*Supporting Information*

# IDP-Specific Force Field *ff14IDPSFF* Improves the Conformer Sampling of Intrinsically Disordered Proteins

Dong Song[1], Ray Luo[2,*], and Hai-Feng Chen[1,3,*]

[1]State Key Laboratory of Microbial metabolism, Department of Bioinformatics and Biostatistics, National Experimental Teaching Center for Life Sciences and Biotechnology, College of Life Sciences and Biotechnology, Shanghai Jiaotong University, Shanghai, 200240, China
[2]Departments of Molecular Biology and Biochemistry, Chemical Engineering and Materials Science, and Biomedical Engineering, University of California, Irvine, CA 92697-3900, USA
[3]Shanghai Center for Bioinformation Technology, Shanghai, 200235, China

Corresponding authors
Email addresses: haifengchen@sjtu.edu.cn; rluo@uci.edu
Tel: 86-21-34204348
Fax: 86-21-34204348.

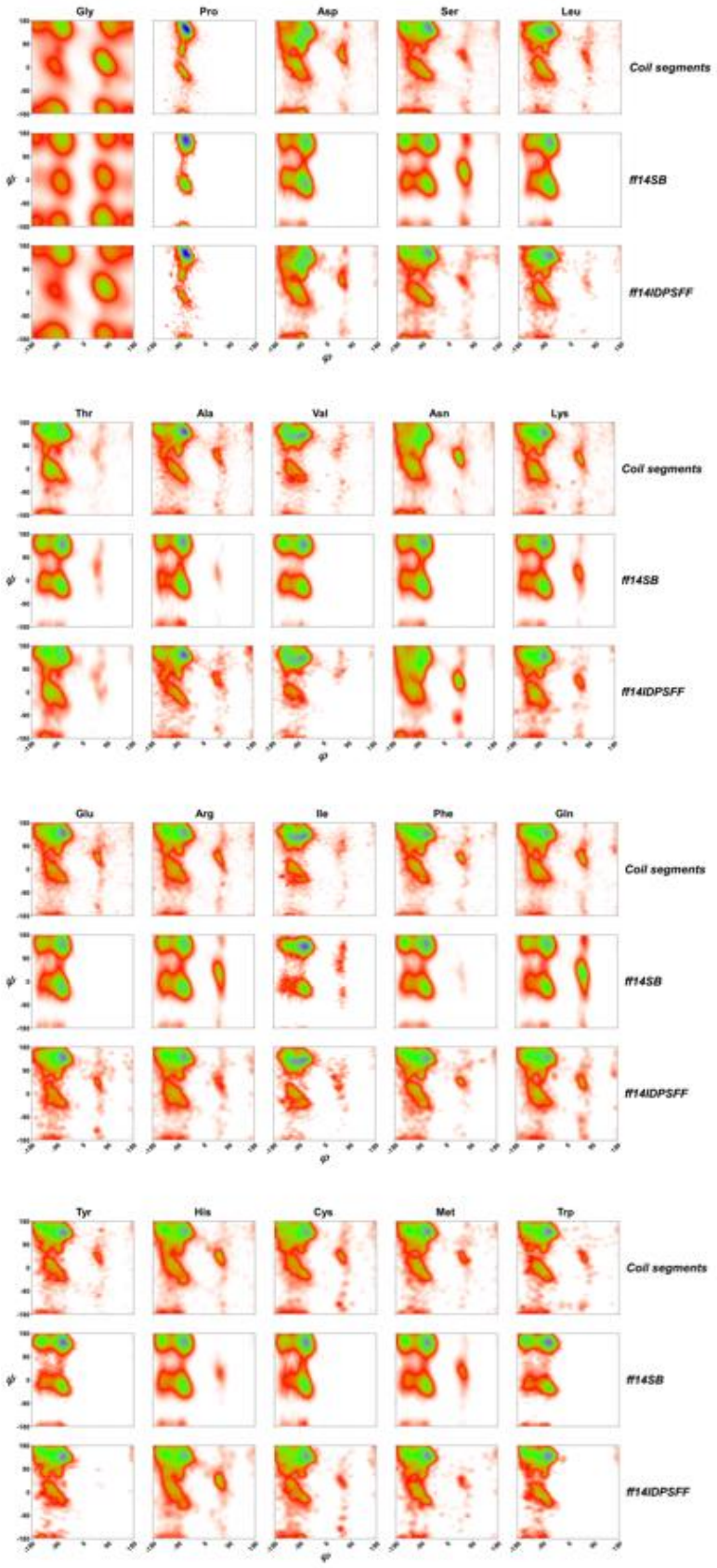


Figure S1. The distribution of phi/psi dihedral for coil segments, ff14SB, and ff14IDPSFF of 20 amino acids.

