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Protein solution-state structure, intermolecular interactions, and tracking aggregation using small-angle x-ray scattering CRYSTAL RODRIGUEZ, RAUL HIGUERA, JACQUELYN KIM, EMMANUEL ZUBIA, MAHESH NARAYAN, JOSE BANUELOS , University of Texas El Paso — Investigating the structural properties of proteins during their folding/unfolding may elucidate the reasons why debilitating protein mis-folding diseases occur. In solution, protein concentration, solvent properties, and the presence of other molecular species impact protein intermolecular interactions including binding events and aggregation. Small-angle x-ray scattering experiments over a Q-range of 0.01 – 0.6 Åˆ-1 are being used to investigate the nanoscale shape and interactions of the proteins hen egg-white lysozyme and human serum albumin at concentrations of 0.01, 0.1, 1 and 10 mg/ml. As concentration increases, interactions increase and this approach allows us to distinguish protein shape from interactions. The ATSAS analysis software suite allow us to apply models to the SAXS data and obtain the structure of the proteins, including their size, as well as generating solution-state SAXS profiles from protein data base (PDB) files. This preliminary work will set the stage for structural studies of temperature induced aggregation, fibril formation of amyloid fragments (amyloid-beta fibrils are prevalent in Alzheimer's disease), and the possibility of fibril disruption by tanshinone compounds.

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