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.

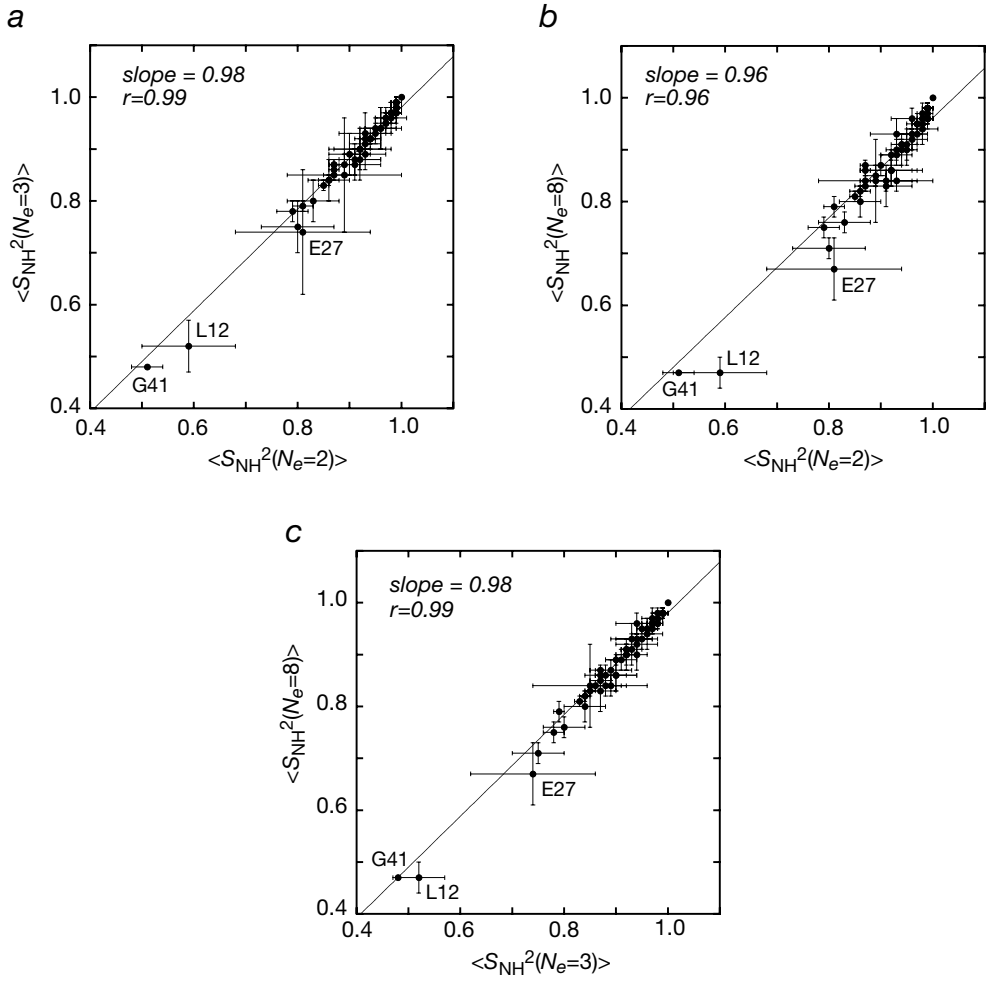

Fig. S1

Fig. S2 Correlation between the ω 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.

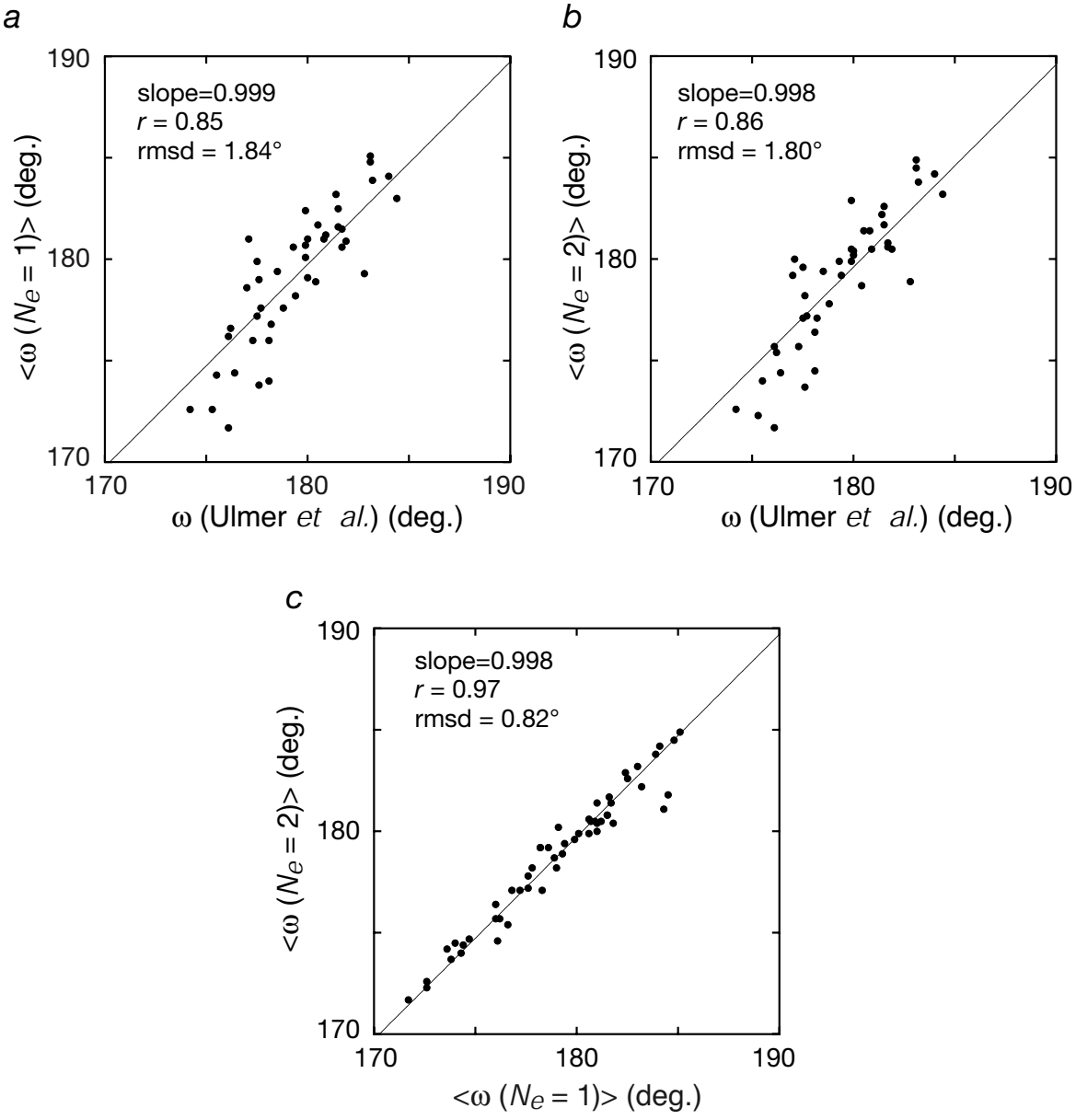

Fig. S2