

Supplementary Information

Deuterium Spin Probes of Backbone Order in Proteins: A ^2H NMR Relaxation Study of Deuterated Carbon α Sites

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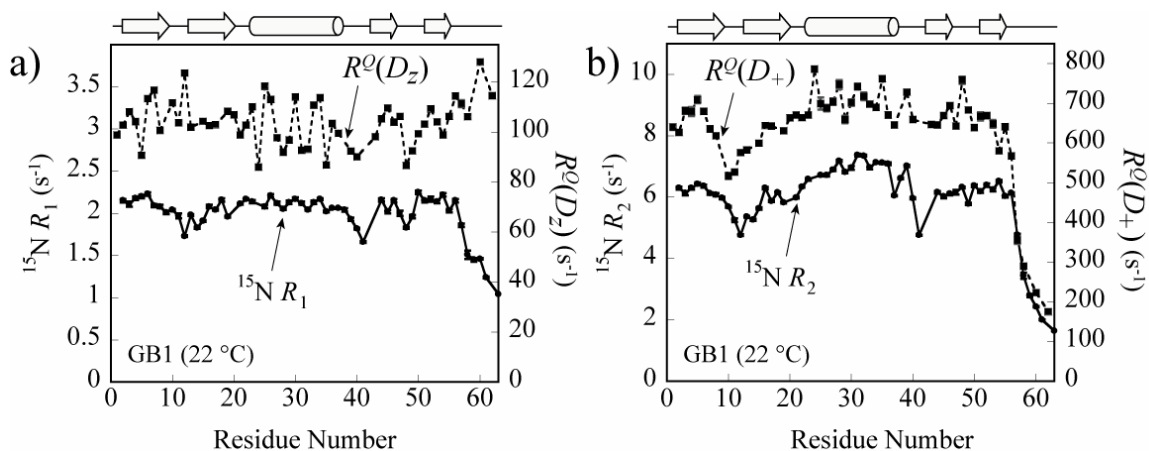


Figure S1. Plots of D^α (black rectangles and dashed lines) and ^{15}N (black circles and solid lines) relaxation rates in GB1 (22°C) shown as a function of the protein sequence: **a)** $R^Q(D_z)$ and $^{15}\text{N } R_1$ rates; **b)** $R^Q(D_+)$ and $^{15}\text{N } R_2$ rates. Schematic representation of the secondary structure is shown at the top of the plots: β -strands are depicted with arrows, while α -helices are represented with cylinders.

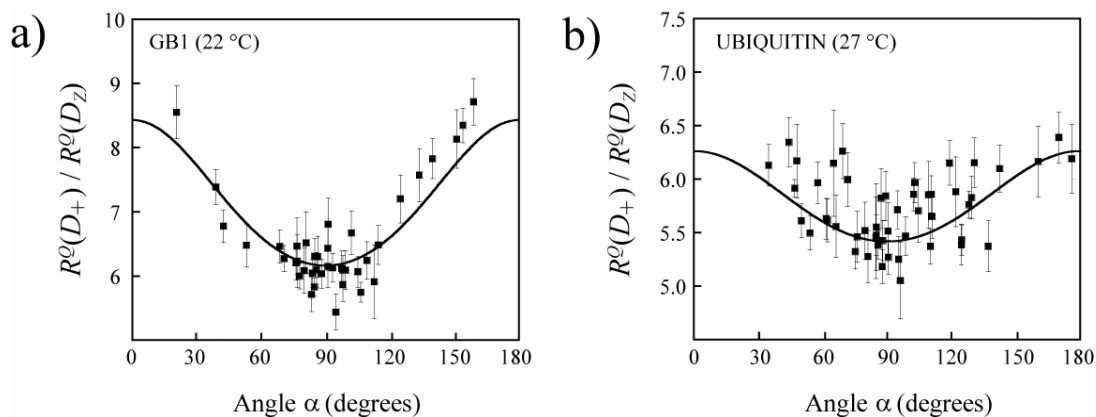


Figure S2. Plots of $R^O(D_+)/R^O(D_z)$ as a function of the angle α that each of the C^α - D^α bond vectors subtends with respect to the unique axis of the diffusion tensor, along with the best fits of the data for **a)** GB1 (22°C), and **b)** ubiquitin (27°C). Direction cosines have been extracted from C^α - H^α vector coordinates using protonated crystallographic structures of ubiquitin and GB1 with respective pdb accession codes 1ubq.pdb¹ and 2qmt.pdb².

