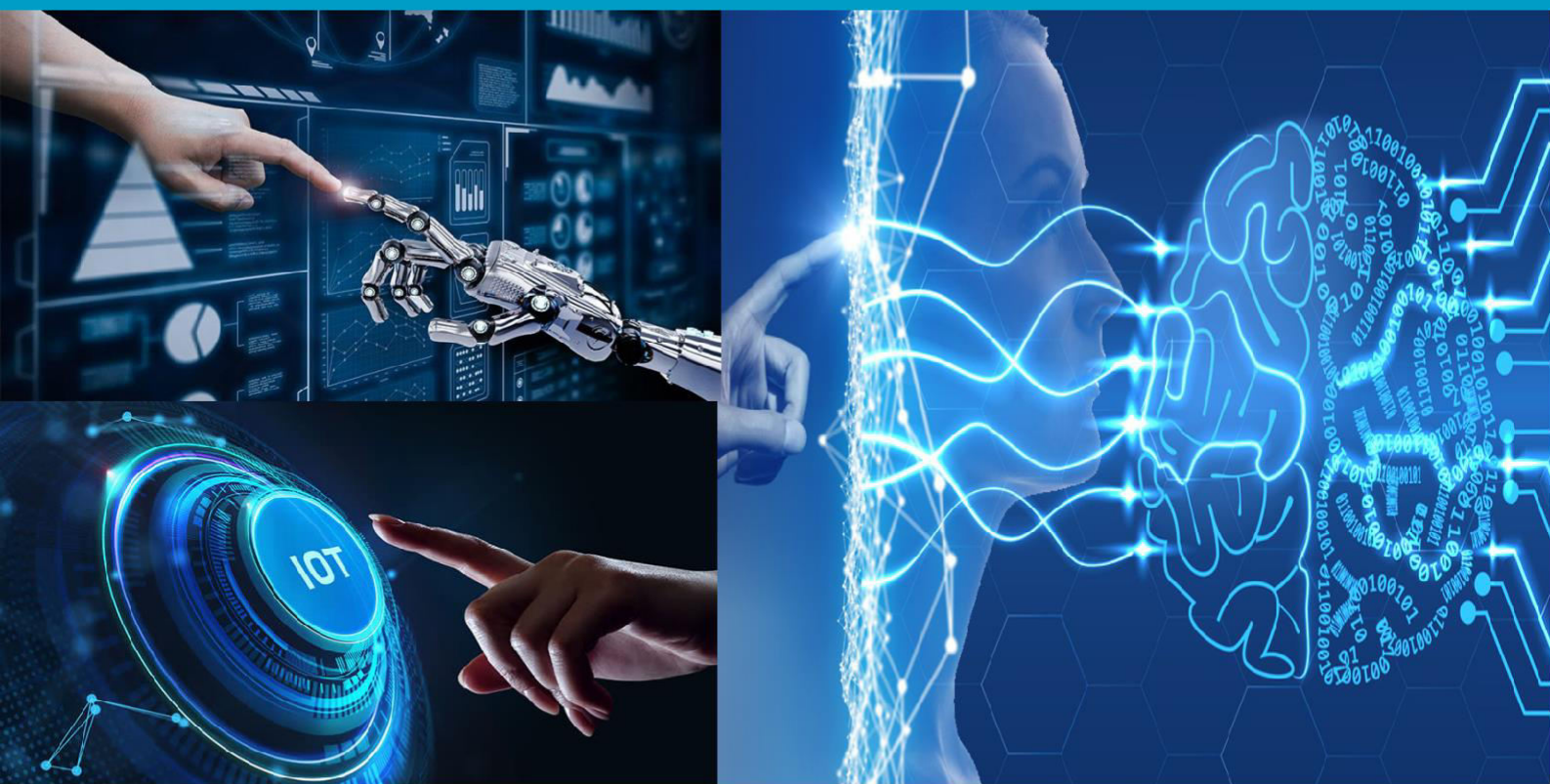




INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH

IN SCIENCE, ENGINEERING, TECHNOLOGY AND MANAGEMENT

Volume 8, Issue 8, August 2021



INTERNATIONAL
STANDARD
SERIAL
NUMBER
INDIA

Impact Factor: 7.580



+91 99405 72462



+9163819 07438



ijmrsetm@gmail.com



www.ijmrsetm.com

Structure, Classification and Functions of Proteins

Dr. Suresh Kumar Meena

Assistant Professor, Dept. of Chemistry, Government College, Kota, Rajasthan, India

ABSTRACT: Proteins are very large molecules composed of basic units called amino acids. Proteins contain carbon, hydrogen, oxygen, nitrogen, and sulphur. Protein molecules are large, complex molecules formed by one or more twisted and folded strands of amino acids. Proteins are highly complex molecules that are actively involved in the most basic and important aspects of life. These include metabolism, movement, defense, cellular communication, and molecular recognition. Positive negative attractions between different atoms in the long amino acid strand cause it to coil on itself again and again to form its highly complex shape. Folded proteins may combine with other folded proteins to form even larger more complicated shapes. The folded shape of a protein molecule determines its role in body chemistry. Structural proteins are shaped in ways that allow them to form essential structures of the body. Collagen, a protein with a fibre shape, holds most of the body tissues together. Keratin, another structural protein forms a network of waterproof fibres in the outer layer of the skin. Functional proteins have shapes that enable them to participate in chemical processes of the body. Functional proteins include some of hormones, growth factors, cell membrane receptors, and enzymes.

KEYWORDS: proteins, shapes, structure, types, functions, classification, enzymes, hormones

I. INTRODUCTION

Protein molecules are large, complex molecules formed by one or more twisted and folded strands of amino acids. Each amino acid is connected to the next amino acid by covalent bonds.^{1,2}

1. **Primary (first level)** – Protein structure is a sequence of amino acids in a chain.
2. **Secondary (secondary level)** – Protein structure is formed by folding and twisting of the amino acid chain.
3. **Tertiary (third level)** – Protein structure is formed when the twists and folds of the secondary structure fold again to form a larger three dimensional structure.
4. **Quaternary (fourth level)** – Protein structure is a protein consisting of more than one folded amino acid chain.

