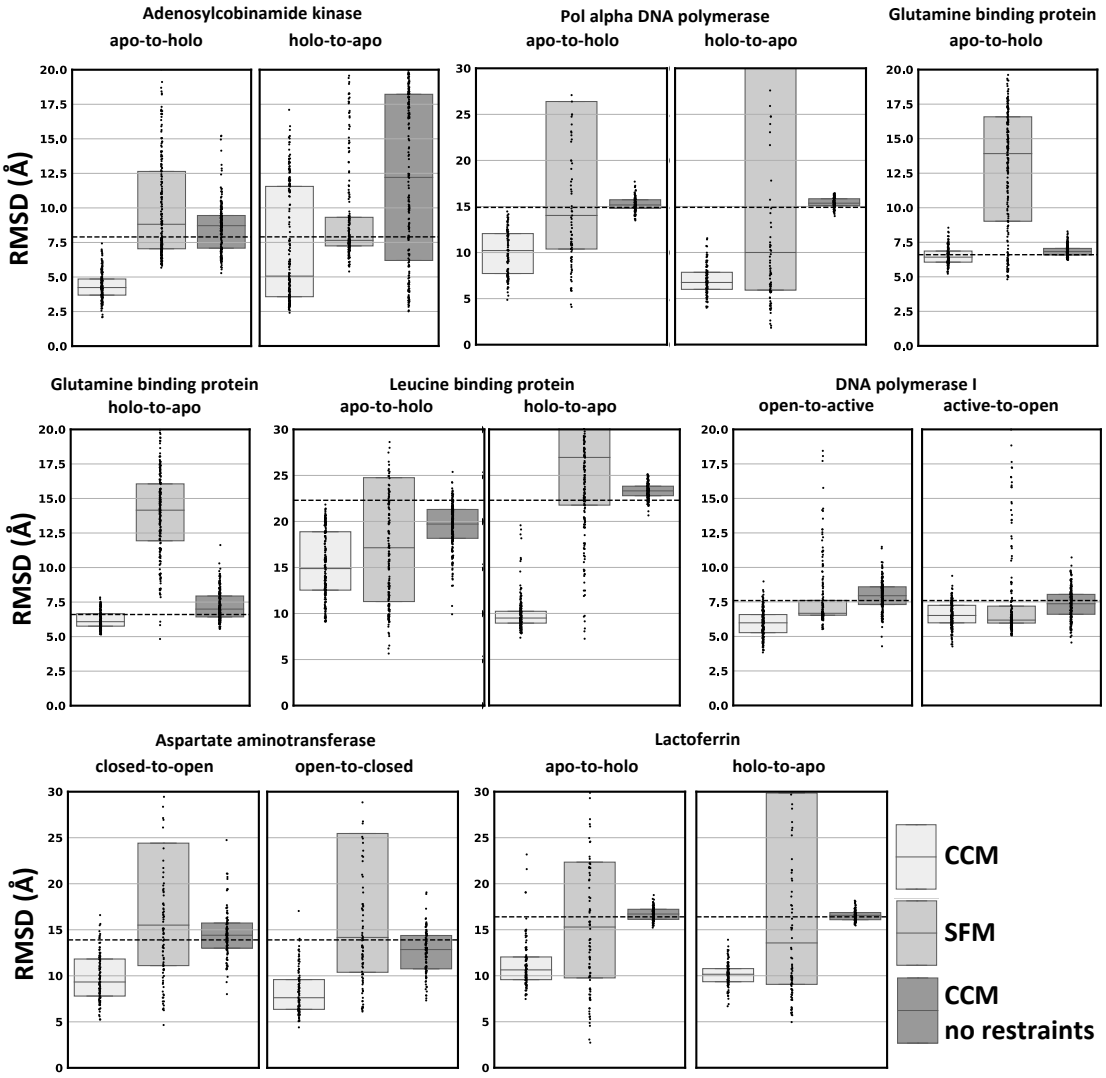

Figure S1. CCM modeled conformational changes of soluble proteins SSEs and loops using simulated Cα-Cα distance restraints, related to Figure 2. Dots represent the real distribution of RMSD values from the target structure. RMSD between the two native conformations is represented as a dashed line.

