

Serve the global community by curing all chronic diseases through a complete understanding of biological complexity at the molecular level.

Core Values and Culture

Meaningful Relationships

A great community fosters creativity and ambition that drives us closer to our vision each day.

Thinking Big

We aim for 10x improvements and the only way to do that is by imagining the future.

Collaboration > Competition

We encourage sharing ideas, and see failures as necessary steps towards success.

Attention to Detail

Aiming for high resolutions of < 1Å drives us to perfection at the molecular level.

Embrace Skepticism

Changing the world and pushing innovation requires going against conventional beliefs.

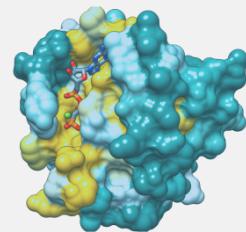
Curiosity

We encourage the pursuit of knowledge and consider it a result in and of itself.

The Problem

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.

The Applications are Our Mission

1

Protein Therapeutics

Our technology can be leveraged to **develop novel protein** therapeutics for the treatment of **chronic diseases such as Alzheimer's and cancer**, saving millions of lives.

2

Protein Structurome Project

We hope to launch the protein structureome project to **catalog >80% of the protein structures in the human proteome**. This will be invaluable for other scientists and biomedical researchers.

3

Clinical Trial Simulations

With high resolution spatial information, we will be able to **more accurately perform clinical trial simulations**. This can shorten the lengthy process between drug discovery and public release.

Our Technology

Nanopores



As ionic current passes through the nano-scale hole, the protein is fed through and disrupts the signal. **These perturbations can be used to gain sequence and structure information.**

They have so far been used to sequence DNA and identify all 20 amino acids.



Rotation with ATP Synthase

For a 3d protein, a single pass through the nanopore is insufficient, so we propose **repeated measurements at different angles to give a full image**.

ATP Synthase can provide that multi-dimensional rotational function.

Gold Nanoparticles



Gold nanoparticles within the nanopore will be better able to identify specific amino acids. **They have been proven to have different binding affinities for each amino acid.**



These binding affinities will be conveyed to the researcher via a fluorescent signal.

Analysis

The electrical signal data from the nanopore (from multiple angles) will be combined with measurements from the gold nanoparticles. This will enable us to gain a comprehensive sequential and structural representation.

Further, we will use **ML algorithms to detect motifs** within proteins such as alpha helices and beta pleated sheets.