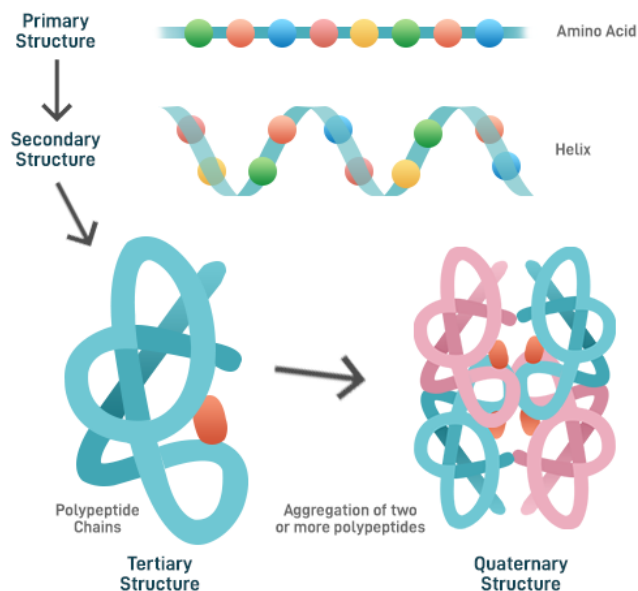
Proteins can bond with other organic compounds and form “mixed” molecules. For example, glycoproteins embedded in cell membranes are proteins with sugars attached. Lipoproteins are lipid-protein combinations.^{3,4}

Nucleic Acids

The two forms of nucleic acid are deoxyribonucleic acid and ribonucleic acid. The basic building blocks of nucleic acids are called nucleotides. Each nucleotide consists of a phosphate unit, a sugar and a nitrogen base. DNA nucleotide bases include adenine, thymine, guanine and cytosine. RNA uses the same set of bases, except for the substitution of uracil for thymine.

Nucleotides bind to one another to form strands or other structures. In the DNA molecule, nucleotides are arranged and twisted, and a double strand called a double helix. The sequence of different nucleotides along the DNA double helix is the “master code” for assembling proteins and other nucleic acids.^{5,6}

PROTEIN STRUCTURE



Primary structure

In the primary structure of proteins, the polypeptide chain consists of a sequence of amino acids. This primary structure has a unique protein structure. The primary structure of this level contains mainly amino acids which are present anywhere in the chain. Peptide bonds are present in the primary structure of the protein. If two amino acids are there to form a chain of proteins it is called a dipeptide bond. Similarly, if three amino acids are ready to form a link it is called tripeptide.^{7,8}

Characteristics of peptide bond:

- A peptide bond is rigid and planar
- It is not able to charge but it is polar.
- It has a partial double bond character.

Secondary structure

This secondary structure is formed by the H-bonds. This secondary structure is formed mostly with the alpha helix and beta pleated sheets. Example: Myoglobin. There are some types of secondary structure^{9,10}

- Alpha Helix
- Beta pleated sheet
- Strand
- Loops

Tertiary structure

The tertiary structure of proteins is in the form of a 3Dimensional structure of the monomeric and multimeric structures. Three dimension structure of a polypeptide is simply called the tertiary structure of the protein. This tertiary structure is because of the lowest energy and greatest stability state of the polypeptide chain. The tertiary structure came from folding secondary structure of the protein.^{11,12}

Functions of Tertiary structure:

- It has a unique function like interacting with other molecules.

Quaternary structure

The quaternary structure of proteins is in the form of a 3Dimensional structure of macromolecules which is a combination of individual polypeptide chains. This quaternary structure is also formed from a special combination of tertiary structures. Quaternary structure is also known as oligomeric proteins. Example: Hemoglobin

Functions of quaternary structure:

- It helps in the chromosome replication process.

- It helps in metabolism

Importance

- Protein helps in maintaining good shape and fit for our body.
- Protein repairs the body's damaged tissues.
- Protein is used to build bones, skin, and muscles.

Classification

Classification of proteins is based on the

- Based on the shape
- Based on Constitution
- Based on the Nature of molecules^{13,14}

Based on shape

- Fibrous protein
- Globular proteins

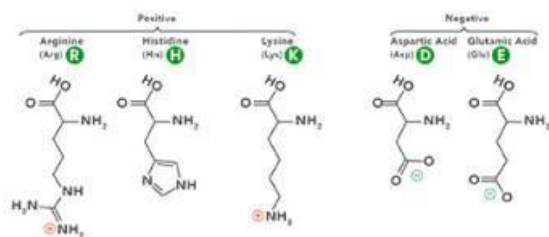
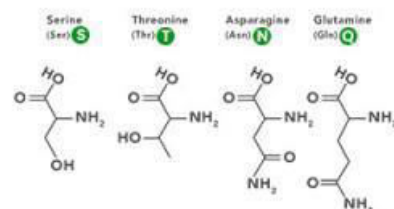
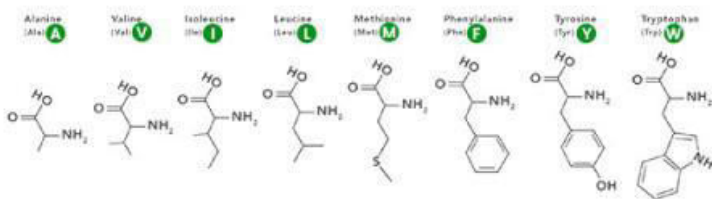
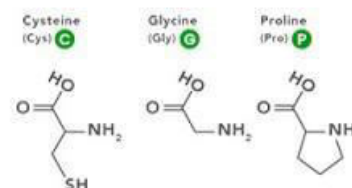
Based on the constitution

- Simple proteins
- Conjugated proteins

The basic unit of protein-amino acids:

Amino acids are the basic structural unit of protein. Amino acids consist of the carbon atom, a carboxyl group (COOH), and a hydrogen atom.

Amino acids are classified as follows

A. Amino Acids with Electrically Charged Side Chains**B. Amino Acids with Polar Uncharged Side Chains****D. Amino Acids with Hydrophobic Side Chains****C. Special Cases**

- **Aromatic:** Tyrosine, Tryptophan, Phenylalanine.
- **Positively charged:** Lysine, Arginine, Histidine.
- **Negatively charged:** Aspartate, Glutamate.
- **Nonpolar, aliphatic:** Leucine, Methionine, Isoleucine.

