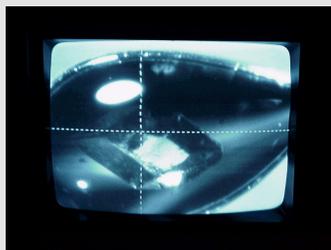
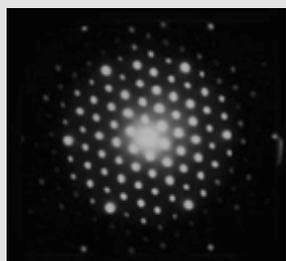


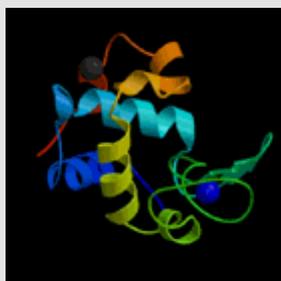
## Crystals



This is a picture of a lysozyme protein crystal.



This is an X-ray diffraction pattern of a crystal.



This is the molecular structure of lysozyme.

### Introduction

Crystals are solids formed by atoms arranged in a certain pattern. The study of crystals is known as crystallography. Many crystals are found naturally such as diamonds while others such as salt and protein crystals can be obtained from solutions. Protein crystals, unlike salt crystals are extremely delicate and cannot be carried around.

### Why do we study them?

We study crystals in order to learn about the arrangement of atoms and molecules in the crystal. This helps us to cut jewels, make better electronics, and has a significant contribution in the development of new drugs. Another reason why we study crystals is to minimize the defects in the structure. When crystals grow in nature or in the laboratory, they tend to have many defects. When we grow them in the lab, the goal is to grow a perfect crystal that does not have any defects. Some of the many defects found in crystals are impurities, cracks, or too many clusters. An impurity can be anything that should not be inside of the crystal. Sometimes, when growing crystals, many of them start growing in the same area right on top of each other. This causes a cluster of crystals to grow. The perfect crystal is one single crystal without any cracks or impurities. This is the type of protein we try to grow because the protein crystal needs to be perfect in order to be used in x-ray diffraction.

### How can we study the crystals at the NSLS?

The crystals can be studied at the Light Source by using x-ray diffraction topography. Although the name sounds way too sophisticated and complicated, the idea is quite simple. It is the same concept as shining a white light through a small hole. When that beam of white light comes out the other end of the hole, it is diffracted and gets bent towards all different directions. In x-ray diffraction, a beam of x-ray is passed through a crystal. When it comes out the other end, there are many beams of x-ray diffracted in different directions. Each one of these beams makes a different spot on a screen. This is the data that the scientist uses to see if the structure of the crystal

shows a perfect crystal. If the data does not represent a perfect structure, the scientist can go back and grow the same kind of crystal in different conditions to see if he can get closer to the perfect crystal with no defects.

### How does all this help?

This all probably seems useless until we realize what it has accomplished for us. So we make the perfect crystal and use x-ray diffraction to see if the structure looks perfect. Well that is very important because that perfect crystal is the reason of the high tech electronics we have today. Scientists had to grow the perfect semi-conductor crystal such as silicon so it could be used in electronics such as the computer chips or the T.V that we use everyday. Then again, the perfect crystal always comes up in talk about jewels. Its always the most expensive diamond in the showcase that has the perfect structure with no defects. Also, jewelers can use the molecular structure of the crystal to know where to cut the gem so it has smooth edges with no cracks. Here at the NSLS, we are interested in making the perfect protein crystals for better results in x-ray diffraction and finding technological applications for such crystals.

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