SUPPLEMENTARY MATERIAL

Amplitudes of Protein Backbone Dynamics and Correlated Motions in a Small α/β Protein: Correspondence of dipolar coupling and heteronuclear relaxation measurements

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2 Figures
**Fig. S1** Correlation between $<S^2_{NH}(jump)>$ derived from the two-, three- and eight-structure ensembles. The angle brackets denote averaging over 100 calculated ensembles.
Fig. S2 Correlation between the $\omega$ peptide bond torsion angle derived from the one- and two-structure ensemble calculations and those reported by Ulmer et al. (J. Am. Chem. Soc. 2003, 125, 9179-9191). The structure of Ulmer et al. was refined with a different procedure using a single-structure representation against the same set of RDCs, excluding those for the following 10 residues (residues 11-12, 24-26, 39-41 and 43). The angle brackets denote averaging over 100 calculated ensembles.

\[ \langle \omega \rangle_{(N_e = 1)} \text{ (deg.)} \]

\[ \omega \text{ (Ulmer et al.) (deg.)} \]

\[ \langle \omega \rangle_{(N_e = 2)} \text{ (deg.)} \]

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\[ \langle \omega \rangle_{(N_e = 1)} \text{ (deg.)} \]