Proteins

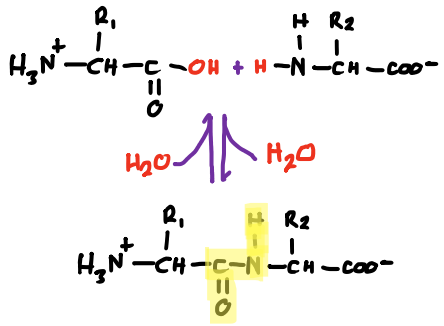
Saturday, 7 April 2018 12:34 pm

Proteins do "things"

- There are 4 main classes of proteins
  - Catalysis
  - Transport
  - Structural
  - Motor

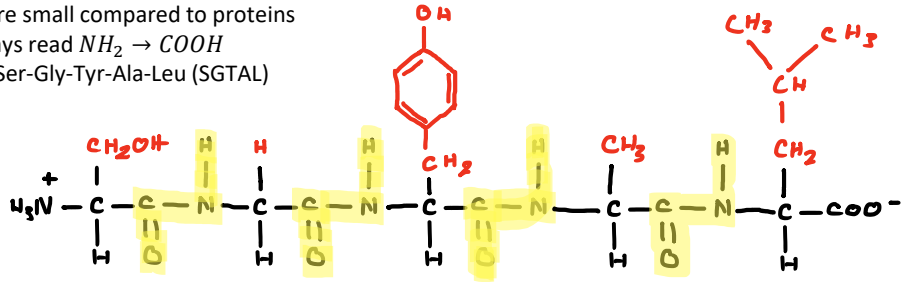
Peptides form when the COOH bonds with the NH_2 in a condensation reaction

- These form amine bonds or "peptide bonds"



Peptides are small compared to proteins

- Always read $NH_2 \rightarrow COOH$
- E.g. Ser-Gly-Tyr-Ala-Leu (SGTAL)



Serine Glycine Tyrosine Alanine Leucine

- Number of possible structures - 20^n structures where $n =$ length of the peptide

Construction of Peptides

1. DNA is transcribed to mRNA (template for the peptide chain)
2. mRNA is fed through the ribosome (rRNA)
3. tRNA carries AA to bind to form the polypeptide
4. tRNA is released

Structure of Proteins

- Proteins have specific 3D structures
- The structure specifies the function
- There are up to 4 levels of structure
- The structure is held together by four types of interaction forces
  - Hydrophobic Effect - Hydrophobic regions group together forcing out H_2O. These regions take energy to separate
  - H Bonds - Polar groups bind together when their dipoles interact. NH_3^+ and COO^- groups interact to form secondary structures
  - London Dispersion Forces - Medium to weak range interaction between all matter as spontaneous dipoles exist from quantum uncertainty.
  - Electrostatic Interactions - Long range, strong interaction between acidic and basic R-groups

The Layers of Structure

1. Primary - The sequence of amino acids
2. Secondary - Backbone interactions of amino acids forming bulk H Bonds (α helicies and βsheets
3. Tertiary - Protein folding, interaction between R-Groups
4. Quaternary - Multiple proteins, organic compounds and inorganic compounds binding together to form the final structure

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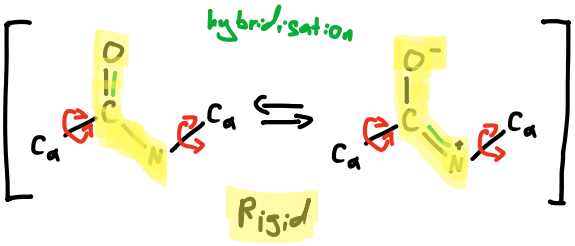
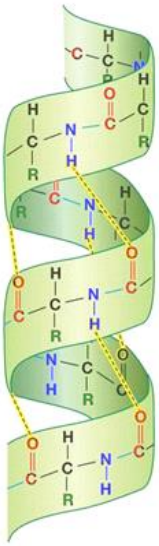
Primary Structure



