INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH & REVIEWS
journal homepage: www.ijmrr.online/index.php/home

Proteins: Structure and Role in Biological Systems

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How to Cite the Article: Shailja, Parul Singh, Proteins: Structure and Role in Biological Systems. *International Journal of Multidisciplinary Research & Reviews , 2(1).*

Keyword

Proteins, structure, function, determination, roles, biological systems, disease, drug design

Abstract

Proteins are fundamental biomolecules that play diverse and critical roles in biological systems. Their three-dimensional structure is intricately linked to their functions, making protein structure-function relationships a central focus of scientific research. This research paper aims to provide an overview of protein structure, its determination methods, and the essential roles proteins play in various biological processes. By understanding protein structure and its functional implications, scientists can gain valuable insights into the mechanisms underlying cellular processes, drug design, and disease pathology.

1. Introduction

Proteins are vital macromolecules that perform a diverse array of functions within biological systems. Deciphering proteins' functions in cellular processes, disease causes, and medication development requires a thorough understanding of the complex link between protein structure and function. The importance of a protein's structure in defining how it functions was highlighted by Anfinsen's observation in 1973 that "the native structure of a protein is determined by its amino acid sequence."

The fundamental structure of a protein is governed by the linear arrangement of amino acids, but the secondary, tertiary, and quaternary structures of a protein are dictated by folding, spatial organisation, and interactions between amino acid residues (Berg et al., 2015). In order to perform their unique biological tasks, proteins must assume various three-dimensional conformations.

The advancement of protein structure determination methods such as X-ray crystallography, Nuclear Magnetic Resonance (NMR) spectroscopy, Cryo-Electron Microscopy (Cryo-EM), and computational approaches has revolutionised the ability to elucidate protein structures in unprecedented detail (Fernández-Recio, 2019). These methods have greatly contributed to our understanding of protein functions and have paved the way for rational drug design and therapeutic interventions (Keskin et al., 2016).

This research paper provides a comprehensive overview of protein structure and its determination methods. Additionally, it explores the essential roles that proteins play in enzymatic catalysis, structural support, molecular transport, hormonal signaling, immune response, cellular regulation, motor function, and storage. Furthermore, the paper discusses the link between protein misfolding and diseases, including neurodegenerative disorders, highlighting the critical role of protein folding and chaperone proteins (Chiti and Dobson, 2017). Finally, the paper explores the emerging field of protein engineering and its applications in drug design.

1.1 Importance of Protein Structure-Function Relationship

Understanding the various functions that proteins perform in biological systems and how they relate to one another is crucial. A protein's unique activities are determined by its three-dimensional structure, and any changes or disruptions to that structure may degrade or eliminate those functions. Therefore, understanding the link between protein structure and function is crucial for identifying the mechanisms underpinning cellular functions, developing therapeutic approaches, and examining disease pathologies.

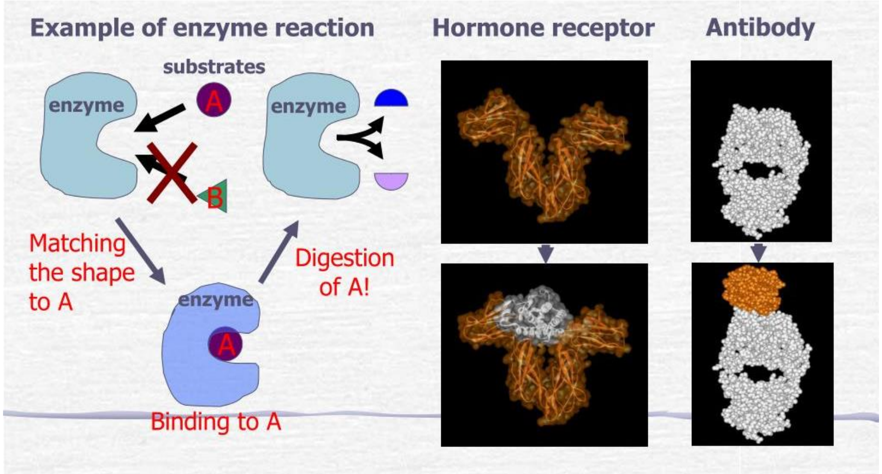

Fig 1- Protein Structure-Function Relationship

The ability of a protein to interact with other molecules, such as ligands, substrates, and other proteins, is determined by the protein structure. Enzymatic proteins must have a specific arrangement of amino acids in their active region in order to catalyse particular biological events.(2015) Berg et al. The complimentary fit between the ligand and the protein's three-dimensional structure, also known as the lock-and-key or induced fit model, is crucial for the binding of a ligand to a protein's active site (Alberts et al., 2002). For instance, the structural compatibility between the antigen and the antibody's binding site is essential for the antibody-antigen interaction, which plays a key role in immune responses.

Proteins are made more stable and resilient by their protein structure, which enables them to maintain their functional shape under a variety of physiological circumstances. A few of the many interactions that regulate how proteins fold into their native forms include hydrogen bonds, disulfide bridges, hydrophobic contacts, and electrostatic forces (Berg et al., 2015). Any protein disruptions or misfolding can result in function loss and may even be a factor in the development of illnesses like neurodegenerative disorders.

In the development and design of pharmaceuticals, comprehension of the structure-function link of proteins is also essential. To control their activity and cure certain disorders, several medications target particular proteins. The logical design of medications that can bind to particular areas or active sites of the protein and modulate its activity is made possible by knowledge of the protein's structure. This method is especially pertinent to the creation of enzyme inhibitors, receptor antagonists, and agents that prevent protein-protein interactions. Insights into the three-dimensional structures of protein targets have been made possible by protein structure determination techniques such X-ray crystallography, NMR spectroscopy, and cryo-EM (Berg et al., 2015).

