Abstract Submitted
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A Unified Model of Protein Folding Cooperativity[1] OLEG VOROV, DENNIS LIVESAY, DONALD JACOBS, UNC at Charlotte — Polypeptide and protein folding are cooperative processes currently modeled by different types of microscopic mechanisms. We apply the Distance Constraint Model (DCM) that explains the origin of cooperativity through nonadditivity of conformational entropy. Within the mean-field approximation of uniform constraint density given by Maxwell counting, a unified model emerges that is solved by a transfer matrix method valid for any type of geometry. Heat capacity for the helix/coil transition and protein folding are described markedly well. This work is supported by NIH R01 GM073082 O. K. Vorov, D. R. Livesay, and D. J. Jacobs, Biophysical Journal Volume 97 December 2009 1-10. O. K. Vorov, D. R. Livesay, and D. J. Jacobs, submitted to Phys. Rev. Lett.

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