

Abstract Submitted
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Some Recent Developments in Structure and Glassy Behavior of Proteins¹

CHIN-KUN HU, Institute of Physics of Academia Sinica, Taipei, Taiwan — We have used ARVO developed by us to find that the ratio of volume and surface area of proteins in Protein Data Bank distributed in a very narrow region [1]. Such result is useful for the determination of protein 3D structures. It has been widely known that a spin glass model can be used to understand the slow relaxation behavior of a glass at low temperatures [2]. We have used molecular dynamics and simple models of polymer chains to study relaxation and aggregation of proteins under various conditions and found that polymer chains with neighboring monomers connected by rigid bonds can relax very slowly and show glassy behavior [3]. We have also found that native collagen fibrils show glassy behavior at room temperatures [4]. The results of [3] and [4] about the glassy behavior of polymers or proteins are useful for understanding the mechanism for a biological system to maintain in a non-equilibrium state, including the ancient seed [5], which can maintain in a non-equilibrium state for a very long time. (1) M.-C. Wu, M. S. Li, W.-J. Ma, M. Kouza, and C.-K. Hu, EPL, in press (2011); (2) C. Dasgupta, S.-K. Ma, and C.-K. Hu. Phys. Rev. B 20, 3837-3849 (1979); (3) W.-J. Ma and C.-K. Hu, J. Phys. Soc. Japan 79, 024005, 024006, 054001, and 104002 (2010), C.-K. Hu and W.-J. Ma, Prog. Theor. Phys. Supp. 184, 369 (2010); S. G. Gevorgian, A. E. Allahverdyan, D. S. Gevorgyan and C.-K. Hu, EPL 95, 23001 (2011); S. Sallon, et al. Science 320, 1464 (2008).

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