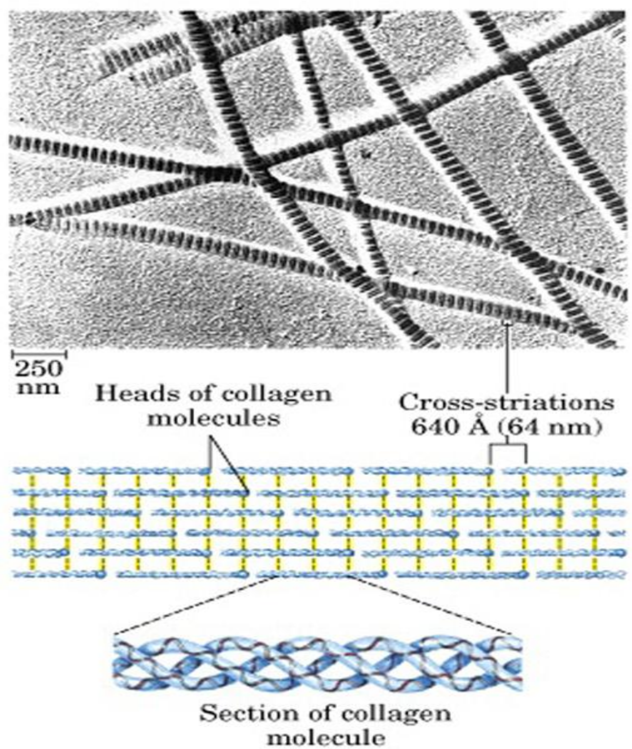


Collagen



(a) (c)





- Collagen is a fibrous protein made of 3 polypeptide helices held together by hydrogen bonding
- Every 3rd amino acid in the chain is a glycine (very small to let the chains lie close to each other)
- Collagen molecules are found side by side forming fbres
- The staggered ends help to give collagen fibres great tensile strength

Levels Of Protein Organization
Quaternary Structure

- Quaternary structure results from the interaction of independent polypeptide chains
- Factors influencing quaternary structure include:
- Hydrophobic interactions
- Hydrogen bonding
- The shape and charge distribution on amino acids of associating polypeptides

