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Vital Protein:The Structure and Function of Protein

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Abstract:

Protein engineering has shown significant growth in recent years, resulting in the development of various advanced goods generated from proteins, including biosensors, antibiotics, vaccines, and genetic scissors.These products are developed by extensive analysis of protein structure and function.The exceptional benefits of protein diversity have been highly regarded for its exciting technological prospects.If the mystery of protein can be revealed definitely as the precision of protein structure contains countless development potential,the protein's autonomous repair ability and strong replication ability can be used for biological and pharmaceutical engineering.This essay,by collecting the research literature and published essays on the structure and function of proteins,it explores the polypeptides folding,the structure of amino acids--the monocase of protein,the function determined by the structure of protein ,the transition metal in the protein and biosensor with diagnostics.

Keywords: biosensor, structure of protein, function of protein , amino acid, diagnosis of disease, protein folding

1.Introduction

The innovation of new proteinaceous products in recent years has focused on diseases that were previously undetectable or difficult to detect. Scientists have made a constellation of research on folding patterns, constituent groups of amino acids, protein receptor and varieties of animal proteins, such as albumin, fibrin, and gelatin[1].The basic unit of amino acid is amino acid and it is essential to find out the combination of amino acid because of the storage of protein's information.[2]Chemical interactions also play an important role of the determination of the characteristics of protein, which include electrostatic forces, hydrogen bonding and the hydrophobic effect. These interactions have been studied with many approaches from different points:biochemistry, quantum chemistry, molecular dynamics, signal transduction, among others.[4][5][6] Additionally,the decision of a complete protein is made by the folding patterns in polypeptides, which permit the protein to have biological functions[7].Proteins are the chief actors within the cell, carrying the task of encoding the information in genes[8],acting as enzymes and involving the cell signaling and ligand binding, which is closely linked with the selection of biosensor and the diagnosis of some rare but difficult to cure diseases, the same as Parkinson.

The paper will focus on the basic information of protein and the initiatives and mechanism of the biosensor to detect disease and the industry prospects.

2 Basic Information of Protein

2.1 Amino Acid

Amino acid plays a crucial part in the construction of protein, which is the monocase of protein. It is an organic compound containing both amino and carboxylic acid functional groups[9].The two groups are bonded with the central carbon atom that contains a side chain.In the form of proteins, amino-acid residues form the second-largest component (water being the largest) of human muscles and other tissues.[10] The polarity can be standard of the classification of different amino acid.The polarity is related to distributions of electrons and thus dipoles, for example,Serine is the one kind of polar amino acid as the existence of a side chain consisting of a hydroxymethyl group. From another perspective, the amino acid with partial charges is polar, whereas, it is non-polar.Amino acid can be classified with Acid-base condition.The criterion is the side chain.The amino acid containing acid side chain is called acidic amino acid, on the contrary, one containing base side chain is called basic amino acid.Amino acids are the precursors to proteins.[11] They combine through condensation processes to create brief polymer chains known as peptides or longer chains referred to as either polypeptides or proteins.Twenty-two amino acids are naturally incorporated into polypeptides and are called proteinogenic or natural amino acids.[12]

2.2 Polypeptide Folding

2.2.1 Chemical Interactions in Amino acid

There are four kinds of chemical interactions in polypeptides, which are hydrophobic interactions, electrostatic interactions, hydrogen bonding and Van der Waals bonds. The sequence of these bonding is decided by the combination pattern.For instance, mitochondrial oxidative phosphorylation chain system components cytochrome c-reductase / cytochrome c / cytochrome c oxidase; microsomal and mitochondrial P450 systems.[13]Changing the polypeptide chain from one dimensional to three dimensional is the value of these chemical interactions. Due to that non-polar amino acids do not prefer contacting with water because it is not electrogenic so this category of amino acid will be inside. As for the amino acid with polarity, they will act as the external unit in protein.

