



2025 Summer Scholar Profile: Molly Goldwasser



My name is Molly Goldwasser, and I am a rising senior at the University of Michigan. I am majoring in Biochemistry with a minor in Computer Science. At the University of Michigan, I am a member of Dr. Nils Walter's lab, which aims to uncover the mechanisms behind the vast roles of RNA molecules in the gene expression process to advance therapeutics. Under the guidance of Dr. Adrien Chauvier, I study sequences of bacterial mRNA, called riboswitches, to characterize how they control gene expression in response to specific molecules. I am excited by the application of biomedical research to advance treatments of disease.

At the Buck Institute, I work in the Metabolomics Core, led by Dr. Prasanna Ashok Kumar. Metabolomics provides a window into the status of a variety of metabolic processes through characterization of the small molecules within a biological sample. Through both internal and external collaborations, the Core has identified metabolic signatures of aging and diseases with its state-of-the-art mass spectrometry technology and data analysis platforms. However, metabolomics is just one type of omics data and can be integrated with other datasets, like proteomics, to provide a more comprehensive view into changes in biological pathways.

My project focused on analyzing lipidomic data, which is still an emerging area of research compared to genomics, proteomics, and metabolomics. Lipids are an important group of molecules involved in energy storage, cell membranes, and signaling. However, studying them is difficult because **lipid analysis is still underdeveloped**—there are no consistent systems for classifying or naming lipids, and the biological roles of many lipid molecules are still unknown. These gaps made it challenging to interpret lipid data and connect it to biological meaning. My work focused on overcoming these challenges to gain a better understanding of the role of lipids in Alzheimer's Disease (AD), a neurodegenerative disease with an unknown pathology.

The APOE gene is strongly associated with AD risk, and different APOE variants (ApoE2, ApoE3 and ApoE4) can either increase or reduce that risk. The Metabolomics Core quantified the relative abundances of different lipids in iPSC-derived-ApoE2, ApoE3 and ApoE4 neurons and pericytes, two brain cell types that help maintain the blood–brain barrier, across different APOE genotypes. To address the challenge of lipid identification, I first **compiled standard identifiers** for all lipids in the dataset by combining information from several public lipid databases. Because most lipids do not have clear pathway annotations, I then **integrated lipidomics data with proteomics data** to use known protein pathways to help interpret the lipid changes. This approach helped identify **important relationships between proteins and lipids** that varied by APOE genotype.

I also used **computational tools** to classify lipids based on their structural features rather than just broad categories. This gave a more detailed view of lipid patterns and how they changed between cell types and genotypes. My findings suggested that the **APOE genotype influenced lipid metabolism in different ways**, revealing key lipid molecules that might help explain how APOE affects Alzheimer's disease risk.

Overall, my project showed how lipidomics can provide valuable biological insights despite current challenges in the field. While I focused on APOE and AD, expanding this kind of analysis to other biological samples will be important to better understand the role of lipids in health and disease.