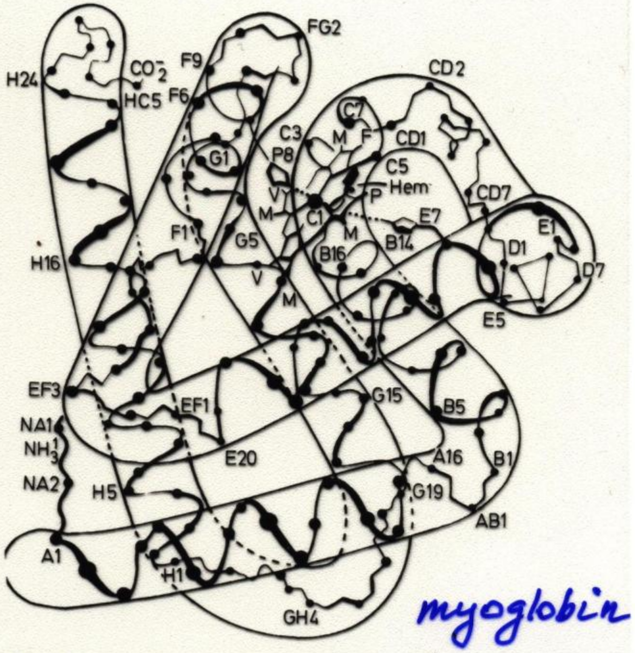
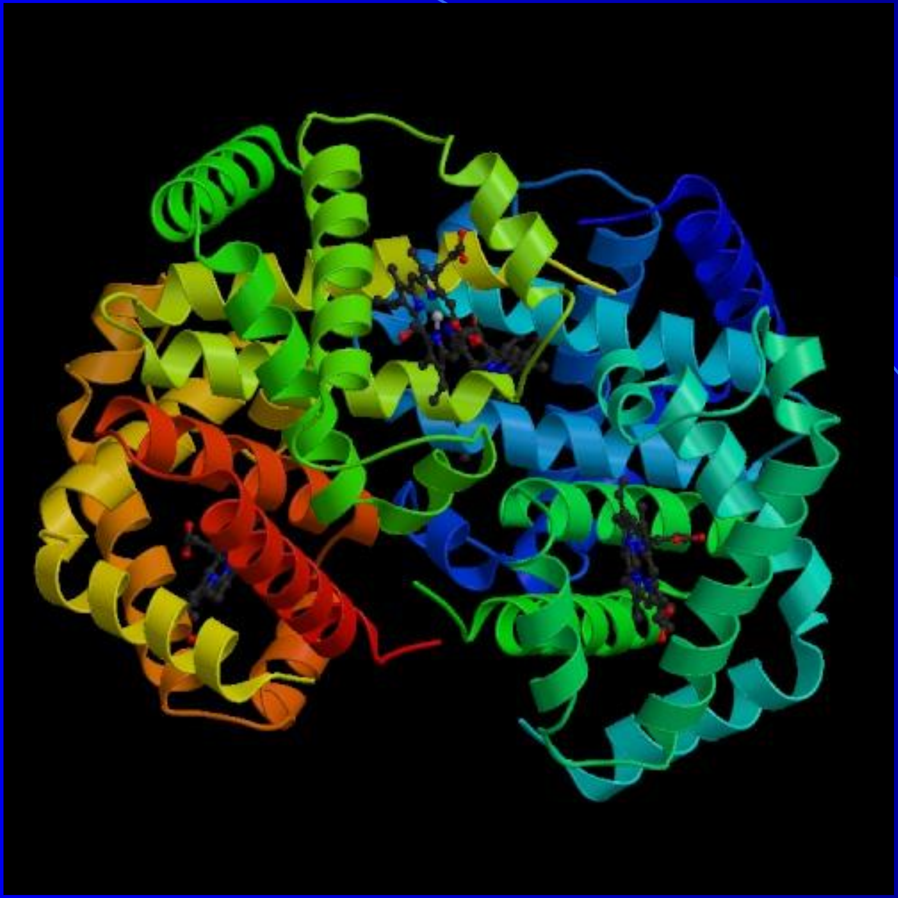


Fig. 2.31. Spatial structure and order of the eight helices of myoglobin from X-ray analysis with 2 nm resolution. [After Perutz, M. F.: Nature (Lond.) **167**, 1053 (1951)]

