

# Proteins

## The shape and structure of proteins

- **Alpha helix:** A common folding pattern in proteins, in which a linear sequence of amino acid folds into a right handed helix stabilized by hydrogen bonding between backbone atoms.
- **Amyloid fibril:** Self propagating, stable beta- sheets that become layered one over the other to create a continuous stack of beta sheets. The unbranched fibrous structure can contribute to human disease when not controlled.
- **Beta sheet:** Common structural motif in proteins in which different sections of the polypeptide chain run alongside each other, joined together by hydrogen-bonding between beta pleated sheet.
- **Binding site:** Region on the surface of one molecule (usually a protein or nucleic acid) that can interact with another molecular through noncovalent bonding.
- **Coiled coil:** Especially stable rod like protein structure formed by two more alpha helices coiled around each other.
- **Conformation:** The folded, three-dimensional structure of a polypeptide chain.
- **Polypeptide backbone:** Repeating sequence of atoms along the core of the polypeptide chain.
- **Primary structure:** A linear sequence of monomer units in a polymer, such as the amino acid sequence in a protein.
- **Prion disease:** A transmissible spongiform encephalopathy- such as Kuru and Creutzfeldt- Jakob disease (CJD) in humans, scrapie in sheep, and bovine spongiform encephalopathy (BSE or “mad cow

disease”) in cows – that is caused and transmitted by an infectious, abnormally folded protein (prion).

- **Protein:** The major macromolecular constituent of cells. A linear polymer of amino acids linked together by peptide bonds in a specific sequence.
- **Protein domain:** Portion of a protein that has a tertiary structure of its own. Larger proteins are generally composed of several domains, each connected to the next by short flexible regions of polypeptide chain. Homologous domains are recognized in many different domains.
- **Protein subunit:** An individual protein chain in a protein composed of more than one chain.
- **Quaternary structure:** Three-dimensional relationship of the different polypeptide chains in a multisubunit protein or protein complex.
- **Secondary structure:** Regular local folding pattern of a polymeric molecule; in proteins alpha helices and beta sheets.
- **Side chain:** The part of the amino acid that differs between amino acid types. The side chain gives each amino acid its unique chemical and physical properties.
- **Tertiary structure:** Complex three-dimensional form of a folded polymer chain, especially a protein or RNA molecule.

## Part two

### Protein function

- **Active site:** A region of an enzyme surface to which a substrate molecule binds in order to undergo a catalyzed reaction.
- **Allosteric protein:** A protein that can adopt at least two distinct conformations, and for which the binding of a ligand at one site causes a conformational change that alters the activity of the protein at a second site; this allows one type of molecule in a cell to alter the fate of a molecule of another type, a feature widely exploited in enzyme reaction.
- **Antibody:** Protein secreted by activated B cells in response to a pathogen or foreign molecule. It binds tightly to the pathogen or foreign molecule inactivating it or marking it for destruction by phagocytosis or complement-induced lysis.
- **Antigen:** A molecule that can induce an adaptive immune response or that can bind to an antibody or T cell receptor.
- **Catalyst:** A substance that can lower that activation energy of a reaction (thus increasing it's rate), thus without itself being consumed by the reaction.

- **Coenzyme:** A small molecule tightly associated with an enzyme that participates in the reaction that the enzyme catalysis, often by forming covalent bonds to the substrate. Ex. NAD<sup>+</sup> or coenzyme A.
- **Equilibrium constant:** Sometimes called *K*. This is the ratio of forward and reverse rate for a reaction. Equal to the association or the affinity constant ( $K_a$ ) for a simple binding reaction ( $A + B \approx AB$ ).
- **Enzyme:** A protein that catalysis a specific chemical reaction.
- **Feedback inhibition:** The process in which a product of a reaction feeds back to inhibit a previous reaction in the same pathway.
- **GTP-binding protein (GTPase):** This is an enzyme that converts GTP to GDP.
- **Ligand:** A molecule that binds to a specific site on a protein or molecule.
- **Linkage:** In ligand bonding, the confirmation coupling between two separate ligand-binding sites on a protein, such that a conformational change in the protein induced by binding of one ligand affects the binding of a second ligand.

- **Lysozyme:** A membrane-enclosed organelle in eukaryotic cells contain digestive enzymes, which are typically most active at the acid pH found in the lumen of lysosomes.
- **Motor protein:** A protein that uses energy derived from nucleoside triphosphate hydrolysis to propel itself along a linear track (protein filament or other polymeric molecule).
- **Protein Kinase:** An enzyme that transfers the terminal phosphate group of ATP to one or more specific amino acids (serine, threonine, or tyrosine) of a target protein.
- **Protein Phosphatase:** An enzyme that catalyzes phosphate removal from amino acids of a target protein.
- **Proteomics:** The study of all proteins, including all the covalently modified forms of each, produced by the cell, tissue, or organism. Proteomics often investigates changes in this larger set of proteins- in “the proteome”- caused by changes in the environment or by extracellular signals.
- **Regulatory site:** Region of an enzyme surface to which a regulatory molecule binds and thereby influences the catalytic site at the separate active site.

- **Scaffold protein:** Protein that binds a group of intracellular signaling proteins into a signaling complex, often anchoring the complex at a specific location in the cell.
- **Substrate:** Molecule in which an enzyme acts.
- **Transition state:** Structure that forms transiently in the course of a chemical reaction and has the highest free energy of any reaction intermediate. Its formation is a rate-limiting step in the reaction.
- **Ubiquitin:** A small highly conserved protein present in all eukaryotic cells that becomes covalently attached to lysines of other proteins. Attachment of a short chain of ubiquitin to such a lysine can tag a protein for intracellular proteolytic destruction by a proteasome.
- **Ubiquitin ligase:** Any one of a large number of enzymes that attach ubiquitin to a protein, often marking it for destruction in a proteasome. The process catalyzed by ubiquitin ligase is called ubiquitination.