Jason Swails Abstract for Sanibel Symposium, 2012

Including pH Effects in Simulation Using Discrete Constant pH Molecular Dynamics

Enzyme and ribozyme function is often dependent on the protonation states of ionizable residues either because the catalytic mechanism requires a general acid or base for proton transfers or because it affects the stability of the system's native state. This strong dependence on protonation state makes these catalysts' activity highly susceptible to changes in solvent pH. It is therefore desirable to include pH as a tunable thermodynamic parameter in molecular simulations that aim to model these systems. Constant pH molecular dynamics (CpHMD) is a technique that can study the coupled behavior of the protein (or RNA) environment and the conformational flexibility inherent to these systems with the protonation states of its ionizable residues. This work shows how CpHMD using Monte Carlo jumps to sample the protonation state equilibria can be a powerful tool to probe the pH-dependence of protein or ribozyme activity.