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Polyglycine in Solution, Random or Ordered? SERGEI BYKOV, SANFORD ASHER, University of Pittsburgh — According to the existing theories during folding, the protein backbone undergoes a transition from unordered (random coil) to ordered (native) conformations. Understanding the nature of the unordered state is one of the key problems in protein folding. Some recent investigations indicate that unfolded peptides and proteins in solution form structures close to PPII helices. Glycine based peptides possess greater conformational freedom due to the lack of the side chains. This high flexibility makes polyglycine an important model system for investigating of the conformational preferences of the polypeptides backbone in solution in general and for understanding the nature of the unfolded states in particular. We utilized UV Resonance and Visible Raman spectroscopy to investigate conformational preferences of glycine based peptides of different lengths in water solution at different conditions. We will discuss conformational preferences of the glycine based peptides in solution, and define the major factors which govern these conformational preferences.

Prefer Oral Session
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Sergei Bykov
bykov@pitt.edu

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