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Supporting Information

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Solid-State Protein Structure Determination with Proton-Detected Triple Resonance 3D Magic-Angle Spinning NMR Spectroscopy**

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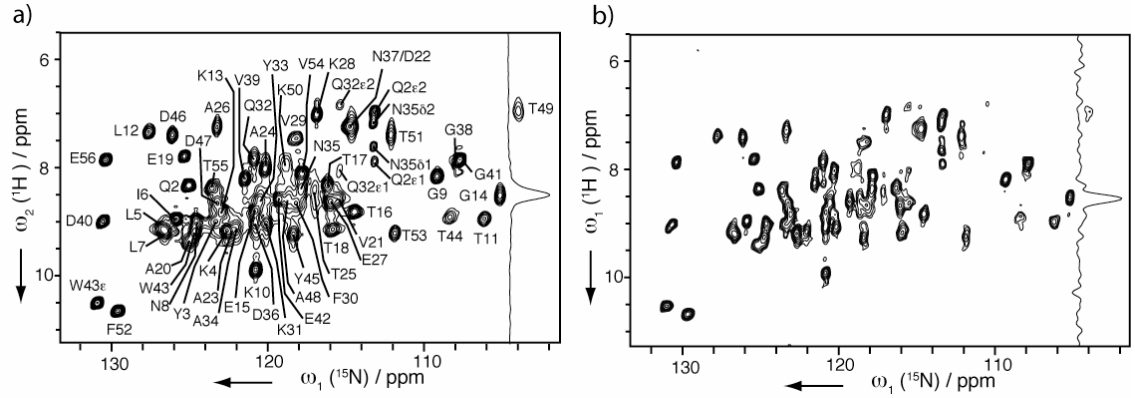

Figure S1. Solid-state 2D HETCOR spectra of uniformly-^{13}C,^{15}N,^{2}H-labeled GB1, back-exchanged with H_2O at labile sites. (a) ^{1}H-detected, ^{15}N-^{1}H 2D reproduced from Fig. 1. The spectrum was acquired in 30 minutes at 750 MHz ^{1}H frequency with 39 kHz magic-angle spinning, 2 s recycle delay, 2 scans per row, $t_1^{max}(^{15}N)$ = 50 ms, $t_2^{max}(^{1}H)$ = 30 ms. (b) ^{15}N-detected, ^{1}H-^{15}N 2D acquired with 4 scans per row, $t_1^{max}(^{1}H)$ = 20 ms, $t_2^{max}(^{15}N)$ = 60 ms, total 50 min. For both spectra, the ^{15}N dimension was truncated to 25 ms and ^{1}H to 7.2 ms, according to $3T_2^*$, where $T_2^*=1/\pi\Delta$ was the apparent relaxation time calculated from average line widths. Contours start from 60 and 6 times noise level in (a) and (b), respectively; the spacing factor is 1.4. The common 1D slices from each spectrum for the G14 resonance illustrate the relative sensitivity afforded by ^{1}H-detection.

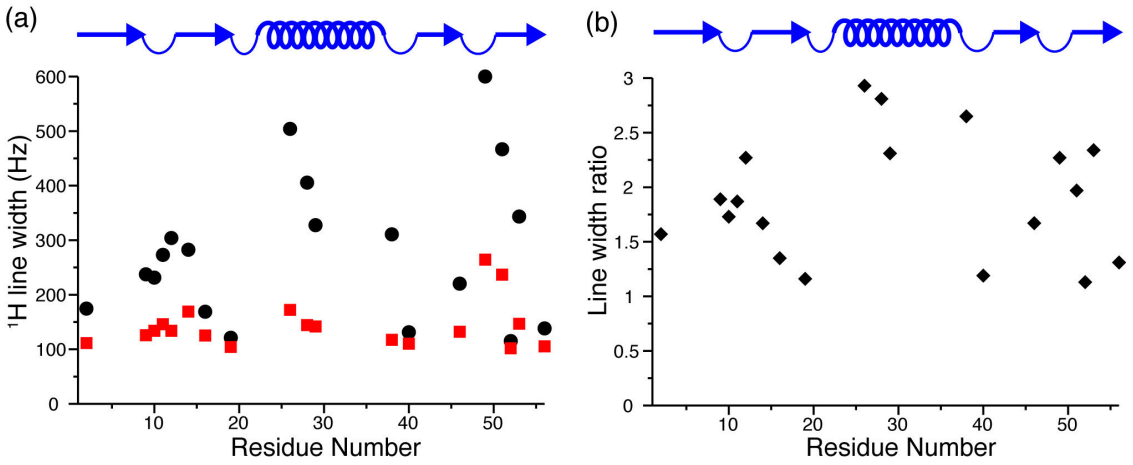

Figure S2. Residue-specific linewidth dependence on MAS rate for protein GB1. (a) Proton linewidths for peaks resolved in ^{15}N-^{1}H 2D spectra acquired at 20 (circle) and 39 kHz (square). (b) The ratio of linewidths at the two sample spinning rates. Secondary structure of the protein is also displayed for reader's convenience.

