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Networks in Protein Folding ERZSÉBET RAVASZ REGAN, Beth Israel Deaconess Medical Center, Harvard Medical School, ZOLTÁN TOROCZKAI, University of Notre Dame, Physics Department, G. GNANAKARAN, Los Alamos National Laboratory, T-10 — We take a networks approach to protein folding by identifying different protein conformations with nodes, while an elementary step of the system (rotation around a bond) that takes one configuration to another is defined as a link. The energies of configurations are scalar quantities associated with each node. Using this approach we can show that the scale-free nature of the observed protein conformation networks can be explained by simple results obtained on gradient networks.

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