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.