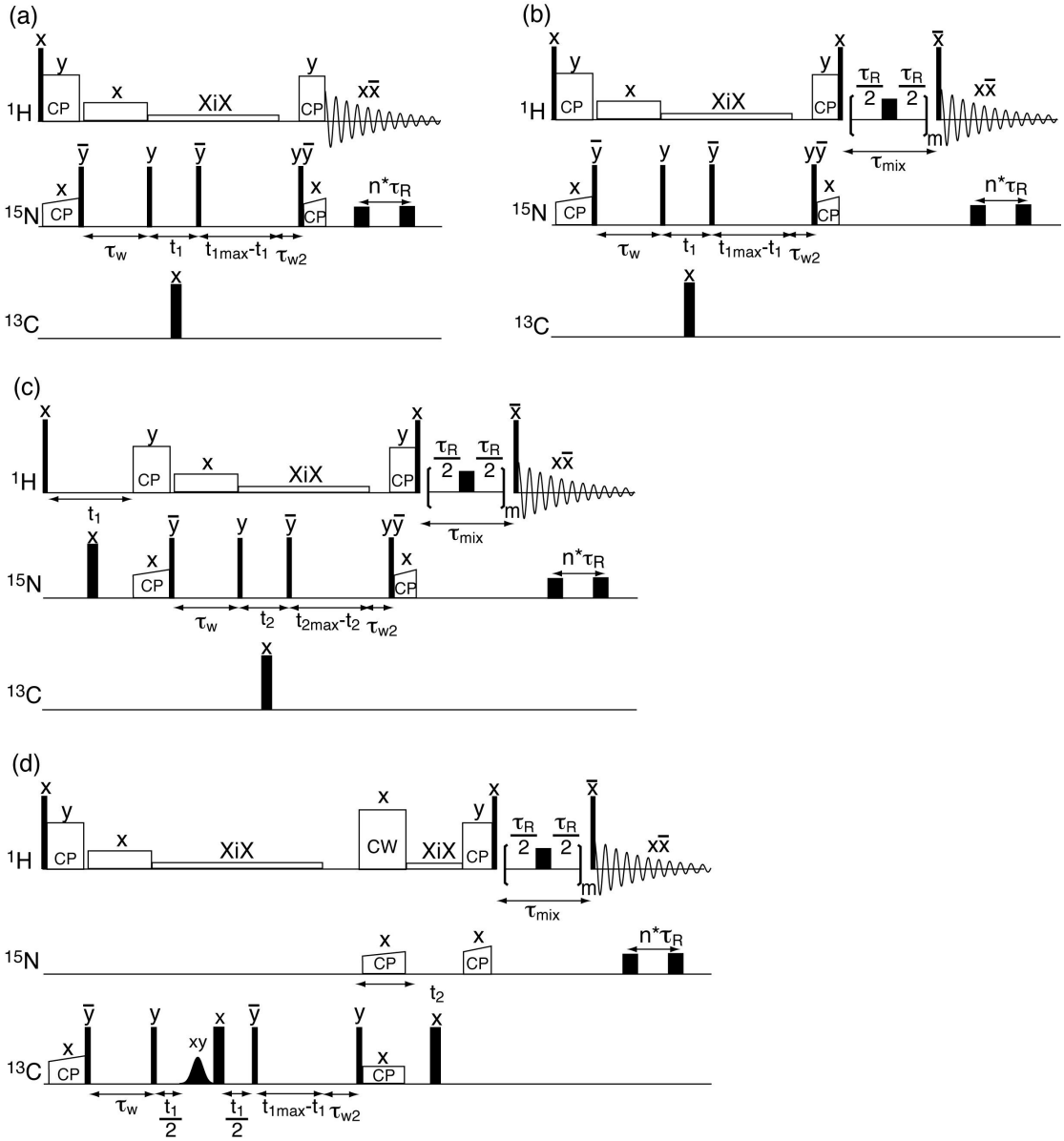

Figure S3. Indirect proton detection pulse sequences used in this study. (a) Sequence for N-H 2D experiments. (b) N(H)H 2D ^{1}H-^{1}H mixing using RFDR dipolar recoupling.[1] (c) HN(H)H 3D. (d) CON(H)H 3D with a pair of soft and hard π pulses in the middle of the t_1 evolution period to remove the $J_{CA\text{-}CO}$ coupling.[2, 3] Narrow and wide rectangles represent π/2 and π pulses, respectively; weaker π pulses were represented with a smaller amplitude. States-TPPI[4, 5] was applied to the π/2 or spin lock pulse immediately following the indirect evolution periods. Two-step phase cycles as indicated on the figure were adequate to ensure proper coherence selection and solvent suppression.

