

**Fig. S1** Comparison of sampling by conventional molecular dynamics (CMD) simulations and replica exchange molecular dynamics (REMD) simulation using force field AMBER99SB-ILDN. For REMD, the conformations sampled at 300k were used for comparison. (A) Distribution of radius of gyration,  $R_g$ , for structural ensembles, (B) Fraction of secondary structure elements based on DSSP algorithm, in which "3-helix" denotes "3<sub>10</sub>-helix".





**Fig. S2** Two-dimensional probability distribution as a function of  $R_g$  and contact order (CO) with five force fields. For CHARMM36m, more than 50% of all sampled conformations are extended without any contact, therefore there is no CO data for those conformations.









Fig. S4



**Fig. S4** The occupancy of secondary structure element (A)  $\beta$ -sheet, (B) Turn, (C) Coil and (D) Bend for each residue in p53 TAD2 based on DSSP algorithm. Standard deviation was obtained from the average values of three independent trajectories for each force field.



**Fig. S5** Ramachandran plot presented by free energy landscape of backbone dihedral angle  $\phi$  and  $\psi$  of p53 TAD2 for each force field. The fee energy was caculated by  $F = -k_B T \times ln(P(\phi,\psi))$ , where  $k_B$  denotes Boltzmann constant, T denotes absolute temperature, and P is population probability. The unit of right vertical color bar is kcal/mol.

## Fig. S5

Fig. S6



**Fig. S6** Comparison between back-calculated RDC profiles with experimental data for p53 TAD2. The calculation was conducted by (A) the –stPales module and (B) bestFit module in program PALES. For each residue, standard deviation was obtained based on the average values of three independent trajectories for each force field.