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Multiple probes of heterogeneous protein kinetics

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Transition state theories break down for very fast folding proteins, where substantial populations exist along the reaction coordinate on a nanosecond to microsecond timescale. For such proteins, different spectroscopic probes yield different dynamics, i.e. there is no well-defined rate coefficient or set of rate coefficients. I will discuss fast relaxation experiments for several such proteins, as well as modeling by Langevin dynamics and molecular dynamics simulations, which now connect with experiment on the 0.1-10 microsecond time scale.