2. Protein Structure:

The hierarchical arrangement of amino acids within a protein, which ultimately defines its form and function, is referred to as protein structure. To fully understand the complexity of protein behaviour and their functions in biological processes, it is imperative to comprehend the various levels of protein structure.

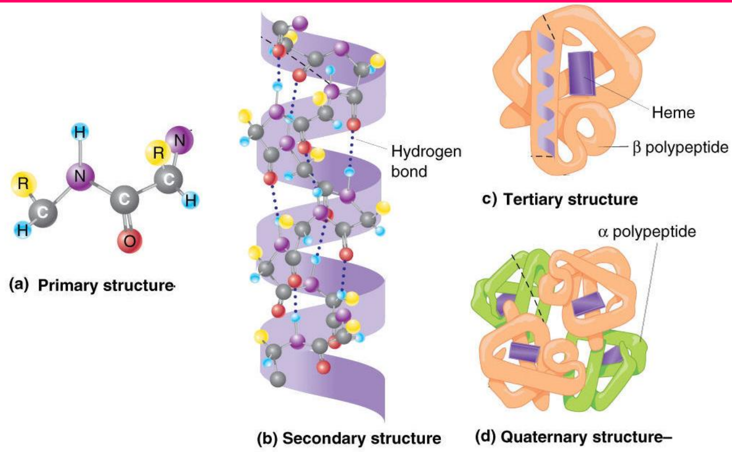

Fig 2- Protein Structure (source- https://newciafrarim.weebly.com/what-is-the-primary-structure-of-a-protein-determined-by.html)

2.1 Primary Structure

A linear sequence of amino acids connected by peptide bonds makes up the basic structure of a protein. The genetic data included in the DNA determines this sequence. Every protein has a unique fundamental structure, according to Nelson and Cox (2017), that has a sequence of amino acids that impacts the protein's overall form and function.

All higher tiers of protein organisation are built upon the core structure. The capacity of a protein to fold into a stable form and communicate with other molecules is influenced by the amino acid sequence (Alberts et al., 2002). The structure and functionality of proteins can be significantly impacted by even minor alterations in the amino acid sequence. For instance, a single amino acid change in the core structure of haemoglobin results in the genetic blood disorder sickle cell anaemia (Nelson and Cox, 2017).

It is usually possible to identify a protein's main structure using DNA sequencing techniques or protein sequencing techniques like mass spectrometry or Edman degradation. Once the primary structure is known, it serves as the starting point for understanding the higher levels of protein organization and their functional implications.

The primary structure of a protein provides important insights into its evolutionary relationships with other proteins. By comparing the amino acid sequences of different proteins, scientists can uncover evolutionary connections and identify conserved regions that contribute to similar functions across species (Nelson and Cox, 2017).

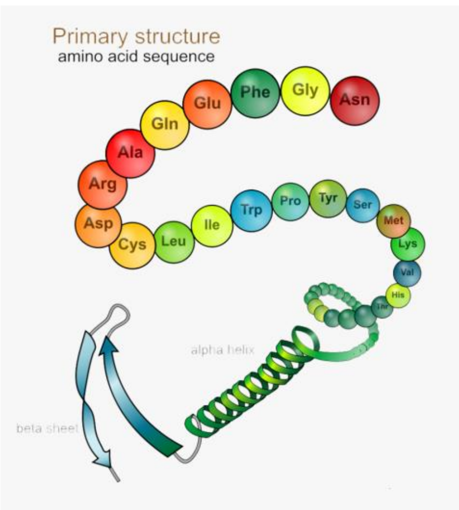

Fig 3- Primary structure of a protein (sources-https://www.pngwing.com/de/free-png-itvcw)

The linear amino acid sequence that dictates a protein's overall structure and function is known as its fundamental structure. It offers information on evolutionary linkages and acts as a key foundation for comprehending protein organisation at higher levels.

2.2 Secondary Structure

The local arrangements and folding patterns of protein segmentation are referred to as secondary structure. It results from special interactions, particularly hydrogen bonding, between amino acids and gives birth to recurrent structural patterns. The secondary structures -helices and -sheets are two popular forms.

The peptide backbone forms a spiral in the right-handed coiled shape known as the -helix. It is stabilised by hydrogen bonds made between the amide hydrogen of an amino acid situated four residues away and the carbonyl oxygen of one amino acid (Berg et al., 2015). A stable and stiff structure is produced as a result of the effective packing of the polypeptide chain made possible by this arrangement. Proteins that bridge membranes or offer structural stability, like keratin, frequently include -helices.

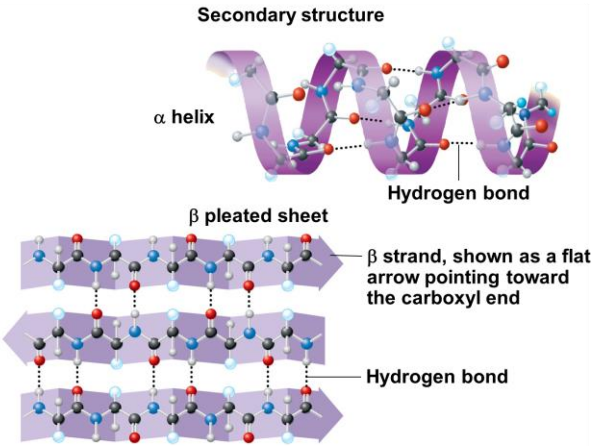

Fig 4- Secondary Structure of Protein (source-http://thebiologs.blogspot.com/2016/09/cape-1-proteins.html)

β-sheets, on the other hand, consist of strands of amino acids connected by hydrogen bonds. The directions of the strands might either be the same (parallel) or different (antiparallel). Proteins that include -sheets are formed as a result of -sheets and are essential for providing structural support, as shown, for example, in the development of the -barrel structure seen in the outer membrane proteins of bacteria (Alberts et al., 2002).