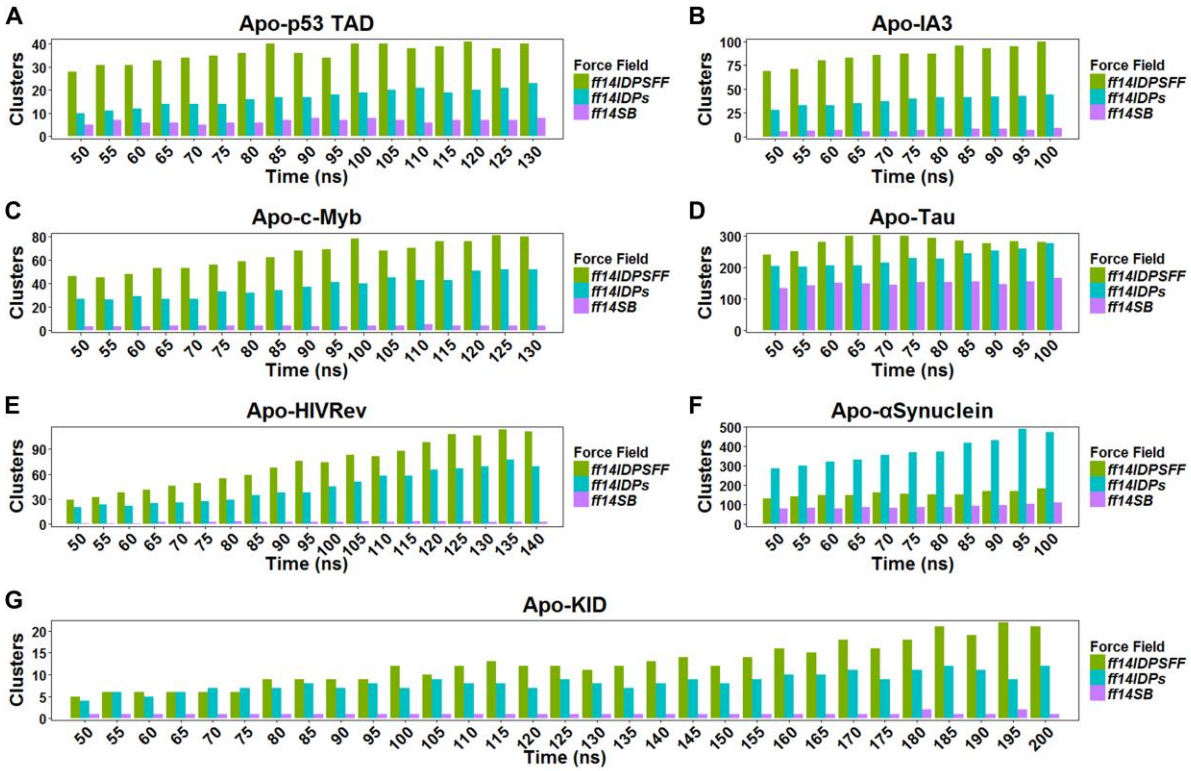


**Figure S2.** Cumulative numbers of conformational clusters over simulation time with tested force fields. A: Apo-p53 TAD ; B: Apo-IA3; C: Apo-c-Myb; D: Apo-Tau; E: Apo-HIVRev; F: Apo-α-Synuclein; G: Apo-KID.

