

Abstract Submitted
for the MAR07 Meeting of
The American Physical Society

Dynamics of DNA bending/unbending in complex with DNA-bending protein IHF ANJUM ANSARI, PAULA VIVAS, SERGUEI KUZNETSOV, University of Illinois at Chicago — Kinetics of conformational changes in proteins and DNA that lead to precise recognition of specific DNA binding sites are difficult to observe with the limited time-resolution of stop-flow and single-molecule techniques. Here we use a ~ 10 ns laser T-jump apparatus to probe the kinetics of a ~ 35 -bp DNA substrate bound to *E. coli* Integration Host Factor (IHF) and end-labeled with a FRET pair. These T-jump measurements, in combination with stop-flow, provide the first direct observation of the DNA bending/unbending kinetics in a protein-DNA complex (Sugimura and Crothers, PNAS, in press; Kuznetsov et al., PNAS, in press). The rates and activation energy of DNA bending are similar to that of a single A:T base pair opening inside uncomplexed DNA, suggesting that spontaneous thermal disruption in base-pairing nucleated at an A:T site may be sufficient to overcome the free energy barrier needed to partially bend/kink DNA. An unusual salt dependence of the binding affinity observed previously for IHF/DNA complex, and explained in terms of DNA binding coupled with disruption of a network of salt bridges within the protein (Holbrook et al., 2001, JMB, **310**, 379), is reflected in the salt dependence of the observed bending rates. These results suggest that salt-dependent protein conformational changes may be playing a role in the DNA bending process.

Anjum Ansari
University of Illinois at Chicago

Date submitted: 01 Dec 2006

Electronic form version 1.4