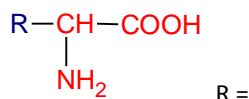


AMINOACIDS + PEPTIDES

AMINOACIDS = *substitutional/functional* derivatives of carboxylic acids
= basic units of proteins (2-aminoacids)

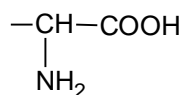
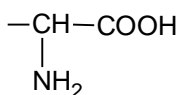
General formula of 2-aminoacids (α -aminoacids):



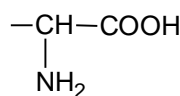
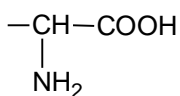
There are 20 aminoacids in our bodies used for the synthesis of proteins.

Classification of aminoacids according to the character of the **side group**:

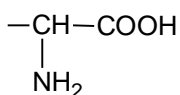
- Non-polar = hydrophobic



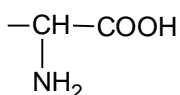
- Polar =



- Acidic = negatively charged at neutral pH



- Basic = charged at neutral pH



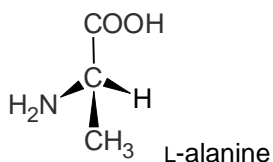
1. Classify the following side groups as non-polar, polar, acidic or basic:

$\text{HO}-\text{CH}_2^-$, $\text{NH}_2-(\text{CH}_2)_4^-$, H^- , $\text{HOOC}-\text{CH}_2^-$, CH_3^- , $\text{CH}_3-\text{CH}(\text{OH})-$

2. See the structures of the examples of aminoacids above. What kind of isomerism do they exhibit?

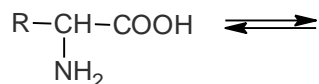
All aminoacids except show isomerism because α -carbon is a centre. Each aminoacid (except) has two All aminoacids that form proteins are-aminoacids.

3. Use the structure of L-alanine to draw the structure of D-alanine.



Physical properties

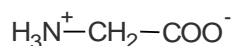
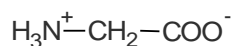
Aminoacids have different properties than non-substituted carboxylic acids, especially a higher melting point and better solubility in water. They form dipolar ions = ZWITTERION = AMFION



Chemical properties

Aminoacids possess both acidic (.....) and basic (.....) group, they have character.

4. Write down the two equations where glycine behaves as an acid or base respectively.



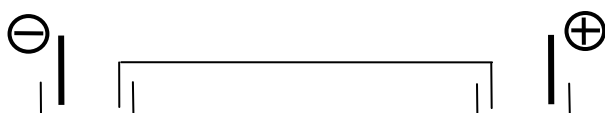
In alkaline conditions: an aminoacid behaves as, it getscharge.

In acidic conditions: an aminoacid behaves as, it getscharge.

At certain pH the two ionizations are balanced and an aminoacid forms zwitterions. This pH = ISOELECTRIC POINT. No net overall charge on the aminoacid at this pH \Rightarrow the aminoacid does not move in the electric field at this pH.

Separation and detection of aminoacids

ELECTROPHORESIS



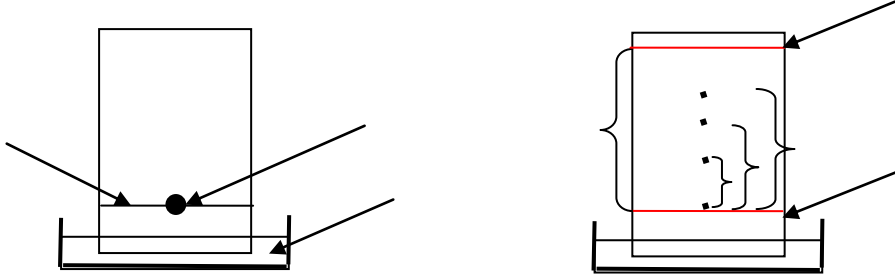
Paper soaked with a solution of a certain (constant) pH (buffer solution).

- Aminoacids with the isoelectric point $\text{pH}_i = \text{pH}$ of the buffer don't move in the electric field.
- Aminoacids with $\text{pH}_i < \text{pH}(\text{buffer})$ are more *acidic/basic*, are *negatively/positively* charged and move to the *anode/cathode* in the electric field.
- Aminoacids with $\text{pH}_i > \text{pH}(\text{buffer})$ are more *acidic/basic*, are *negatively/positively* charged and move to the *anode/cathode* in the electric field.

The speed of the movement depends on their masses.

