

Proteins under Pressure

Angel E. Garcia, Center for NonLinear Studies (CNLS), Los Alamos National Laboratory, Los Alamos, NM 87545.

Proteins are heteropolymers that self-assemble into a compact ordered structure known as the folded state. Although the folded state is a compact state, proteins will unfold under high hydrostatic pressure. This effect seems contradictory, given that high pressures should drive the system toward lower volume states. However, pressure denaturation can be easily explained in terms of the pressure effects of hydrophobic interactions (i.e., how non polar molecules interact with water). We use molecular simulations to model pressure folding/unfolding equilibrium of small peptides that form alpha helices, beta sheets, and a model protein (the trp-cage mini protein). These calculations show a rich P-T stability diagram in which a protein can unfold at high pressures, or can unfold upon cooling (cold denature) at elevated pressures. I will describe the role of the interactions of water with proteins in describing these effects. The simulation results in small, model proteins will be used to interpret experimental data in larger, complex protein systems.