Abstract Submitted
for the MAR11 Meeting of
The American Physical Society

Tracking the Growth Transitions of A Solvent-Charged Model Globular Protein JEREMIAH BABCOCK, JACOB FRIDAY, LORENZO BRANCALEON, University of Texas at San Antonio — Biophysical studies have shown that solutes like proteins undergo aggregation through specific pathways that often lead to long polymeric structures called fibrils. The knowledge of the size of early-stage protein aggregates (oligomers) has an important bearing on the elucidation of the dynamics of the process of protein unit combinations. In this study, bovine serum albumin, a well-characterized model protein known to polymerize in alkaline and acidic conditions in the normal (N) to basic (B) or (N) to (E) transition, was incubated at pH 9.0 and pH 3.1 for longer than eight days. Particle growth in solution was monitored by absorption, fluorescence and circular dichroism spectroscopy and concurrently measured by atomic force microscopy (AFM) methods to yield BSA oligomer size distributions. Results show that the BSA aggregation pathway is concentration-dependent and rapidly forms spherical aggregates, which preferentially come together to form flexible polymers.

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Date submitted: 28 Nov 2010 Electronic form version 1.4