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The University of Chicago, USA

The topographies of energy landscapes of real proteins

Exploration of the energy landscapes of two relatively small proteins, protein G and srcSH3 and of two random peptides containing the same amino acids reveals the kind of topography that can be expected for real proteins, the topographies that proteins must traverse as they fold to their native states. The most significant characteristic of those landscapes is probably the multiplicity of funnels that they display; the simple single "folding funnel" model is quite unlike the energy landscapes of these real proteins. The folding processes that bring these proteins to their native state follow varieties of trajectories, some of which avoid the "wrong" funnels while others visit those misfolded structures and then leave them and go to the funnel of the native state. A network analysis reveals some of what seem to be common characteristics of the folding process.

Biography

R Stephen Berry has completed his Undergraduate and Graduate studies at Harvard. He was a Member of the Chemistry Faculty at The University of Michigan then at Yale and from 1964 at The University of Chicago. His research has covered a wide range within physical chemistry, from protein dynamics to atomic scattering and photo-ionization, to atomic and molecular clusters and to finite-time thermodynamics.

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