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Probing Single-Molecule Protein Conformational Folding-Unfolding Dynamics: The multiple-State and Multiple-Channel Energy Landscape H. PETER LU, ZHIJIANG WANG, YUFAN HE, Bowling Green State University — The folding-unfolding dynamics of protein provides an important understanding of the protein conformational dynamics and functions. We have used single-molecule fluorescence resonance energy transfer combined with statistical data analysis to characterize enzyme and signaling protein fundamental conformational dynamics of Calmodulin (CaM) and kinase (6-Hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK). The concentration dependence of FRET efficiency of GdmCl indicates the unfolding conformational transition of the proteins. At 2M of denaturant solvent, the majority of the HPPK and CaM protein molecules are under fluctuating folding-unfolding conformational changes, spending about half time in their native state and half time in their unfolded state. We obtained the fluctuation rates from the autocorrelation function analyses of the protein conformational fluctuation trajectories, and we have identified multiple intermediate states involving in bunched time dynamics and the related energy landscape. We had also analyzed the protein folding-unfolding pathways using detailed balance theoretical model analysis in order to understand the complex multiple-state and multiple-channel protein dynamics.

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