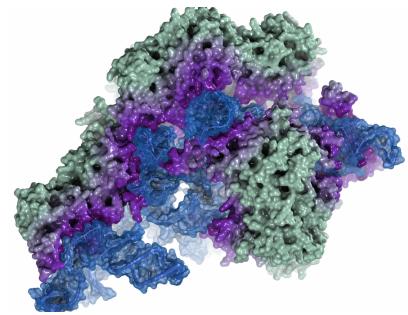


Macula Imaging

Reimagining the future of protein imaging

Protein imaging -

High resolution spatial imaging of proteins is essential to understanding protein structure. With the ability to image proteins using **small and cost efficient devices**, researchers will better be able to **understand protein interactions** and develop therapeutics targeting specific proteins.



Current Limitations -

Current protein imaging techniques are imprecise, time consuming, or expensive (costing anywhere from \$1-\$7 million dollars)

X-ray Crystallography relies on arranging several instances of a protein in a crystal lattice structure and using x-ray diffraction to create an electron density map. **It breaks down when analyzing an unstable protein that doesn't form a clear crystal shape and reports a fuzzy image.**

Cryo Electron Microscopy freezes a protein at -180 °C to form vitreous ice, and then fires electron beams at it to determine the scattering patterns. **This method is expensive and time consuming; the freezing process is error prone and it is difficult to keep the samples frozen throughout the analysis process.**

Our Solution

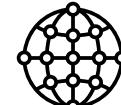


Nanopore to Identify Amino Acids

Nanopores have been used to sequence DNA and **identify all 20 amino acids**. They measure the blockage of ionic current.



Rotation



Analysis

Use ATP synthase to rotate the protein through various angles and repetitively feed it through the nanopore.

Analyze **electrical signal data from nanopores** from multiple angles to determine sequence and structure of the protein.

This gives enough information to understand the full structure.

Train recognition using ML for repeated protein formations such as alpha helices and pleated sheets.

By feeding the protein through the nanopore, we can gain information on the sequence and structure, bringing down costs to \$10K.