1041-92-220 **Graham L. Randall**, **Jonathan M. Fogg**, **Daniel J. Catanese**, **B. Montgomery Pettitt** and **Lynn Zechiedrich*** (elz@bcm.edu), Molecular Virology & Microbiology, Baylor College of Medicine, Houston, TX 77025. *Elastic polymer models for DNA: where they work and where they fail.*

The predominant protein-centric perspective in protein-DNA binding studies assumes that the protein drives the interaction and DNA is left the passive polymer to be manipulated. Our computational and biochemical studies of supercoiling, knotting, and linking of DNA reveal that DNA is not just a passive participant and explain well data from single molecule manipulations of DNA. DNA curvature and underwinding drive sequence-dependent kinking, base flipping, and denaturing that relax the rest of the molecule to B-form. Such bimodal behavior with DNA underwinding does not follow elastic rod models in which the underwinding would be evenly distributed over the length of the DNA helix. In stark contrast, DNA that is overwound behaves as an elastic chain until extreme overwinding, which forms Pauling-like (P-DNA). Therefore, relative to the acrobatics of DNA, proteins are relatively passive in comparison. The extraordinary deformations of the B-form structure arise from the massive amounts of energy– structural energy in the form of supercoiling and electrostatic energy arising from its -2 charge per base pair– that are innate to DNA, and can be harnessed to influence sequence-specific protein-DNA interactions. (Received August 11, 2008)