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Perspectives on Structural Molecular Biology and its Prevention Strategies in COVID-19

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Abstract

Visualization has been a key technology in the progress of structural molecular biology for as long as the field has existed. This perspective describes the nature of the visualization process in structural studies, how it has evolved over the years, and its relationship to the changes in technology that have supported and driven it. It focuses on how technical advances have changed the way we look at and interact with molecular structure, and how structural biology has fostered and challenged that technology.

Keywords: COVID-19 • DNA • RNA • Molecular Biology

Introduction

Coronavirus Disease 2019 (COVID19) is an extreme acute respiratory syndrome caused by a new beta coronavirus called Coronavirus 2 (SARSCoV2), a severe acute respiratory syndrome reported to be the seventh coronavirus to infect humans. Appears as a disease. Like other SARSCoVs, it has a large positive-strand RNA genome. However, specific furin sites of peplomer proteins that are susceptible to mutations and phylogenetically disrupt the open reading frame 1ab (Orf1ab) isolate SARSCoV2 from other RNA viruses. Since its outbreak, researchers, scientists, and medical professionals have studied all kinds of facts and aspects, including replication, detection, and prevention strategies. This quickly identified functional information based on the basic biology of the protein, genomic characterization, structure and expression, and used this information to optimize strategies to prevent its spread. This overview summarizes the latest updates on the basic molecular biology of SARSCoV2 and the preventive strategies being implemented around the world to combat COVID19. Structural biology is a branch of molecular biology, biochemistry, and biophysics, and the molecular structure of biological macromolecules (particularly proteins consisting of amino acids, RNA or DNA consisting of nucleotides, membranes consisting of lipids). Handles. How do they acquire the structure they have, and how changes in their structure affect their functioning [1]. This topic is of great interest to biologists, as macromolecules perform most of the functions of cells and can only perform those functions by being wrapped in a particular three-dimensional shape. This structure, the "tertiary structure" of a molecule, depends intricately on the basic composition or "primary structure" of each molecule [2]. In recent years, it has become possible to complement in silico investigations of biological structures with highly accurate physical molecular models. Examples of these models can be found in the protein database. Computational techniques such as molecular dynamics simulations can be used in combination with empirical structure elucidation strategies to extend and study the structure, conformation, and function of proteins. In 1912, Max von Laue irradiated crystallized copper sulphate with X-rays to create a diffraction pattern [3]. These experiments have led to the development of X-ray crystallography and its use in the study of biological structure. In 1951, Rosalind Franklin and Maurice Wilkins used an X-ray diffraction pattern to take the first image of deoxyribonucleic acid (DNA). Francis Crick and James Watson used the same technique in 1953 to model the double helix structure of DNA and, along with Wilkins, received the Nobel Prize in Medicine in 1962 and the Nobel Prize in Chemistry in 1962[4]. The first tertiary protein structure of myoglobin was published by John Kendrew in 1958 [5]. During this time, the protein structure was modeled on balsa wood or wire models. With the invention of modeling software such as CCP4 in the late 1970s, modeling is now computer-backed. Recent developments in this area include the generation of X-ray free electron lasers that enable the analysis of previously hidden structures and the use of structural biology to support synthetic biology. Will be. From the late 1930s to the early 1940s, nuclear magnetic resonance (NMR) was developed by a combination of studies by Izidol Rabbi, Felix Bloch, and Edward Mills Purcell. Solid NMR is now widely used in structural biology to determine the structure and dynamic properties of proteins (protein NMR). In 1990, Richard Henderson used a cryo-electron microscope (KryoEM) to create the first three-dimensional high-resolution image of bacteriorhodopsin.

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