Abstract: Spontaneous transitions between the native and non-native protein conformations are normally rare events that hardly take place in typical unbiased molecular dynamics simulations. It was recently demonstrated that such transitions can be well described by a reaction coordinate, Q, that represents the collective fraction of the native contacts between the protein atoms. Here we attempt to use this reaction coordinate to enhance the conformational sampling. We perform umbrella sampling simulations with biasing potentials on Q for two model proteins, Trp-Cage and BBA, using the CHARMM force field. Hamiltonian replica exchange is implemented in these simulations to further facilitate the sampling. The simulations appear to have reached satisfactory convergence, resulting in unbiased free energies as a function of Q. In addition to the native structure, multiple folded conformations are identified in the reconstructed equilibrium ensemble. Some conformations without any native contacts nonetheless have rather compact geometries and are stabilized by hydrogen bonds not present in the native structure. Whereas the enhanced sampling along Q reasonably reproduces the equilibrium conformational space, we also find that the folding of an α-helix in Trp-Cage is a slow degree of freedom orthogonal to Q and therefore cannot be accelerated by biasing the reaction coordinate. Overall, we conclude that whereas Q is an excellent parameter to analyze the simulations, it is not necessarily a perfect reaction coordinate for enhanced sampling, and better incorporation of other slow degrees of freedom may further improve this reaction coordinate.