- Not particularly reactive
- Planar structure within the peptide bond
- Rigid
- Large dipole moment

Secondary Structure

Common α Helix

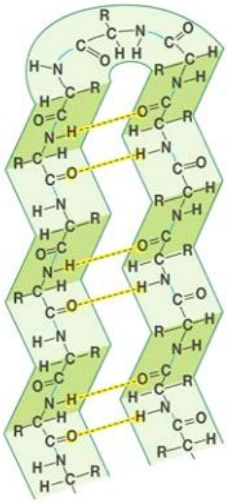


- Right handed helix - (Rotates clockwise from the NH_3^+ terminus)
- Stabilised by H bonds between nearby residues
- Form from residues 4 AA apart in primary structure
- Peptide bonds are parallel to the helix

Features

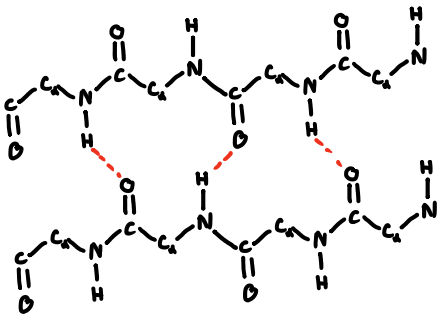
- Structure is too small for pretty much anything to fit inside of
- Outer dimensions of α helix are the same as the major groove of DNA
- It's possible to have properties on one side of the helix and not the other (e.g. hydrophobic on one side)
- Typically formed from small hydrophobic residues
- Proline and glycine break an α helix
- Attractive or repulsive forces 3-4 residues part also break the α helix

Common β sheets

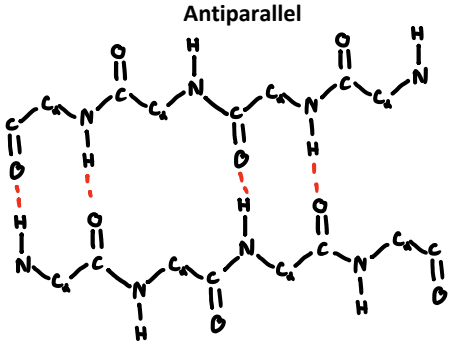


- H bonds between distant (primary) residues
- Formed by the combination of tetrahedral α carbon and planar peptide bonds
- R-groups stick up and down alternating per amino acid
- Multiple β sheets can H bond with each other
    - Can be parallel or antiparallel
    - Antiparallel have shorter H bonds and are therefore a stronger structure

Parallel



Antiparallel



- β turns occur when β sheets do a 180° turn, requires one of two AA to occur
    - Proline - forces the bend because of its shape
    - Glycine - allows it to bend because of it's small functional group
- Takes 4 AA to form a turn, AA 2 or 3 in that sequence must be Pro or Gly

Tertiary Structure

- The overall spacial arrangement between individual polypeptides
- Stabilised by many interactions
    - Hydrophobic interactions
    - Disulphide bonds between cysteine
    - These residues can be far apart in the primary structure
- Two major classes of tertiary structure
    - Fibrous - water soluble
    - Globular - lipid soluble

Motifs

- Secondary structure interactions that create complex tertiary structures
- They form globular proteins

E.g. β-α-β loop

α-α corner

E.g. β-α-β loop

α-α corner

twisted β sheet

β barrel

Quaternary Structure

- Multiple proteins, organic compounds and inorganic compounds binding together to form the final structure

Protein Modification

- Cofactors (non AA molecules) can be added to the quaternary structure
- Often inorganic, particularly metals
- Coenzymes - organic cofactors
- Prosthetic groups - covalently attached cofactors

Analysis

- Proteins can be separated for analysis based on
  - Charge
  - Size
  - Affinity for ligands
  - Solubility
  - Hydrophobicity
- Proteins can be sequenced using mass spectrometry
  - Involves breaking up the molecule and measuring it's constituent parts