Levels of Protein Structure (Interactions)

(a) Primary Structure

Sequence of amino acids bonded together by peptide bonds.

Peptide bonds have "partial double bond character", i.e. there is no rotation around them.

(b) Secondary Structure

Repeating structures held together by H-bonds along the backbone of the protein.

Tend to form α -helix sections: Ala, Cys, Leu Met, Glu, Gln, His, Lys

Tend to form β -sheet sections: Val, Ser, Asp, Asn, Pro, Arg

Triple Helix – 3 strands. Collagen has this structure. (Collagen is the most abundant protein. Found in skin, connective tissue, blood vessels, tendons, ligaments, cartilage, etc.) 3 strands twisted together – H bonds between the strands.

(c) Tertiary Structure

It refers to the overall shape of the protein due to interactions among R groups.

- 1. Hydrophobic interactions nonpolar side chains cluster together in the interior of the protein, away from water.
- 2. Hydrophilic interactions attractions between polar or charged side chains and water. (H-bonding, ion-dipole forces) The outside surface of the protein contains polar and charged side chains.
- 3. Salt bridges (ionic attractions) attractions between + and charged side chains (on basic and acidic groups.)
- 4. Hydrogen bonds between polar side chains (or side chains and backbone.)
- 5. Disulfide bridges covalent bonds between cysteine residues on different parts of the protein.

$$R-CH_2-S-S-CH_2-R$$

Globular proteins – compact, roughly spherical (soluble in water). Ex: enzymes, myoglobin

Fibrous proteins – long, stretched out (insoluble in water). Mostly structural. (3 α -helixes coiled together.) Ex. α -Keratins in hair, wool, skin and nails.

(d) Quaternary Structure

Interactions that hold together separate polypeptide chains. (Same interactions as 3° structure.)

Proteins can be Hydrolyzed or Denatured

Proteins can be hydrolyzed – catalyzed by acid, base or digestive enzymes.

Peptide +
$$H_2O \xrightarrow{H^+}$$
 amino acids

(This happens during digestion of proteins. The amino acids can be absorbed through the intestinal walls, carried to cells and used to make new proteins.)

Proteins can be denatured – their normal folding is disrupted and the protein loses its activity. (It <u>does not</u> break the peptide bonds.)

Denaturing agents:

Heat – disrupts H-bonds and hydrophobic interactions (cooking eggs or other food, disinfecting surgical instruments).

Acids or bases – Change the charges on acidic or basic side chains, thereby disrupting salt bridges.

If acid is added: negative charged side chains \rightarrow Ø charge (no longer attracted to

positive side chains)

If base is added: positive charged side chains $\rightarrow \emptyset$ charge (no longer attracted to

negative side chains)

Organic compounds.

Polar ones (ethanol, isopropyl alcohol) – form H-bonds with the protein. (Alcohols is used to disinfect – coagulates proteins in bacteria)

Nonpolar ones – disrupt hydrophobic and hydrophilic interactions.

Heavy metal ions (Ag^+, Pb^{2+}, Hg^{2+}) – They are <u>toxic</u>, can react with the sulfur in proteins and the denatured protein solidifies.

Agitation (whipping egg whites) – stretches polypeptide chains and disrupts all types of interactions.

Salts – In high concentration can disrupt salt bridges. (NaCl)

Detergents – disrupt hydrophobic and hydrophilic interactions.