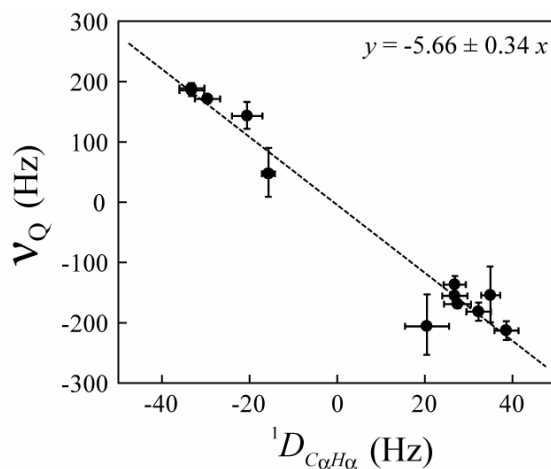


Figure S3. The correlation plot of the ^2H quadrupolar splitting, ν_Q (y -axis, Hz), with the $^1D_{C\alpha-H\alpha}$ residual dipolar couplings (x -axis, Hz) in the subset of 11 residues of GB1. The best fit is shown with a dashed line. The values of ν_Q and $^1D_{C\alpha-H\alpha}$ have been assumed to have opposite signs.

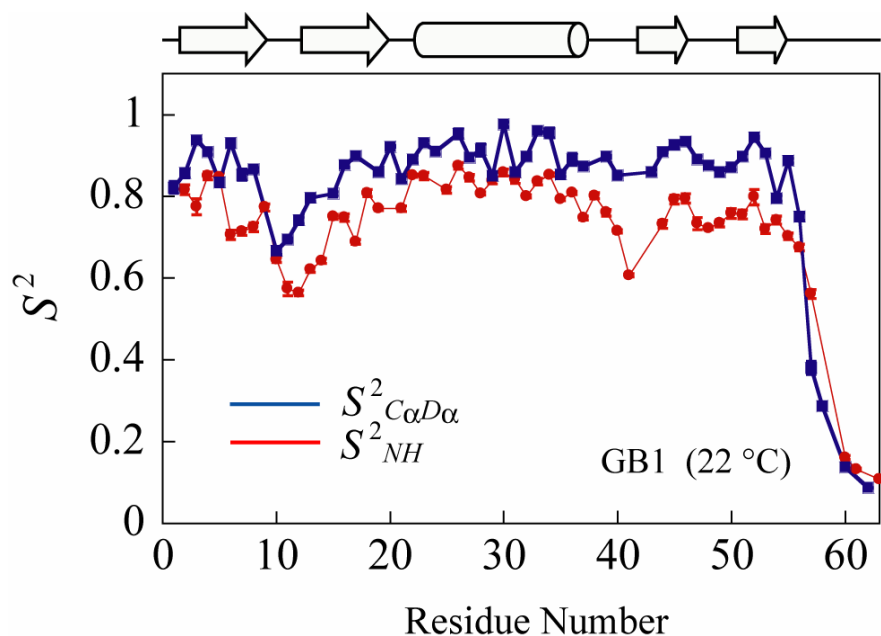


Figure S4. D^α-derived $S^2_{C\alpha D\alpha}$ (blue rectangles and lines) and ¹⁵N-derived S^2_{NH} (red circles and lines) in GB1 (22°C) plotted as a function of protein sequence. A schematic representation of the secondary structure of GB1 is shown at the top of the plot: β-strands are depicted with arrows, while α-helices are represented with cylinders.

