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Protein folding microenvironments within the cytoplasm of living cells MINGHAO GUO, APRATIM DHAR, MARTIN GRUEBELE, University of Illinois at Urbana-Champaign — The protein folding kinetics in a living cell strongly depends on the local environment. Viscosity of cytoplasm and crowding by macromolecules modulate stability, folding rates and folding mechanism in the folding progresses. We use Fast Relaxation Imaging (FReI) to map out the stability and folding kinetics of a FRET-labeled phosphoglycerate kinase (PGK) in the cytoplasm of individual eukaryotic cells with 500 nm spatial resolution. It shows that this modulation results in large variation of folding mechanism compared to in vitro experiment. We have developed the folding-diffusion model of protein folding in cell with hetergenous microenvironment, which includes spatial hetergenous of folding rates of the multiple-state folding of PGK and diffusion between pixels. It is shown that diffusion contributes little to the large variation of folding kinetics, which can only result from the change of folding mechanism due to microenvironment.

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