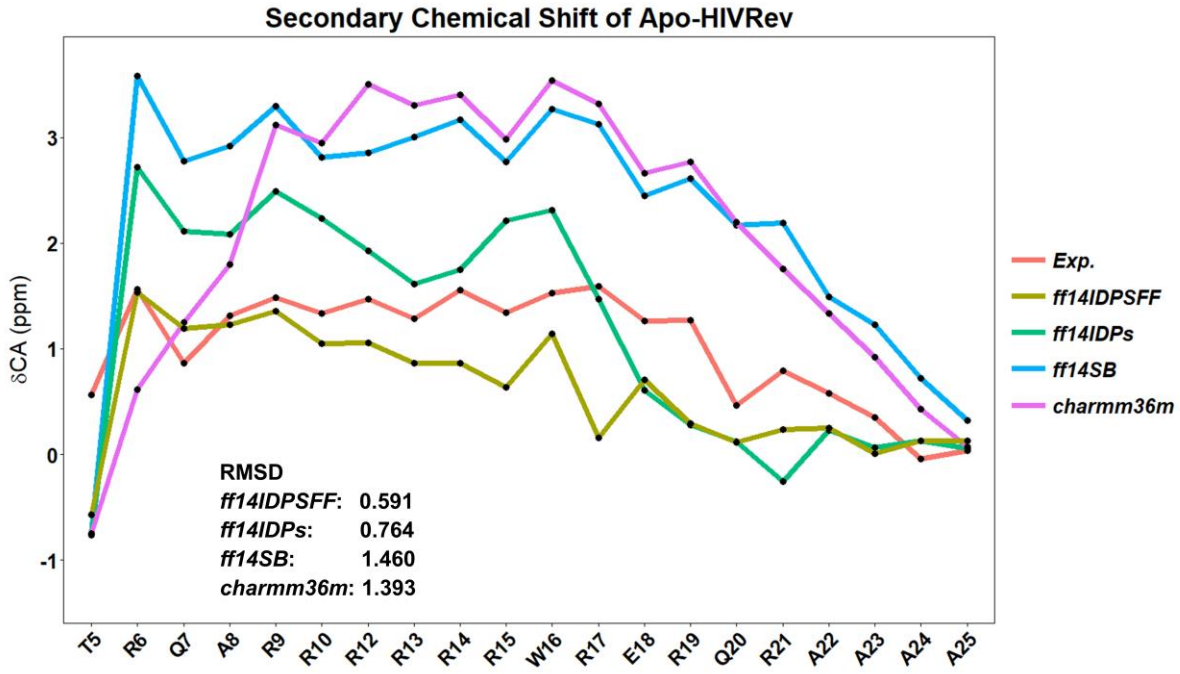


Figure S3. The secondary chemical shift of experiment and simulation of different force fields for Apo-HIVRev.

