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Mini Review

Nuclear Pore Complex

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Abstract

The only bidirectional entry and exit point for macromolecules into and out of the nucleus is the nuclear pore complex (NPC). The NPC has remained one of the biggest problems for structure determination because of its size and complexity (1,000 protein subunits, 110 MDa in humans). The majority of nucleoporins now have atomic-resolution crystal structures thanks to structural research. With the help of biochemical reconstitution experiments, cross-linking mass spectrometry, and cryo-electron tomography, the acquisition of these structures has made it easier to determine the near-atomic overall architecture of the symmetric core of the human, fungus, and algal NPCs (Elmlinger MW et al., 2002). Here, we go over the knowledge obtained from these recent developments and unresolved problems with relation to NPC form and operation. The potent combination of top-down and bottom-up methods used to determine the NPC's structure provides a framework for identifying the architectures of other complex biological machines with almost atomic precision (Elmlinger MW et al., 2005).

Keywords: Nuclear pore complex, Nucleocytoplasmic transport, mRNA export, Integrative structural biology, X-ray crystallography, Electron microscopy

INTRODUCTION

One distinguishing characteristic of eukaryotic cells is the existence of organelles with membranes, such as the nucleus. Genomic DNA is contained in the nucleus by a double lipid bilayer known as the nuclear envelope, which isolates it from the rest of the cell. In addition to protecting the genome from damage-causing agents, its design offers chances for gene regulation. At the same time, macromolecules like transcription factors or messenger RNAs (mRNAs) need to be able to go back and forth between the nucleus and cytoplasm (Soldin OP et al., 2005). Nuclear pore complexes (NPCs), which are large, proteinaceous macromolecular machineries, are responsible for nuclear cytoplasmic transport, which is the movement of macromolecules into and out of the nucleus. One of the biggest macromolecular assemblies in cells, the nucleoporin complex (NPC) is made up of approximately 1,000 protein subunits called nucleoporins in humans. By preventing macromolecules from freely diffusing into or out of the nucleus, NPCs protect the integrity of the nuclear compartment. However, unlike the majority of other membrane transporters, NPCs transport payloads in their naturally folded state. This characteristic enables macromolecules to function as soon as they have completed their transit, for as when signal transduction activates a transcriptional programme. Basic molecular building blocks make up macromolecules (Owen WE et al., 2010). They consist of lipids (with a variety of modular ingredients), nucleic acids (polymers of nucleotides), carbohydrates (polymers of sugars), and proteins (polymers of amino acids). Proteins, nucleic acids, and lipids are broken down through linear polymerization, and carbohydrates may also branch and debranch during the biosynthesis and destruction of biological macromolecules. Multi-protein complexes with intricate regulation, such as the proteasome and ribosome, may be involved in these activities (Konforte D et al., 2013).

The interaction of X-rays with an atom's electron cloud in a crystal is what causes X-ray diffraction. Major peaks correspond to atomic locations and can be utilised to identify the structure since the atomic core electron density dominates the electron-density distribution (Yang L et al., 2005). The H atom is an exception since it only has one valence electron, and that electron's distribution is pushed towards the covalent bond partner. The Fourier transform

of the amplitude and phase of the scattered X-rays is related to the electron density in the unit cell. Only the wave intensities can be measured, thus the phase information must be deduced using a variety of techniques (Davis GK et al., 2006).

DISCUSSION

An in-depth comprehension of a biological macromolecule's function necessitates an understanding of its three-dimensional structure. The majority of biological macromolecules' atomic-resolution structures have been deduced by nuclear magnetic resonance (NMR) in solution or x-ray diffraction in single crystals. The process of determining NMR structure is covered in this review. An overview of NMR's fundamental ideas is given first. The article's main discussion focuses on the several methods required to determine an NMR structure (Carel JC et al., 2009). At the conclusion, the topic shifts to thoughts on how macromolecules' molecular sizes may affect how their structures are determined by NMR. The potential for using NMR on large molecular systems has been substantially increased by the development of new techniques, which are reviewed. Great macromolecular assemblages made up of several proteins arranged precisely are found in great numbers in cells and are essential for carrying out biological processes. Biologists wish to know these structures' atomic-level details in order to fully comprehend their roles. However, several technologies now make this possible, and scientists are starting to use an integrated strategy to study these huge structures (Zec I et al., 2012).

A biological macromolecule's three-dimensional structure must be understood in detail in order to fully comprehend its function. Nuclear magnetic resonances (NMR) in solution or X-ray diffraction in single crystals have both been used to solve the majority of the atomic-resolution structures of biological macromolecules. This review explores the process of determining NMR structure. First, a succinct explanation of NMR's foundational ideas is provided. The majority of the article focuses on the distinct processes required to determine an NMR structure. The subject then shifts to questions regarding the impact of macromolecules' molecular sizes on NMR's ability to determine their structures. The use of NMR to large molecule systems is substantially improved by the new methods that are outlined (Chan MK et al., 2009).

CONCLUSION

An in-depth comprehension of a biological macromolecule's function necessitates an understanding of its three-dimensional structure. The majority of the atomic-resolution structures of biological macromolecules have been determined either using nuclear magnetic resonance (NMR) in solution or by X-ray diffraction in single crystals. The process of determining NMR structure is covered in this review. An overview of NMR and its fundamental ideas is given first. The article's main discussion focuses on the several methods required to determine an NMR structure. At the end, the topic shifts to thoughts on how macromolecules' molecular sizes may affect how their structures are determined by NMR. The application of NMR to large molecule systems has been substantially improved by the development of new techniques, which are reviewed. Since neutron diffraction is based on the same formalisation as X-ray diffraction and depends on the interaction of neutrons with atomic nuclei, it directly determines the positions of individual atoms. The scattering lengths of light atoms like hydrogen and deuterium (D) atoms are comparable to those of the heavier atoms (C, O, and N), as the neutron scattering cross-section varies with element (or isotope) in a nonlinear manner.

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