Table S1. $S^2_{C\alpha D\alpha}$ and τ_f Values in Human Ubiquitin Derived from Analysis of D^α ²H Relaxation rates at 10°C, 27°C and 40°C.^{a)}

| | $S^2_{C\alpha-D\alpha}$ 10°C | $\tau_f(\text{ps})^b$ 10°C | $S^2_{C\alpha-D\alpha}$ 27°C | $\tau_f(\text{ps})^b$ 27°C | $S^2_{C\alpha-D\alpha}$ 40°C | $\tau_f(\text{ps})^b$ 40°C |
|-----|---------------------------------|-------------------------------|---------------------------------|-------------------------------|---------------------------------|-------------------------------|
| M1 | 0.89 (0.01) | - | 0.85 (0.01) | - | 0.82 (0.01) | - |
| Q2 | 0.89 (0.01) | - | 0.81 (0.01) | - | 0.82 (0.01) | - |
| I3 | - | - | 0.89 (0.01) | 82.7 (43.1) | 0.93 (0.01) | - |
| F4 | 0.94 (0.01) | - | 0.92 (0.01) | - | 0.83 (0.05) | 232.3 (51.3) |
| V5 | 0.85 (0.01) | - | 0.82 (0.02) | 136.9 (71.2) | 0.83 (0.01) | - |
| K6 | 0.87 (0.01) | - | 0.84 (0.01) | - | - | - |
| T7 | 0.89 (0.01) | - | 0.86 (0.01) | - | 0.77 (0.01) | - |
| L8 | 0.73 (0.02) | 204.1 (11.7) | - | - | - | - |
| T9 | 0.74 (0.01) | 69.5 (5.1) | 0.78 (0.01) | - | - | - |
| K11 | 0.86 (0.01) | - | 0.86 (0.01) | - | 0.87 (0.02) | - |
| T12 | 0.82 (0.01) | - | 0.87 (0.02) | - | 0.83 (0.01) | - |
| I13 | 0.91 (0.02) | 154.0 (68.2) | 0.86 (0.01) | 90.3 (35.7) | 0.82 (0.02) | 150.4 (30.0) |
| T14 | 0.86 (0.01) | - | 0.90 (0.02) | - | 0.85 (0.01) | - |
| E16 | 0.91 (0.01) | - | 0.86 (0.02) | 95.9 (42.7) | 0.84 (0.01) | - |
| V17 | - | - | 0.89 (0.01) | - | 0.88 (0.01) | - |
| P19 | 0.89 (0.01) | - | 0.86 (0.01) | - | 0.81 (0.01) | - |
| S20 | 0.87 (0.01) | 51.2 (22.9) | 0.85 (0.01) | - | 0.82 (0.01) | - |
| D21 | 0.92 (0.01) | 213.8 (53.4) | 0.94 (0.01) | - | - | - |
| T22 | - | - | 0.86 (0.01) | 112.0 (62.8) | 0.92 (0.01) | - |
| E24 | - | - | 0.91 (0.01) | - | 0.89 (0.01) | - |
| V26 | - | - | 0.91 (0.01) | - | 0.79 (0.02) | 266.8 (31.4) |
| K27 | 0.88 (0.03) | - | 0.87 (0.02) | - | - | - |
| A28 | 0.97 (0.01) | - | 0.92 (0.01) | - | 0.87 (0.01) | - |
| K29 | 0.92 (0.04) | - | 0.85 (0.01) | 105.1 (53.6) | 0.90 (0.01) | - |