A protein's overall conformation and function are frequently significantly influenced by its secondary structure. It may affect the protein's resiliency, ability to bind, and ability to interact with other molecules. Due to their compatibility with the hydrogen bonding patterns involved, some amino acid residues are also frequently found in particular secondary structure elements (Berg et al., 2015).

Experimental methods like X-ray crystallography, NMR spectroscopy, or circular dichroism (CD) spectroscopy are frequently used to identify secondary structure. Secondary structural components can also be predicted with a respectable degree of accuracy using computational approaches that analyse protein sequences and patterns of amino acids.

2.3 Tertiary Structure

The entire three-dimensional configuration of one protein molecule is referred to as tertiary structure. The connections among residues of amino acids that are distant from one another in the linear sequence but converge close to one another in the folded protein have a major role in determining it. The distinctive shape and functional characteristics of a protein are strongly influenced by its tertiary structure (Berg et al., 2015).

Numerous forces contribute to the stabilization of the tertiary structure, including hydrophobic interactions, electrostatic interactions, hydrogen bonds, and disulfide bridges. Hydrophobic interactions occur between nonpolar amino acid residues, causing them to cluster together in the protein's interior, shielded from the surrounding aqueous environment. Electrostatic interactions involve the attraction or repulsion between charged amino acid residues. Polar amino acids join together to generate hydrogen bonds, which aid in protein folding and stabilisation. In the presence of oxidative circumstances, disulfide bridges, covalent connections between two cysteine residues, can develop and offer further stability to the structure of proteins (Berg et al., 2015).

The hydrophilic effect, which permits nonpolar amino acids to reduce their interaction with water, and the development of the stabilising interactions stated above are what cause a protein to fold into its particular tertiary structure. The protein's conformation is intricately linked to its biological function. For instance, enzymes have active sites with specific shapes that allow them to bind substrates and catalyze chemical reactions. Receptors have binding sites that recognize and interact with signaling molecules, initiating cellular responses (Alberts et al., 2002).

Proteins can adopt a variety of tertiary structures, such as globular structures, fibrous structures, or a combination of both. Globular proteins typically have a compact, spherical shape, while fibrous proteins tend to have elongated, thread-like structures. Examples of globular proteins include myoglobin and hemoglobin, while collagen and keratin are examples of fibrous proteins (Alberts et al., 2002).

It can be difficult to determine a protein's tertiary structure and calls for sophisticated methods like X-ray crystallisation, NMR spectroscopy, or cold electron microscopy (Cryo-EM). These techniques enable a better knowledge of how amino acids are arranged spatially and how proteins operate (Berg et al., 2015).

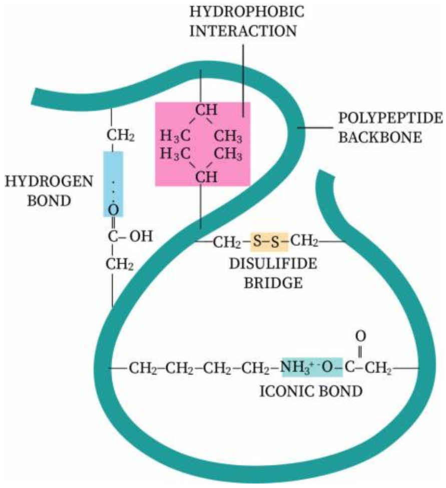

Fig 5- Tertiary Structure of Protein (source-http://fayllar.org/proteins-are-a-class-of-diverse-macromolecules-that-determine.html)

A protein's overall three-dimensional shape, which is necessary for its function, is referred to as the tertiary framework of a protein. The interactions between the amino acid residue that are spaced apart in the linear sequence determine it. The distinctive shape, security, and function characteristics of a protein are strongly influenced by its tertiary structure.

2.4 Quaternary Structure

The organisation and interactions of many protein subunits to create a useful protein complex are referred to as quaternary structure. Many proteins are made up of several polypeptide chains that come together to form a quaternary structure, especially those with higher molecular weights. According to Berg et al. (2015), these protein complexes' overall stability and functionality depend heavily on their quaternary structure.

One or more noncovalent interactions, including as hydrogen bonds, electrostatic charges, van der Waals forces, and hydrophilic contacts, control how the individual subunits of a protein in a quaternary structure are arranged. The quaternary structure's stability and integrity are influenced by these interactions.

Fig 6- Quaternary Structure of protein (sources- https://www.biologybrain.com/4-four-levels-of-protein-structure-examples/)

The assembly of protein subunits into a functional quaternary structure expands the functional repertoire of proteins. It can provide increased catalytic activity, substrate specificity, allosteric regulation, or enable the formation of binding sites that are inaccessible in individual subunits. Examples of proteins with quaternary structures include hemoglobin, which consists of four subunits, and the ribosome, which is composed of multiple subunits (Berg et al., 2015).

2.5 Protein Folding and Stability

The process through which a protein assumes its useful three-dimensional structure is known as protein folding. Newly created polypeptide chains go through a variety of folding processes during synthesis, which results in the acquisition of their native structure. The information included in a protein's amino acid sequence serves as a guide for protein folding, which is further aided by molecular chaperones and folding catalysts (Dobson, 2003).

The hydrophobic effect, which allows nonpolar amino acids to assemble in the inside of the protein, protected from the surrounding aqueous environment, is what drives the folding process. Other stabilizing interactions, including hydrogen bonds, electrostatic interactions, and disulfide bridges, contribute to the proper folding and stability of the protein.

Protein stability refers to the tendency of a protein to maintain its native structure and resist denaturation or misfolding. Stable proteins exhibit robust folding properties that enable them to withstand changes in temperature, pH, and other environmental conditions. However, destabilizing factors such as mutations, extreme conditions, or the presence of denaturing agents can disrupt the protein's stability, leading to misfolding, aggregation, and loss of function (Dobson, 2003).