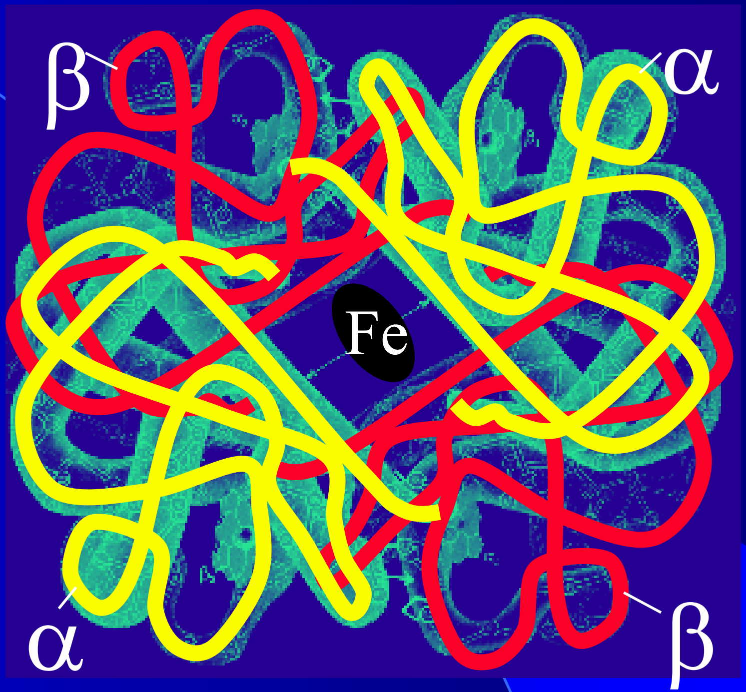
Kvartérna štruktúra
hemoglobin

Haemoglobin

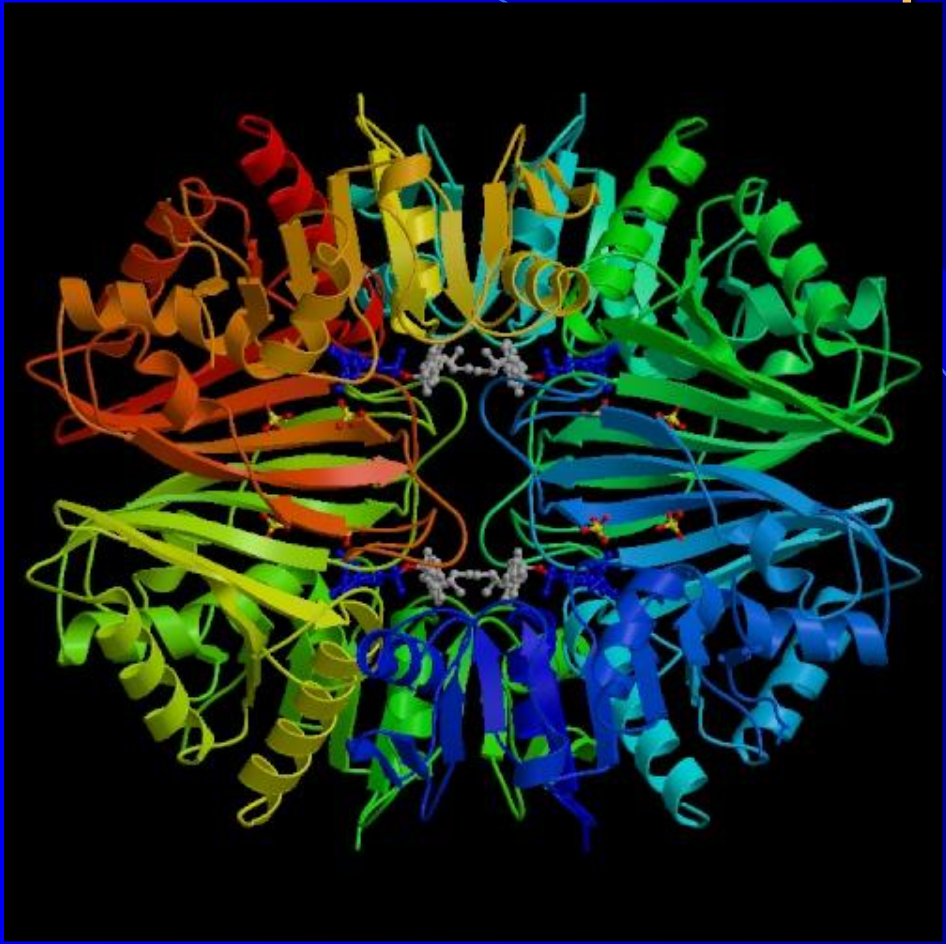


Haemoglobin

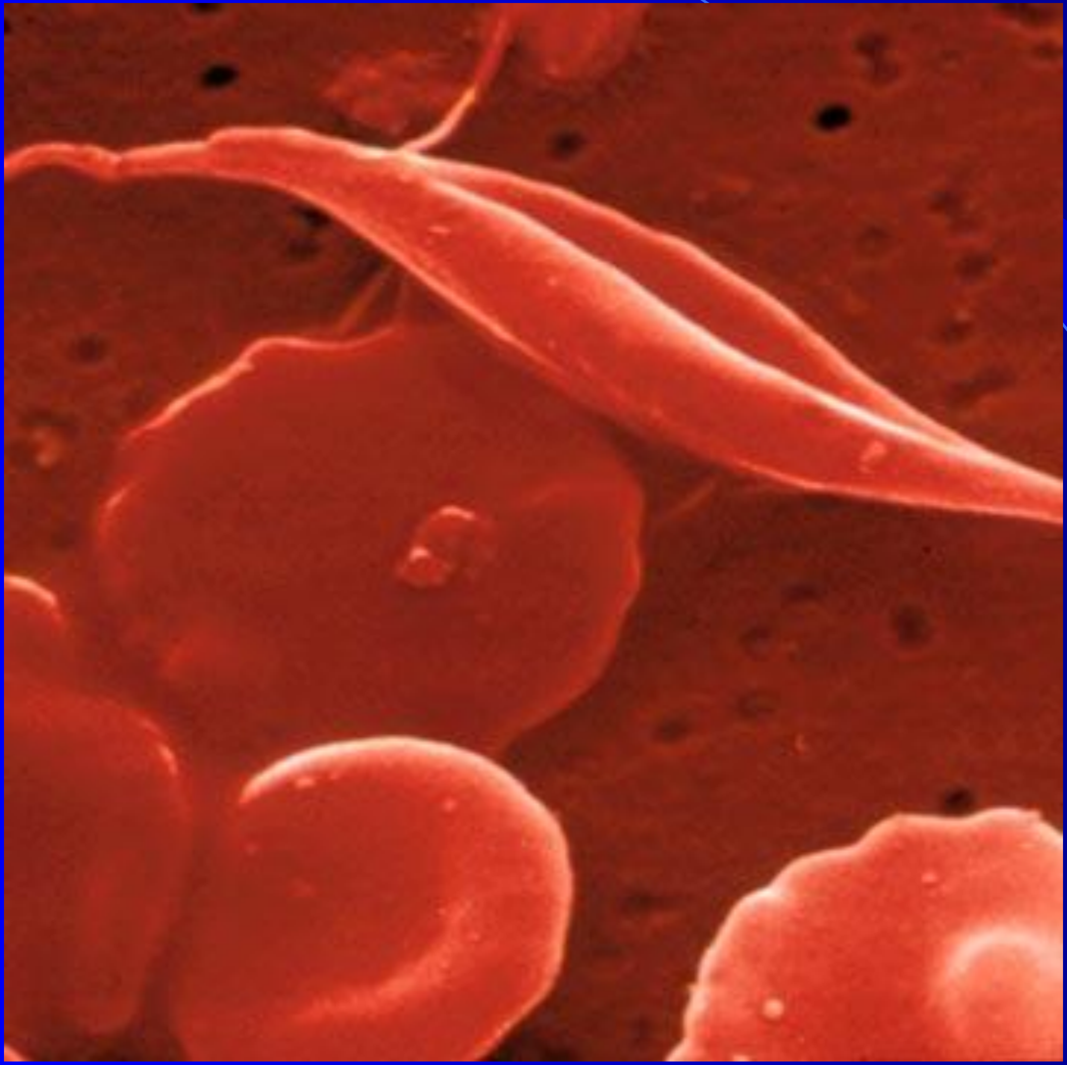
- Haemoglobin is a globular protein with a prosthetic 'iron' group
- In adults, hemoglobin is made up of 4 polypeptides (2 α polypeptide chains and 2 β polypeptide chains)
- Each polypeptide surrounds a prosthetic 'haem' group
- Hydrophobic interactions between side groups pointing inwards maintain the structure
- Hydrophilic side chains point outwards making it soluble

