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Crowding Effects on the Thermodynamics of Apoflavodoxin Folding. DIRAR AL HOMOUZ, Univ of Houston — The thermodynamics of folding in Apoflavodoxin protein are studied using coarse-grained molecular dynamics simulations as a function of volume fraction of crowding agents. The stability of the folded state is enhanced in the presence of crowding agents as can be seen from the free energy diagrams. The changes in the transition state ensemble are analyzed under different crowding conditions.

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