

Abstract Submitted
for the MAR13 Meeting of
The American Physical Society

Low resolution structures of cold, warm, and chemically denatured cytochrome-c via SAXS CHRISTOPHER ASTA, ANTHONY BANKS, MARGARET ELMER, TREVOR GRANDPRE, ERIC LANDAHL¹, DePaul University — The results of a small-angle x-ray scattering (SAXS) study of equine cytochrome-c protein under different unfolding conditions are discussed. Although the measured radius of gyration of this protein over a wide range of temperatures and GuHCl concentrations conform to a two-state model, we find different levels of residual structure present depending on whether the protein is cold- or warm-denatured. We present DAMMIF reconstructions of these different unfolded states using 1532 dummy atoms with a 1.5 Angstrom radius, and suggest ways that these different states may be described by the same folding free energy.

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Date submitted: 09 Nov 2012

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