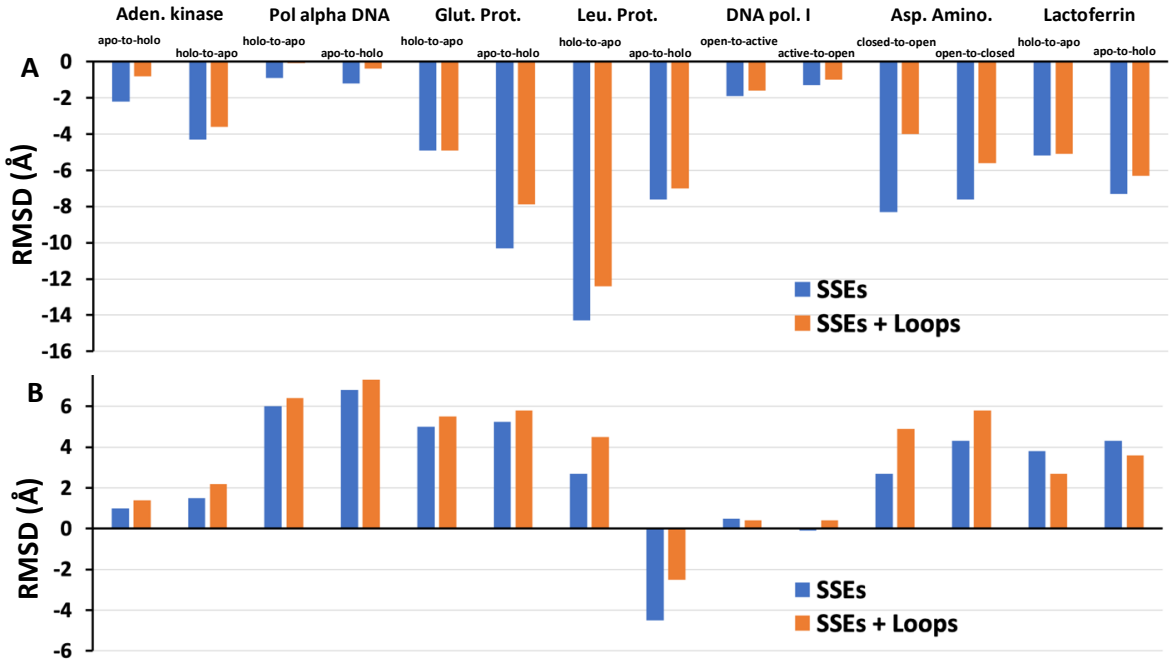

Figure S2. CCM was generally more accurate in modeling SSEs rather than unfolded regions, related to Figure 2. Each bar represents the difference between the RMSD median value of each ensemble of models and the value between native conformations. Lower is the number and closer each ensemble of models is to the target structure, where the absolute value indicates how much in angstrom the ensemble is closer with respect the initial conformation to model. A) CCM. B) SFM.

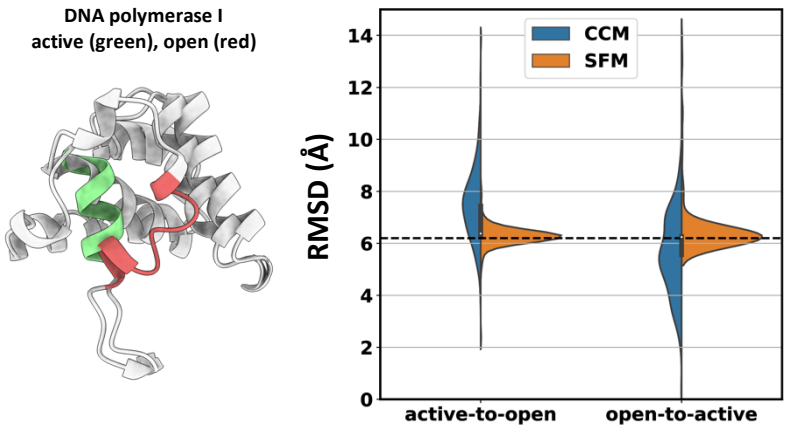

Figure S3. CCM successfully modeled an unfolded-to-folded helix transition but failed in doing the opposite, related to Figure 2. Folding states of the region of interest are shown with colored cartoons. RMSD between native states is shown as a dashed line.

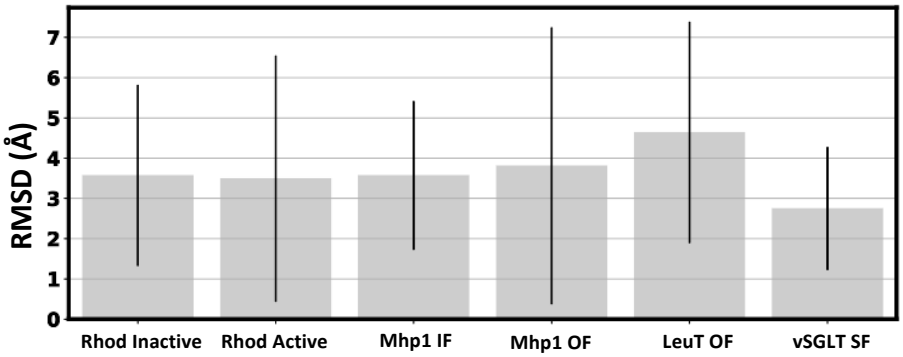

Figure S4. Accuracy of experimental DEER distances datasets, related to Figure 5 and Figure 6. Bars indicate average RMSD between experimental and simulated DEER distances. Black lines represent standard deviations.