| | | | | | | |
|-----|-------------|--------------|-------------|--------------|-------------|--------------|
| I30 | 0.87 (0.02) | - | 0.92 (0.01) | - | - | - |
| Q31 | 0.93 (0.02) | - | 0.90 (0.01) | - | 0.89 (0.01) | - |
| D32 | 0.92 (0.01) | - | 0.89 (0.01) | - | 0.87 (0.01) | - |
| K33 | 0.90 (0.01) | - | 0.86 (0.02) | - | - | - |
| E34 | 0.91 (0.01) | - | 0.88 (0.01) | - | 0.85 (0.01) | - |
| P38 | - | - | 0.89 (0.01) | - | 0.85 (0.01) | - |
| D39 | 0.91 (0.01) | - | 0.86 (0.01) | - | 0.84 (0.01) | - |
| Q40 | 0.94 (0.02) | - | 0.90 (0.01) | - | 0.88 (0.01) | - |
| Q41 | - | - | 0.94 (0.01) | - | - | - |
| R42 | 0.89 (0.01) | - | 0.92 (0.01) | - | 0.89 (0.02) | - |
| L43 | 0.87 (0.01) | - | 0.94 (0.01) | - | 0.82 (0.02) | - |
| I44 | - | - | 0.82 (0.01) | - | 0.84 (0.01) | - |
| F45 | 0.89 (0.01) | 128.0 (68.6) | - | - | - | - |
| A46 | 0.82 (0.02) | 112.7 (26.5) | 0.79 (0.01) | - | 0.71 (0.03) | 137.9 (26.7) |
| K48 | - | - | 0.81 (0.01) | - | - | - |
| Q49 | 0.90 (0.01) | - | 0.86 (0.01) | - | 0.84 (0.01) | - |
| L50 | - | - | 0.89 (0.01) | - | 0.87 (0.01) | - |
| E51 | 0.91 (0.01) | - | 0.86 (0.01) | - | 0.86 (0.01) | - |
| R54 | 0.92 (0.01) | - | 0.88 (0.01) | - | 0.89 (0.01) | - |
| T55 | 0.84 (0.01) | - | 0.88 (0.01) | - | 0.88 (0.01) | - |
| L56 | - | - | - | - | 0.94 (0.01) | - |
| S57 | 0.92 (0.02) | - | 0.92 (0.01) | - | 0.91 (0.02) | - |
| D58 | 0.97 (0.02) | - | 0.92 (0.01) | - | 0.91 (0.01) | - |
| Y59 | 0.88 (0.02) | - | 0.92 (0.01) | - | 0.89 (0.01) | - |
| N60 | 0.87 (0.02) | - | 0.81 (0.01) | - | 0.81 (0.01) | - |
| I61 | 0.88 (0.01) | - | 0.87 (0.01) | - | 0.84 (0.01) | - |
| Q62 | - | - | 0.81 (0.01) | 53.0 (27.8) | 0.81 (0.01) | - |
| K63 | 0.92 (0.01) | - | 0.88 (0.02) | - | 0.83 (0.01) | - |
| E64 | 0.87 (0.01) | - | 0.83 (0.01) | - | 0.85 (0.01) | - |
| S65 | 0.90 (0.01) | - | 0.90 (0.01) | - | 0.85 (0.01) | - |
| T66 | 0.85 (0.01) | - | 0.84 (0.01) | - | 0.81 (0.01) | - |
| L67 | 0.92 (0.01) | - | 0.90 (0.01) | - | 0.92 (0.01) | - |
| H68 | 0.94 (0.01) | - | 0.89 (0.01) | - | 0.90 (0.01) | - |
| L69 | 0.93 (0.02) | - | 0.91 (0.01) | - | 0.86 (0.01) | - |
| V70 | 0.91 (0.01) | 107.7 (16.5) | 0.83 (0.01) | 204.3 (20.6) | - | - |
| L71 | 0.81 (0.02) | 208.1 (21.2) | 0.77 (0.02) | 167.5 (17.7) | - | - |
| R72 | 0.62 (0.02) | 306.1 (11.7) | 0.57 (0.02) | 329.9 (35.6) | - | - |
| L73 | 0.43 (0.01) | 384.6 (6.3) | 0.33 (0.01) | 339.6 (26.3) | - | - |
| R74 | 0.28 (0.01) | 319.7 (5.3) | - | - | - | - |

^{a)}Errors in $S^2_{CaD\alpha}$ and τ_f as established from Monte-Carlo simulations³ are shown in parentheses. ^{b)} τ_f values (in picoseconds) are reported only for the residues that could not be fit to the single-parameter ($S^2_{CaD\alpha}$ only) Lipari-Szabo spectral density function^{4,5} with 5% probability of exceeding χ^2 .⁶

