X-Ray Diffraction and Characterization of Crystalline Materials

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Abstract: X-ray crystallography is a tool used for determining the atomic and molecular structure of a crystals .Although Bragg's law $n\lambda = 2d \sin\Theta$ was used to explain the interference pattern of X rays scattered by crystals, diffraction has been developed to study the structure of all states of matter with any beam, e.g., ions, electrons, neutrons, and protons, with a wavelength similar to the distance between the atomic or molecular structures of interest. The method also revealed the structure and function of many biological molecules, including vitamins, drugs, proteins and nucleic acids such as DNA. X respectively is still the chief method for characterizing the atomic structure of new materials and indiscerning materials that appear similar by other experiments.

Key Words: X-ray diffraction. Crystals , Characterization, Bragg's law

1 Introduction

X-ray crystallography is a tool used for determining the nomic and molecular structure of a crystal, in which the crystalline atoms cause a beam of incident is asys to diffract into many specific directions. By measuring the angles and intensities of these diffracted beams, a crystallographer can produce a three-dimensional picture of the density of electrons which the crystal. From this electron density, the mean positions of the atoms in the crystal can be determined, as well as their chemical bonds, their disorder and various other information.





2 Principles

Bragg's Law $n\lambda = 2d \sin\Theta$ derived by the English physicists Sir W.H. Bragg and his son Sir W.L. Bragg in 1913 to explain why the cleavage faces of crystals appear to reflect X-ray beams at certain angles of incidence (Θ, λ) . The variable *d* is the distance between atomic layers in a crystal, and the variable lambda is the **wavelength** of the incident X-ray beam n is an integer.

This observation is an example of X-ray **wave interference** (Roentgenstrahlinterferenzen), commonly known as X-ray diffraction (XRD), and was direct evidence for the periodic atomic structure of cristals postulated for several centuries. The Braggs were awarded the Nobel Prize in physics in 1915 for their work in determining crystal structures beginning with NaCl, ZnS and diamond. Although Bragg's law waves used to explain the interference pattern of X-rays scattered by crystals, diffraction has been developed to study the structure of all states of matter with any beam, e.g., ions, electrons, neutrons, and process, with a wavelength similar to the distance between the atomic or molecular structures of interest.



Figure 2 : Bruker D5005 Wice angle X-ray diffractometer with variable temperature for the study of covallinity and detection of polymorphisms.

3. Experimental Procedure

In an X-ray diffraction measurement, a crystal is mounted on a goniometer and gradually rotated while being bombarded with X-rays, producing a diffraction pattern of regularly spaced spots known as *reflections*. The two-dimensional images taken at different rotations are converted into a three-dimensional model of the lensity of electrons within the crystal using the mathematical method of Fourier transforms, combined with chemical data known for the sample. Poor resolution (fuzziness) or even errors may result if the crystals are too small, or not uniform enough in their internal makeup.

X-ray crystallography is related to several other methods for determining atomic structures. Similar diffraction patterns can be produced by scattering electrons or neutrons, which are likewise interpreted as a Fourier transform. If single crystals of sufficient size cannot be obtained, various other X-ray methods can be applied to obtain less detailed information; such methods include fiber diffraction, powder diffraction and small-angle X-ray scattering (SAXS). If the material under investigation is only available in the form of nanocrystalline powders or suffers from poor crystallinity, the methods of electron crystallography can be applied for determining the atomic structure. Since many materials can form crystals—such as salts, metals, minerals, semiconductors, as well as various inorganic, organic and biological molecules

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X-ray crystallography has been fundamental in the development of many scientific fields. In its first decades of use, this method determined the size of atoms, the lengths and types of chemical bonds, and the atomic-scale differences among various materials, especially minerals and alloys. The method also revealed the structure and function of many biological molecules, including vitamins, drugs, proteins and nucleic acids such as DNA. X-ray crystallography is still the chief method for characterizing the atomic structure of new materials and in discerning materials that appear similar by other experiments. X-ray crystal structures can also account for unusual electronic or elastic properties of a material, shed light on chemical interactions and processes, or serve as the basis for designing pharmaceuticals against diseases.



Workflow for solving the structure of a molecule by X-ray crystallography.

The oldest and most precise method of X-ray crystallography is *single-crystal X-ray diffraction*, in which a beam of X-rays strikes a single crystal, producing statured beams. When they land on a piece of film or other detector, these beams make a *diffraction pattern* of spots; the strengths and angles of these beams are recorded as the crystal is gradually rotated.^[93] Each spot is called a *reflection*, since it corresponds to the reflection of the X-rays from one set of availy spaced planes within the crystal. For single crystals of sufficient purity and regularity, X-ray diffraction data can determine the mean chemical bond lengths and angles to within a few thousandths of an angestrom and to within a few tenths of a degree, respectively. The atoms in a crystal are not static, but occluate about their mean positions, usually by less than a few tenths of an angestrom. X-ray crystallograph, allows measuring the size of these oscillations.

5. Results & Discussion

The technique of single crystal X-ray crystallography has three basic steps. The first—and often most difficult—step is to obtain an adequate crystal of the material under study. The crystal should be sufficiently large typically larger than 0.1 mm in all dimensions), pure in composition and regular in structure, with no significant internal imperfections such as cracks or twinning.

In the second step, the crystal is placed in an intense beam of X-rays, usually of a single wavelength (*non-circomatic X-rays*), producing the regular pattern of reflections. As the crystal is gradually rotated, privides reflections disappear and new ones appear; the intensity of every spot is recorded at every orientation of the crystal. Multiple data sets may have to be collected, with each set covering slightly more than half a full rotation of the crystal and typically containing tens of thousands of reflections.

In the third step, these data are combined computationally with complementary chemical information to produce and refine a model of the arrangement of atoms within the crystal. The final, refined model of the atomic arrangement—now called a *crystal structure*—is usually stored in a public database.



Applications of XRD

XRD is a nondestructive technique, fast, easy sample preparation To identify crystalline phases and orientation To determine structural prorenies Lattice parameters (10 Å), strain, grain size, expitaxy, phase composition, preferred orientation (leuc) order disorder transformation, thermal expansion. To measure thickness of thin films and multi layers to determine atomic arrangement High accuracy ford spacing calculations Single crystal, poly and amorphous materials

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