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Effect of negative curvature on the interaction of amphipathic α-helix model protein with an oil/buffer interface MONA MIRHEYDARI, ELIZABETH K. MANN, Department of Physics, Kent State University, EDGAR E. KOOIJMAN, Department of Biological Sciences, Kent State University — Lipid droplets, are dynamic cell organelles that play roles in biological processes. The biophysics of lipid droplets are studied with a model system consisting of a triolein drop formed in a physiologically-relevant buffer and covered with phospholipid monolayer. Interfacial tension is used to characterize the droplet surface after addition of the protein to the buffer. ApoLp-III serves as a model protein for the amphipathic α-helix bundle domain in proteins associated with lipid droplets. Previous work use POPC to form the phospholipid monolayer surrounding the oil droplet. Here, we used POPC, and mixtures of POPC and other lipids to study the effect of effective molecular shape, headgroup charge and size in protein binding to the oil/buffer interface. Our data shows that the affinity of the protein binding to the interface increases for monolayer made up of POPC lipid mixed with negatively charged lipids. We compared the results for native and folded apoLp-III (which contains a disulfide bond) to explore the role of unfolding on the protein affinity with a POPC monolayer. Experiments are done using our home-build droplet tensiometer in a temperature controlled room.

Mona Mirheydari
Department of Physics, Kent State University

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