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Towards a Model of Cold Denaturation of Proteins

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Proteins/enzymes can undergo *cold denaturation* or cold deactivation. In the active or natured state, a protein exists in a unique folded/ordered state. In the deactivated (denatured) state, a protein unfolds and exists in a disordered expanded state. This protein folding/unfolding or order/disorder transition can be triggered by a temperature change. What seems paradoxical is that the active (ordered) state can be induced by heating, or equivalently, the disordered inactive state can be induced by cooling. This is equivalent to an Ising spin model passing from a disordered array of spins to an ordered array by increasing temperature! Hydrogels and their corresponding polyelectrolyte chains behave similarly, i.e., the swollen disordered state can be induced by cooling while the more ordered collapsed or globular state is induced by heating (an entropically driven phase transition). In a living cell at the physiological temperature of 37 C, activation and deactivation of proteins is triggered by local environmental changes in pH, salinity, etc. The important physics is that the denaturation temperature can be moved up or down relative to 37 C by these stimuli. Moving the transition temperature up can destabilize the active protein while moving it down leads to stabilization. An analytical polymer model will be described that exhibits cold denaturation behavior.