Functions**Enzymatic protein**

The function of enzymatic protein:

- It accelerates the metabolic process in our cells.
- It also accelerates the metabolic process in stomach digestion, liver functions, and blood clotting.^{15,16}

Hormonal protein

The function of hormonal protein

- Hormonal proteins are protein-based chemicals secreted by endocrine glands.
- By using hormonal protein each hormone affects particular cells in the body.

Structural protein

The function of structural protein

- Structural proteins are very important for the body because they are fibrous proteins.
- It helps in developing muscles, bones, skin, and cartilage.^{17,18}

Defensive protein

The function of defensive protein

- These defensive proteins help in developing antibodies for attacking.
- These antibodies are developed in white blood cells to attack bacteria.

Storage protein

The function of storage protein

- Storage protein stores minerals like potassium.
- Storage protein contains ovalbumin and casein found in milk, and egg whites.

Transport protein

The function of transport protein

- Transport protein called calbindin which is useful for absorption of calcium from intestinal walls.
- Transport proteins carry important materials to the cells of the body.^{19,20}

Receptor protein

- It controls the substances which enter and leave the cells.

Contractile protein.

The function of contractile protein

- It helps in regulating the strength, speed of the heart, and muscle contractions.
- Contractile proteins cause heart complications if the heart produces severe contractions.^{21,22}

II.DISCUSSION

Proteins were recognized as a distinct class of biological molecules in the eighteenth century by Antoine Fourcroy and others, distinguished by the molecules' ability to coagulate or flocculate under treatments with heat or acid.^[1] Noted examples at the time included albumin from egg whites, blood serum albumin, fibrin, and wheat gluten.

Proteins were first described by the Dutch chemist Gerardus Johannes Mulder and named by the Swedish chemist Jöns Jacob Berzelius in 1838.^{[2][3]} Mulder carried out elemental analysis of common proteins and found that nearly all proteins had the same empirical formula, $C_{400}H_{620}N_{100}O_{120}P_1S_1$.^[4] He came to the erroneous conclusion that they might be composed of a single type of (very large) molecule. The term "protein" to describe these molecules was proposed by Mulder's associate Berzelius; protein is derived from the Greek word *πρωτεϊος* (proteios), meaning "primary",^[5] "in the lead", or "standing in front",^[6] + -in. Mulder went on to identify the products of protein degradation such as the amino acid leucine for which he found a (nearly correct) molecular weight of 131 Da.^[4] Prior to "protein", other names were used, like "albumins" or "albuminous materials" (Eiweisskörper, in German).^[7]

Early nutritional scientists such as the German Carl von Voit believed that protein was the most important nutrient for maintaining the structure of the body, because it was generally believed that "flesh makes flesh."^[8] Karl Heinrich Ritthausen extended known protein forms with the identification of glutamic acid. At the Connecticut Agricultural Experiment Station a detailed review of the vegetable proteins was compiled by Thomas Burr Osborne. Working with Lafayette Mendel and applying Liebig's law of the minimum in feeding laboratory rats, the nutritionally essential amino acids were established. The work was continued and communicated by William Cumming Rose. The understanding of proteins as polypeptides came through the work of Franz Hofmeister and Hermann Emil Fischer in 1902.^{[9][10]} The central role of proteins as enzymes in living organisms was not fully appreciated until 1926, when James B. Sumner showed that the enzyme urease was in fact a protein.^[11]

The difficulty in purifying proteins in large quantities made them very difficult for early protein biochemists to study. Hence, early studies focused on proteins that could be purified in large quantities, e.g., those of blood, egg white, various toxins, and digestive/metabolic enzymes obtained from slaughterhouses. In the 1950s, the Armour Hot Dog Co. purified 1 kg of pure bovine pancreatic ribonuclease A and made it freely available to scientists; this gesture helped ribonuclease A become a major target for biochemical study for the following decades.^[4]

Linus Pauling is credited with the successful prediction of regular protein secondary structures based on hydrogen bonding, an idea first put forth by William Astbury in 1933.^[12] Later work by Walter Kauzmann on denaturation,^{[13][14]} based partly on previous studies by Kaj Linderstrøm-Lang,^[15] contributed an understanding of protein folding and structure mediated by hydrophobic interactions.

The first protein to be sequenced was insulin, by Frederick Sanger, in 1949. Sanger correctly determined the amino acid sequence of insulin, thus conclusively demonstrating that proteins consisted of linear polymers of amino acids rather than branched chains, colloids, or cyclols.^[16] He won the Nobel Prize for this achievement in 1958.^[17]

With the development of X-ray crystallography, it became possible to sequence protein structures.^[18] The first protein structures to be solved were hemoglobin by Max Perutz and myoglobin by John Kendrew, in 1958.^{[19][20]} The use of computers and increasing computing power also supported the sequencing of complex proteins. In 1999, Roger Kornberg succeeded in sequencing the highly complex structure of RNA polymerase using high intensity X-rays from synchrotrons.^[18]

Since then, cryo-electron microscopy (cryo-EM) of large macromolecular assemblies^[21] has been developed. Cryo-EM uses protein samples that are frozen rather than crystals, and beams of electrons rather than x-rays. It causes less damage to the sample, allowing scientists to obtain more information and analyze larger structures.^[18] Computational protein structure prediction of small protein domains^[22] has also helped researchers to approach atomic-level resolution of protein structures. As of 2017, the Protein Data Bank has over 126,060 atomic-resolution structures of proteins.^[23]

III.RESULTS

Proteins are assembled from amino acids using information encoded in genes. Each protein has its own unique amino acid sequence that is specified by the nucleotide sequence of the gene encoding this protein. The genetic code is a set of three-nucleotide sets called codons and each three-nucleotide combination designates an amino acid, for example AUG (adenine–uracil–guanine) is the code for methionine. Because DNA contains four nucleotides, the total number of possible codons is 64; hence, there is some redundancy in the genetic code, with some amino acids specified by more than one codon.^[30] Genes encoded in DNA are first transcribed into pre-messenger RNA (mRNA) by proteins such as RNA polymerase. Most organisms then process the pre-mRNA (also known as a primary transcript) using various forms of Post-transcriptional modification to form the mature mRNA, which is then used as a template for protein synthesis by the ribosome. In prokaryotes the mRNA may either be used as soon as it is produced, or be bound by a ribosome after having moved away from the nucleoid. In contrast, eukaryotes make mRNA in the cell nucleus and then translocate it across the nuclear membrane into the cytoplasm, where protein synthesis then takes place. The rate of protein synthesis is higher in prokaryotes than eukaryotes and can reach up to 20 amino acids per second.^[34]

