

Functional Proteins and Genes

Summary

Week 2 - Lipids & Sugars

- Characteristic and function of lipids:
 - have a charge
 - make up cell membranes
 - efficient energy reserves (they don't hold water)
 - some are hormones (sterols and sex hormones)
 - aid in digestion (bile acids)
- **Fatty acid** → carboxylic acid + long chain hydrocarbon
- **Palmitic acid** → carboxylic acid + 16 carbon long hydrocarbon chain (16:0)
 - C₁ is the carbon in carboxyl group
 - C₂ is the **α (alpha)** carbon
 - C₃ is the **β (beta)** carbon
 - Last carbon is **ω (omega)** carbon
- **Saturated fatty acid** → only single bonds (linear)
- **Unsaturated fatty acid** → 1 or more double bonds (bent)
 - 16:0 → 16 carbons long with no double bonds (saturated)
 - 18:2 → 18 carbons long with 2 double bonds (unsaturated)
- e.g. omega-6-fatty acid → distance between ω carbon and double bond is 6 carbons
- Fatty acids are always even numbered
- Double bonds are represented by **Δ (delta)**
 - e.g. cis-Δ⁹ → a double bond is at carbon 9-10, with the methyl groups (carbons) on the same side
- **Essential fatty acids** → our body cannot make them, have to get it from food:
 - **Linoleic acid** → 18:2^(9,12) → 18 carbons long, 2 double bonds at carbon 9-10 and 12-13
 - **Linolenic acid** → 18:3^(9,12,15) → 18 carbons long, 3 double bonds at carbon 9-10, 12-13 and 15-16

- **Arachidonic acid** → 20:4^(5,8,11,14) → 20 carbons long, 4 double bonds at carbon 5-6, 8-9, 11-12 and 14-15
 - Our bodies can make these:
 - Miristic acid → 14:0
 - **Palmitic acid** → 16:0
 - Stearic acid → 18:0
 - Cis double bond would make the chain bent — trans double bond would keep it straight
 - More double bonds (unsaturated) → lower the melting point → can't pack together closely
 - e.g. olive oil → lots of **unsaturated fatty acids** → liquid at even room temperature
 - e.g. butter → lots of **saturated fatty acids** → can maintain its structure at higher temperatures → harder to melt than olive oil
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Week 2 - Carbohydrates

- $(\text{CH}_2\text{O})_n$ → $n = 3$ or more
- **Glycerol** → has 3 carbons with OH on each carbon
- The furthest chiral carbon from C_1 → determines if D or L sugar
 - If OH on right → D sugar
- **Isomer** → same number of atoms just in different combination
- **Enantiomer** → an isomer that has a mirror image
- **Pyra ring** → 5 carbons + 1 oxygen
- Actual name for glucose: e.g. α -D-glucopyranose
- **Glucose** → down-up-down
- **Galactose** → down-up-up
- **Mannose** → down-up-up
- **Ribose** → 5 carbon sugar in the form of a furan ring
- **Fructose** → 6 carbon sugar in the form of a furan ring → C_2 joints to C_5
- **Glyceraldehyde** → glycerol + aldehyde group at C_1

Week 3 - Proteins I (amino acids)

- **Functional proteins** —> enzymes (globular)
- **Structural proteins** —> keeping us together (fibrous)
- **Glycine** is the only amino acid that is achiral (doesn't have chiral carbon)
- **Proline** is the only amino acid that has NH_2 instead of NH_3^+ —> the ring attaches back on itself
- **Anion** (-ve) —> **zwitterion** (neutral) —> **cations** (+ve)
- Hydrogen (proton) first attaches to the amine group and then to the carboxyl group
- Amino acids are categorised into 4 groups:
 - **non-polar**
 - **polar**
 - **+ve charge**
 - **-ve charge**
- Cystine has sulfhydryl (thiol) group which allows it to form disulphide bonds
- **Lysine** is an essential amino acid
- Protein structure levels:
 - **primary** —> linear amino acid sequence
 - **secondary** —> α -helix and β -sheets
 - **tertiary** —> polypeptide chain of α -helix and β -sheets
 - **quaternary** —> having 2 or more tertiary structure subunits
- Peptide bonds are all in trans (opposite) configuration
- Even though peptide bonds are single bond —> acts like a double bond —> can't bend

Week 4 - Proteins II (structure)

- Looking at a primary structure → go from N to C terminus
 - N terminal goes in ribosome first
- Different types of bonds in proteins:
 - **Covalent bonding** (sharing electrons) → peptide and disulphide bond
 - **Hydrogen bonds** → weak interactive of electronegative atoms (polar interactions)
 - **Ionic bonds** (giving electrons) → attracting opposite charges
 - **Non-bonding interactions** → e.g. hydrophobic interactions, where they hang out together since they all hate water
- There can be disulphide bonds between side chains → bending the peptide backbone
- Peptide bonds can form by the backbone folding back on itself
- **Cystine** and **methionine** both have **sulphur**
- When primary structure → α -helix: $R_i \rightarrow R_i + 4$
 - the carboxyl on the first carbon will attach to the amino group on the 5th amino acid, which is 4 amino acids away from it
- α -helices are usually 12-40 residues long

Forming an α -helix

- too large (tryptophan, tyrosine) and too small (glycine) residues won't work
- branched [at β carbon] amino acids (valine, isoleucine, threonine) can destabilise by clashing
- polar or charged amino acids won't work due to hydrogen bonding competition
- proline also wouldn't work as it lacks a hydrogen in its amino group

Forming a β -sheet

- Can be parallel, antiparallel or mix (both)
- Antiparallel is much stronger as the hydrogen bonds align perfectly
- Beta sheets can be up to 4-5 strands