

Abstract Submitted
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Protein Dynamics Studied by Quasi-elastic Neutron Scattering¹

XIANG-QIANG (ROSIE) CHU, EUGENE MAMONTOV, Oak Ridge National Lab, MARCO LAGI, SOW-HSIN CHEN, MIT, MANAVALAN GAJAPATHY, JOSEPH NG, University of Alabama in Huntsville, KEVIN WEISS, LEIGHTON COATES, Oak Ridge National Lab, EMILIANO FRATINI, PIERO BAGLIONI, University of Florence — The biological function and activities of proteins are intimately related to their structures and dynamics. Nowadays, neutron scattering is one of the most powerful tools to study the protein dynamics. In this study, we use quasielastic neutron scattering (QENS) at the Spallation Neutron Source, ORNL, to study relaxational dynamics of two structurally different proteins — hen egg white lysozyme and an inorganic pyrophosphatase from a hyperthermophile, in the time range of 10ps to 1ns. We experimentally prove that the slow dynamics of globular proteins can be described by the mode-coupling theory (MCT) that was originally developed for glass-forming molecular liquids. The MCT predicts the appearance of a logarithmic decay for a glass-forming liquid. Such dynamic behavior is also observed by recent molecular dynamics (MD) simulations on protein molecules. In addition, we compare the temperature dependence of the dynamics of the two proteins with completely different activity profiles. Our results greatly help understanding the relation between protein dynamics and their biological functions.

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Xiang-qiang Chu
Oak Ridge National Lab

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