3. Methods for Determining Protein Structure:

Accurately determining the three-dimensional structure of proteins is crucial for understanding their functions and exploring their roles in biological systems. Several methods have been developed to elucidate protein structures, each with its strengths and limitations. The following sections describe some of the commonly used methods for protein structure determination.

3.1 X-ray Crystallography

A popular method for identifying protein structures at the atomic level is X-ray crystallography. It entails producing superior protein crystals and analysing them using X-ray diffraction (Drenth, 1994). X-ray beam interactions with the protein crystal cause X-rays to scatter in recognisable ways. The protein's electron density may be recreated by examining the diffraction pattern, which enables the identification of the protein's three-dimensional structure.

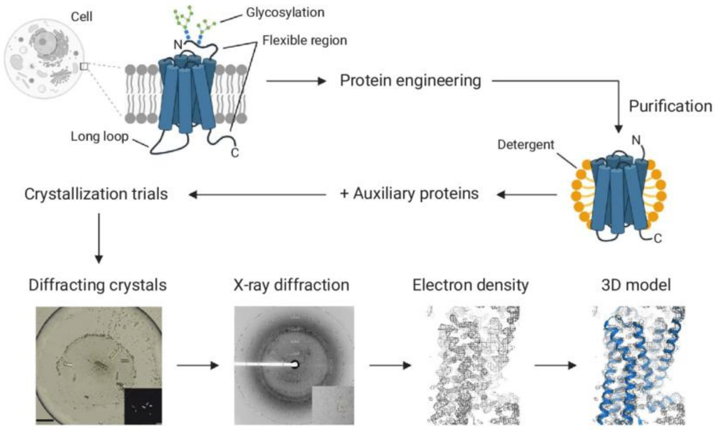

Fig 7- X-ray Crystallography

X-ray crystallography provides detailed information about the position of individual atoms within the protein molecule, allowing for a precise understanding of its structure and interactions. This method has been instrumental in uncovering numerous protein structures and has contributed significantly to our understanding of protein function (Henderson, 1995).

3.2 Nuclear Magnetic Resonance (NMR) Spectroscopy

Nuclear Magnetic Resonance (NMR) spectroscopy is another powerful technique for determining protein structures, particularly for smaller proteins or those that are challenging to crystallize. NMR spectroscopy relies on the behavior of atomic nuclei in a magnetic field and their interaction with radiofrequency pulses (Riek et al., 2002).

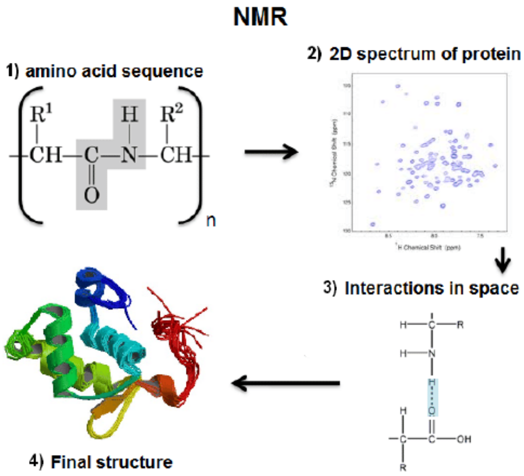

Fig- 8 Nuclear Magnetic Resonance (NMR) Spectroscopy for determining protein structures

In NMR spectroscopy, the protein is dissolved in a suitable solvent and subjected to a strong magnetic field. The NMR spectrum obtained provides information about the chemical shifts and couplings of the atomic nuclei, which can be used to deduce the protein's structure. By analyzing the NMR data and performing computational calculations, a three-dimensional model of the protein can be generated.

NMR spectroscopy is advantageous as it can provide insights into protein dynamics and flexibility, which are crucial for understanding protein function. It can also be applied to study protein-protein interactions and ligand binding events (Riek et al., 2002).

3.3 Cryo-Electron Microscopy (Cryo-EM)

Large protein complexes and membrane proteins may now be structurally determined using cryo-electron microscopy (Cryo-EM). Using an electron microscope, protein sample samples are imaged after being quickly frozen in vitreous ice (Cheng, 2018).

The protein sample is prepared in a thin layer of ice for Cryo-EM, and pictures are taken using an electron microscope while it is in a cryogenic environment. Following processing, a three-dimensional density map of the protein complex is created from these pictures. Recent advancements in Cryo-EM technology, such as direct electron detectors and advanced image processing algorithms, have greatly improved its resolution and applicability.

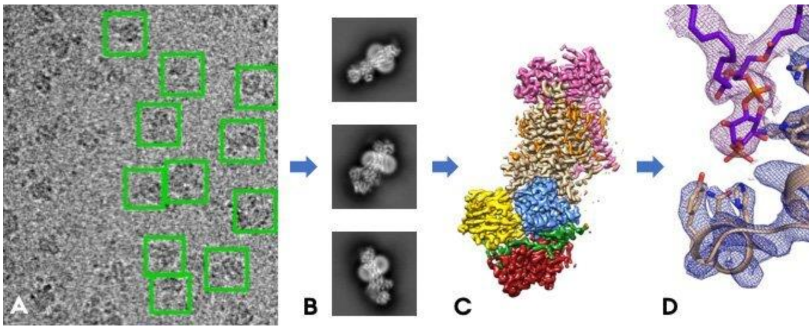

Fig 9- Cryo-electron microscopy reveals structures of protein

Cryo-EM has revolutionized the structural biology field by enabling the determination of high-resolution structures of previously challenging targets, including large macromolecular complexes. It has provided valuable insights into protein-protein interactions, conformational changes, and membrane protein structures (Cheng, 2018).

3.4 Computational Approaches

Computational approaches have become integral to protein structure determination and prediction. These methods utilize algorithms, statistical potentials, and computational modeling to generate protein structures based on experimental data and theoretical principles.

Homology modeling, also known as comparative modeling, is a computational approach that predicts protein structures based on their similarity to known structures. By utilizing the evolutionary conservation of protein sequences and structures, homology modeling can generate accurate models for proteins that share sequence similarity with already solved structures (Martí-Renom et al., 2000).