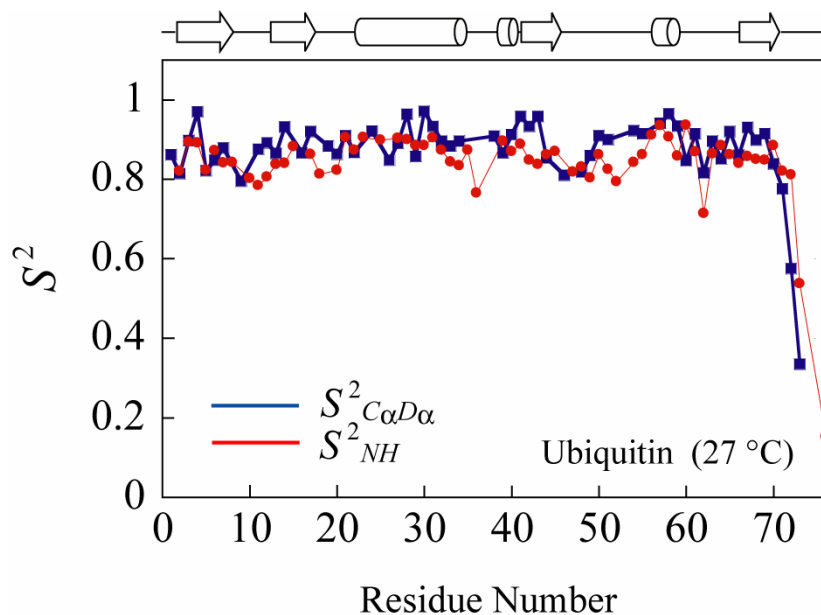


Figure S5. D^α-derived $S^2_{C\alpha D\alpha}$ (blue rectangles and lines) and ¹⁵N-derived S^2_{NH} (red circles and lines) in ubiquitin (27°C) obtained using common global diffusion tensor parameters ($\tau_{c,eff} = (2D_{||} + 4D_{\perp})^{-1} = 4.05$ ns; $D_{||}/D_{\perp} = 1.20$; $\theta = 7^\circ$; $\phi = -12^\circ$) and $QCC = 171$ kHz, plotted as a function of the protein sequence. A schematic representation of the secondary structure of ubiquitin is shown at the top of the plot: β -strands are depicted with arrows, while α -helices are represented with cylinders.

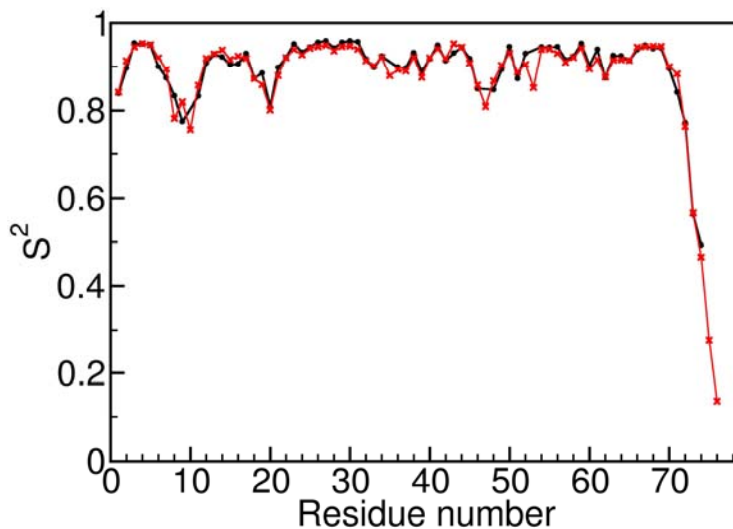


Figure S6. Comparison of $S^2_{C\alpha D\alpha}$ (red, 'x' symbols) with $S^2_{C\alpha C\beta}$ (black, filled circles) order parameters derived from the 1- μ s MD trajectory of ubiquitin (27°C) averaged over a 5-ns time window. See 'Materials and Methods' for the details of MD simulations.

References

- (1) Vijay-Kumar, S.; Bugg, C. E.; Cook, W. J. *J. Mol. Biol.* **1987**, *194*, 531-544.
- (2) Frericks-Schmidt, H. L.; Sperling, L. J.; Gao, Y. G.; Wylie, B. J.; Boettcher, J. M.; Wilson, S. R.; Rienstra, C. M. *J. Phys. Chem. B* **2007**, *111*, 14362-14369.
- (3) Kamith, U.; Shriver, J. W. *J. Biol. Chem.* **1989**, *264*, 5586-5592.
- (4) Lipari, G.; Szabo, A. *J. Am. Chem. Soc.* **1982**, *104*, 4546-4559.
- (5) Lipari, G.; Szabo, A. *J. Am. Chem. Soc.* **1982**, *104*, 4559-4570.
- (6) Bevington, P. R.; Robinson, D. K. *Data Reduction and Error Analysis for the Physical Sciences*; WCB/McGraw-Hill, New York, 1992.