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Relationship between peptide amino acid sequence and membrane curvature generation NATHAN SCHMIDT, DAVID KUO, GHEE HWEE LAI, ABHIJIT MISHRA, GERARD WONG, Bioengineering Dept, UCLA — Amphipathic peptides and amphipathic domains in proteins can perturb and restructure biological membranes. For example, it is believed that the cationic, amphipathic motif found in membrane active antimicrobial peptides (AMPs) is responsible for their membrane disruption mechanisms of action. And ApoA-I, the main apolipoprotein in high density lipoprotein contains a series of amphipathic α -helical repeats which are responsible for its lipid associating properties. We use small angle x-ray scattering (SAXS) to investigate the interaction of model cell membranes with prototypical AMPs and consensus peptides derived from the helical structural motif of ApoA-I. The relationship between peptide sequence and the peptide-induced changes in membrane curvature and topology is examined. By comparing the membrane rearrangement and corresponding phase behavior induced by these two distinct classes of membrane restructuring peptides we will discuss the role of amino acid sequence on membrane curvature generation.

Nathan Schmidt
Bioengineering Dept, UCLA

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