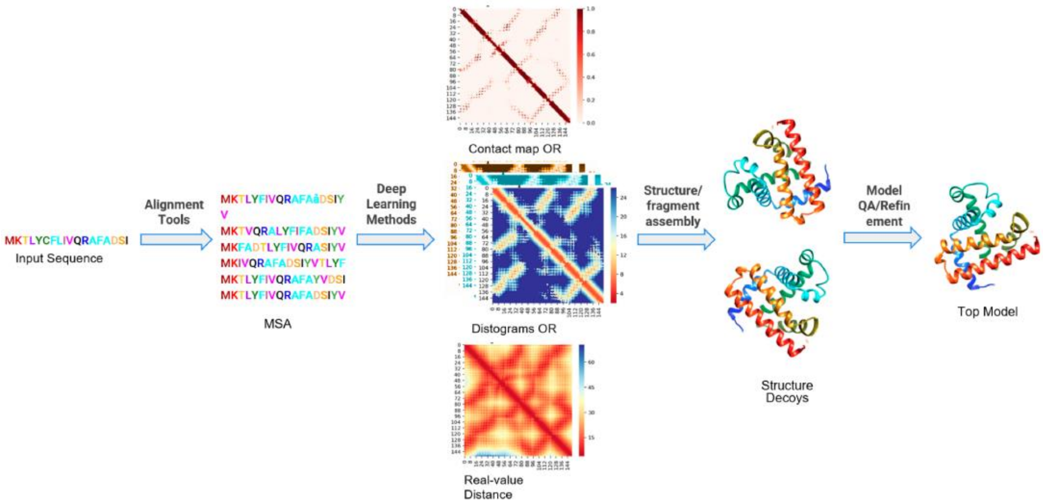

Fig 10 - Computational Approach

Ab initio methods, on the other hand, aim to predict protein structures from scratch, without relying on known templates. These methods employ physical principles and statistical potentials to explore the conformational space and identify the most energetically favorable structures (Raman et al., 2009).

4. Protein Functions:

Proteins are involved in a multitude of functions within living organisms, enabling the execution of essential biological processes. The diverse range of protein functions is a result of their structural versatility and ability to interact with other molecules. The following sections describe several key protein functions.

4.1 Enzymatic Proteins

Enzymatic proteins, known as enzymes, are catalysts that facilitate and accelerate biochemical reactions in cells (Berg et al., 2015). Enzymes lower the activation energy required for a reaction, enabling it to occur at a faster rate. Each enzyme is specialized for a particular reaction or set of reactions, and their specificity is due to the precise arrangement of amino acids within their active sites. Enzymes play crucial roles in metabolic pathways, DNA replication, protein synthesis, and many other cellular processes.

4.2 Structural Proteins

Structural proteins provide support and stability to cells, tissues, and organs. They have a fibrous or filamentous structure, forming networks or scaffolds that maintain the shape and integrity of biological structures (Alberts et al., 2002). Examples of structural proteins include collagen, which gives strength and flexibility to connective tissues, and keratin, which forms the structural framework of hair, nails, and skin.

4.3 Transport Proteins

Transport proteins facilitate the movement of molecules, ions, or other substances across cellular membranes or throughout the body. These proteins have specific binding sites that recognize and transport molecules, ensuring their efficient delivery to their target destinations. Examples of transport proteins include channels, carriers, and pumps involved in the transport of ions, nutrients, and signaling molecules across cell membranes.

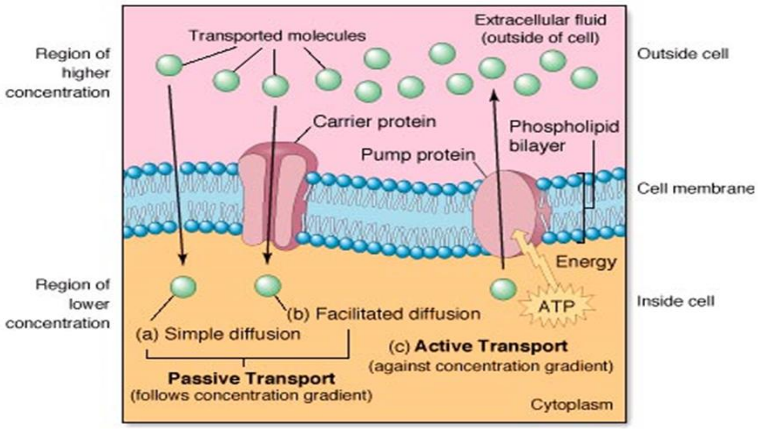

Fig 11 - Examples of Transport Proteins

4.4 Hormonal Proteins

Growth hormones and other hormonal proteins function as chemical transmitters in the body, controlling a variety of physiological activities. Specialized cells produce these proteins, which then move via the circulatory system to target organs or cells. Hormonal proteins bind to specific receptors on target cells, initiating cellular responses and coordinating functions such as metabolism, growth, and reproduction.

Fig 12 -Structure of Some hormonal protein (a) Growth hormone (b) prolactin

4.5 Immunoglobulins

Antibodies and immunoglobulins are essential elements of the immune system. They identify and attach to foreign things like infections or poisons, designating them for the immune system to eliminate. Immunoglobulins are essential for immunological responses that protect the body from illnesses and infections (Alberts et al., 2002).

