



Determining Protein Structure of HsRio2 Using X-Ray Crystallography



Kashif Rahman

College Park Scholars – Science & Global Change Program

Computer Science Major

krahman@umd.edu

College Park Scholars Academic Showcase - May 3, 2019

Background

The HsRio2 protein is a structure that makes up a larger group of structures related to the function of ribosomes in the human body. The exact mechanics of this structure is a mystery, and only guesses can be made based on the product of materials that go through this structure. By creating a crystal lattice of the structure, x-ray crystallography can be used to generate a very accurate model. Based on this model, analysis can reveal interaction with other structures and other mechanisms that can help lead to the full understanding of how this structure works.

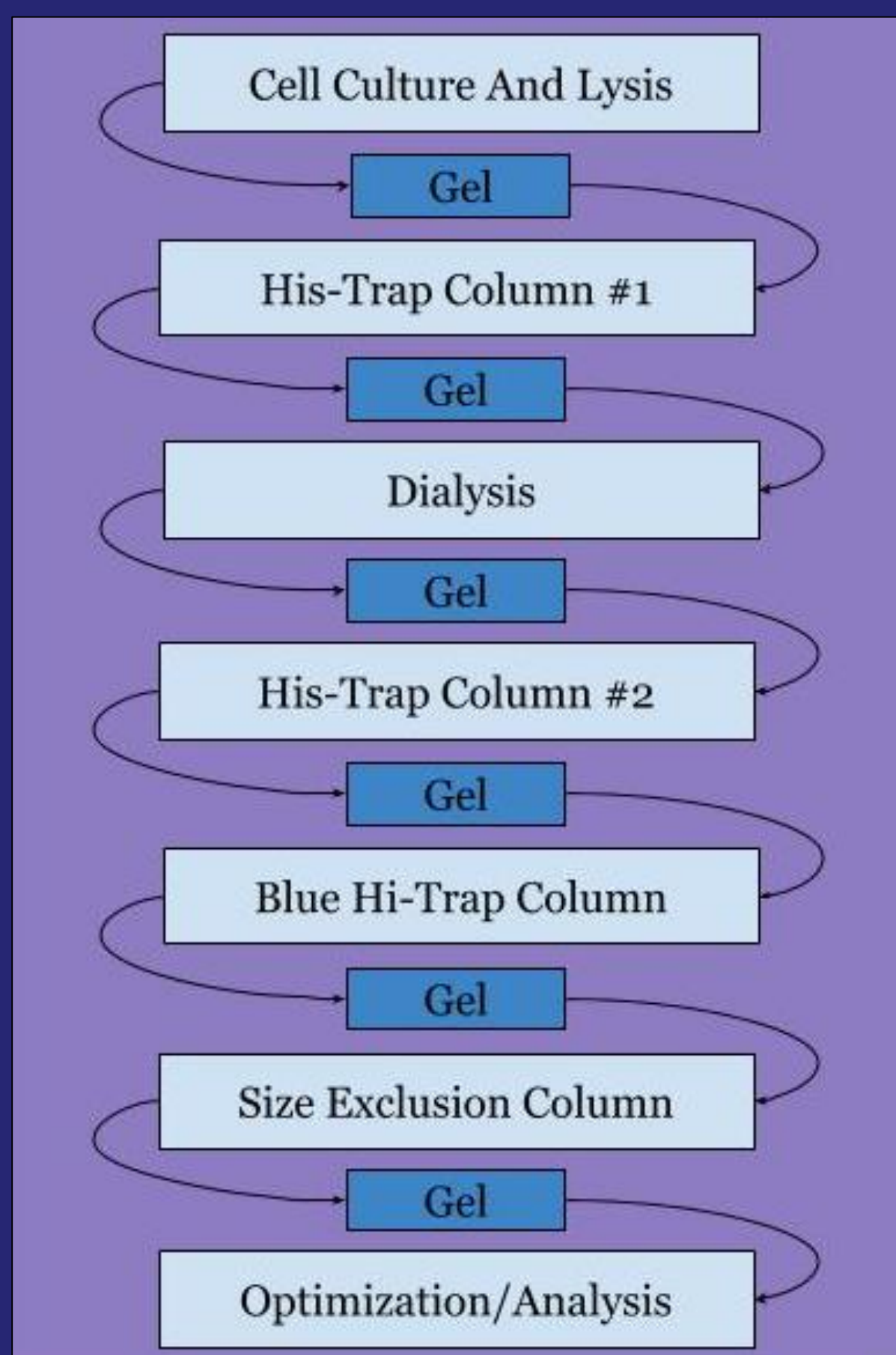


Figure 1 – The process that my lab used for purification. Gels are run after every step to check the purity and general quantity.

