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The Glassy State of Crambin and the THz Time Scale Fluctuations Related to Protein Function KRISTINA WOODS, BEDIHA BESER, Carnegie Mellon University — THz experiments have been used to characterize the picosecond time scale fluctuations taking place in the model protein crambin. Using both hydration and temperature as an experimental parameter, we have successfully identified the collective fluctuations ( $\leq 200 \text{ cm}^{-1}$ ) in the protein (Figure 1). Observation of the transition of the protein dynamics in the THz spectrum from both below and above the glass transition temperature ( $T_g$ ) provides unique insight into microscopic interactions and modes that allow the solvent to couple with the protein dynamics (Figure 2). Our findings suggest that the solvent dynamics on the picosecond time scale not only contribute to the flexibility of the protein but also provides a dynamical parameter that allows the protein to modulate local regions of its structure that are distinct from the protein whole. These distinct dynamical regions of the protein may be important for energy transport and hence, linked with protein function.

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