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Scale Invariant Fluctuations of Proteins Native States[1] QIAN-YUAN TANG, YANG-YANG ZHANG, JUN WANG, WEI WANG, Collaborative Innovation Center of Advanced Microstructures, National Laboratory of Solid State Microstructure, Nanjing University, China, DANTE R CHIALVO, Consejo Nacional de Investigaciones Científicas y Tecnológicas (CONICET), Argentina — Long-range correlations in biological systems often hints for the presence of universal mechanism at work. Here we study protein native dynamics by analyzing a large set of structure ensembles determined by solution NMR. For proteins of diverse sizes, the average distance-dependent cross-correlation functions $\phi(r)$ and its correlation length ξ_ϕ are analyzed. The analysis uncovered the presence of nontrivial scaling in the proteins' equilibrium dynamics around native states. We show that the correlation length is proportional to the gyration radius of the molecule, implying that the motion of any residue could influence all the others, up to the entire molecule. In addition, it is found that certain shapes are favored, such that for any given protein size the folding process "chooses" the shape with the maximum susceptibility. These results suggest that the proteins native state is critical in the same sense with other slowly built self-organized critical systems, which once posed near the minimum of the energy landscape, preserve their dynamic flexibility.

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