2.2.2 Folding Patterns

It is essential that the folding of polypeptide must be correct to ensure no malfunction of the protein, although some parts of functional proteins may remain unfolded[14]. Failure to fold a correct structure of protein might make protein toxic.Additionally, the failure might cause some allergies, although some parts of functional proteins may remain unfolded[15].The primary structure of a protein will decide the its native conformation.[16]an occur as the polypeptide chain is being synthesized within the ribosome (Wilson et al., 2010). The concerted action of the ribosome and the associated chaperone trigger factor has been shown to confine nascent polypeptide folding, suggesting that the conformational space and kinetics of folding are restricted in close proximity to the ribosome .

2.3 The Structure of A Protein

Proteins are essential biological molecules that play a crucial role in various cellular functions. Understanding protein function and interactions within the cell requires knowledge of their three-dimensional structure [17] (Wetlaufer et al., 1973).Circular dichroism is a spectroscopic technique used to study protein structure and predict secondary structure [18] (Hennessey et al., 1981; Louis-Jeune et al., 2011).Using sequence homologies to predict protein structure has revealed that even identical pentapeptides can have various conformations, demonstrating the intricacy of protein folding [19] (Kabsch et al., 1984). The crystal structure analysis of the 30 S ribosomal subunit from Thermus thermophilus has shown that ribosomal proteins share similar alpha+beta sandwich folds, but the topology of this domain varies considerably, impacting their interactions with RNA[20] (Brodersen et al., 2002). Efforts have been made to predict protein structures from amino acid sequences, with the Rosetta protein modeling suite being a valuable tool for biochemical and biomedicinal studies[21] (Kaufmann et al., 2010). However, predicting the three-dimensional structure of proteins remains a challenging task in biophysics and computational biology, with recent advancements such as AlphaFold showing promise in highly accurate protein structure prediction[21] (Deng et al., 2017; Jumper et al., 2021). New methods have been developed to improve the speed and accuracy of protein structure prediction, opening the door for more effective and thorough studies of protein structures [22] (Lin et al., 2022). One such method is evolutionary-scale prediction of atomic-level protein structure using language models.According to Chandrapala et al. (2010), ultrasound has also been demonstrated to influence the thermal and structural properties of proteins, offering insights into the dynamic nature of protein folding and stability [23]. All things considered, the study of protein structure is still a dynamic and developing area, with advances in computational techniques and technology helping us better comprehend the intricate three-dimensional arrangements of proteins and the functional consequences of these configurations.

3. Diagnosis using biochemical sensors

3.1 Biosensors

3.1.1 Receptive Surface

A biosensor is an analytical device, which is used for detecting a chemical substance, that combines a biological component with a physicochemical detector.[24][25][26][27] The match of antibodies and antigens is a vital process of the attraction and detection because only the antigen will bond to the antibody with a correct conformation.

There are several receptors on the receptive surface that is used to capture specific proteins, in most situation, we will use protein-protein bonding.And antibody is a paramount receptor.Antibody is a molecule in Y shape, which has an area for the use of antigen-bonding.Antigens can be proteins, peptides (amino acid chains), polysaccharides (chains of simple sugars), lipids, or nucleic acids[28][29].In addition, the antigen-bonding area is a region where there are positive, negative, and hydrophobic amino acids and they will have interactions with our target protein, containing Electrostatic force and hydrophilicity.The process will come across the whole antibody so it will perfectly combine with the target protein.And there is no restriction of shape and size for target protein.

For example,Sandwich ELISA, a widely used technique in immunoassays, has been employed in various studies to detect different analytes.[30]demonstrated the effectiveness

of sandwich ELISA in detecting staphylococcal enterotoxins in foods, highlighting the ability to detect all known enterotoxins.[31]investigated the interference of human anti-mouse antibodies in sandwich ELISAs, emphasizing the importance of considering species-specific antibodies to avoid interference.

