

# Dynamical Self-organization in Protein Folding

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We propose that protein folding is due to a self-organization process, that can be described in terms of solitons, the paradigm self-organizers in numerous physical scenarios. We present a simple Hamiltonian energy function that supports solitons, and show how these solitons can be utilized to describe protein collapse. As an example, we consider two proteins, the myoglobin and a mainly-beta-stranded protein with PDB code 3LL1 and show how in both cases the process of collapse can be modeled, with sub-atomic precision, in terms of explicit soliton profiles.