CHROMATOGRAPHY

= paper chromatography



As the solvent ascends the sheet of paper, different aminoacids move at different rates \Rightarrow the mixture separates.

A_1, A_2, A_3 aminoacids

a_1, a_2, a_3 distance travelled by the acid

b distance travelled by the solvent

$$R_{F(A_1)} = \frac{a_1}{b}$$

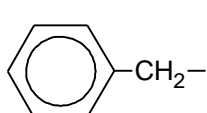
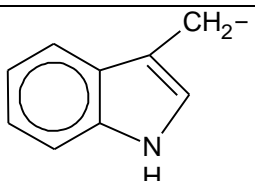
$$R_{F(A_2)} = \frac{a_2}{b}$$

$$R_{F(A_3)} = \frac{a_3}{b}$$

Each aminoacid has a specific value of R_f .

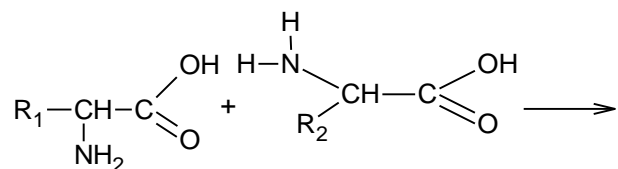
Aminoacids and diet

Our body uses 20 aminoacids for the synthesis of proteins. The aminoacids are accepted in a diet in the form of proteins. However most of them can be synthesised by our body. Only EIGHT aminoacids cannot be synthesised by our body and they must be accepted in a diet = ESSENTIAL AMINOACIDS.

$\begin{array}{c} \text{H}_3\text{C} \\ \diagdown \\ \text{CH} \\ \diagup \\ \text{H}_3\text{C} \end{array} -$	Valine	$\text{H}_2\text{N}-(\text{CH}_2)_4-$	Lysine
$\begin{array}{c} \text{H}_3\text{C} \\ \diagdown \\ \text{CH} \\ \diagup \\ \text{H}_3\text{C} \end{array} - \text{CH}_2-$	Leucine	$\text{H}_3\text{C}-\text{S}-(\text{CH}_2)_2-$	Methionine
$\begin{array}{c} \text{H}_3\text{C}-\text{CH}_2 \\ \diagdown \\ \text{CH} \\ \diagup \\ \text{H}_3\text{C} \end{array} -$	Isoleucine		Phenylalanine
$\begin{array}{c} \text{H}_3\text{C}-\text{CH} \\ \\ \text{OH} \end{array} -$	Threonine		Tryptophan

PEPTIDES

= substances made by condensation of aminoacids



Two aminoacids may form 2 dipeptides.

5. Write the two possible structures made by the condensation of alanine and glycine.

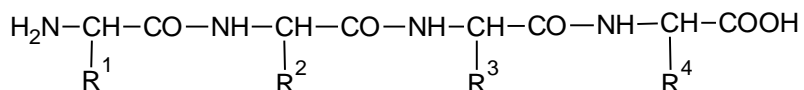
Three aminoacids form

2-10 aminoacids \Rightarrow OLIGOPEPTIDES

10 - 100 aminoacids \Rightarrow POLYPEPTIDES

>100 aminoacids \Rightarrow

A peptide chain consists of a peptide BACKBONE and SIDE CHAINS.



Important peptides:

- Antibiotics, produced by microorganisms (may contain D- α -aminoacids)
- Toxins of mushrooms, e.g. α -amanitin (amanita phalloides) is a cyclic octapeptide
- Hormons, e.g. glucagon (29 aminoacids)
- Artificial sweetener Aspartam is a methylester of a dipeptide made from aspartic acids and phenylalanine

PROTEINS

= macromolecular substances made by condensation of

Types of proteins according to their function:

- **Structural proteins**, e.g.
- **Contractile proteins**, in muscles, e.g.
- **Enzymes + many hormones**, control metabolism
- **Transport proteins**, carry vital substances through an organism, e.g.
- **Immunoproteins**, bind to substances, which are foreign to a mammal

Structure of proteins

- several levels of structure

1. primary structure = the sequence of aminoacids in the protein chain, found by hydrolysis of proteins + electrophoresis or

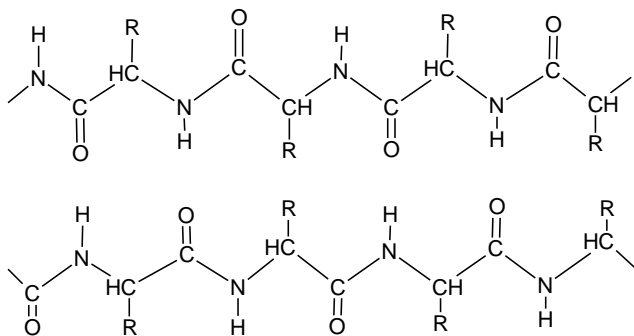
2. secondary structure

- **α -helix** = regular spiral

Side chains point towards the outside of the helix.

