Abstract Submitted
for the MAR14 Meeting of
The American Physical Society

Using engineered intra-molecular disulfide bonds to identify FIMs that matter WOUTER HOFF, MASATO KUMAUCHI, Oklahoma State University, EEFEI CHEN, University of California Santa Cruz — The realization that proteins are not the static structures derived from crystallographic structure determination, but instead undergo conformational dynamics on a wide range of length- and time-scales started a novel field of research that has remained active to the present day. Protein dynamics have been shown to occur on a complex energy landscape, and can be divided into equilibrium fluctuations (EFs) and non-equilibrium functionally important motions (FIMs). Much effort has been spent on the complex task of discovering and describing such FIMs. However, if a region of a protein is found to undergo conformational changes during function, this is not sufficient to conclude that this motion is important for protein function. We use engineered intra-molecular disulfide bonds as an experimental tool to examine functionally critical conformational changes. In this approach the effect of preventing large-scale motions in a specific region of the protein by the introduction of an intramolecular covalent crosslink on protein functional dynamics is examined. We will report results of the application of this approach to photoactive yellow protein, a bacterial photosensor.

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Date submitted: 17 Nov 2013 Electronic form version 1.4