ULTRAFAST SOLVATION DYNAMICS OF HUMAN SERUM ALBUMIN: CORRELATION WITH CONFORMATIONAL TRANSITIONS AND SITE-SELECTED RECOGNITION

WEIHONG QIU, LUYUAN ZHANG, OGHAGHARE OKOBIAH, YI YANG, LIJUAN WANG, DONGPING ZHONG, *Departments of Physics, Chemistry, and Biochemistry, Programs of Biophysics, Chemical Physics, and Biochemistry, The Ohio State University, Columbus, OH 43210*; AHMED H. ZEWAIL, *Laboratory of Molecular Science, Noyes Laboratory of Chemical Physics, California Institute of Technology, Pasadena, CA 91125 (Email to D.Z.: dongping@mps.ohio-state.edu).*

Human serum albumin (HSA), the most abundant protein in blood plasma, transports numerous ligands in the circulation and undergoes reversible conformational transitions over wide pH values. We report here our systematic studies of solvation dynamics and local rigidity in these conformers using the single intrinsic tryptophan residue as a local molecular probe with femtosecond resolution. Under physiological pH of 7.0, we observed the decay of solvation correlation function of 100 ps and a large wobbling motion of the tryptophan probe within the deeply buried binding site, revealing the softness of the binding pocket and conformational plasticity of native HSA. At acidic pH, the albumin molecule transforms to an extended conformation with a large charge distribution at the surface, and we observed a similar temporal profile of solvation correlation function. However, the solvation dynamics at the basic pH conditions are significantly faster (25-45 ps) as the protein opens the originally buried crevice while tightens its global structure. These changes in the solvation dynamics are well correlated with the conformational transitions and related to the structural integrity of the protein.