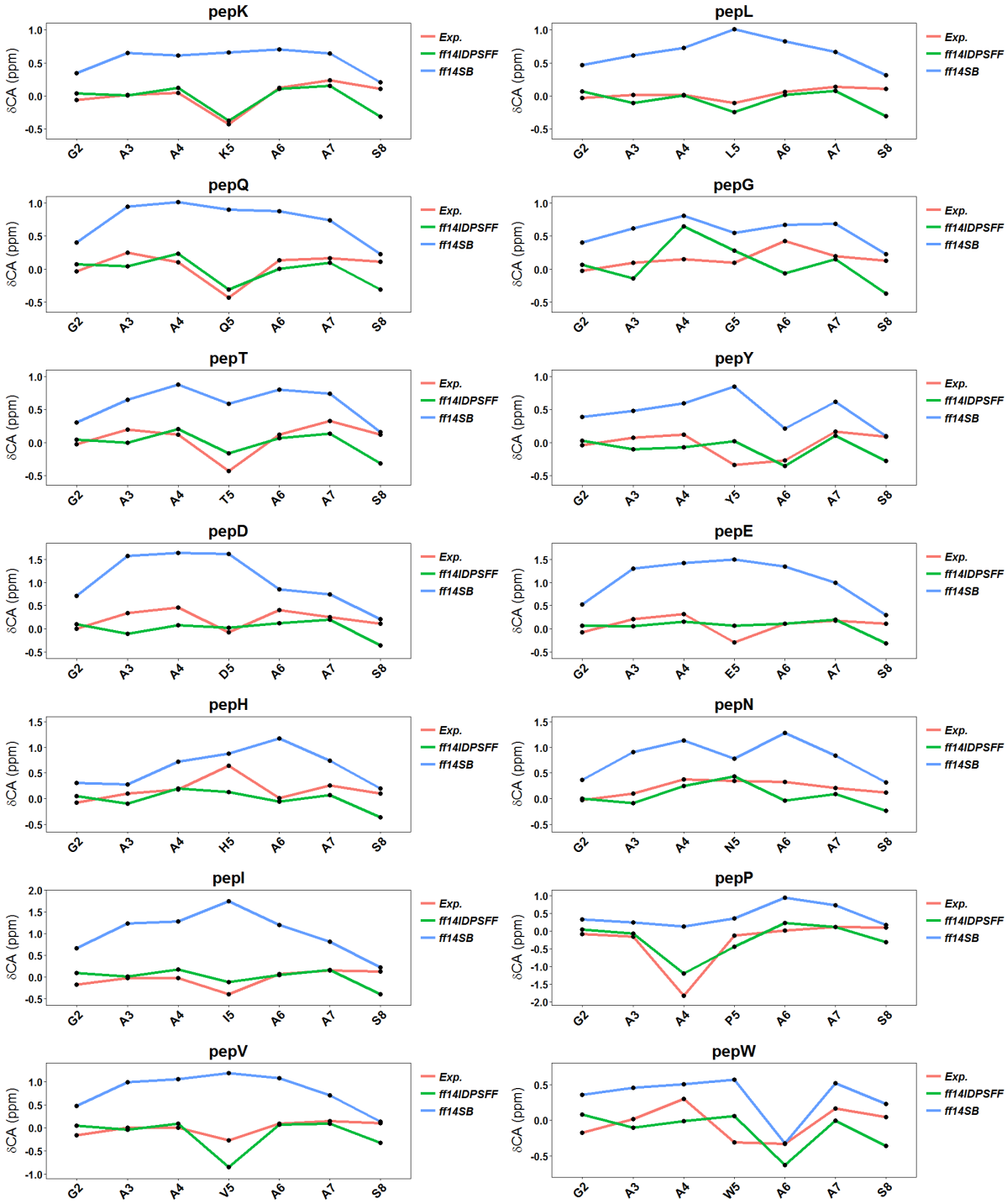


**Figure S4.** Cα chemical shifts between MD in *ff14SB* and *ff14IDPSFF* and NMR for unstructured short peptides.

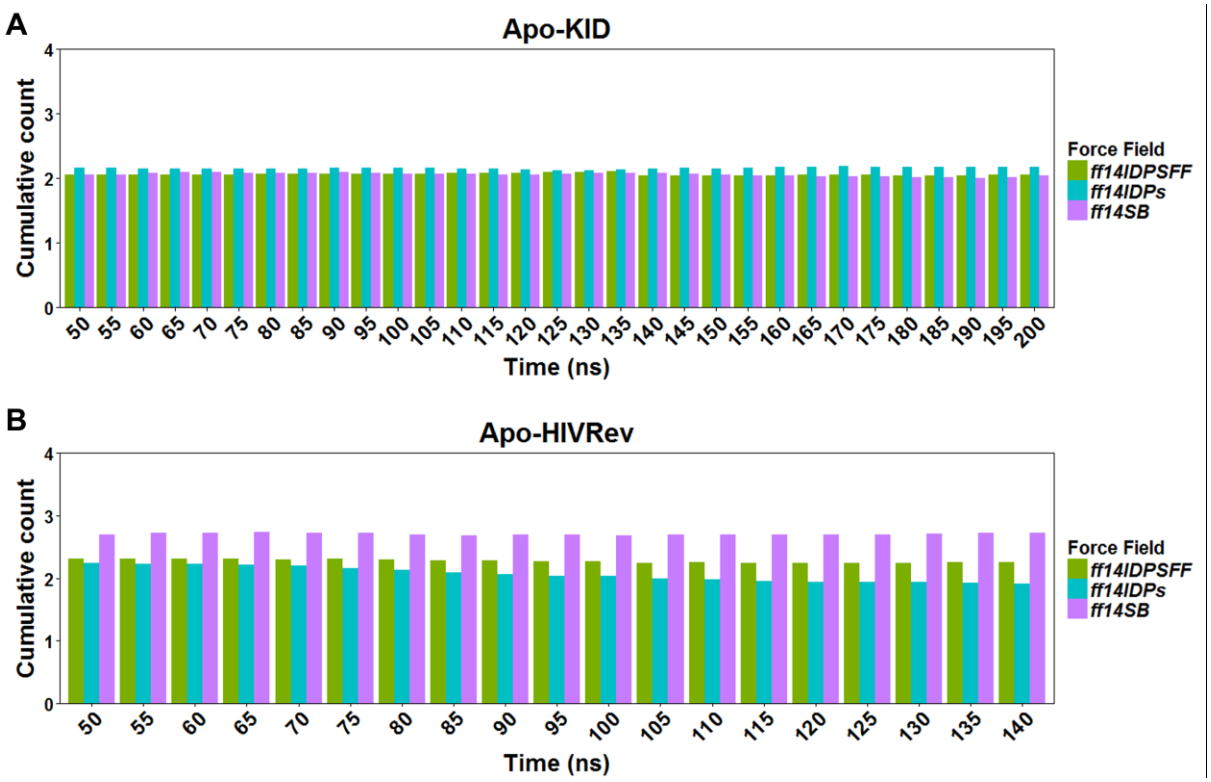


**Figure S5.** Convergences of salt bridge interactions over accumulative simulation time. A: Apo-KID; B: Apo-HIVRev.

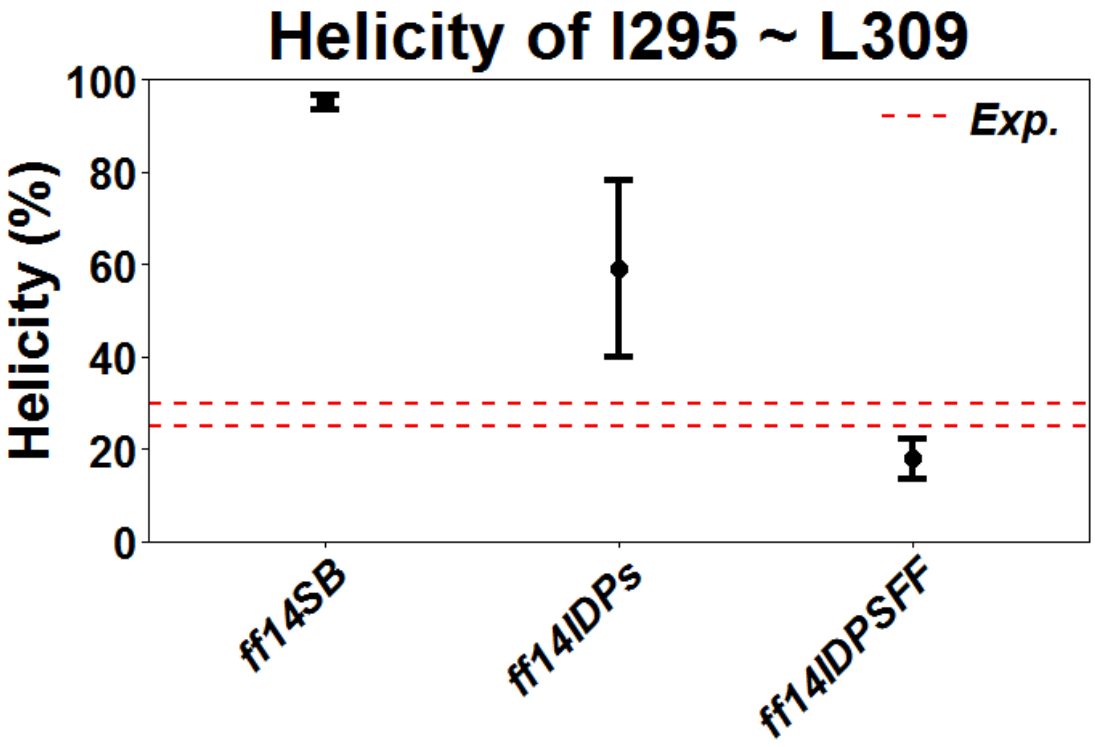


**Figure S6.** Comparison of simulated helicity for Apo-c-Myb in three tested force fields versus experiment.

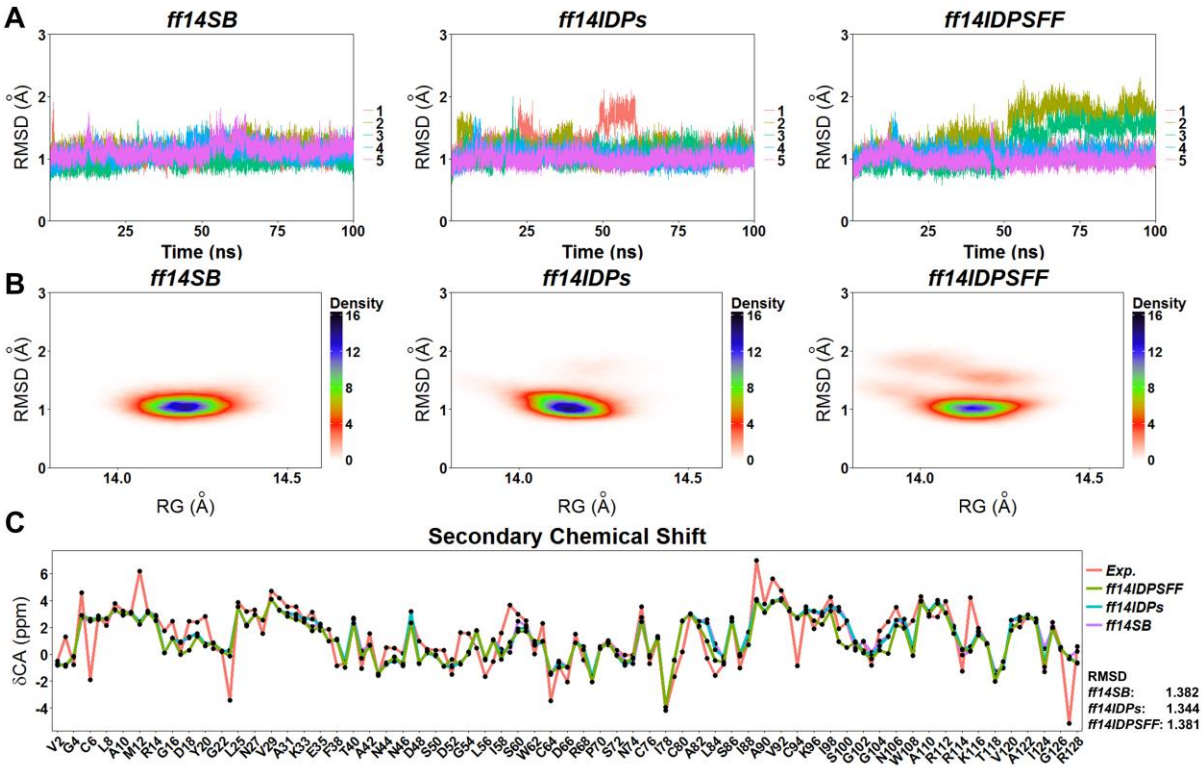


**Figure S7.** Simulation properties, sequence-dependent helicity, and Cα chemical shifts from experiment from MD in *ff14IDPSFF*, *ff14IDPs* and *ff14SB* for lysozyme. (A) Cα RMSD for five trajectories. (B) Free energy landscape on 2D space of radius gyration (Rg) and RMSD, showing *ff14IDPSFF* could sample wider and more flexible conformation space. (C) Comparison of Ca chemical shift over sequence.

