ESRP: Attempted Crystallization of Gallus Gallus Domesticus Riboflavin Binding Protein and the Collection of Diffraction Data from Lysozyme Protein

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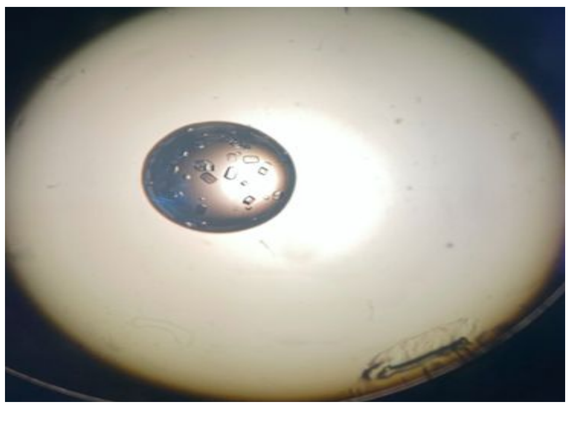
MOTIVATION

Initially, the purpose of this research project was to crystallize a riboflavin binding protein that was not yet entered into the protein database. This project was the first time many of the researchers would be working with crystallization and also have the chance to work with a state of the art electron accelerator. This experimental process is a great opportunity to educate high school students in research opportunities while also influencing the science community by collecting a previously unrecorded molecule structure.

MAJOR ACCOMPLISHMENTS

The crystallization of the protein unfortunately failed. During the hanging-drop procedure, the protein (dried form) was implemented in the hanging drop solutions; there were no riboflavin binding protein crystals that formed. This prevented us from being able to use X-ray diffraction since there would be no consistent ray patterns to suggest the protein's structure. In light of this, lysosome crystals provided by Dr. Duguid were used instead. The Argonne synchrotron and other lab machinery was used to successfully find light diffraction data. This data helped us understand the structure of this protein and gave us a look at how correct and successful crystallography can lead to the accurate interpretation of a protein's structure.



IMPACT

We were unable to successfully crystallize the intended riboflavin protein, however, we were provided lysozyme crystals from Dr. Erica Duguid. From the data that was collected on the lysozyme crystals, Argonne workers were able to create a def.SciFile with a program that can be utilized by future users of the Argonne beamline. This project also influenced us, helping feed our interest in the sciences and lab research.

FUTURE DIRECTIONS

We are now better equipped for future crystallization attempts because we have experience with the techniques for mounting and freezing crystals. Being able to examine the crystal samples that we collected allowed us to recognize our errors: namely taking too long to submerge the crystals in the liquid nitrogen. This resulted in significant amounts of ice crystals around the samples due to atmospheric water condensing on the surface. Thus, we saw diffraction from both the crystals and water when hit with X-rays. This limited our ability to properly analyze the protein data. For future crystallizations, we will be aware of this potential interference.

[1] M. S. Miller, H. B. White, III. *Isolation of Avian Riboflavin-Binding Protein.* Academic Press, 1986.
[2] Hampton Research. *Hanging Drop Vapor Diffusion Crystallization*. Hampton Research Corp., 2020.

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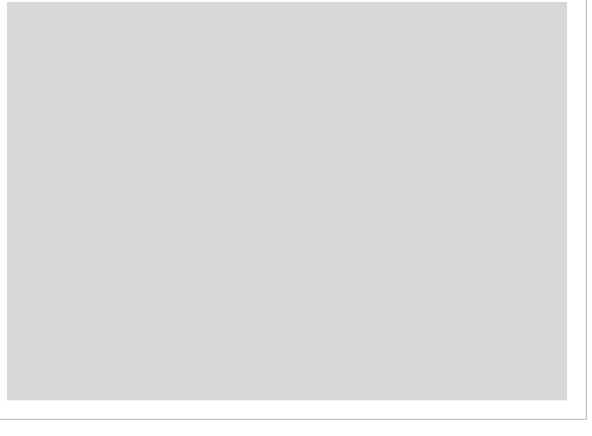

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