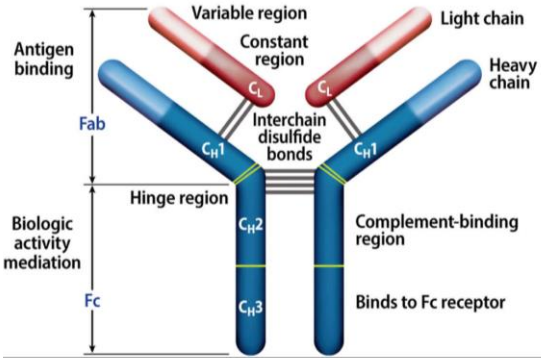

Fig 13 - Immunoglobulins Structure

4.6 Signaling Proteins

Signaling proteins transmit signals and information within and between cells, regulating various cellular processes and coordinating physiological responses. These proteins can function as receptors on cell surfaces, intracellular messengers, or components of signaling cascades. Examples include protein kinases, which control biological functions via phosphorylation events, and receptors linked to G proteins, which participate in signal transduction.

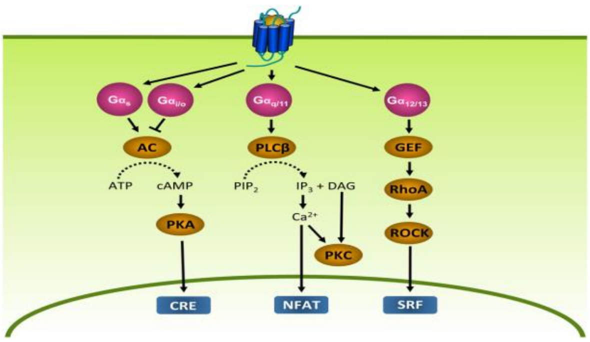

Fig 14- Signaling Proteins

4.7 Regulatory Proteins

Regulatory proteins control gene expression and modulate cellular processes by interacting with DNA, RNA, or other proteins. They can act as transcription factors, binding to specific DNA sequences and influencing the transcription of target genes. Regulatory proteins also play roles in cell cycle regulation, cell differentiation, and development.

4.8 Motor Proteins

Motor proteins are responsible for generating movement within cells and tissues. They use energy derived from ATP hydrolysis to perform mechanical work, such as transporting organelles along microtubules or causing muscle contraction. Examples of motor proteins include myosin and kinesin, which are involved in muscle contraction and intracellular transport, respectively.

4.9 Storage Proteins

Storage proteins serve as reservoirs of amino acids or essential nutrients in organisms. These proteins accumulate and store molecules, such as ions, metal ions, or amino acids, to be utilized when needed. Examples of storage proteins include ferritin, which stores iron, and casein, which stores essential amino acids in milk.

5. Protein Misfolding and Diseases:

Protein misfolding refers to the abnormal folding of proteins, leading to the adoption of incorrect conformations. Misfolded proteins often form aggregates and can contribute to the development of various diseases. The following sections discuss the implications of protein misfolding in different disease contexts.

5.1 Protein Misfolding and Aggregation

Multiple misfolded proteins can gather and clump together to create protein aggregates as a result of protein misfolding. These aggregates can impair organelle function, cause cellular toxicity, and disturb cellular processes (Chiti and Dobson, 2017). Numerous illnesses, including Alzheimer's, Parkinson's, and Huntington's disorders, have been linked to aggregated proteins.

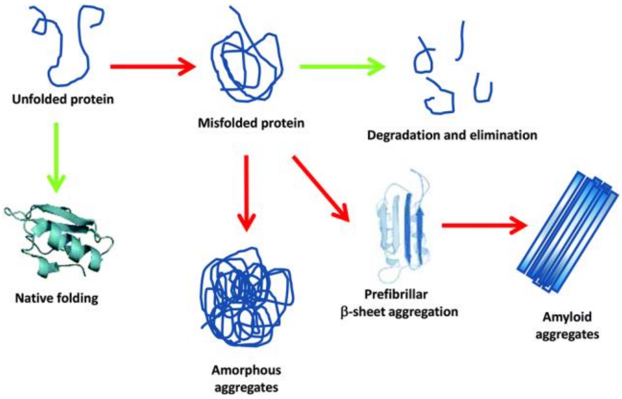

Fig 15- Protein Misfolding and Aggregation

5.2 Prions and Prion Diseases

Prions are misfolded proteins that have the ability to convert other normally folded proteins into the misfolded conformation. According to Prusiner (1998), this conversion process has the potential to spread across tissues and cause the emergence of prion disorders like Creutzfeldt-Jakob syndrome and mad cow disease. Prion disorders are characterized by the buildup of aberrant prion proteins, which cause progressive neurological symptoms and neurodegeneration.

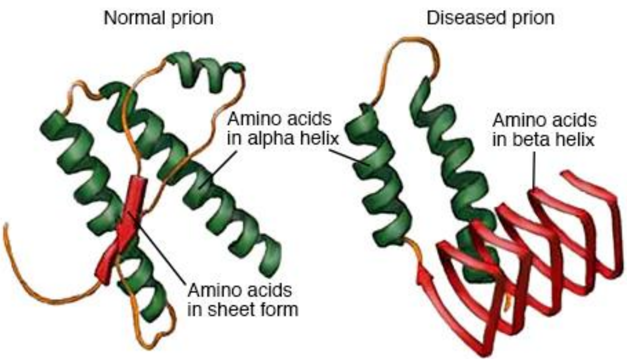

Fig 16- How Prions Folds (sources- https://www.mayoclinic.org/diseases-conditions/creutzfeldt-jakob-disease/multimedia/normal-and-diseased-prions/img-20007478)

5.3 Protein Misfolding in Neurodegenerative Disorders

Many neurodegenerative diseases, such as Alzheimer's disease, Parkinson's disease, and ALS (amyotrophic lateral sclerosis), are characterised by protein misfolding. These diseases cause a number of proteins to misfold and clump together in the brain, notably amyloid-beta, tau, alpha-synuclein, and the superoxide dismutase enzyme 1 (SOD1) (Ross and Poirier, 2004), misfold and clump together in the brain as a result of these illnesses (Ross and Poirier, 2004). The aggregates, such as amyloid plaques and Lewy bodies, are associated with neuronal dysfunction and cell death, contributing to the progressive degeneration of the nervous system.