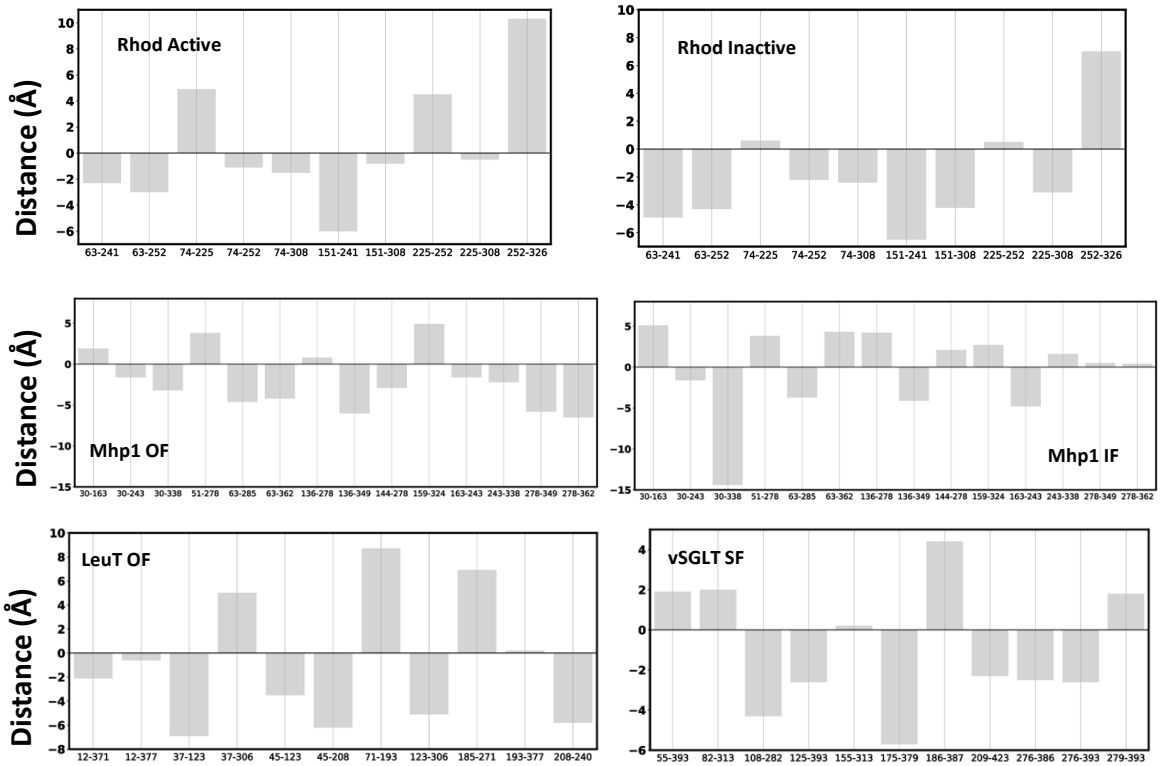

Figure S5. Few experimental DEER distance restraints have shown a great discrepancy with the corresponding simulated value, related to Figure 6. The difference between experimental DEER distance and the corresponding simulated value was measured for each restrained residue pair.

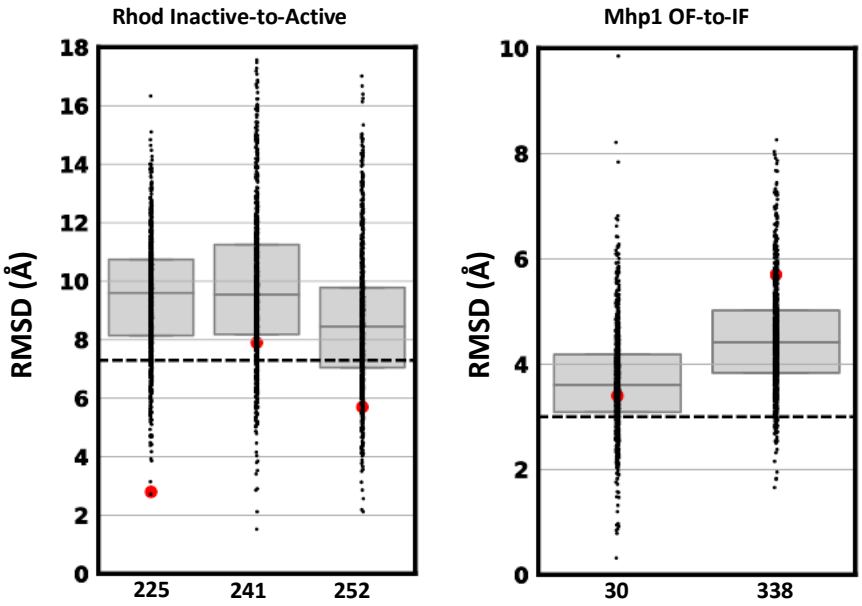

Figure S6. Residues involved in the most inaccurate experimental restraints of Rhodopsin and Mhp1 belong to protein regions poorly modeled, related to Figure 6. Black dots represent real data values. Per-residue RMSD between native conformations is shown as red dot. The median value of the global RMSD distribution of models is shown as dashed line.