Commentary

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A Brief Note on Proteins

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Description

Proteins are huge biomolecules and macromolecules that are made up of one or more long chains of amino acids. Proteins play a variety of roles in organisms, including catalysing metabolic events, DNA replication, responding to stimuli, giving cells and organism's structure, and moving materials from one place to another. Proteins differ primarily in their amino acid sequence, which is governed by their genes' nucleotide sequence and usually culminates in protein folding into a specific 3D structure that dictates its activity. A polypeptide is a linear chain of amino acid residues. At least one lengthy polypeptide can be found in a protein. Short polypeptides (less than 20–30 residues) are generally referred to as peptides and are rarely considered proteins [1].

Peptide bonds and neighboring amino acid residues bind the individual amino acid residues together. A gene's sequence, which is encoded in the genetic code, determines the amino acid residue sequence in a protein. In general, the genetic code specifies 20 conventional amino acids; nevertheless, selenocysteine and pyrrolysine can be found in the genetic code of some organisms. The residues in a protein are frequently chemically transformed by post-translational modification shortly after or even during synthesis, altering the physical and chemical characteristics, folding, stability, activity and ultimately, the function of the proteins. Non-peptide groups, often known as prosthetic groups or cofactors, are connected to some proteins.

Proteins only persist for a short time once they are created, and then they are destroyed and recycled by the cell's machinery through the protein turnover process. The longevity of a protein is measured in terms of its half-life, which can vary greatly. In mammalian cells, they can live for minutes or years, with an average lifespan of 1–2 days. Proteins that are abnormal or misfolded degrade more quickly, either because they are targeted for destruction or because they are unstable. Proteins, like other biological macromolecules like polysaccharides and nucleic acids, are vital elements of organisms that play a role in nearly every function within cells. Enzymes are proteins that catalyse biological reactions and are essential for metabolism [2].

Actin and myosin in muscle and the proteins in the cytoskeleton, which constitute a scaffolding framework that keeps cells in shape, are examples of proteins with structural or mechanical activities. Cell signalling, immunological responses, cell adhesion, and the cell cycle all require other proteins. Proteins are required in the diet of animals in order to give vital amino acids that cannot be produced. Proteins are broken down during digestion and used in the metabolism. Proteins can be separated from other cellular components using a range of techniques, including ultracentrifugation, precipitation, electrophoresis, and chromatography; the advent of genetic engineering has made a number of purification approaches available. Immunohistochemistry, site-directed mutagenesis, and X-ray crystallography are all common methods for studying protein structure and function [3].

The majority of proteins are linear polymers made up of up to 20 distinct L amino acids. A common structural property of all protein genic amino acids is a carbon to which an amino group, a carboxyl group, and a variable side chain are attached. Only praline deviates from this fundamental structure because it has a unique ring attached to the N-end amine group that pushes the CO–NH amide moiety into a fixed conformation. The side chains of the standard amino acids, detailed in the list of standard amino acids, have a great variety of chemical structures and properties; it is the combined effect of all of the amino acid side chains in a protein that ultimately determines its three-dimensional structure and its chemical reactivit [4].

Peptide bonds connect the amino acids in a polypeptide chain. An individual amino acid is known as a residue once it has been linked in the protein chain, and the linked series of carbon, nitrogen, and oxygen atoms is known as the main chain or protein backbone. The alpha carbons are roughly coplanar because the peptide bond has two resonance forms that provide some double-bond character and inhibit rotation along its axis. The protein backbone's local shape is determined by the other two dihedral angles in the peptide bond. The N-terminus, or amino terminus, of a protein is known as the amino terminus, whereas the C-terminus, or carboy terminus, is known as the carboxy terminus.

The information contained in genes is used to construct proteins from amino acids. The nucleotide sequence of the gene that encodes this protein specifies the amino acid sequence of each protein. The genetic code is made up of three-nucleotide sets called codons, each of which indicates an amino acid. For example, the code for methionine is AUG (adenine–uracil–

guanine). Because DNA has four nucleotides, there are a total of 64 potential codons; as a result, the genetic code has considerable redundancy, with some amino acids being specified by more than one codon [5].

RNA polymerase and other proteins convert DNA-encoded genes into pre-messenger RNA (mRNA). Most organisms then utilise various forms of Post-transcriptional modification to convert the pre-mRNA (also known as a primary transcript) into mature mRNA, which is then used as a template for protein synthesis by the ribosome. In prokaryotes, mRNA can be used just after it is made, or it can be bound by a ribosome after it has travelled away from the nucleoid. Eukaryotes, on the other hand, produce mRNA in the nucleus and then transport it across the nuclear membrane into the cytoplasm, where protein synthesis occurs.

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Translation is the process of producing a protein from an mRNA template. The ribosome loads the mRNA, which is then read three nucleotides at a time by matching each codon to its base pairing anticodon on a transfer RNA molecule, which carries the amino acid corresponding to the codon it recognises. Aminoacyl tRNA synthetase is an enzyme that "charges" tRNA molecules with the right amino acids. The nascent chain is a word used to describe a developing polypeptide. From the N-terminus to the C-terminus, proteins are always biosynthesized.

