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Exact analytical solution in the Extended Zwanzig Model (EZM) for linear protein denaturation LUIS OLIVARES-QUIROZ, Universidad Autonoma de la Ciudad de Mexico — The elucidation of the physical mechanisms underlying protein's folding and unfolding in a variety of physico-chemical conditions is one of the most challenging problems faced by molecular biology and biophysics. The *Extended Zwanzig Model* (EZM) is a formalism that relates protein denaturation profiles with the energy spectrum $\{E_k\}$ accessible to the system. In this work, an exact analytical solution for the EZM in the case of a protein following a linear denaturation profile as function of a reactive coordinate \mathcal{C} is presented. The relevance for this solution is two fold. Given the complex functional form followed by the energy spectrum $\{E_k\}$ in terms of the reactive coordinates, there is a lack of analytical solutions for the MEZ even in the most simplest cases. On the other hand, it is known that most proteins exhibit a sigmoidal denaturation pattern in terms of physical variables like temperature, pressure or concentration of chemical compounds. It is shown here that the sigmoidal denaturation profile can be approximated by a sum of linear terms and therefore, an approximate solution for the general denaturation profile can be generated from a superposition of exact linear cases.

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