

# Conformational dynamics in modular enzyme systems studied by SAXS and cryo-EM

Maxwell Watkins<sup>1</sup>, Nozomi Ando<sup>2</sup>

<sup>1</sup>N/A <sup>2</sup>Cornell University

*mbw3@princeton.edu*

Although proteins are often depicted by a single conformation or set of discrete conformations, they are constantly in motion. In solution, proteins adopt ensembles of conformations as described by a continuous thermodynamic landscape. Some, including those involved in the biosynthesis of small molecules, require large-scale domain rearrangements during turnover, and thus a high degree of flexibility is intrinsic to these systems. These types of systems are especially challenging to study, and a multi-faceted approach is required to describe how their dynamics relate to their function. In this talk, I will discuss how information from high-resolution techniques and computational modeling is most powerful when combined with solution techniques, such as small-angle X-ray scattering (SAXS), that measures the full solution conformational ensemble. I will show how structural data from AlphaFold2 predictions, fragment crystal structures, and single-particle cryo-electron microscopy (cryo-EM) can be effectively used concurrently with direct measurements of protein conformational ensembles by SAXS to capture the full extent of motions in a flexible, multi-domain enzyme.