## Classical nucleation theory from a dynamical approach to nucleation

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## Abstract-

shown that diffusion-limited classical nucleation theory (CNT) can be recovered as simple limit of the recently proposed dynamical theory of nucleation based on fluctuating hydrodynamics [J. F. Lutsko, J. Chem. Phys. 136, 034509 (2012)] https://doi.org/10.1063/1.3677191.. The same framework is also used to construct a more realistic theory in which clusters have finite interfacial width. When applied to the dilute solution/dense solution transition in globular proteins, it is found that the extension gives corrections to the nucleation rate even for the case of small supersaturations due to changes the monomer distribution function and to the excess free energy. It also found is the monomer attachment/detachment picture breaks down at high supersaturations corresponding to clusters smaller than about 100 molecules. The results also confirm the usual assumption that most important corrections to CNT can be achieved by means of improved estimates of the free energy barrier. The theory also illustrates two topics that have received considerable attention in the recent literature on nucleation: the importance sub-dominant corrections to the capillary model for the free energy and of the correct choice of the reaction coordinate.

## **Index Terms-**

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