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More than one dynamic crossover in protein hydration water<sup>1</sup> GIANCARLO FRANZESE, Universitat de Barcelona, Spain, MARCO G. MAZZA, TU Berlin, Germany, KEVIN STOKELY, Center for Polymer Studies, Boston University, MA, SARA PAGNOTTA, Centro de Fisica de Materiales, Donostia-San Sebastian, Spain, FABIO BRUNI, Università di Roma Tre, Italy, H. EUGENE STANLEY, Center for Polymer Studies, Boston University, MA — We study by theory, simulations and experiments, the dynamics of the hydrogen bond (HB) network of a percolating layer of water hydrating lysozyme powder. Using dielectric spectroscopy we measure the temperature dependence of the relaxation time of proton charge fluctuations. These fluctuations are associated with the dynamics of the HB network of water molecules adsorbed on the protein surface. Using Monte Carlo simulations and mean-field calculations, we study the dynamics and thermodynamics of a coarse-grained model that successfully reproduces the properties of hydration water. Both experimental and model analyses are consistent with the interesting possibility of two dynamic crossovers, (i) at  $\approx 252$  K, and (ii) at  $\approx 181$ K. Because the experiments agree with the model, we can relate the two crossovers to the presence at ambient pressure of two specific heat maxima. The first is caused by fluctuations in the HB formation, and the second, at a lower temperature, is due to the reordering of the HB network.

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