Abstract Submitted
for the MAR08 Meeting of
The American Physical Society

Statistical features of the rough energy landscape of proteins emerging from single molecule force-clamp spectroscopy[1] JASNA BRUJIC, MAXIME CLUSEL, ERIC CORWIN, New York University — Following the complete folding trajectories of single ubiquitin molecules opens an unique window into the detailled mechanisms of protein folding. The biological importance of this problem motivated extensive studies using macroscopic biochemistry experiments and molecular dynamics simulations at the atomic scale, while little is known about the mesoscopic mechanisms of folding. To this end, our recent experiments combined with the tools of modern statistical mechanics reveal a wealth of new information. Using this single molecule approach, we have observed physical features reminiscent of glassy systems, exemplified by a power-law distribution of the rates of protein unfolding under a stretching force [1]. To further probe the signs of complexity in protein dynamics, we investigate memory effects and the influence of force on the folding trajectories, and more specifically the mechanism of formation of native interactions. The general aim of this research is to build a self-consistent picture of the free energy landscape of proteins. [1] J. Brujic *et al.*, Nature Physics, vol 2, 282 (2006).

[1]Carrier Award at the Scientific Interface from the Burroughs Wellcome Fund (J.B.)

Jasna Brujic
New York University

Date submitted: 27 Nov 2007 Electronic form version 1.4