An Integrative Approach to Exploring the Role of Oligomerization in Enzyme Function

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Almost 50% of all proteins form homooligomers. The preponderance of self-association by enzymes implies that oligomerization and quaternary structure are important for catalytic function. This presentation will explore the fundamental theme of how oligomerization underlies enzyme catalysis, with an emphasis on the integration of multiple structural and biophysical techniques. SAXS plays an important role in this endeavor. Notably, the oligomeric states that are present in solution can be obtained from SAXS data collected on a relative scale. Furthermore, when combined with X-ray crystallography, SAXS provides a powerful tool for determining the quaternary structure of proteins in solution. Examples demonstrating the integration of SAXS, crystallography, hot spot mutagenesis, and analytical ultracentrifugation to understand the role of oligomerization in enzyme function will be described.