Abstract Submitted
for the MAR09 Meeting of
The American Physical Society

Modeling the behavior of DNA-loop-extruding enzymes ELNAZ A. BAUM-SNOW, JOHN F. MARKO, Northwestern University — Condensin proteins are large complexes belonging to a family of ATP hydrolyzing proteins known as SMC (Structural Maintenance of Chromosomes). Condensins are believed to play a vital role in chromosomal assembly and segregation in eukaryotic cells but the details of their function along chromatin are poorly understood. Here, we propose a model to describe the behavior of DNA-loop-inducing proteins, such as type I restriction enzymes, which we believe can be used to understand condensin's function. We assume an effective motor behavior for these enzymes in which the bias of the two dimer heads is to travel away from each other, which results in loop formation along the DNA lattice. Processivity causes the enzymes to stack on top of each other. We further discuss the results of theory and computer simulations for different values of motor bias and processivity.

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Date submitted: 15 Dec 2008

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