The process of synthesizing a protein from an mRNA template is known as translation. The mRNA is loaded onto the ribosome and is read three nucleotides at a time by matching each codon to its base pairing anticodon located on a transfer RNA molecule, which carries the amino acid corresponding to the codon it recognizes. The enzyme aminoacyl tRNA synthetase "charges" the tRNA molecules with the correct amino acids. The growing polypeptide is often termed the nascent chain. Proteins are always biosynthesized from N-terminus to C-terminus.^[30] The size of a synthesized protein can be measured by the number of amino acids it contains and by its total molecular mass, which is normally reported in units of daltons (synonymous with atomic mass units), or the derivative unit kilodalton (kDa). The average size of a protein increases from Archaea to Bacteria to Eukaryote (283, 311, 438 residues and 31, 34, 49 kDa respectively) due to a bigger number of protein domains constituting proteins in higher organisms.^[35] For instance, yeast proteins are on average 466 amino acids long and 53 kDa in mass.^[27] The largest known proteins are the titins, a component of the muscle sarcomere, with a molecular mass of almost 3,000 kDa and a total length of almost 27,000 amino acids.^[36]

The best-known role of proteins in the cell is as enzymes, which catalyse chemical reactions. Enzymes are usually highly specific and accelerate only one or a few chemical reactions. Enzymes carry out most of the reactions involved in metabolism, as well as manipulating DNA in processes such as DNA replication, DNA repair, and transcription. Some enzymes act on other proteins to add or remove chemical groups in a process known as posttranslational modification. About 4,000 reactions are known to be catalysed by enzymes.^[46] The rate acceleration conferred by enzymatic catalysis is often enormous—as much as 10^{17} -fold increase in rate over the uncatalysed reaction in the case of orotate decarboxylase (78 million years without the enzyme, 18 milliseconds with the enzyme).^[47]

The molecules bound and acted upon by enzymes are called substrates. Although enzymes can consist of hundreds of amino acids, it is usually only a small fraction of the residues that come in contact with the substrate, and an even smaller fraction—three to four residues on average—that are directly involved in catalysis.^[48] The region of the enzyme that binds the substrate and contains the catalytic residues is known as the active site.

Dirigent proteins are members of a class of proteins that dictate the stereochemistry of a compound synthesized by other enzymes.^[49]

Many proteins are involved in the process of cell signaling and signal transduction. Some proteins, such as insulin, are extracellular proteins that transmit a signal from the cell in which they were synthesized to other cells in distant tissues. Others are membrane proteins that act as receptors whose main function is to bind a signaling molecule and induce a biochemical response in the cell. Many receptors have a binding site exposed on the cell surface and an effector domain within the cell, which may have enzymatic activity or may undergo a conformational change detected by other proteins within the cell.^{[29]:251–81}

Antibodies are protein components of an adaptive immune system whose main function is to bind antigens, or foreign substances in the body, and target them for destruction. Antibodies can be secreted into the extracellular environment or anchored in the membranes of specialized B cells known as plasma cells. Whereas enzymes are limited in their binding affinity for their substrates by the necessity of conducting their reaction, antibodies have no such constraints. An antibody's binding affinity to its target is extraordinarily high.^{[30]:275–50}

Many ligand transport proteins bind particular small biomolecules and transport them to other locations in the body of a multicellular organism. These proteins must have a high binding affinity when their ligand is present in high concentrations, but must also release the ligand when it is present at low concentrations in the target tissues. The canonical example of a ligand-binding protein is haemoglobin, which transports oxygen from the lungs to other organs and tissues in all vertebrates and has close homologs in every biological kingdom.^{[30]:222–29} Lectins are sugar-binding proteins which are highly specific for their sugar moieties. Lectins typically play a role in biological recognition phenomena involving cells and proteins.^[50] Receptors and hormones are highly specific binding proteins.

Transmembrane proteins can also serve as ligand transport proteins that alter the permeability of the cell membrane to small molecules and ions. The membrane alone has a hydrophobic core through which polar or charged molecules cannot diffuse. Membrane proteins contain internal channels that allow such molecules to enter and exit the cell. Many ion channel proteins are specialized to select for only a particular ion; for example, potassium and sodium channels often discriminate for only one of the two ions.

IV.CONCLUSIONS

Most microorganisms and plants can biosynthesize all 20 standard amino acids, while animals (including humans) must obtain some of the amino acids from the diet.^[42] The amino acids that an organism cannot synthesize on its own are referred to as essential amino acids. Key enzymes that synthesize certain amino acids are not present in animals—such as aspartokinase, which catalyses the first step in the synthesis of lysine, methionine, and threonine from aspartate. If amino acids are present in the environment, microorganisms can conserve energy by taking up the amino acids from their surroundings and downregulating their biosynthetic pathways.

In animals, amino acids are obtained through the consumption of foods containing protein. Ingested proteins are then broken down into amino acids through digestion, which typically involves denaturation of the protein through exposure to acid and hydrolysis by enzymes called proteases. Some ingested amino acids are used for protein biosynthesis, while others are converted to glucose through gluconeogenesis, or fed into the citric acid cycle. This use of protein as a fuel is particularly important under starvation conditions as it allows the body's own proteins to be used to support life, particularly those found in muscle.^[88]

In animals such as dogs and cats, protein maintains the health and quality of the skin by promoting hair follicle growth and keratinization, and thus reducing the likelihood of skin problems producing malodours.^[89] Poor-quality proteins also have a role regarding gastrointestinal health, increasing the potential for flatulence and odorous compounds in dogs because when proteins reach the colon in an undigested state, they are fermented producing hydrogen sulfide gas, indole, and skatole.^[90] Dogs and cats digest animal proteins better than those from plants, but products of low-quality animal origin are poorly digested, including skin, feathers, and connective tissue.^[90]