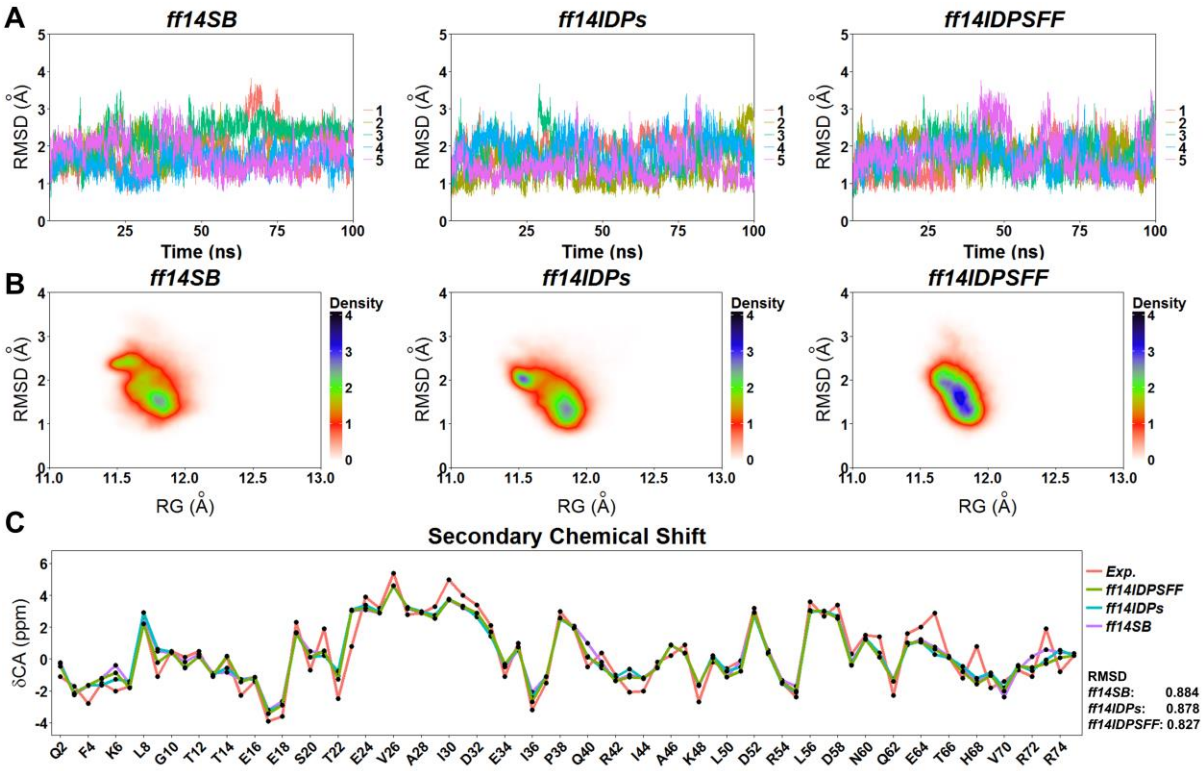


**Figure S8.** Simulation properties, sequence-dependent helicity, and Cα chemical shifts from experiment from MD in *ff14IDPSFF*, *ff14IDPs* and *ff14SB* for ubiquitin. (A) Cα RMSD for five trajectories. (B) Free energy landscape on 2D space of radius gyration (Rg) and RMSD, showing *ff14IDPSFF* could sample wider and more flexible conformation space. (C) Comparison of Ca chemical shift over sequence.

