Abstract Submitted
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Resolution of the unfolded state. GREGORY BEAUCAGE, University of Cincinnati — The unfolded states in proteins and nucleic acids remain weakly understood despite their importance to protein folding; misfolding diseases (Parkinson's & Alzheimer's); natively unfolded proteins ($\sim 30\%$ of eukaryotic proteins); and to understanding ribozymes. Research has been hindered by the inability to quantify the residual (native) structure present in an unfolded protein or nucleic acid. Here, a scaling model is proposed to quantify the *degree of folding* and the unfolded state (Beaucage, 2004, 2007). The model takes a global view of protein structure and can be applied to a number of analytic methods and to simulations. Three examples are given of application to small-angle scattering from pressure induced unfolding of SNase (Panick, 1998), from acid unfolded Cyt c (Kataoka, 1993) and from folding of *Azoarcus* ribozyme (Perez-Salas, 2004). These examples quantitatively show 3 characteristic unfolded states for proteins, the statistical nature of a folding pathway and the relationship between extent of folding and chain size during folding for charge driven folding in RNA. Beaucage, G., *Biophys. J.*, in press (2007). Beaucage, G., *Phys. Rev. E.* **70**, 031401 (2004). Kataoka, M., Y. Hagihara, K. Mihara, Y. Goto *J. Mol. Biol.* **229**, 591 (1993). Panick, G., R. Malessa, R. Winter, G. Rapp, K. J. Frye, C. A. Royer *J. Mol. Biol.* **275**, 389 (1998). Perez-Salas U. A., P. Rangan, S. Krueger, R. M. Briber, D. Thirumalai, S. A. Woodson, *Biochemistry* **43** 1746 (2004).

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