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Combining Protein Dynamics and Aggregation Measurements

CURTIS MEUSE, NIST - Natl Inst of Stds & Tech — Infrared spectroscopy has long been used to deduce concentration and structural descriptions of proteins in a variety of static and time resolved experiments. We have developed an infrared order parameter to describe protein conformation variations around the average molecular values. Here, we combine our order parameter measurements with circular dichroism, light scattering and atomic force microscopy measurements to clarify the characterization of protein structure and aggregation. By combining the information from our suite of methods, we explore the relationship between protein stability, dynamics and aggregation. Our focus is on developing new methods to compare the structure, dynamics and function of nearly identical biopharmaceutical protein ensembles. Examples include lysozyme, albumin cytochrome *c* and the characterization of amyloid beta during aggregation.

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