REFERENCES

1. Thomas Burr Osborne (1909): The Vegetable Proteins Archived 2016-03-22 at the Wayback Machine, History pp 1 to 6, from archive.org
2. ^ Mulder GJ (1838). "Sur la composition de quelques substances animales". *Bulletin des Sciences Physiques et Naturelles en Néerlande*: 104.
3. ^ Harold H (1951). "Origin of the Word 'Protein.'" *Nature*. **168** (4267): 244. Bibcode:1951Natur.168..244H. doi:10.1038/168244a0. PMID 14875059. S2CID 4271525.
4. ^ Perrett D (August 2007). "From 'protein' to the beginnings of clinical proteomics". *Proteomics: Clinical Applications*. **1** (8): 720–38. doi:10.1002/prca.200700525. PMID 21136729. S2CID 32843102.
5. ^ New Oxford Dictionary of English
6. ^ Reynolds JA, Tanford C (2003). *Nature's Robots: A History of Proteins* (Oxford Paperbacks). New York, New York: Oxford University Press. p. 15. ISBN 978-0-19-860694-9.
7. ^ Reynolds and Tanford (2003).
8. ^ Bischoff TL, Voit C (1860). *Die Gesetze der Ernährung des Pflanzenfressers durch neue Untersuchungen festgestellt* (in German). Leipzig, Heidelberg.
9. ^ "Hofmeister, Franz". *encyclopedia.com*. Archived from the original on 5 April 2017. Retrieved 4 April 2017.
10. ^ "Protein, section: Classification of protein". *britannica.com*. Archived from the original on 4 April 2017. Retrieved 4 April 2017.
11. ^ Sumner JB (1926). "The isolation and crystallization of the enzyme urease. Preliminary paper" (PDF). *Journal of Biological Chemistry*. **69** (2): 435–41. doi:10.1016/S0021-9258(18)84560-4. Archived from the original on 2011-03-25. Retrieved 2011-01-16.
12. ^ Pauling L, Corey RB (May 1951). "Atomic coordinates and structure factors for two helical configurations of polypeptide chains" (PDF). *Proceedings of the National Academy of Sciences of the United States of America*. **37** (5): 235–40. Bibcode:1951PNAS...37..235P. doi:10.1073/pnas.37.5.235. PMC 1063348. PMID 14834145. Archived (PDF) from the original on 2012-11-28. Retrieved 2009-04-14.
13. ^ Kauzmann W (May 1956). "Structural factors in protein denaturation". *Journal of Cellular Physiology*. **47** (Suppl 1): 113–31. doi:10.1002/jcp.1030470410. PMID 13332017.
14. ^ Kauzmann W (1959). "Some factors in the interpretation of protein denaturation". *Advances in Protein Chemistry* Volume 14. *Advances in Protein Chemistry*. Vol. 14. pp. 1–63. doi:10.1016/S0065-3233(08)60608-7. ISBN 978-0-12-034214-3. PMID 14404936.
15. ^ Kalman SM, Linderstrøm-Lang K, Ottesen M, Richards FM (February 1955). "Degradation of ribonuclease by subtilisin". *Biochimica et Biophysica Acta*. **16** (2): 297–99. doi:10.1016/0006-3002(55)90224-9. PMID 14363272.
16. ^ Sanger F (1949). "The terminal peptides of insulin". *The Biochemical Journal*. **45** (5): 563–74. doi:10.1042/bj0450563. PMC 1275055. PMID 15396627.
17. ^ Sanger F. (1958), Nobel lecture: The chemistry of insulin (PDF), *Nobelprize.org*, archived (PDF) from the original on 2013-03-19, retrieved 2016-02-09
18. ^ Stoddart, Charlotte (1 March 2020). "Structural biology: How proteins got their close-up". *Knowable Magazine*. doi:10.1146/knowable-022822-1. Retrieved 25 March 2020.
19. ^ Muirhead H, Perutz MF (August 1963). "Structure of hemoglobin. A three-dimensional fourier synthesis of reduced human hemoglobin at 5.5 Å resolution". *Nature*. **199** (4894): 633–38. Bibcode:1963Natur.199..633M. doi:10.1038/199633a0. PMID 14074546. S2CID 4257461.
20. ^ Kendrew JC, Bodo G, Dintzis HM, Parrish RG, Wyckoff H, Phillips DC (March 1958). "A three-dimensional model of the myoglobin molecule obtained by x-ray analysis". *Nature*. **181** (4610): 662–66. Bibcode:1958Natur.181..662K. doi:10.1038/181662a0. PMID 13517261. S2CID 4162786.
21. ^ Zhou ZH (April 2008). "Towards atomic resolution structural determination by single-particle cryo-electron microscopy". *Current Opinion in Structural Biology*. **18** (2): 218–28. doi:10.1016/j.sbi.2008.03.004. PMC 2714865. PMID 18403197.
22. ^ Keskin O, Tuncbag N, Gursoy A (April 2008). "Characterization and prediction of protein interfaces to infer protein-protein interaction networks". *Current Pharmaceutical Biotechnology*. **9** (2): 67–76. doi:10.2174/138920108783955191. hdl:11511/32640. PMID 18393863.
23. ^ "RCSB Protein Data Bank". Archived from the original on 2015-04-18. Retrieved 2017-01-19.
24. ^ Nelson DL, Cox MM (2005). *Lehninger's Principles of Biochemistry* (4th ed.). New York, New York: W. H. Freeman and Company.
25. ^ Gutteridge A, Thornton JM (November 2005). "Understanding nature's catalytic toolkit". *Trends in Biochemical Sciences*. **30** (11): 622–29. doi:10.1016/j.tibs.2005.09.006. PMID 16214343.



