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Protein Unfolding Energy Determined by Jarzynski's Equality
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— The dynamic response of single protein molecules to mechanical forces and the relation of dynamics to equilibrium properties of biomolecules has been a subject of intense recent study. Characterization of the fluctuations in these small systems plays an important role in successful application of Jarzynski's equality to determine equilibrium free energies from nonequilibrium measurements. Here we used the atomic force microscope to manipulate single titin I27 molecules to unfold the protein, and we have applied Jarzynski's equality to calculate the free energy landscape for stretching this heart muscle protein.

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