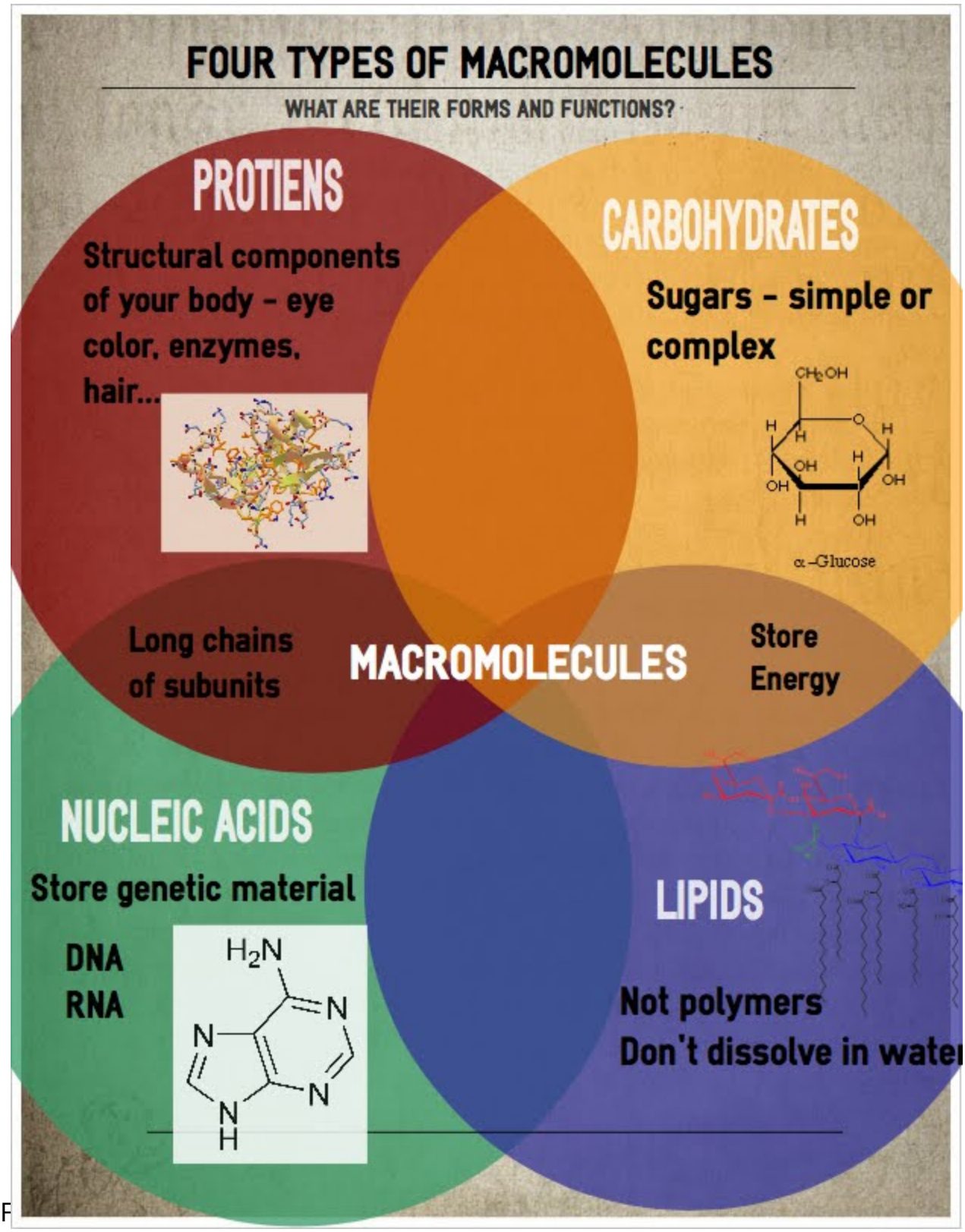
Paravastu Lab work from my understanding

Protein **Background:**

> Proteins, lipids, carbohydrates, and nucleic acids are the four essential classes of biological macromolecules (biomolecules) that constitute the structure and functions of all living cells.



Proteins work by connecting their molecules to different cells causing functions

The basic structure is called a monomer which is a simple basic string of these molecules

However sometimes to do more complex jobs, this structure just dosent work... hence the **protein folds**

BUT protein folding can go wrong

Amyloids & Misfolding

Protein misfolding is the process where proteins fail to achieve their functional three-dimensional shape, often forming toxic, stable aggregates like amyloids

Why? = Errors can stem from genetic mutations, environmental stressors (heat, pH changes, oxidative stress), or failures in the cell's quality control machinery (chaperones).

Amyloids = colections of misfolded proteins that start despoiting in tissues and organs

This is very toxic and dangerous (think of it as random blocks of code grouping up and spawning in your code, its not very good)

Amyloids lead to a group of diseases known as **amyloidosis** and these deposits often accumulate in the heart, kidneys, liver, and nerves.

Some of these diseases include Alzheimer's, Parkinson's, Huntington's, and cystic fibrosis.

Paravastu Lab

The Paravastu Lab uses biophysical techniques, primarily solid-state NMR, paired with computational simulations to characterize and understand the assembly of disease-related amyloids and de novo peptide assemblies.

structural characterization is critical to our understanding of how these structures form and how to develop targeted therapeutics.

NMR