Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Mapping the temperature-dependent conformational landscapes of the dynamic enzymes cyclophilin A and urease[1] ROBERT THORNE, Cornell University, DANIEL KEEDY, University of California, San Francisco, MATTHEW WARKENTIN, Cornell University, JAMES FRASER, University of California, San Francisco, DAVID MOREAU, HAKAN ATAKISI, PETER RAU, Cornell University — Proteins populate complex, temperature-dependent ensembles of conformations that enable their function. Yet in X-ray crystallographic studies, roughly 98% of structures have been determined at 100 K, and most refined to only a single conformation. A combination of experimental methods enabled by studies of ice formation and computational methods for mining low-density features in electron density maps have been applied to determine the evolution of the conformational landscapes of the enzymes cyclophilin A and urease between 300 K and 100 K. Minority conformations of most side chains depopulate on cooling from 300 to ∼200 K, below which subsequent conformational evolution is quenched. The characteristic temperatures for this depopulation are highly heterogeneous throughout each enzyme. The temperature-dependent ensemble of the active site flap in urease has also been mapped. These all-atom, site-resolved measurements and analyses rule out one interpretation of the protein-solvent glass transition, and give an alternative interpretation of a dynamical transition identified in site-averaged experiments. They demonstrate a powerful approach to structural characterization of the dynamic underpinnings of protein function.

[1]Supported by NSF MCB-1330685

Robert Thorne
Cornell University

Date submitted: 06 Nov 2015 Electronic form version 1.4