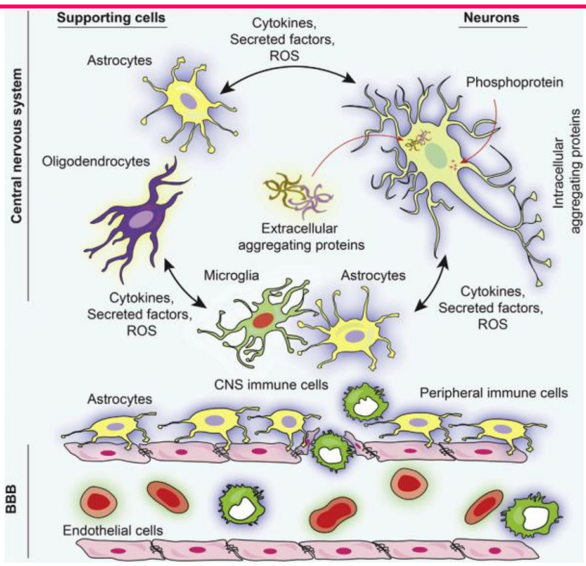

Fig 17 - Protein Misfolding in Neurodegenerative Disorders (source-Article in press (B.D. Kevadiya et al. / Advanced Drug Delivery Review)

5.4 Protein Folding Diseases and Chaperone Proteins

Specific proteins misfold and aggregate, resulting in protein folding illnesses, also known as conformational diseases. These illnesses include familial amyloidosis in various forms, Huntington's disease, and cystic fibrosis (Dobson, 1999). Molecular chaperones, also known as chaperone proteins, aid in protein folding by avoiding improper conformation and misfolding (Balch et al., 2008). These chaperones are essential for preserving protein homeostasis and avoiding the buildup of abnormally folded proteins, which can cause illness.

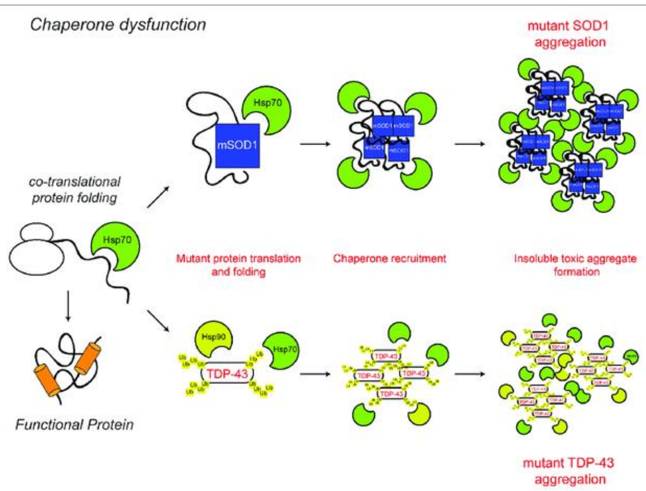

Fig 18-Chaperone Dysfunction in protein folding (sources-https://www.researchgate.net/publication/316633007_Protein_Homeostasis_in_Amyotrophic_Lateral_Sclerosis_Therapeutic_Opportunities)

6. Protein Engineering and Drug Design

Protein engineering involves modifying and designing proteins to enhance their properties or create novel functionalities for various applications, including drug design. Numerous techniques, such as computational protein design, guided the theory of evolution, and logical protein design, have been created to achieve these goals.The fundamentals and uses of protein engineering in drug development are covered in the sections that follow.

6.1 Rational Protein Design

Rational protein design utilizes the knowledge of protein structure-function relationships to make specific modifications in protein sequences or structures (Kuhlman and Baker, 2009). This approach involves a systematic and targeted design based on a deep understanding of protein folding, stability, and interaction mechanisms. Rational protein design can be used to improve protein stability, alter substrate specificity, or create novel functions by introducing specific amino acid substitutions or structural modifications.

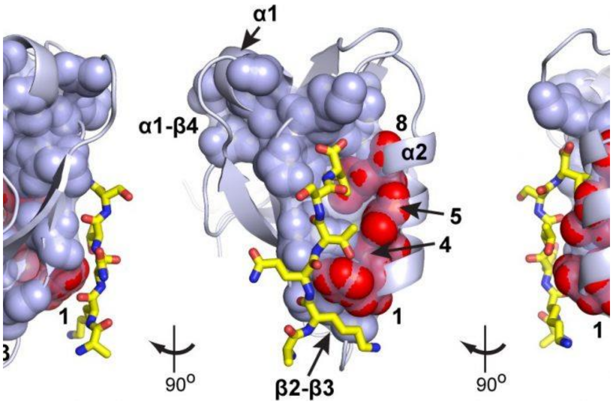

Fig 19- Rational Protein Engineering (source- https://datascience.uchicago.edu/research/rational-protein-engineering-using-data-driven-generative-models/)

6.2 Directed Evolution

Directed evolution is a powerful technique that mimics the process of natural evolution to create proteins with desired properties (Arnold, 2018). It involves generating a diverse population of protein variants through random mutagenesis or DNA shuffling and subjecting them to a selection or screening process to identify variants with improved properties. Directed evolution can be used to enhance enzymatic activity, increase protein stability, or confer new functions not present in the original protein.

