182 Lecture 3 Proteins

Amino acid = monomers joined in a linear chain.
Polypeptides = polymers
Contain: Carbon, hydrogen, oxygen, nitrogen & sulfur
Amino Acid R groups: 20 side chains, which determine folding, charge and grouping (due to polarity) of the polypeptide. R group is what determines the Amino Acid.

Side chain types

Polar: Hydrophilic, electrons not shared, neutral charge
Non-Polar: Hydrophobic, electrons shared
Acidic: negatively charged
Basic: positively charged

Acidic and basic form ionic bonds, holding the folded protein structure together

Polypeptide chain – amino end (N-terminus) is the beginning and carboxyl end (C- terminus) is the end.

Polypeptide Bonds

- Link amino acids together via condensation reactions
- Covalent bonds (Very strong)

Cysteine bonds

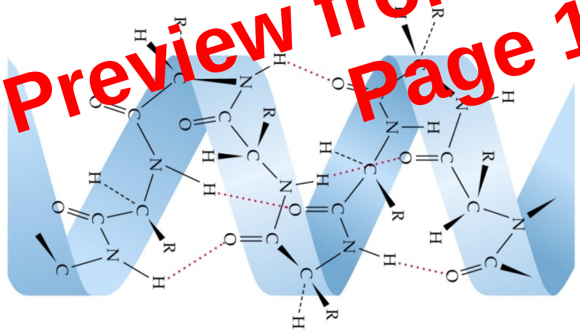
- Sulfhydryl group – SH group attached to R group
  - 2SH groups attached to cysteines can interact to form a Disulphide bridge under oxidizing conditions. – Create folds in protein chain

Proline bonds

- Cyclic structures that cause the bend in a protein.
- Are stable at high temperatures

Protein structure levels

Primary: sequencing of amino acids into polypeptide
Secondary: folding or coiling of alpha helix or beta pleated sheets – Hydrogen bonds
Tertiary: final 3D shape of polypeptide – R group interactions
Quaternary: several protein structures come together. 2 heavy chains (4 blobs each) and 2 light chains (2 blobs each).



Direction = NCC with C double bonded to O furthest away. Same with beta pleated sheets.

Protein activation

Effected by:

- Sequence of amino acids (mutations),
- The chemical conditions (pH, temperature, salts),
- Binding
  - Co-factor: all non-amino acids eg. Zinc (what you need to get from food: vitamins)
  - Co-enzyme: anything that contains carbon
- Energy (ATP, and phosphorylation; transfer of phosphate to the protein)
- Post translational modification
  - Glycosylation, lipidation, methylation, phosphorylation, acetylation, ubiquitination, SUMOylation, NEDDylation, proteolysis