MAR08-2007-001520

Abstract for an Invited Paper
for the MAR08 Meeting of
the American Physical Society

Rare returns on lost effort! Dynamic refolding (after unfolding) of protein domains.[1]

EVAN EVANS, Boston University

Dynamic force loading is an established technique for probing the forward kinetics in unfolding of single protein domains. Examined over several orders of magnitude in force rate, the unfolding forces often exhibit a linear dependence on the logarithm of loading rate, revealing the dynamic truncation of a precipitous activation barrier. The slope and force-rate intercept of the linear response characterize the critical molecular length gained in the barrier transition and the force-free rate of barrier passage. On the other hand, if reversed and probed with negative force rates, refolding of a stretched polypeptide chain has been found to yield a linear relation between the squares of the refolding forces and the logarithms of (reverse) force rates. Revealing here the dynamic elevation of a deep harmonic well that confines the unfolded states, the slope and force-rate intercept of the linear response characterize the effective spring constant of the harmonic well and the unstretched refolding rate. Representing a dynamical corollary to predictions of fluctuation theorems for small systems, the most-frequent amount of mechanical work recovered (from the thermal environment) in refolding increases with each decade reduction in the force-unloading rate and approaches the limit set by near-equilibrium transitions over a logarithmic span related to the free energy of transition.

[1] Acknowledgement: supported by USPHS NIH Grants HL31579 and HL65333.