Abstract Submitted
for the MAR09 Meeting of
The American Physical Society

Interaction of Defensins with Model Cell Membranes LORI K. SANDERS, Dept. of Materials Science and Engineering, UIUC, NATHAN W. SCHMIDT, Dept. of Physics, UIUC, LIHUA YANG, ABHIJIT MISHRA, Dept. of Materials Science and Engineering, UIUC, VERNITA D. GORDON, Dept.of Materials Science and Engineering, UIUC, MICHAEL E. SELSTED, Dept. of Pathology and Laboratory Medicine, UCI, GERARD C. L. WONG, Dept. of Materials Science and Engineering, UIUC — Antimicrobial peptides (AMPs) comprise a key component of innate immunity for a wide range of multicellular organisms. For many AMPs, activity comes from their ability to selectively disrupt and lyse bacterial cell membranes. There are a number of proposed models for this action, but the detailed molecular mechanism of selective membrane permeation remains unclear. Theta defensins are circularized peptides with a high degree of selectivity. We investigate the interaction of model bacterial and eukaryotic cell membranes with theta defensins RTD-1, BTD-7, and compare them to protegrin PG-1, a prototypical AMP, using synchrotron small angle x-ray scattering (SAXS). The relationship between membrane composition and peptide induced changes in membrane curvature and topology is examined. By comparing the membrane phase behavior induced by these different peptides we will discuss the importance of amino acid composition and placement on membrane rearrangement.

Nathan W. Schmidt
Dept. of Physics, UIUC

Date submitted: 21 Nov 2008 Electronic form version 1.4