1020-92-110 **Stephen D Levene*** (sdlevene@utdallas.edu), Institute of Biomed. Sci. and Technology, University of Texas at Dallas, PO Box 830688, Richardson, TX 75083, **Abbye E McEwen**, Institute of Biomed. Sci. and Technology, University of Texas at Dallas, PO Box 830688, Richardson, TX 75083, and **Yongli Zhang**, Physical Biosciences Division, Lawrence Berkeley National Laboratory, University of California, Berkeley, CA 94720. *Understanding Gene-regulatory Mechanisms in vivo: Lessons from the Mechanics of Protein-DNA Complexes.*

The repression of genes mediated by *E. coli lac* repressor (LacR) is a major paradigm for bacterial gene regulation. In its normal gene-regulatory context, LacR interacts simultaneously with two cognate DNA sequences, called operators, along a single DNA molecule to form a DNA loop. Based on our statistical-mechanical theory for DNA looping (Zhang *et al. Biophys J* **90**, 1903-1912 (2006)), we have developed a model for LacR-mediated gene repression that integrates operator-LacR affinity, spacing between operator sequences, and DNA flexibility. Gene repression calculated as a function of operator spacing gives excellent agreement with independent sets of *in-vivo* data and shows that loop-mediated repression in wild-type *E. coli* strains is facilitated by decreased DNA rigidity and high levels of flexibility in the LacR tetramer. Repression data for strains lacking the architectural DNA-binding protein HU gave a near-normal value of the DNA persistence length. Our findings underscore the importance of both protein conformation and elasticity in the formation of small DNA loops widely observed *in vivo*, and demonstrate the utility of analyzing gene regulation based on the mechanics of nucleoprotein complexes. (Received August 21, 2006)