26. ^ Murray RF, Harper HW, Granner DK, Mayes PA, Rodwell VW (2006). Harper's Illustrated Biochemistry. New York: Lange Medical Books/McGraw-Hill. ISBN 978-0-07-146197-9.
27. ^ Lodish H, Berk A, Matsudaira P, Kaiser CA, Krieger M, Scott MP, Zipurksy SL, Darnell J (2004). Molecular Cell Biology (5th ed.). New York, New York: WH Freeman and Company.
28. ^ Ardejani MS, Powers ET, Kelly JW (August 2017). "Using Cooperatively Folded Peptides To Measure Interaction Energies and Conformational Propensities". *Accounts of Chemical Research*. **50** (8): 1875–1882. doi:10.1021/acs.accounts.7b00195. PMC 5584629. PMID 28723063.
29. ^ Branden C, Tooze J (1999). Introduction to Protein Structure. New York: Garland Pub. ISBN 978-0-8153-2305-1.
30. ^ Van Holde KE, Mathews CK (1996). Biochemistry. Menlo Park, California: Benjamin/Cummings Pub. Co., Inc. ISBN 978-0-8053-3931-4.
31. ^ Milo R (December 2013). "What is the total number of protein molecules per cell volume? A call to rethink some published values". *BioEssays*. **35** (12): 1050–55. doi:10.1002/bies.201300066. PMC 3910158. PMID 24114984.
32. ^ Beck M, Schmidt A, Malmstroem J, Claassen M, Ori A, Szymborska A, Herzog F, Rinner O, Ellenberg J, Aebersold R (November 2011). "The quantitative proteome of a human cell line". *Molecular Systems Biology*. **7**: 549. doi:10.1038/msb.2011.82. PMC 3261713. PMID 22068332.
33. ^ Wu L, Candille SI, Choi Y, Xie D, Jiang L, Li-Pook-Than J, Tang H, Snyder M (July 2013). "Variation and genetic control of protein abundance in humans". *Nature*. **499** (7456): 79–82. Bibcode:2013Natur.499...79W. doi:10.1038/nature12223. PMC 3789121. PMID 23676674.
34. ^ Dobson CM (2000). "The nature and significance of protein folding". In Pain RH (ed.). *Mechanisms of Protein Folding*. Oxford, Oxfordshire: Oxford University Press. pp. 1–28. ISBN 978-0-19-963789-8.
35. ^ Kozlowski LP (January 2017). "Proteome-pl: proteome isoelectric point database". *Nucleic Acids Research*. **45** (D1): D1112–D1116. doi:10.1093/nar/gkw978. PMC 5210655. PMID 27789699.
36. ^ Fulton AB, Isaacs WB (April 1991). "Titin, a huge, elastic sarcomeric protein with a probable role in morphogenesis". *BioEssays*. **13** (4): 157–61. doi:10.1002/bies.950130403. PMID 1859393. S2CID 20207314.
37. ^ Bruckdorfer T, Marder O, Albericio F (February 2004). "From production of peptides in milligram amounts for research to multi-tons quantities for drugs of the future". *Current Pharmaceutical Biotechnology*. **5** (1): 29–43. doi:10.2174/1389201043489620. PMID 14965208.
38. ^ Schwarzer D, Cole PA (December 2005). "Protein semisynthesis and expressed protein ligation: chasing a protein's tail". *Current Opinion in Chemical Biology*. **9** (6): 561–69. doi:10.1016/j.cbpa.2005.09.018. PMID 16226484.
39. ^ Kent SB (February 2009). "Total chemical synthesis of proteins". *Chemical Society Reviews*. **38** (2): 338–51. doi:10.1039/b700141j. PMID 19169452. S2CID 5432012.
40. ^ Fernández A, Scott R (September 2003). "Dehydron: a structurally encoded signal for protein interaction". *Biophysical Journal*. **85** (3): 1914–28. Bibcode:2003BpJ....85.1914F. doi:10.1016/S0006-3495(03)74619-0. PMC 1303363. PMID 12944304.
41. ^ Davey NE, Van Roey K, Weatheritt RJ, Toedt G, Uyar B, Altenberg B, Budd A, Diella F, Dinkel H, Gibson TJ (January 2012). "Attributes of short linear motifs". *Molecular BioSystems*. **8** (1): 268–81. doi:10.1039/c1mb05231d. PMID 21909575.
42. ^ Voet D, Voet JG. (2004). Biochemistry Vol 1 3rd ed. Wiley: Hoboken, NJ.
43. ^ Sankaranarayanan R, Moras D (2001). "The fidelity of the translation of the genetic code". *Acta Biochimica Polonica*. **48** (2): 323–35. doi:10.18388/abp.2001_3918. PMID 11732604.
44. ^ Copland JA, Sheffield-Moore M, Koldzic-Zivanovic N, Gentry S, Lamprou G, Tzortzatou-Stathopoulou F, Zoumpourlis V, Urban RJ, Vlahopoulos SA (June 2009). "Sex steroid receptors in skeletal differentiation and epithelial neoplasia: is tissue-specific intervention possible?". *BioEssays*. **31** (6): 629–41. doi:10.1002/bies.200800138. PMID 19382224. S2CID 205469320.
45. ^ Samarin S, Nusrat A (January 2009). "Regulation of epithelial apical junctional complex by Rho family GTPases". *Frontiers in Bioscience*. **14** (14): 1129–42. doi:10.2741/3298. PMID 19273120.
46. ^ Bairoch A (January 2000). "The ENZYME database in 2000" (PDF). *Nucleic Acids Research*. **28** (1): 304–05. doi:10.1093/nar/28.1.304. PMC 102465. PMID 10592255. Archived from the original (PDF) on June 1, 2011.
47. ^ Radzicka A, Wolfenden R (January 1995). "A proficient enzyme". *Science*. **267** (5194): 90–3. Bibcode:1995Sci...267...90R. doi:10.1126/science.7809611. PMID 7809611.
48. ^ EBI External Services (2010-01-20). "The Catalytic Site Atlas at The European Bioinformatics Institute". Ebi.ac.uk. Archived from the original on 2013-08-03. Retrieved 2011-01-16.
49. ^ Pickel B, Schaller A (October 2013). "Dirigent proteins: molecular characteristics and potential biotechnological applications". *Applied Microbiology and Biotechnology*. **97** (19): 8427–38. doi:10.1007/s00253-013-5167-4. PMID 23989917. S2CID 1896003.



