

- Tertiary structure – interactions between fully folded polypeptide chains to make a protein.
- Domain: globular, autonomously folding unit within a protein's overall structure.
- Most proteins: one to four domains.
- Quaternary structure: interactions between different proteins.
- Protein folding:
 - Each protein is surrounded by an aqueous environment.
 - Water molecules engage in hydrogen bonds with polar groups in polypeptide.
 - Folding causes some of these to be replaced with intra-molecular hydrogen bonds.
 - Number may not change, but quality improves.
 - Van der Waals also favours folding.
 - Entropy of the polypeptide decreases, but must also consider water molecules.
 - Random coils expose non-polar side chains. Structured pockets of water form around these side chains.
 - Burial of the non-polar side chains upon folding breaks up these structures, favouring folding as entropy is increased.
 - Term: hydrophobic effect.
 - The Gibbs Free Energy of a folded protein is smaller than that of the unfolded form, but is easily disturbed.
- i. Elevate temperature
- ii. pH values one unit above or below physiological pH
- iii. Chemical denaturants (urea, guanidinium chloride)
- iv. Temp and pH – often irreversible. Guanidinium chloride – reversible
 - Levinthal's Paradox – An unfolded polypeptide chain has an astronomical number of possible configurations, but folds within seconds.
 - A random search for conformation is not feasible.
 - Inferred that folding pathways exist. Proteins go through distinct intermediates.
 - Misfolded proteins are often self-destructed by antibodies.
 - Chaperonins – proteins that assist other proteins escape their misfolded shape.
 - Prosthetic groups – non-amino acid components of a polypeptide chain. Cofactors – vitamins, metal ions etc.
- Post-translation modifications
 - Permanent: hydroxyproline in collagen
 - Temporary: phosphorylation of serine in signaling cascade
- Antibodies: extracellular glycoproteins produced by beta-lymphocytes. Must be able to bind to antigen intended for immune attack and then trigger cellular and molecular effector mechanism in immune system to eradicate invader.
 - Must be able to distinguish between self and invader
 - Effector mechanism must only be activated by target-bound antibodies, not free-circulating antibodies
- IgG Antibodies
 - Y shaped
 - 4 polypeptide chains
 - Two heavy chains (440 amino acids)