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Protein folding in a force-clamp MAREK CIEPLAK, Polish Academy of Sciences, PIOTR SZYMCZAK, Warsaw University — Kinetics of folding of a protein held in a force-clamp are compared to an unconstrained folding. The comparison is made within a simple topology-based dynamical model of ubiquitin. We demonstrate that the experimentally observed rapid changes in the end-to-end distance mirror microscopic events during folding. However, the folding scenarios in and out of the force-clamp are distinct.

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