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A two-parameter extension of classical nucleation theory

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Abstract-

A two-variable stochastic model for diffusion-limited nucleation is developed using a formalism derived from fluctuating hydrodynamics. The model is a direct generalization of the standard classical nucleation theory (CNT). The nucleation rate and pathway are calculated in the weak-noise approximation and are shown to be in good agreement with direct numerical simulations for the weak-solution/strong-solution transition in globular proteins. We find that CNT underestimates the time needed for the formation of a critical cluster by two orders of magnitude and that this discrepancy is due to the more complex dynamics of the two variable model and not, as often is assumed, a result of errors in the estimation of the free energy barrier.

Index Terms- nucleation, classical nucleation theory, proteins, Fokker–Planck equation

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