Replica Exchange Constant pH Molecular Dynamics Simulation in Biomolecules

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Solution pH is a very important thermodynamic variable that affects protein structure and function. Both constant-pH molecular dynamics (MD) method and replica exchange molecular dynamics (REMD) methodology are necessary in modeling pH-dependent processes. In this work, replica exchange constant pH molecular dynamics method is applied to the study of hen egg white lysozyme (HEWL). Simulations are performed in acidic range and only aspartate and glutamate are selected to be titratable. Restraints on alpha carbons are put for each replica in order not to destroy secondary structures at high temperatures. pKa of aspartate and glutamate residues are calculated and compared with experimental values. Structural features such as hydrogen bond network are showed. The coupling between conformation and protonation states is demonstrated in order to emphasize the importance of accurate sampling of the coupled conformations and protonation states.