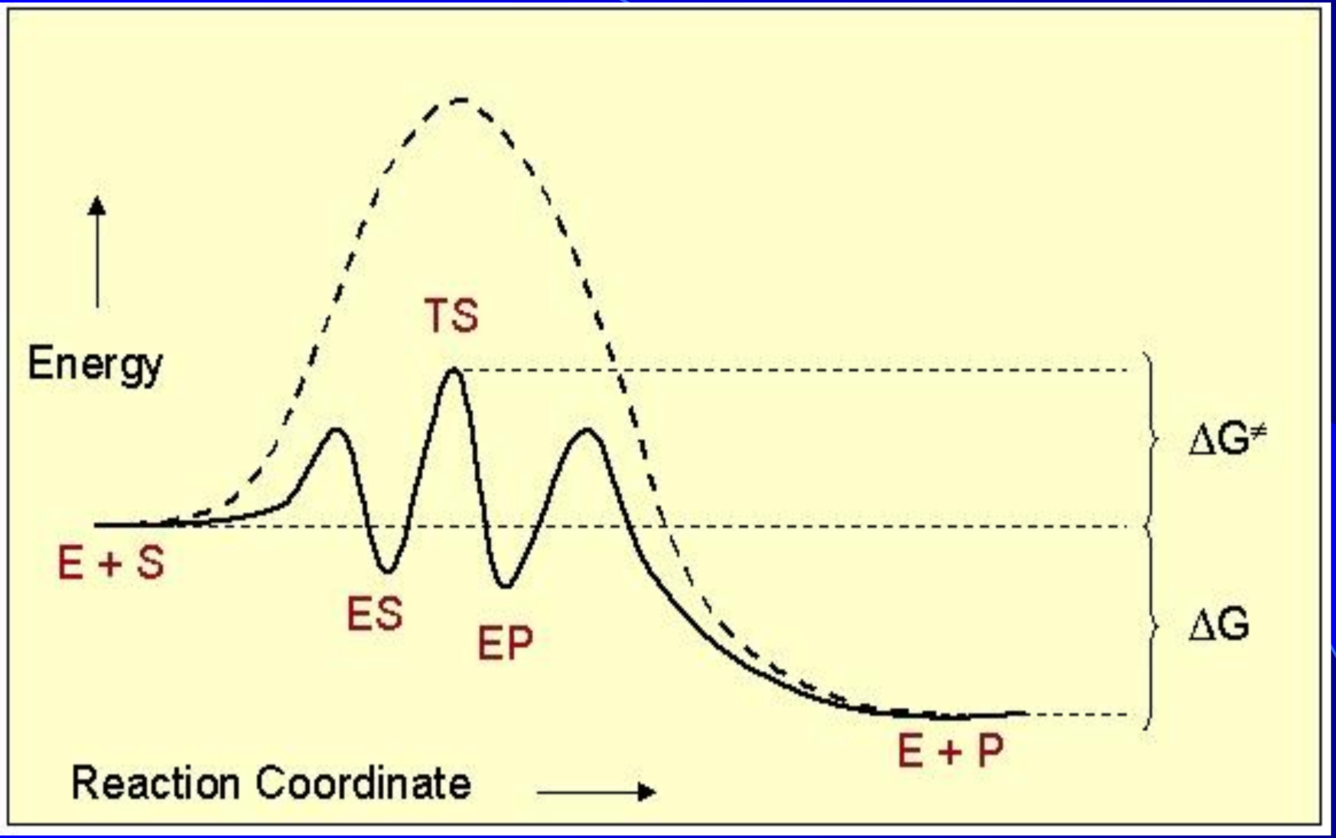


G-3-P Dehydrogenase
from Bacillus stearothermophilus



Sickle Cell Anaemia





E + S → ES → EP → E + P

Arrheniov vzťah pre rýchlostn. konštantu :