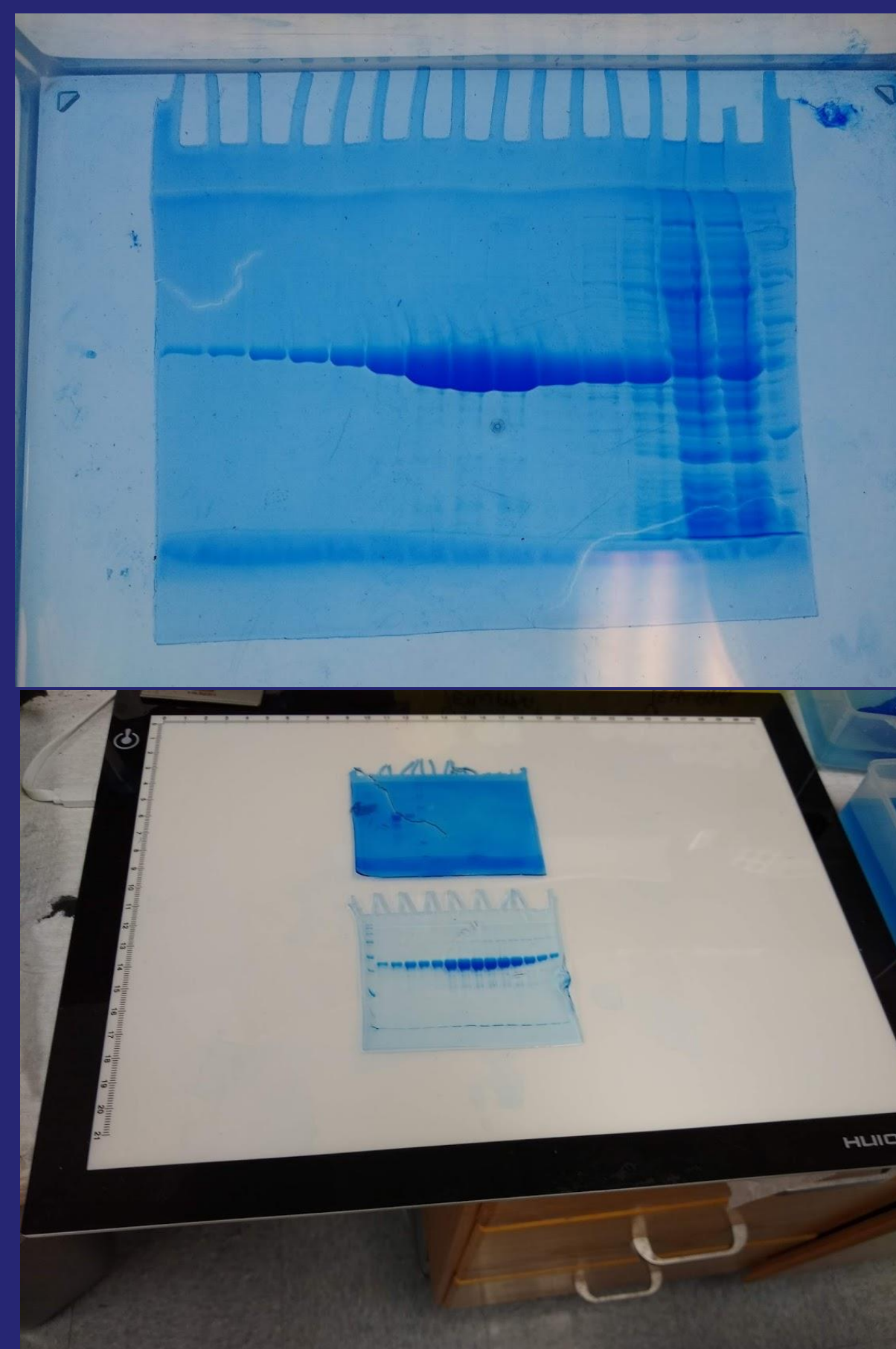


Figure 2 – One of the gels that I ran. Each well ran a different fraction of a sorting column, and the large dark blue area contains the fractions with the most protein.

Activities

As an intern, my primary job was to work on the wet lab component of research, involving a lot of column purification using the machine in Figure 3. First, we start by creating a new culture of cells that contain the protein we are looking for, HsRio2. Then we run various columns in order to remove everything beyond the proteins we are looking for. Figure 1 names the processes that are used typically during a full cycle, which can take 1 week to run. My job also involved running a lot of gels to check on the amount of protein in our samples. Once the proteins are purified, we can begin to run the proteins under different conditions to see in what solution the protein crystallizes the best. This is different for every protein, so as much protein as possible must be preserved. A crystal can be sent to a secondary lab to run x-ray crystallography on.

