The Unfolding Action of GroEL on a Protein Substrate

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Conformational transitions are crucial for the functioning of many proteins. To simulate these processes in timescales accessible to atomistic molecular dynamics, biasing techniques need to be used that guide the trajectory towards the desired state. We will discuss the application of biasing molecular dynamics to the GroEL chaperone, a protein that helps other proteins fold. Simulations of the opening transition of GroEL with a bound denatured protein substrate showed the presence of a stretching force, which led to the increased unfolding of the substrate. The origins of the stretching force, and the implications of the results for mutation experiments and the action of GroEL will be discussed.