$$k = A e^{-\frac{\Delta G^{\neq}}{RT}}$$

$\Delta G^{\neq}$ - aktivačná energia

$$A \underset{k_{-1}}{\overset{k_1}{\rightleftarrows}} B$$

$$\frac{d[B]}{dt} = \vec{v} = k_1[A]$$

$$\frac{d[A]}{dt} = \overleftarrow{v} = k_{-1}[B]$$

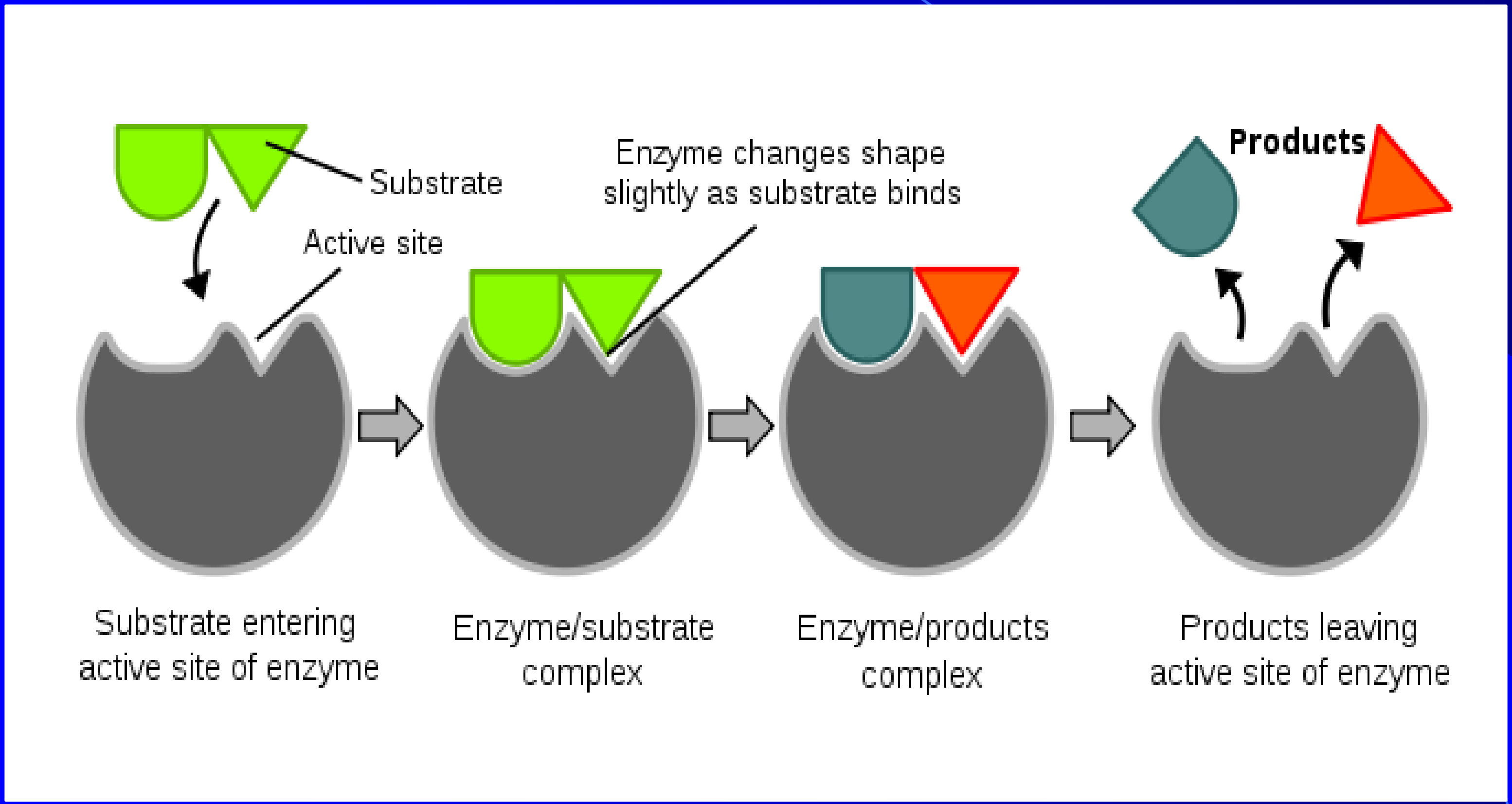
rovnováž. stav :

