## Abstract Submitted for the MAR16 Meeting of The American Physical Society

Quantifying the DNA binding characteristics of ruthenium based threading intercalator  $\Lambda$   $\Lambda$ -P with optical tweezers NICHOLAS BRYDEN, Bridgewater State University, MA, MICAH MCCAULEY, Northeastern University, MA, FREDRIK WESTERLUND, PER LINCOLN, Chalmers University of Technology, Sweden, IOULIA ROUZINA, Ohio State University, OH, MARK WILLIAMS, Northeastern University, MA, THAYAPARAN PARAMANATHAN, Bridgewater State University, MA — Utilizing optical tweezers, biophysics researchers have been able to study drug-DNA interactions on the single molecule level. Binuclear ruthenium complexes are a particular type of drug molecule that have been found to have potential cancer-fighting qualities, due to their high binding affinity and low dissociation rates. These complexes are threading intercalators, meaning that they must thread their bulky side chains through DNA base pairs to allow the central planar moiety to intercalate between the bases. In this study, we explored the binding properties of the binuclear ruthenium complex,  $\Lambda\Lambda$ -P ( $\Lambda\Lambda$ -[-bidppz(phen)<sub>4</sub>Ru<sub>2</sub>]<sup>4+</sup>). A single DNA molecule is held at a constant force and the  $\Lambda\Lambda$ -P solution introduced to the system in varying concentrations until equilibrium is reached. DNA extension data at various concentrations of  $\Lambda\Lambda$ -P recorded as a function of time provide the DNA binding kinetics and equilibrium binding affinity. Preliminary data analysis suggests that  $\Lambda\Lambda$ -P exhibits fast binding kinetics compared to the very similar  $\Delta\Delta$ -P. These complexes have the same chemical structure and only differ in their chirality, which suggests that the left handed  $(\Lambda\Lambda)$  threading moieties require less DNA structural distortion for threading compared with the right handed  $(\Delta\Delta)$ threading moieties.

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