3.2 Electrochemical Diagnostics

Electrochemical diagnostics have been a subject of significant research and development in various fields. [32] discussed the use of in-situ electrochemical diagnostics in Proton Exchange Membrane Fuel Cells (PEFCs), highlighting the importance of real-time monitoring in improving performance.[33]focused on electrochemical diagnostics and modeling in developing the cathode of PEFCs, emphasizing the need for accurate diagnostic tools in fuel cell technology. [34] provided new insights into electrochemical diagnostics related to the high current density performance of Pt-based catalysts, shedding light on the importance of understanding catalyst behavior under different conditions.[35]The study focused on developing materials and electrochemical diagnostics for fuel cell-based ethanol sensors, highlighting their potential uses in sensor technology. [36] explored the potential of electrochemical diagnostics to identify bacterial infectious diseases, emphasizing the specificity, speed, and simplicity of sensors that detect whole organisms. [37] examined the problems and trends in electrochemical diagnostics for infectious viral illnesses, emphasizing the importance of transferring laboratory research into real-world applications. Furthermore, [38] focused on the efficiency of nanomaterials in electrochemical diagnostics for non-invasive oral cancer biomarkers. This demonstrates the promise of nanotechnology in point-of-care detection. [39]

Conclusion:

Overall, the prospect of protein and biosensor is promising due to the various function in different areas. If biosensors can be designed for all the uncommon diseases discovered so far, the difficulty of tracking and detecting these diseases will be greatly reduced, providing a brighter future for mankind

References

1.Tanford C (2001). Nature's robots: a history of proteins. Internet Archive. Oxford ; Toronto: Oxford University Press. ISBN 978-0-19-850466-5.

2.Journal of Medicinal Plants Research Vol. 5(17), pp. 3997-4000, 9 September, 2011 ISSN 1996-0875 ©2011 Academic Journals

3.Titeca K, Lemmens I, Tavernier J, Eyckerman S (January 2019). "Discovering cellular protein-protein interactions: Technological strategies and opportunities". Mass Spectrometry Reviews. 38 (1): 79–111. doi:10.1002/mas.21574. PMID 29957823.

4.Herce HD, Deng W, Helma J, Leonhardt H, Cardoso MC (2013). "Visualization and targeted disruption of protein interactions in living cells". Nature Communications. 4: 2660. Bibcode:2013NatCo...4.2660H. doi:10.1038/ncomms3660. PMC 3826628. PMID 24154492

5. Isa NF, Bensaude O, Murphy S (February 2022). "Amber Suppression Technology for Mapping Site-specific Viral-host Protein Interactions in Mammalian Cells". Bio-Protocol. 12 (3): e4315. doi:10.21769/bioprotoc.4315. PMC 8855090. PMID 35284605.

6. Alberts B, Johnson A, Lewis J, Raff M, Roberts K, Walters P (2002). "The Shape and Structure of Proteins". Molecular Biology of the Cell; Fourth Edition. New York and London: Garland Science. ISBN 978-0-8153-3218-3.

7.Lodish H, Berk A, Matsudaira P, Kaiser CA, Krieger M, Scott MP, et al. (2004). Molecular Cell Biology (5th ed.). New York, New York: WH Freeman and Company.

8.Bischoff TL, Voit C (1860). Die Gesetze der Ernaehrung des Pflanzenfressers durch neue Untersuchungen festgestellt (in German). Leipzig, Heidelberg.

9. Nelson DL, Cox MM (2005). Principles of Biochemistry (4th ed.). New York: W. H. Freeman. ISBN 0-7167-4339-6.

10. Latham MC (1997). "Chapter 8. Body composition, the functions of food, metabolism and energy". Human nutrition in the developing world. Food and Nutrition Series – No. 29. Rome: Food and Agriculture Organization of the United Nations. Archived from the original on 8 October 2012. Retrieved 9 September 2012.