50. ^ Rüdiger H, Siebert HC, Solís D, Jiménez-Barbero J, Romero A, von der Lieth CW, Diaz-Mariño T, Gabius HJ (April 2000). "Medicinal chemistry based on the sugar code: fundamentals of lectinology and experimental strategies with lectins as targets". *Current Medicinal Chemistry*. **7** (4): 389–416. doi:10.2174/0929867003375164. PMID 10702616.
51. ^ Mulder NJ (2007-09-28). "Protein Family Databases". eLS. Chichester, UK: John Wiley & Sons, Ltd. pp. a0003058.pub2. doi:10.1002/9780470015902.a0003058.pub2. ISBN 978-0-470-01617-6.
52. ^ Sisu C, Pei B, Leng J, Frankish A, Zhang Y, Balasubramanian S, et al. (September 2014). "Comparative analysis of pseudogenes across three phyla". *Proceedings of the National Academy of Sciences of the United States of America*. **111** (37): 13361–6. Bibcode:2014PNAS..11113361S. doi:10.1073/pnas.1407293111. PMC 4169933. PMID 25157146.
53. ^ Guzmán GI, Sandberg TE, LaCroix RA, Nyerges Á, Papp H, de Raad M, et al. (April 2019). "Enzyme promiscuity shapes adaptation to novel growth substrates". *Molecular Systems Biology*. **15** (4): e8462. doi:10.15252/msb.20188462. PMC 6452873. PMID 30962359.
54. ^ Roohi, Bano K, Kuddus M, Zaheer MR, Zia Q, Khan MF, Ashraf GM, Gupta A, Aliev G (2017). "Microbial Enzymatic Degradation of Biodegradable Plastics". *Current Pharmaceutical Biotechnology*. **18** (5): 429–440. doi:10.2174/1389201018666170523165742. PMID 28545359.
55. ^ Hey J, Posch A, Cohen A, Liu N, Harbers A (2008). "Fractionation of complex protein mixtures by liquid-phase isoelectric focusing". *2D PAGE: Sample Preparation and Fractionation. Methods in Molecular Biology*. Vol. 424. pp. 225–39. doi:10.1007/978-1-60327-064-9_19. ISBN 978-1-58829-722-8. PMID 18369866.
56. ^ Terpe K (January 2003). "Overview of tag protein fusions: from molecular and biochemical fundamentals to commercial systems". *Applied Microbiology and Biotechnology*. **60** (5): 523–33. doi:10.1007/s00253-002-1158-6. PMID 12536251. S2CID 206934268.
57. ^ Stepanenko OV, Verkhusha VV, Kuznetsova IM, Uversky VN, Turoverov KK (August 2008). "Fluorescent proteins as biomarkers and biosensors: throwing color lights on molecular and cellular processes". *Current Protein & Peptide Science*. **9** (4): 338–69. doi:10.2174/138920308785132668. PMC 2904242. PMID 18691124.
58. ^ Yuste R (December 2005). "Fluorescence microscopy today". *Nature Methods*. **2** (12): 902–4. doi:10.1038/nmeth1205-902. PMID 16299474. S2CID 205418407.
59. ^ Margolin W (January 2000). "Green fluorescent protein as a reporter for macromolecular localization in bacterial cells". *Methods*. **20** (1): 62–72. doi:10.1006/meth.1999.0906. PMID 10610805.
60. ^ Walker JH, Wilson K (2000). *Principles and Techniques of Practical Biochemistry*. Cambridge, UK: Cambridge University Press. pp. 287–89. ISBN 978-0-521-65873-7.
61. ^ Mayhew TM, Lucocq JM (August 2008). "Developments in cell biology for quantitative immunoelectron microscopy based on thin sections: a review". *Histochemistry and Cell Biology*. **130** (2): 299–313. doi:10.1007/s00418-008-0451-6. PMC 2491712. PMID 18553098.
62. ^ Hohsaka T, Sisido M (December 2002). "Incorporation of non-natural amino acids into proteins". *Current Opinion in Chemical Biology*. **6** (6): 809–15. doi:10.1016/S1367-5931(02)00376-9. PMID 12470735.
63. ^ Cedrone F, Ménez A, Quéméneur E (August 2000). "Tailoring new enzyme functions by rational redesign". *Current Opinion in Structural Biology*. **10** (4): 405–10. doi:10.1016/S0959-440X(00)00106-8. PMID 10981626.
64. ^ Görg A, Weiss W, Dunn MJ (December 2004). "Current two-dimensional electrophoresis technology for proteomics". *Proteomics*. **4** (12): 3665–85. doi:10.1002/pmic.200401031. PMID 15543535. S2CID 28594824.
65. ^ Conrotto P, Souchelnytskyi S (September 2008). "Proteomic approaches in biological and medical sciences: principles and applications". *Experimental Oncology*. **30** (3): 171–80. PMID 18806738.
66. ^ Koegl M, Uetz P (December 2007). "Improving yeast two-hybrid screening systems". *Briefings in Functional Genomics & Proteomics*. **6** (4): 302–12. doi:10.1093/bfpg/elm035. PMID 18218650. Archived from the original on 2017-09-11. Retrieved 2017-07-23.
67. ^ Plewczynski D, Ginalski K (2009). "The interactome: predicting the protein-protein interactions in cells". *Cellular & Molecular Biology Letters*. **14** (1): 1–22. doi:10.2478/s11658-008-0024-7. PMC 6275871. PMID 18839074.
68. ^ Zhang C, Kim SH (February 2003). "Overview of structural genomics: from structure to function". *Current Opinion in Chemical Biology*. **7** (1): 28–32. doi:10.1016/S1367-5931(02)00015-7. PMID 12547423. Archived from the original on 2018-11-19. Retrieved 2019-06-29.
69. ^ Gonen T, Cheng Y, Sliz P, Hiroaki Y, Fujiyoshi Y, Harrison SC, Walz T (December 2005). "Lipid-protein interactions in double-layered two-dimensional AQP0 crystals". *Nature*. **438** (7068): 633–38. Bibcode:2005Natur.438..633G. doi:10.1038/nature04321. PMC 1350984. PMID 16319884.



