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Monitoring the uniformity of alpha helices in lipophilic environments[1] ANAHITA ZARE, JIAN XIONG, JASON COOLEY, RENEE JIJI, University of Missouri — It is known that membrane-embedded alpha helices are more uniform structurally than their aqueous counterparts. Despite this uniformity, protein dynamics are thought to be common in these proteins in order for them to conduct their cellular tasks. However, how amino acid sequence facilitates these dynamics remains unknown as methods for investigating structural heterogeneity in transmembrane proteins are limited. Circular dichroism (CD) is often used to characterize the secondary structure of the protein, but its sensitivity to specific non-helical structural configurations is low. Deep-ultraviolet resonance Raman spectroscopy (DUVRR) is a structurally sensitive spectroscopy technique emerging for analyzing membrane protein structures. A set of *de novo* designed peptides have been constructed that contain varying contents of helix breaking residues (HBR) in order to test their role helical instability in lipophilic environments. The secondary structure of each peptide was monitored through the measured by DUVRR spectroscopy, where changes in the Amide III and S modes indicate that HBRs actually cause the "unwinding" or the helix when solubilized in detergent environments. This observation has implications towards the role of water presentation in membrane protein dynamics.

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