Characterizing a Histidine Switch Controlling pH-Dependent Conformational Changes of the Influenza Virus Hemagglutinin

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Fig. S1: RMSD time series during the implicit solvent simulations of systems with either protonated (red lines) or neutral (blue lines) hinge histidine over the first 300 ns of the trajectories of each model.
Fig. S2: Radius of gyration (Rg) time series during the implicit solvent simulations of systems with either protonated (red lines) or neutral (blue lines) hinge histidine over the first 300 ns of the trajectories of each model.