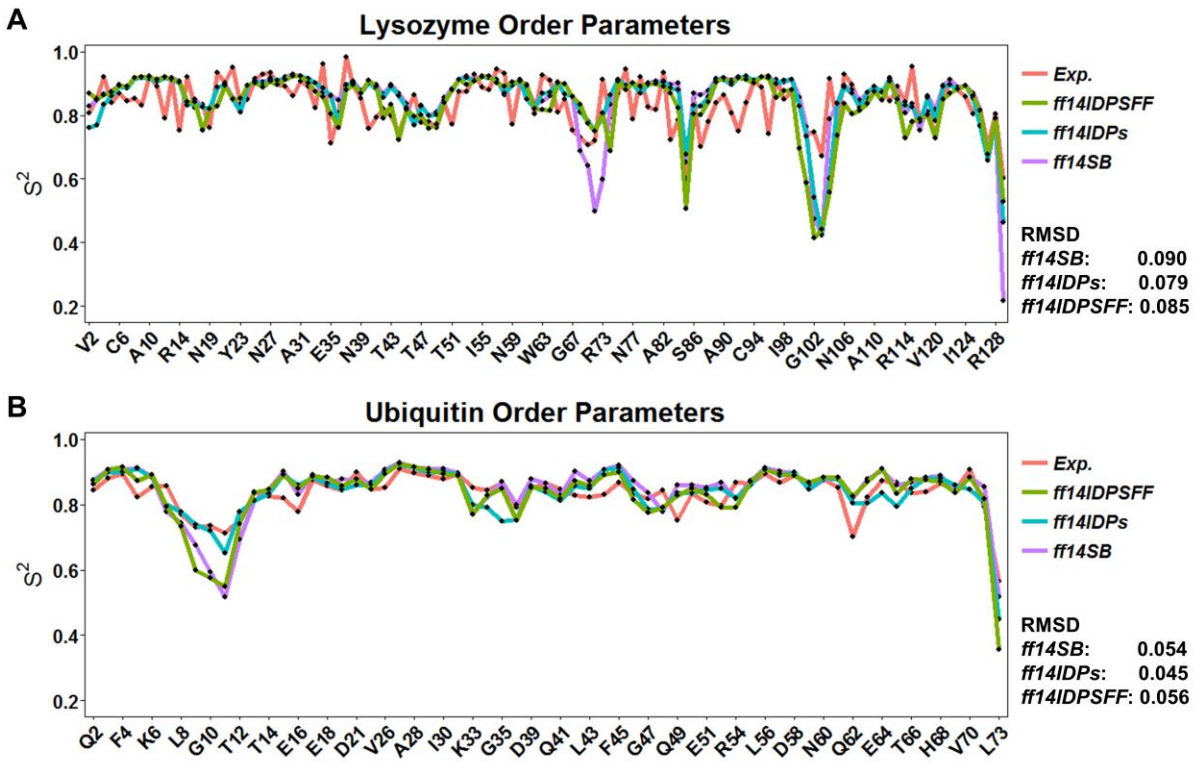


**Figure S9.** Comparison of order parameter ($S^2$) versus sequence for the two tested folded proteins.

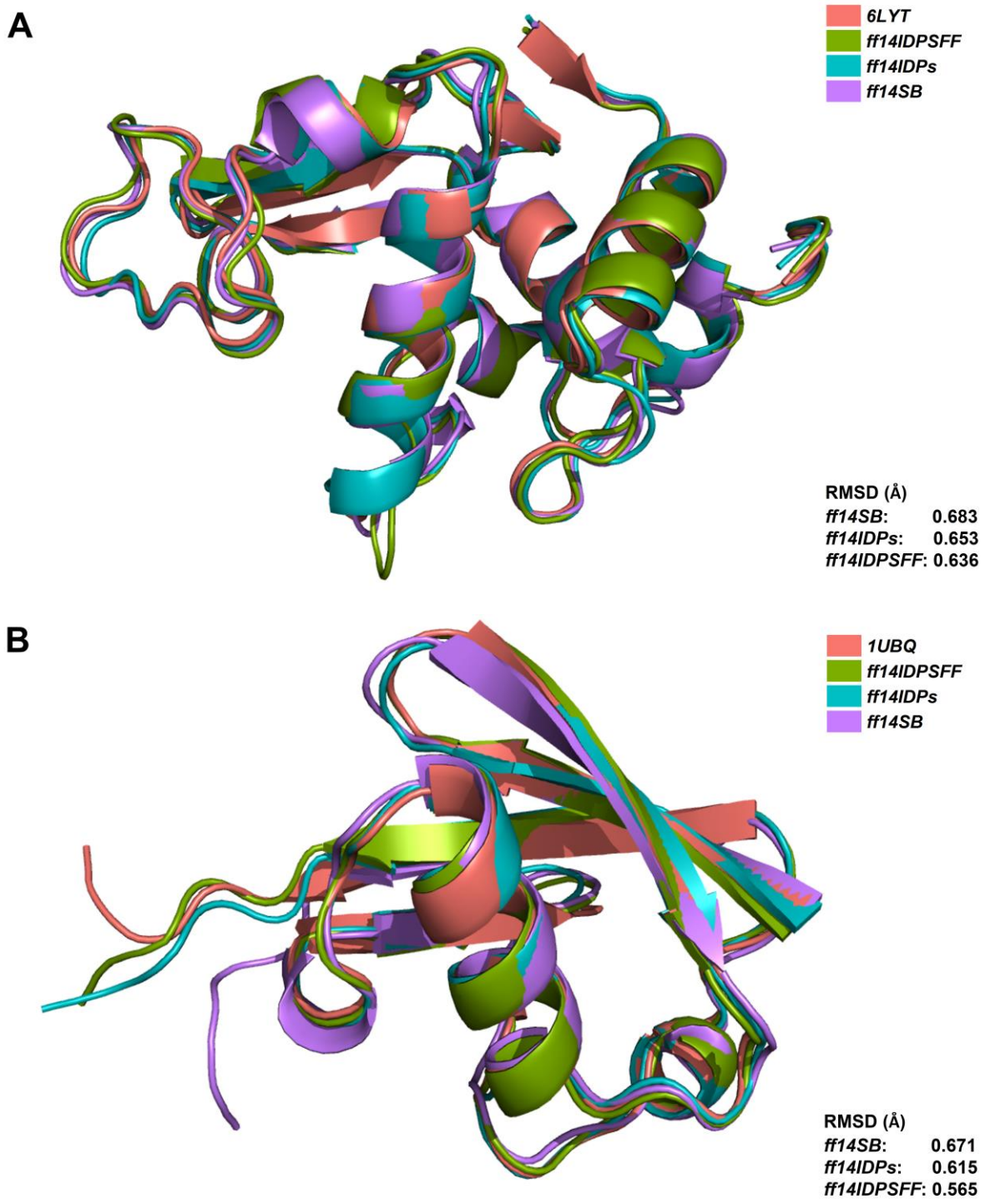


