

Time-resolving biomolecular motions on length scales from single Å to Rg

L Pollack¹

¹*Cornell University, Ithaca, NY*
lp26@cornell.edu

In this talk I will describe new technologies and new analysis methods that can dramatically enhance our understanding of how biological macromolecules fold and function. Solution scattering, in time-resolved modes, can detect conformational changes on length scales of ~ 10 's of Å. When coupled with methods that embrace the ensemble nature of the time-dependent populations, time-resolved SAXS provides powerful new insight into the rearrangement of backbones of nucleic acids. In conjunction with contrast variation methods, SAXS provides a different perspective on the assembly of protein-nucleic acid complexes. Finally, time-resolved crystallography can now be performed with millisecond resolution, allowing us to follow the Å scale structures of enzymes as they process their substrates.