Abstract Submitted
for the MAR09 Meeting of
The American Physical Society

Hydrodynamic and Conformational Properties of Unfolded Proteins GUY BERRY, Carnegie Mellon University — Published data on the characterization of unfolded proteins in dilute solutions in aqueous guanidine hydrochloride are analyzed to show that the data are not fit by either the random-flight or wormlike chain models for linear chains. The analysis includes data on the intrinsic viscosity, root-mean-square radius of gyration, from small-angle x-ray scattering, and hydrodynamic radius, from the translational diffusion coefficient. It is concluded that residual structure consistent with that deduced from nuclear magnetic resonance on these solutions can explain the dilute solution results in a consistent manner through the presence of ring-structures, which otherwise have an essentially flexible coil conformation. The ring-structures could be in a state of continual flux and rearrangement. Calculation of the radius of gyration for the random-flight model gives a similar reduction of this measure for chains joined at their endpoints, or those containing loop with two dangling ends, each one-fourth the total length of the chain. This relative insensitivity to the details of the ring-structure is taken to support the behavior observed across a range of proteins.

Guy Berry
Carnegie Mellon University

Date submitted: 21 Nov 2008 Electronic form version 1.4