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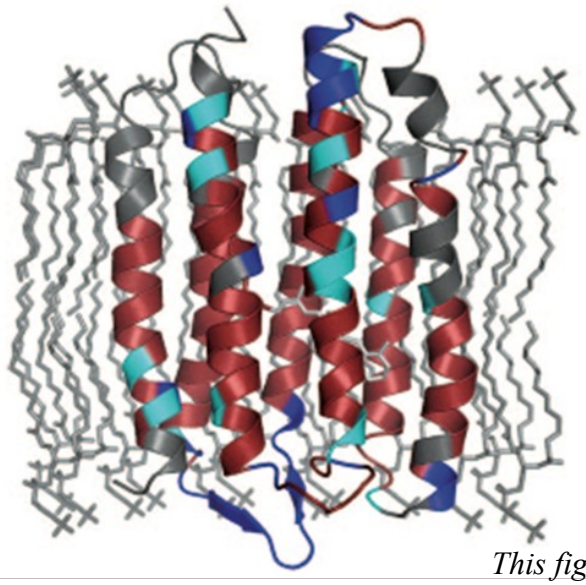
Determining the structure of a rhodopsin protein

What is this research about?

Proteins are present in all organisms and have varying functions. Proteins fold into specific spatial conformations in order to perform their biological functions. To understand the functions of proteins at a molecular level, we need to understand their 3-dimensional structures. This research studies the structure and dynamics of a protein. The protein being studied is a photoreceptor sensory rhodopsin from bacteria called *Anabaena*. Sensory rhodopsin is a protein found in the membrane (the casing) of cells.



This figure shows a structural model of the sensory rhodopsin protein that has been derived from SSNMR and X-ray data.

What you need to know:

Researchers used solid-state nuclear magnetic resonance spectroscopy (SSNMR) to study the structure of a protein. The protein studied was a sensory rhodopsin protein found in the membrane of *Anabaena* bacteria.

They were able to determine the fine details of the seven-helical architecture of the protein. They showed that using SSNMR to characterize a membrane protein in the lipid environment could reveal structures that are non-detectable or distorted by using an X-ray technique.

How can you use this research?

This research expands our knowledge of protein structure, and demonstrates the applicability of a new technique, SSNMR.

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What did the researchers do?

To study the structure and dynamics of the protein, researchers use a tool called solid-state nuclear magnetic resonance (SSNMR) spectroscopy. SSNMR is a technique that uses magnetic fields. This research used magic-angle spinning SSNMR. In this technique researchers spin the sample at the magic angle (54.7°). This increases the resolution for improved structural analysis.

With SSNMR, the membrane proteins can be tested in their natural lipid environment. This is one of the key advantages of SSNMR techniques compared to another structural technique called X-ray crystallography. X-ray crystallography requires large 3D crystals. The environment of 3D crystals may distort structures of membrane proteins. The researchers compared what they found with SSNMR to what had been previously found using X-ray crystallography.

What did the researchers find?

The primary structure of a protein is made up of a chain of amino acid residues. The SSNMR detected the majority (91%) of residues that make up the protein. The secondary structure is the regions of the chains that are organized into regular structures. The secondary structure of the rhodopsin protein consists of seven helices (similar to a spiral shape).

The researchers were able to detect small distortions and kinks at specific locations of the protein. They were also able to detect other shapes and structures that the X-ray technique was unable to detect. Overall, SSNMR of the rhodopsin protein in the lipid environment revealed structures that appear non-detectable or distorted when using X-ray crystallography.

About the Researchers:

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