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An amino acid composition criterion for membrane active antimicrobials NATHAN SCHMIDT, GHEE HWEE LAI, Physics, UIUC, ABHIJIT MISHRA, Bioengineering, UCLA, DENNIS BONG, Chemistry, Ohio State U, PAUL MCCRAY, JR., Pediatrics, U. Iowa, MICHAEL SELSTED, ANDRE OUELLETTE, Pathology, USC, GERARD WONG, Bioengineering, UCLA — Membrane active antimicrobials (AMPs) are short amphipathic peptides with broad spectrum anti microbial activity. While it is believed that their hydrophobic and cationic moieties are responsible for membrane-based mechanisms of action, membrane disruption by AMPs is manifested in a diversity of outcomes, such as pore formation, blebbing, and budding. This complication, along with others, have made a detailed, molecular understanding of AMPs difficult. We use synchrotron small angle xray scattering to investigate the interaction of model bacterial and eukaryotic cell membranes with archetypes from beta-sheet AMPs (e.g. defensins) and alpha-helical AMPs (e.g. magainins). The relationship between membrane composition and peptide induced changes in membrane curvature and topology is examined. By comparing the membrane rearrangement and phase behavior induced by these different peptides we will discuss the importance of amino acid composition on AMP design.

Nathan Schmidt
Physics, UIUC

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