All α -helices found in proteins are right handed (clockwise). They are in flexible and elastic structures, occur in fibrous α -KERATIN (e.g. in,

- **β -pleated sheet** = polypeptide chains are aligned side by side, connected by hydrogen bonds. They are inelastic and flexible, present in SILK fibres.



This is the final level of organisation of many proteins.

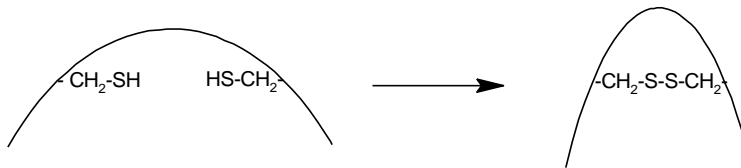
3. tertiary structure = chains or sheets are further folded and coiled into a shape.

- **Fibrous proteins** – long molecules coil round each other \Rightarrow fibres: keratin (in, collagen (in e.g.:.....), insoluble in water

- **Globular proteins** – more extensive folding leads to a spherical shape, soluble in water.

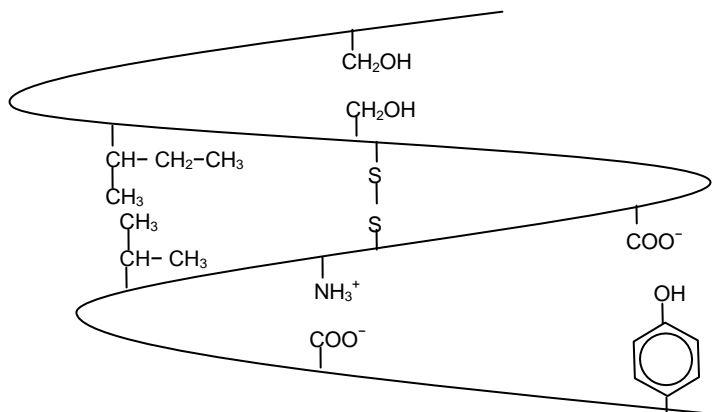
Tertiary structure results from:

- Hydrogen bonding, e.g. between
- Ionic interactions, between the positive charge of and the negative charge of
- Van der Waals forces, between groups
- Sulphide bridges between two residues of cystein



This is a final level of organisation of proteins containing a single polypeptide chain only.

6. *What types of interactions are involved in the following picture of a part of a protein?*



4. quaternary structure

Some proteins:

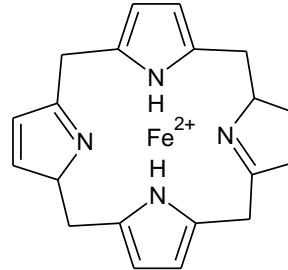
consist of more protein subunits = OLIGOMERIC PROTEINS

or contain also a non-protein unit:

- glycoproteins (..... + protein)
- lipoproteins (..... + protein), transport of lipids (cholesterol)
- metaloproteins
 - storage of metals
 - metalloenzymes
 - haemoproteins (contain a heme group) – haemoglobin, myoglobin, cytochroms
- phosphoproteins – casein

The structure of haemoglobin

- consists of four subunits, which are closely associated to form a stable globular protein.



Heme group

The structure of collagen

= fibrous structural protein (occurs e.g. in)

- three helices which intertwine to form a superhelix.

Tests for proteins:

1. biuret test: protein + CuSO_4 + NaOH \rightarrow purple colour
2. xanthoprotein test: protein + HNO_3 $\xrightarrow{\text{heat}}$ yellow $\xrightarrow{\text{ammonia}}$ orange

Denaturation of proteins

- involves the disruptions of the secondary or tertiary structure of proteins (covalent bonds responsible for the primary structure stay unaffected by the denaturation reactions).
- The secondary structure is caused by between oxygen from CO and hydrogen from NH group. The tertiary structure is caused by:....., and
- The bonds between the side chains may be broken by:
 - Heat
 - Strong acids and alkali
 - Ions of heavy metals
- As the protein loses its structure, it also loses its shape, which is very important for the correct function of the protein.
- 7. *Suggest how the above mentioned factors can destroy the secondary and tertiary structure of proteins.*