DEEP-UV RESONANCE RAMAN SPECTROSCOPY OF MEMBRANE PROTEINS

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ABSTRACT

Despite the various protein structure determination methods in use, a need still exists for adequate resolution of membrane protein structure while remaining rapid and inexpensive. Deep-UV resonance Raman (DUVRR) spectroscopy addresses this need and also offers a high sensitivity to the protein backbone such that membrane proteins require no further modification from their native state in the lipid bilayer. DUVRR spectroscopy is a mature technique for secondary structure determination of aqueous proteins but had not been seriously explored as a means of structure determination for membrane proteins. Early progress in characterizing the secondary structure of the lipid-solvated cytochrome $bc_1$ complex led to exploring other membrane proteins mostly based on the $\alpha$-helix motif. DUVRR is not limited to proper membrane proteins, but also interrogates lipophilic protein-like structures such as the depsipeptide valinomycin. We find DUVRR spectroscopy characterizes membrane protein structure as well as aqueous protein structure. Additionally, it can describe the degree to which the protein backbone is embedded into the membrane. This largely is explained by the absence of hydrogen bonding from water to the amide backbone and its effect on the carbonyl stretching mode in DUVRR spectra. These findings are promising and indicate a need for further investigation of the variety of secondary structures formed in the lipid bilayer.