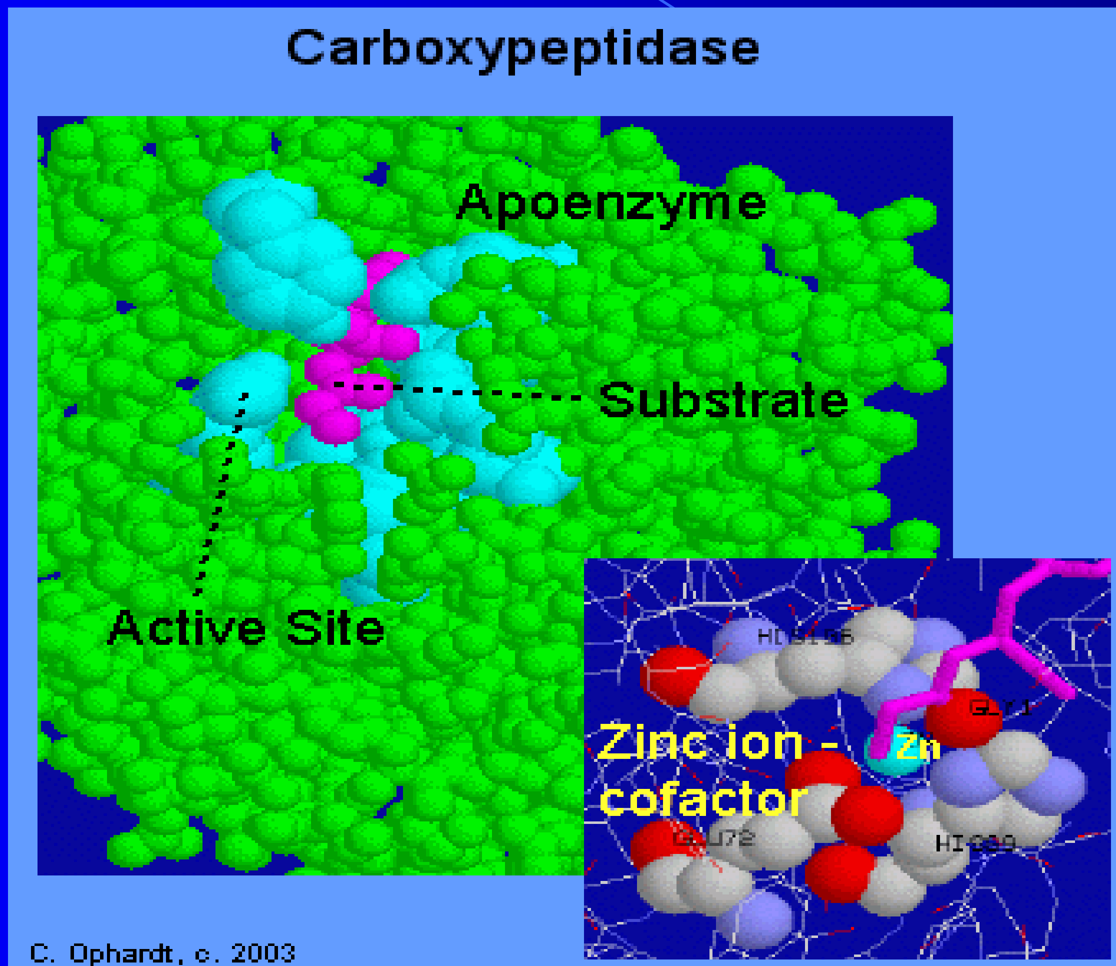
$$\vec{v} = \overleftarrow{v}$$

$$K = \frac{[B]_r}{[A]_r} = \frac{k_1}{k_{-1}}$$

rovnováž. konštanta

$$\Delta G = -RT \ln K = \Delta H - T\Delta S$$


Substrate
Active site
Enzyme changes shape slightly as substrate binds
Products
Substrate entering active site of enzyme
Enzyme/substrate complex
Enzyme/products complex
Products leaving active site of enzyme


Carboxypeptidase
Apoenzyme
Substrate
Active Site
Zinc ion -
cofactor
C. Ophandt, c. 2003