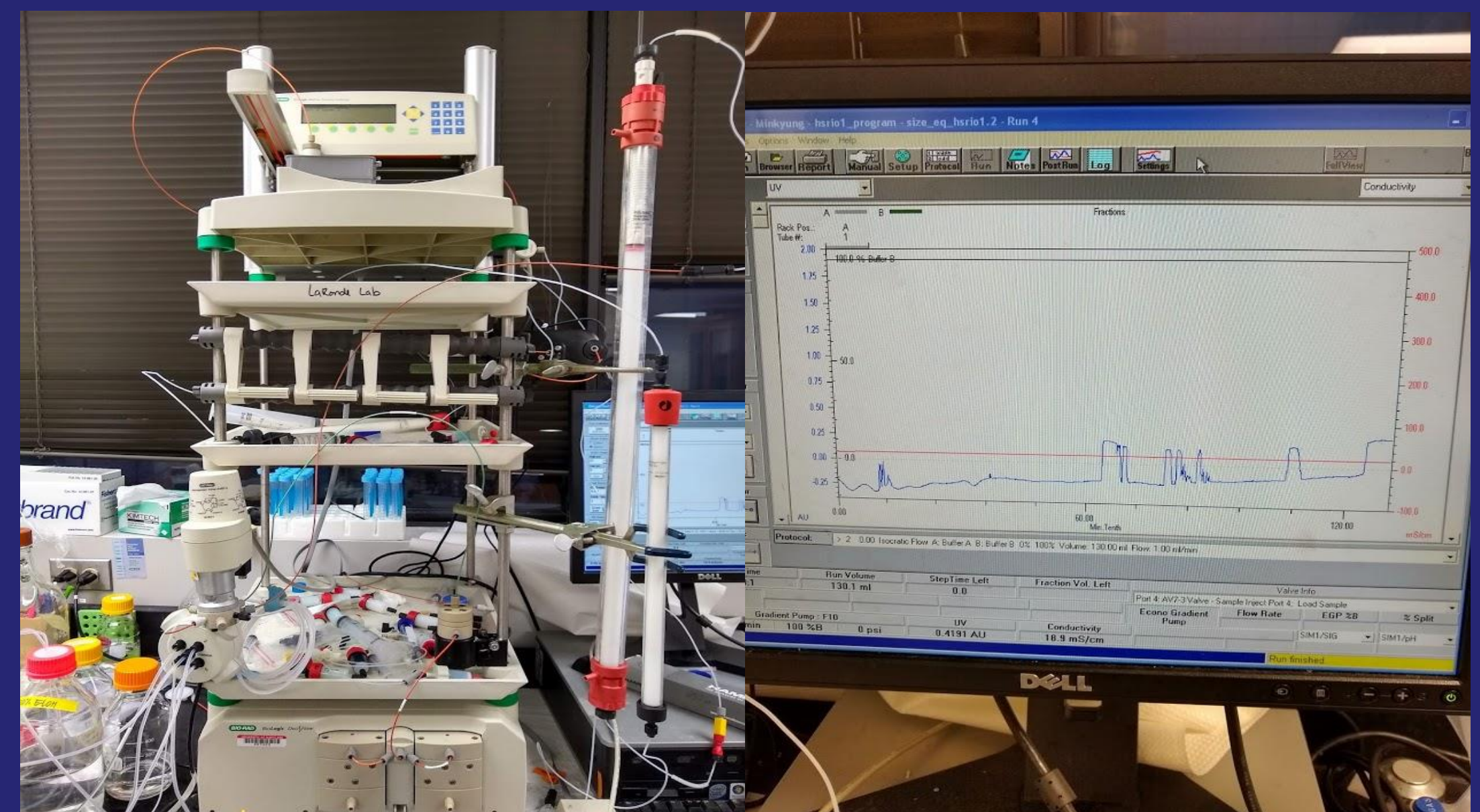


Figure 3 – This machine does column purification, which runs material down a column contain some environment meant to slow specific items down. They then sort the materials into fractions based on how long it spent in the column. Each column contains a different environment.

Site Information

2125 Biomolecular Sciences Bldg.
8314 Paint Branch Dr
College Park, MD 20740

Principal Investigator: Dr Nicole LaRonde

Lab Supervisor: Nishat Seraj

Lab Focus: ribosome proteins, inhibitor design and development, determination of protein structure via x-ray crystallography

My Experience

I thoroughly enjoyed my time in the LaRonde lab, and learned more biochemistry in the lab than in any of my classes. More than that, I also learned that, while enjoyable, it was not something I wanted to do in the long term. It influenced my decision to become a full time Computer Science major instead, which I believe is where my interest currently lies.

Acknowledgements

I would like to thank Dr. Nicole LaRonde for letting me work in her lab, and Nishat Seraj for teaching and supervising me as well as giving me tons of advice. I would also like to thank Dr. John Merck and Dr. Thomas Holtz for all their teaching and helping us through the process of our internship and preparing our poster and presentation.