11.Chapter 1: Proteins are the Body's Worker Molecules". The Structures of Life. National Institute of General Medical Sciences. 27 October 2011. Archived from the original on 7 June 2014. Retrieved 20 May 2008

12.Creighton TH (1993). "Chapter 1". Proteins: structures and molecular properties. San Francisco: W. H. Freeman. ISBN 978-0-7167-7030-5.

13. Hanukoglu I (1996). "Electron transfer proteins of cytochrome P450 systems". In Bittar EE, Jefcoate CR (eds.). Physiological Functions of Cytochrome P450 in Relation to Structure and Regulation. Advances in Molecular and Cell Biology. Vol. 14. JAI Press, Inc. pp. 29–55. doi:10.1016/S1569-2558(08)60339-2

14.Anfinsen CB (July 1972). "The formation and stabilization of protein structure". The Biochemical Journal. 128 (4): 737–49. doi:10.1042/bj1280737. PMC 1173893. PMID 4565129.

15.Berg JM, Tymoczko JL, Stryer L (2002). "3. Protein Structure and Function". Biochemistry. San Francisco: W. H. Freeman. ISBN 978-0-7167-4684-3

16.Anfinsen CB (July 1973). "Principles that govern the folding of protein chains". Science. 181 (4096):

223–30. Bibcode:1973Sci...181..223A. doi:10.1126/science.181.4096.223. PMID 4124164.
\17.Z. Lin; H. Akin; R. Rao; B. Hie; Z. Zhu; W. Lu; N. Smetanin; R. Verkuil; O. Kabeli; Y. Shmueli; A. dos Santos Costa; M. Fazel-Zarandi; T. Sercu; S. Candido; A. Rives; "Evolutionary-scale Prediction of Atomic Level Protein Structure with A Language Model", BIO.SYNTHETIC-BIOLOGY, 2022.
18.John Jumper; Richard Evans; Alexander Pritzel; Tim Green; Michael Figurnov; Olaf Ronneberger; Kathryn Tunyasuvunakool; Russ Bates; Augustin Žídek; Anna Potapenko; Alex Bridgland; Clemens Meyer; Simon A A Kohl; Andrew J Ballard; Andrew Cowie; Bernardino Romera-Paredes; Stanislav Nikolov; Rishub Jain; Jonas Adler; Trevor Back; Stig Petersen; David Reiman; Ellen Clancy; Michal Zielinski; Martin Steinegger; Michalina Pacholska; Tamas Berghammer; Sebastian Bodenstein; David Silver; Oriol Vinyals; Andrew W Senior; Koray Kavukcuoglu; Pushmeet Kohli; Demis Hassabis; "Highly Accurate Protein Structure Prediction with AlphaFold", NATURE, 2021.
19.Caroline Louis-Jeune; Miguel A Andrade-Navarro; Carol Perez-Iratxeta; "Prediction Of Protein Secondary Structure From Circular Dichroism Using Theoretically Derived Spectra", PROTEINS, 2011.
20.Jayani Chandrapala; Bogdan Zisu; Martin Palmer; Sandra Kentish; Muthupandian Ashokkumar; "Effects Of Ultrasound On The Thermal And Structural Characteristics Of Proteins In Reconstituted Whey Protein Concentrate", ULTRASONICS SONOCHEMISTRY, 2010.
21.Jayani Chandrapala; Bogdan Zisu; Martin Palmer; Sandra Kentish; Muthupandian Ashokkumar; "Effects Of Ultrasound On The Thermal And Structural Characteristics Of Proteins In Reconstituted Whey Protein Concentrate", ULTRASONICS SONOCHEMISTRY, 2010.
22.Ditlev E Brodersen; William M Clemons; Andrew P Carter; Brian T Wimberly; V Ramakrishnan; "Crystal Structure of The 30 S Ribosomal Subunit from Thermus Thermophilus: Structure of The Proteins and Their Interactions with 16 S RNA", JOURNAL OF MOLECULAR BIOLOGY, 2002.