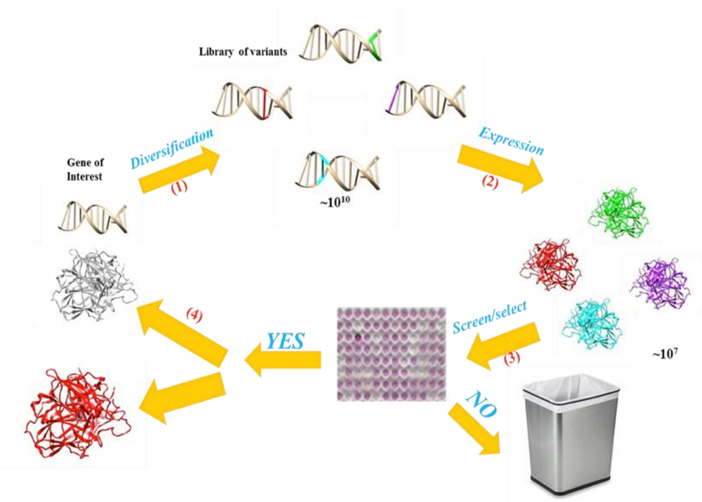

Fig 20- An illustration of directed evolution, a protein engineering method

6.3 Computational Protein Design

Computational protein design combines computational modeling and simulations to design new protein sequences or structures with desired properties (Kuhlman and Baker, 2009). This approach relies on the principles of protein folding and molecular interactions to predict and optimize protein sequences or structures. Computational protein design allows the exploration of vast sequence and structural space, enabling the creation of proteins with novel functions or improved properties.

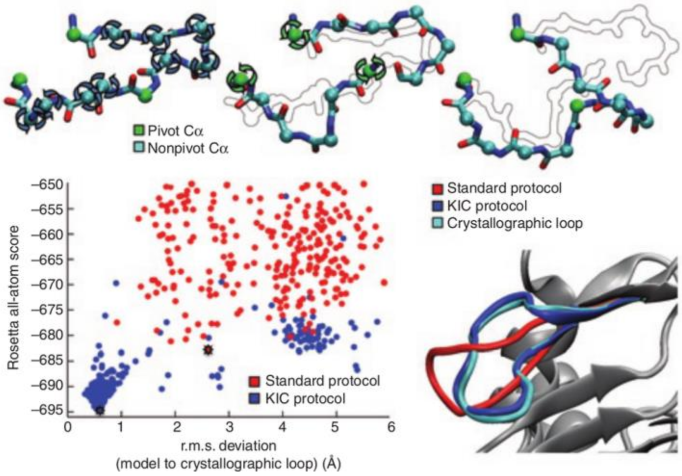

Fig 21- Computational Protein Design

6.4 Applications in Drug Design

Protein engineering plays a crucial role in drug design and development. By modifying or designing proteins, researchers can develop protein-based therapeutics, including antibodies, enzymes, and peptide drugs (Simeon and Shoichet, 2019). Rational protein design and directed evolution can be used to optimize the binding affinity, specificity, and stability of therapeutic proteins, enhancing their efficacy and reducing off-target effects.

When creating protein-based therapeutics, such as de novo created peptides or scaffolds of proteins for delivering drugs and targeted therapy, computational protein design techniques are used (Chevalier et al., 2017). Protein engineering methods are also used to create enzymes for drug production and biocatalysis, as well as protein-based biosensors for identifying and monitoring disease signs.

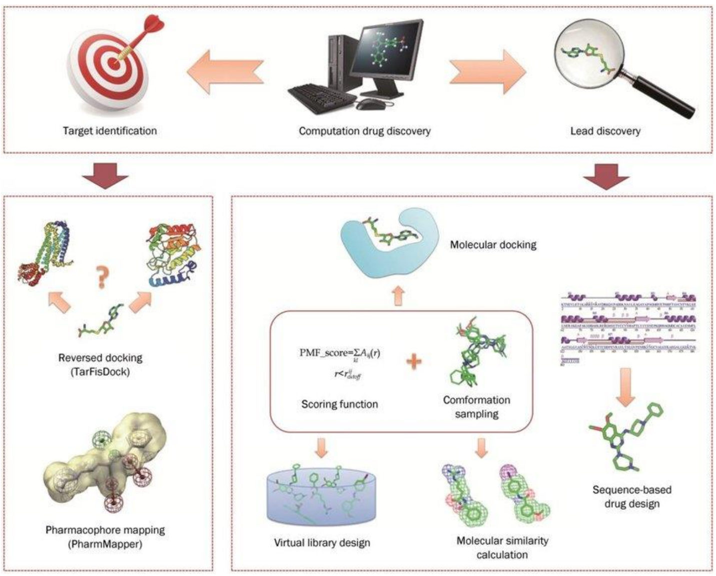

Fig 22- Important methodologies and platforms in Structure-Based Drug Design strategy

7. Conclusion:

In conclusion, proteins play a vital role in biological systems, serving diverse functions essential for life. The structure-function relationship of proteins governs their ability to perform specific tasks within cells and organisms. The secondary structure includes regional folding patterns like -helices and -sheets, whereas the fundamental structure controls the general sequence of amino acids. While quaternary structure entails the synthesis of several protein subunits, tertiary structure refers the three-dimensional organisation of a single protein. Protein folding and stability are crucial for maintaining proper protein function.

Proteins exhibit various functions in biological systems. Enzymatic proteins act as catalysts, facilitating biochemical reactions, while structural proteins provide support and stability to cells and tissues. Transport proteins enable the movement of molecules across membranes, and hormonal proteins serve as chemical messengers. Immunoglobulins play a vital role in the immune response, while signaling proteins transmit signals within and between cells. Regulatory proteins control gene expression and cellular processes, and motor proteins generate movement. Storage proteins store essential molecules for future use.

Protein misfolding can have detrimental effects. Misfolded proteins can aggregate, leading to the development of diseases such as neurodegenerative disorders and prion diseases. Protein engineering techniques, including rational protein design, directed evolution, and computational protein design, have been developed to modify and design proteins for various applications. Protein engineering plays a crucial role in drug design, enabling the optimization of therapeutic proteins and the creation of novel protein-based drugs.

Proteins are multifunctional macromolecules that serve as the workhorses of biological systems. Their structure determines their functions, and advancements in protein structure determination techniques have revolutionized our understanding of their diverse roles. Further research into protein structure and function will unlock new insights into cellular processes, disease mechanisms, and potential therapeutic interventions.

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