70. ^ Standley DM, Kinjo AR, Kinoshita K, Nakamura H (July 2008). "Protein structure databases with new web services for structural biology and biomedical research". *Briefings in Bioinformatics*. **9** (4): 276–85. doi:10.1093/bib/bbn015. PMID 18430752.
71. ^ Walian P, Cross TA, Jap BK (2004). "Structural genomics of membrane proteins". *Genome Biology*. **5** (4): 215. doi:10.1186/gb-2004-5-4-215. PMC 395774. PMID 15059248.
72. ^ Sleator RD (2012). "Prediction of protein functions". *Functional Genomics. Methods in Molecular Biology*. Vol. 815. pp. 15–24. doi:10.1007/978-1-61779-424-7_2. ISBN 978-1-61779-423-0. PMID 22130980.
73. ^ Zhang Y (June 2008). "Progress and challenges in protein structure prediction". *Current Opinion in Structural Biology*. **18** (3): 342–48. doi:10.1016/j.sbi.2008.02.004. PMC 2680823. PMID 18436442.
74. ^ Xiang Z (June 2006). "Advances in homology protein structure modeling". *Current Protein & Peptide Science*. **7** (3): 217–27. doi:10.2174/138920306777452312. PMC 1839925. PMID 16787261.
75. ^ Zhang Y, Skolnick J (January 2005). "The protein structure prediction problem could be solved using the current PDB library". *Proceedings of the National Academy of Sciences of the United States of America*. **102** (4): 1029–34. Bibcode:2005PNAS..102.1029Z. doi:10.1073/pnas.0407152101. PMC 545829. PMID 15653774.
76. ^ Kuhlman B, Dantas G, Ireton GC, Varani G, Stoddard BL, Baker D (November 2003). "Design of a novel globular protein fold with atomic-level accuracy". *Science*. **302** (5649): 1364–68. Bibcode:2003Sci...302.1364K. doi:10.1126/science.1089427. PMID 14631033. S2CID 1939390.
77. ^ Ward JJ, Sodhi JS, McGuffin LJ, Buxton BF, Jones DT (March 2004). "Prediction and functional analysis of native disorder in proteins from the three kingdoms of life". *Journal of Molecular Biology*. **337** (3): 635–45. CiteSeerX 10.1.1.120.5605. doi:10.1016/j.jmb.2004.02.002. PMID 15019783.
78. ^ Tompa P, Fersht A (18 November 2009). *Structure and Function of Intrinsically Disordered Proteins*. CRC Press. ISBN 978-1-4200-7893-0. Archived from the original on 19 April 2017. Retrieved 19 October 2016.
79. ^ Ritchie DW (February 2008). "Recent progress and future directions in protein-protein docking". *Current Protein & Peptide Science*. **9** (1): 1–15. CiteSeerX 10.1.1.211.4946. doi:10.2174/138920308783565741. PMID 18336319.
80. ^ Zagrovic B, Snow CD, Shirts MR, Pande VS (November 2002). "Simulation of folding of a small alpha-helical protein in atomistic detail using worldwide-distributed computing". *Journal of Molecular Biology*. **323** (5): 927–37. CiteSeerX 10.1.1.142.8664. doi:10.1016/S0022-2836(02)00997-X. PMID 12417204.
81. ^ Herges T, Wenzel W (January 2005). "In silico folding of a three helix protein and characterization of its free-energy landscape in an all-atom force field". *Physical Review Letters*. **94** (1): 018101. arXiv:physics/0310146. Bibcode:2005PhRvL..94a8101H. doi:10.1103/PhysRevLett.94.018101. PMID 15698135. S2CID 14771100.
82. ^ Hoffmann M, Wanko M, Strodel P, König PH, Frauenheim T, Schulten K, Thiel W, Tajkhorshid E, Elstner M (August 2006). "Color tuning in rhodopsins: the mechanism for the spectral shift between bacteriorhodopsin and sensory rhodopsin II". *Journal of the American Chemical Society*. **128** (33): 10808–18. doi:10.1021/ja062082i. PMID 16910676.
83. ^ Mendive-Tapia D, Mangaud E, Firmino T, de la Lande A, Desouter-Lecomte M, Meyer HD, Gatti F (2018). "Multidimensional Quantum Mechanical Modeling of Electron Transfer and Electronic Coherence in Plant Cryptochromes: The Role of Initial Bath Conditions". *J. Phys. Chem. B*. **122** (1): 126–136. doi:10.1021/acs.jpcc.7b10412. PMID 29216421.
84. ^ Strümpfer J, Schulten K (2012). "Open Quantum Dynamics Calculations with the Hierarchy Equations of Motion on Parallel Computers". *J. Chem. Theory Comput.* **8** (8): 2808–2816. doi:10.1021/ct3003833. PMC 3480185. PMID 23105920.
85. ^ Scheraga HA, Khalili M, Liwo A (2007). "Protein-folding dynamics: overview of molecular simulation techniques". *Annual Review of Physical Chemistry*. **58**: 57–83. Bibcode:2007ARPC...58...57S. doi:10.1146/annurev.physchem.58.032806.104614. PMID 17034338.
86. ^ Muñoz-Huerta, Rafael F.; Guevara-Gonzalez, Ramon G.; Contreras-Medina, Luis M.; Torres-Pacheco, Irineo; Prado-Olivarez, Juan; Ocampo-Velazquez, Rosalia V. (Aug 16, 2013). "A Review of Methods for Sensing the Nitrogen Status in Plants: Advantages, Disadvantages and Recent Advances". *Sensors (Basel, Switzerland)*. **13** (8): 10823–10843. Bibcode:2013Senso..1310823M. doi:10.3390/s130810823. PMC 3812630. PMID 23959242.
87. ^ Martin, P D; Malley, D F; Manning, G.; Fuller, L. (Nov 1, 2002). "Determination of soil organic carbon and nitrogen at the field level using near-infrared spectroscopy". *Canadian Journal of Soil Science*. **82** (4): 413–422. doi:10.4141/S01-054 – via DOI.org (Crossref).
88. ^ Brosnan JT (June 2003). "Interorgan amino acid transport and its regulation". *The Journal of Nutrition*. **133** (6 Suppl 1): 2068S–72S. doi:10.1093/jn/133.6.2068S. PMID 12771367.
89. ^ Watson TD (1998). "Diet and skin disease in dogs and cats". *The Journal of Nutrition*. **128** (12 Suppl): 2783S–89S. doi:10.1093/jn/128.12.2783S. PMID 9868266.



90. ^ Case LP, Daristotle L, Hayek MG, Raasch MF (2010). Canine and Feline Nutrition-E-Book: A Resource for Companion Animal Professionals. Elsevier Health Sciences.



INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH

IN SCIENCE, ENGINEERING, TECHNOLOGY AND MANAGEMENT



+91 99405 72462



+91 63819 07438



ijmrsetm@gmail.com

www.ijmrsetm.com