23.J P Hennessey; W C Johnson; "Information Content in The Circular Dichroism of Proteins", BIOCHEMISTRY, 1981.
24. Khalilian, Alireza; Khan, Md. Rajibur Rahaman; Kang, Shin-Won (2017). "Highly sensitive and wide-dynamic-range side-polished fiber-optic taste sensor". Sensors and Actuators B. 249: 700–707. doi:10.1016/j.snb.2017.04.088.
25.^ Turner, Anthony; Wilson, George; Kaube, Isao (1987). Biosensors:Fundamentals and Applications. Oxford, UK: Oxford University Press. p. 770. ISBN 978-0198547242.
26.^ Bănică, Florinel-Gabriel (2012). Chemical Sensors and Biosensors:Fundamentals and Applications. Chichester, UK: John Wiley & Sons. p. 576. ISBN 9781118354230.
27.^ Dincer, Can; Bruch, Richard; Costa-Rama, Estefanía; Fernández-Abedul, Maria Teresa; Merkoçi, Arben; Manz, Andreas; Urban, Gerald Anton; Güder, Firat (15 May 2019). "Disposable Sensors in Diagnostics, Food, and Environmental Monitoring". Advanced Materials. 31 (30): 1806739. Bibcode:2019AdM....3106739D. doi:10.1002/adma.201806739. hdl:10044/1/69878. ISSN 0935-9648. PMID 31094032.
28. "Antigen". Cleveland Clinic. 2023. Retrieved 23 May 2023.
29.Abbas AK, Lichtman A, Pillai S (2018). "Antibodies and Antigens". Cellular and Molecular Immunology (9th ed.). Philadelphia: Elsevier. ISBN 9780323523240. OCLC 1002110073
30.R C Freed; M L Evenson; R F Reiser; M S Bergdoll; "Enzyme-linked Immunosorbent Assay for Detection of Staphylococcal Enterotoxins in Foods", APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1982. (IF: 4)
31.A Larsson; H Mellstedt; "Chicken Antibodies: A Tool to Avoid Interference By Human Anti-mouse Antibodies in ELISA After in Vivo Treatment with Murine Monoclonal Antibodies", HYBRIDOMA, 1992.
32. Satheesh Sambandam; Vijay Ramani; "In-situ Electrochemical Diagnostics in PEFCs", 2009.
33. Anusorn Kongkanand; Venkata Yarlagadda; Taylor R. Garrick; Thomas E. Moylan; Wenbin Gu; "Plenary) Electrochemical Diagnostics and Modeling in Developing The PEMFC Cathode", 2016. (IF: 3)
34. K. C. Neyerlin; "New Insights from Electrochemical Diagnostics Pertaining to The High Current Density Performance of Pt-Based Catalysts", 2016.
35.E. Bradley Easton; "Development of Materials and Electrochemical Diagnostics for Fuel Cell-Based Ethanol Sensors", 2020.
36. Amruta A Karbelkar; Ariel L Furst; "Electrochemical Diagnostics for Bacterial Infectious Diseases", ACS INFECTIOUS DISEASES, 2020. (IF: 3)
37. Tanvir R. Tanim; Eric J. Dufek; Sergiy V. Sazhin; "Challenges and Needs for System-level Electrochemical Lithium-ion Battery Management and Diagnostics", MRS BULLETIN, 2021. (IF: 3)
38. Neeraj Kumar; "Efficiency Of Nanomaterials For Electrochemical Diagnostics Based Point-Of-Care Detection Of Non-Invasive Oral Cancer Biomarkers", 2021.
39.K Yugender Goud; K Koteshwara Reddy; Ahmed Khorshed; V Sunil Kumar; Rupesh K Mishra; Mohamed Oraby; Alyaa Hatem Ibrahim; Hern Kim; K Vengatajalabathy Gobi; "Electrochemical Diagnostics of Infectious Viral Diseases: Trends and Challenges", BIOSENSORS & BIOELECTRONICS, 2021. (IF: 3)