

Structure determination of proteins by X ray Crystallography

Biotech Review

X-ray crystallography is a widely used method for determining the structure of a protein. The first step in this method is to grow a crystal of the protein. Unlike table salt, proteins are difficult to crystallize because of their irregular surfaces, so multiple attempts may be required to grow a crystal. Once a crystal is grown, it is exposed to X-rays. The interaction between the X-rays and the atoms in the crystal causes the X-rays to scatter. By analyzing the scattered X-rays, the position of each atom in the crystal can be determined. This information can be used to construct a three-dimensional model of the protein's structure. It's worth noting that X-ray crystallography is just one method for determining protein structure, and it does have its limitations. However, it has been used successfully to determine the structure of many important proteins, including insulin and various enzymes.

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