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How does a protein fold? The effects of structure and many body interactions STEVEN PLOTKIN, University of British Columbia — A theory for how a protein folds up to a biologically functional structure has occupied researchers for the last few decades. The difficulties stem from an incomplete knowledge of an accurate Hamiltonian, as well as non-trivial aspects of polymer physics that complicate the kinetics of folding. Here I will describe some recent results showing that relaxation rates increase significantly as the folding mechanism becomes increasingly heterogeneous. I will go on to discuss the role of many-body interactions in the Hamiltonian, and show how accounting for them is essential for predicting folding rates and mechanisms.

Steven Plotkin
University of British Columbia

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