Short proteins can also be chemically manufactured using a group of techniques known as peptide synthesis, which relies on organic synthesis techniques like chemical ligation to produce high yields of peptides. Chemical synthesis allows non-natural amino acids to be introduced into polypeptide chains, such as fluorescence probes attached to amino acid side chains. These techniques are valuable in laboratory biochemistry and cell biology, but they are not suitable for commercial use. For polypeptides longer than roughly 300 amino acids, chemical synthesis is inefficient, and produced proteins may not immediately adopt their natural tertiary structure. The majority of chemical synthesis processes work in the opposite direction of biological reactions, from C-terminus to N-terminus [7].

Proteins aren't completely rigid atoms. Proteins may change between numerous related configurations while performing their functions, in addition to these levels of structure. These tertiary or quaternary forms are commonly referred to as "conformations" in the context of functional rearrangements and transitions between them are referred to as conformational alterations. The attachment of a substrate molecule to an enzyme's active site, or the physical portion of the protein that participates in chemical catalysis, frequently causes such modifications. Proteins in solution also change structure due to heat vibration and collisions with other molecules.

Tertiary Structures

Proteins are classified informally into three groups based on their tertiary structures: globular proteins, fibrous proteins, and membrane proteins. The vast majority of globular proteins are soluble, and many of them are enzymes. Collagen, the primary component of connective tissue, and keratin, the protein component of hair and nails, are examples of fibrous proteins that are structural. Membrane proteins are frequently used as receptors or as channels via which polar or charged substances can move through the cell membrane.

Dehydrons are a type of intramolecular hydrogen bond inside proteins that is poorly protected from water attack and so promotes their own dehydration. Proteins are classified informally into three groups based on their tertiary structures: globular proteins, fibrous proteins, and membrane proteins. The vast majority of globular proteins are soluble, and many of them are enzymes. Collagen, the primary component of connective tissue, and keratin, the protein component of hair and nails, are examples of fibrous proteins that are structural. Membrane proteins are frequently used as receptors or as channels via which polar or charged substances can move through the cell membrane [8].

Dehydrons are a type of intramolecular hydrogen bond inside proteins that is poorly protected from water attack and so promotes their own dehydration. Proteins are the main players in the cell, and they are believed to carry out the functions dictated by the information encoded in genes. Most biological molecules, with the exception of specific forms of RNA, are relatively inert components upon which proteins function. Proteins account for half of the dry weight of an Escherichia coli cell, while DNA and RNA account for only 3% and 20% of the dry weight, respectively. The proteome is the collection of proteins expressed by a single cell or cell type [9].

Small-Molecule Substrates

Proteins can bind to small-molecule substrates as well as other proteins. Proteins can create fibrils when they bind specifically to other copies of the same molecule; this happens frequently in structural proteins, which are made up of globular monomers that self-associate to form hard fibres. Protein–protein interactions also influence enzymatic activity, cell cycle progression, and the formation of big protein complexes that carry out a number of closely linked processes with a shared biological function. Proteins can bind to cell membranes and even be incorporated into them. Binding partners' ability to cause conformational changes in proteins allows for the creation of massively complex signalling networks [10].

References

1. Anderson LK (1966) High-speed photodetectors. Proceedings of the IEEE. 1966; 54:1335-1349.

2. Beneking H (1976) High-gain wide-gap-emitter Ga1-xAlxAs-GaAs phototransistor. Electron Lett 12: 395-396.
3. Stillman GE (1976) Electroabsorption in GaAs and its application to waveguide detectors and modulators. Appl Phys Lett 28: 544-546.
4. Dupuis RD (1977) Room-temperature operation of Ga(1-x)AlxAs/GaAs double-heterostructure lasers grown by metalorganic chemical vapor deposition. Appl Phys Lett 31: 466-468.
5. Faist J (1994) Quantum cascade laser. Sci 264: 553-556.
6. Burnham RD (1970) AlxGa1-xAs1-y'P y'single bond sign Gas1-yPy Heterostructure laser and lamp junctons. Appl Phys Lett 17: 455–457.
7. Leta G (2013) Desho grass (pennisetum pedicellatum) for livestock feed, grazing land and soil and water management on small-scale farms.
8. Ducat L, Rubenstein A, Philipson LH, Anderson BJ (2015) A review of the mental health issues of diabetes conference. Diab Car 38: 333-8.
9. Powers MA, Richter S, Ackard D, Gerken S, Meier M, et al. (2012) Characteristics of persons with an eating disorder and type 1 diabetes and psychological comparisons with persons with an eating disorder and no diabetes. Int J Eat Disord 45: 252-256.
10. Mairs R, Nicholls D (2016) Assessment and treatment of eating disorders in children and adolescents. Arch Dis Child 101: 1168-1175.