**Figure S10**. Alignment between crystal and simulation structures. A: Lysozyme. B: Ubiquitin.

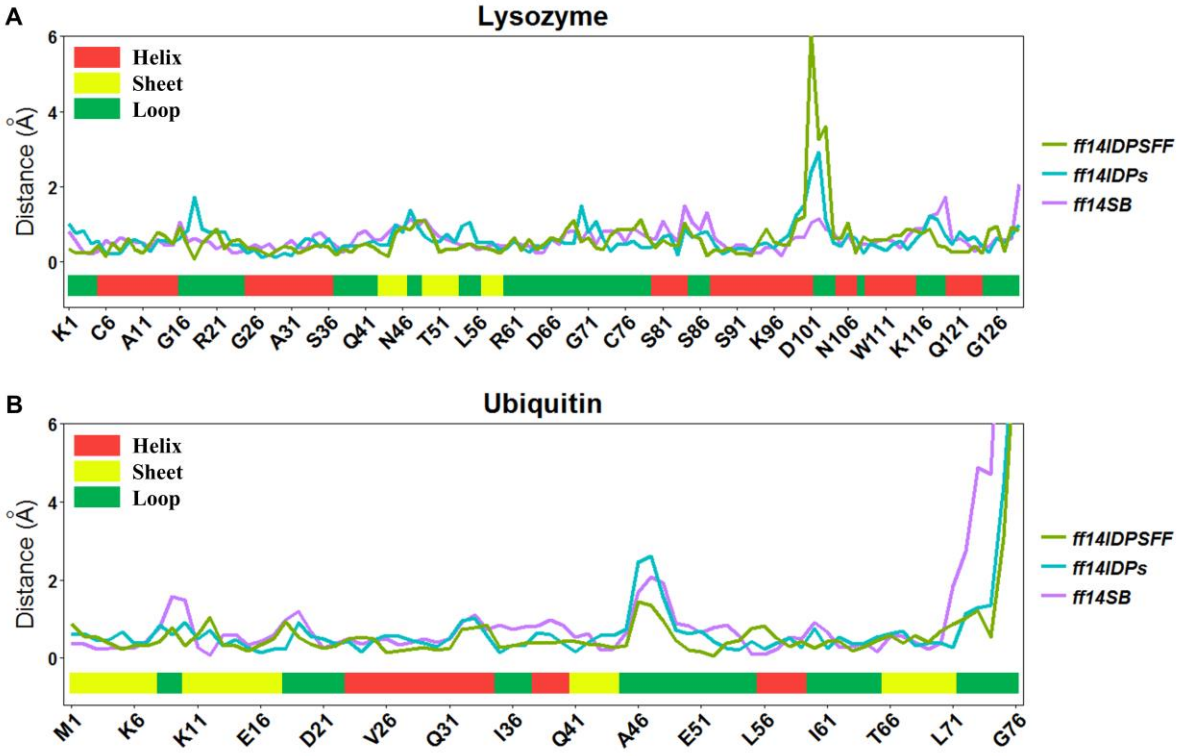


Figure S11. Cα deviations between crystal and simulation structures. A: Lysozyme. B: Ubiquitin.