Abstract Submitted
for the MAR06 Meeting of
The American Physical Society

**Co-operative unfolding of protein domains** BUDDHAPRIYA CHAKRABARTI, Lyman Laboratory of Physics, Harvard University, Cambridge MA 02138, TANNIEMOLA B. LIVERPOOL, Department of Applied Mathematics, University of Leeds, LS2 9JT, UK., ALEX J. LEVINE, Department of Chemistry, University of California at Los Angeles, Los Angeles, CA 90095 — How well does the worm-like chain force extension curve fit single-molecule protein unfolding data? Careful analysis of dynamic force spectroscopy data for different proteins[1] suggests that the compliance of a protein is generically larger than that predicted by the worm-like chain model. We propose that the observed excess compliance is due to pre-transitional conformational rearrangements within the protein domain that occur before the more dramatic failure of the domain as a whole. Using a generalization of the formalism introduced by Evans and Ritchie[2], we study protein–unfolding kinetics in our model where these internal conformational rearrangements are represented by a number of interacting Ising-type variables, which cooperatively escape over a barrier to the unfolded state. From this model, we predict a relation between the statistics of the fluctuations of the peak domain–unfolding force and the deviations of the force extension curves from the worm-like chain prediction. We suggest that, by using this approach, one can extract further details on the domain–unfolding pathway from extant force spectroscopy data.
[1] D. J. Brockwell (private communication).
[2] E. Evans, and K. Ritchie, Biophys. J., **72** 1541 (1997).

Buddhapriya Chakrabarti
Lyman Laboratory of Physics, Harvard University, Cambridge MA 02138

Date submitted: 29 Nov 2005 Electronic form version 1.4