Pulse sequences. The proton-detected sequences (Fig. S1) were based on the water suppression scheme by Zilm and coworkers,[6] but modified for decoupling conditions under fast MAS and to suppress multiple solvent signals. A pulse of moderate power (~35 kHz or less) was applied for a sufficiently long duration (τ_w = 250 ms) to saturate solvent signals throughout the proton spectrum. A short T_2 filter (τ_{w2}=10 ms) was also added to further

attenuate any residual solvent signals. The precise ^{1}H carrier position was not critical but either conveniently placed on one of the solvent resonances, or in the center of amide resonances to allow the use of a narrow bandwidth in HN(H)H 3D. During HX or XH CP, rf fields were 98 kHz and 59 kHz for ^{1}H and X channels, respectively; these nutation frequencies correspond to half-integer multiples of the spinning rate (ω_H = 5/2 ω_R and ω_C = 3/2 ω_R) to avoid rotary resonance recoupling[7] during the CP period. The YX transfer was achieved with SPECIFIC CP,[8] with RF nutation frequencies of ~59, ~20, and 90 kHz for ^{13}C, ^{15}N, and ^{1}H channels, respectively. Low-power XiX decoupling[9] of ~14 kHz was applied during indirect evolution periods. ^{13}C and ^{15}N π pulses during indirect evolution periods were at the maximal field amplitude (according to the π/2 pulses quoted above) and reduced to half the field strength for decoupling during the acquisition period. These π pulses were applied once every 40 rotor periods, with rotor synchronization and *XY*-16 supercycling.[10] The selective π pulse used 484 μs rSNOB to refocus CO.[2, 3, 11]

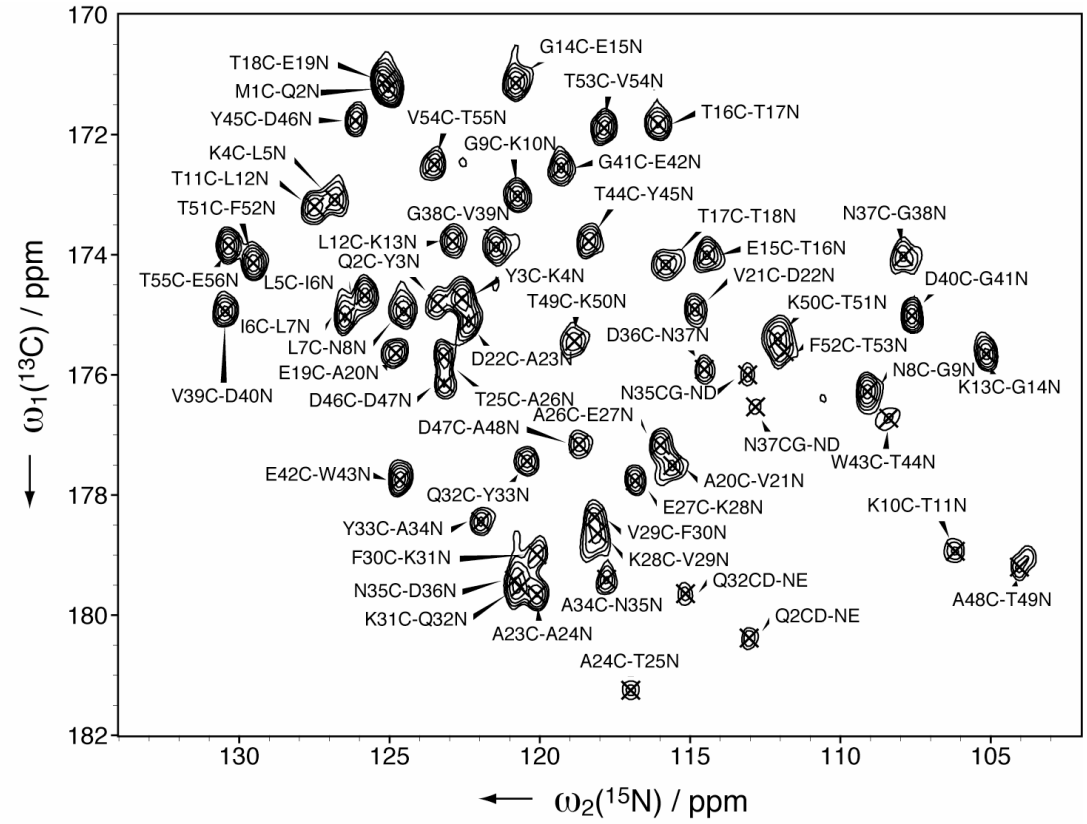

Figure S4. The ^{13}C-^{15}N 2D projection from the CON(H)H 3D spectrum of Fig. 2a (39 kHz MAS, 750 MHz, 2 s recycle delay, 2 scans per row, t_1^{max}(^{13}C) = 18.8 ms, t_2^{max}(^{15}N) = 30 ms, t_3^{max}(^{1}H) = 30 ms, total 36 hours).

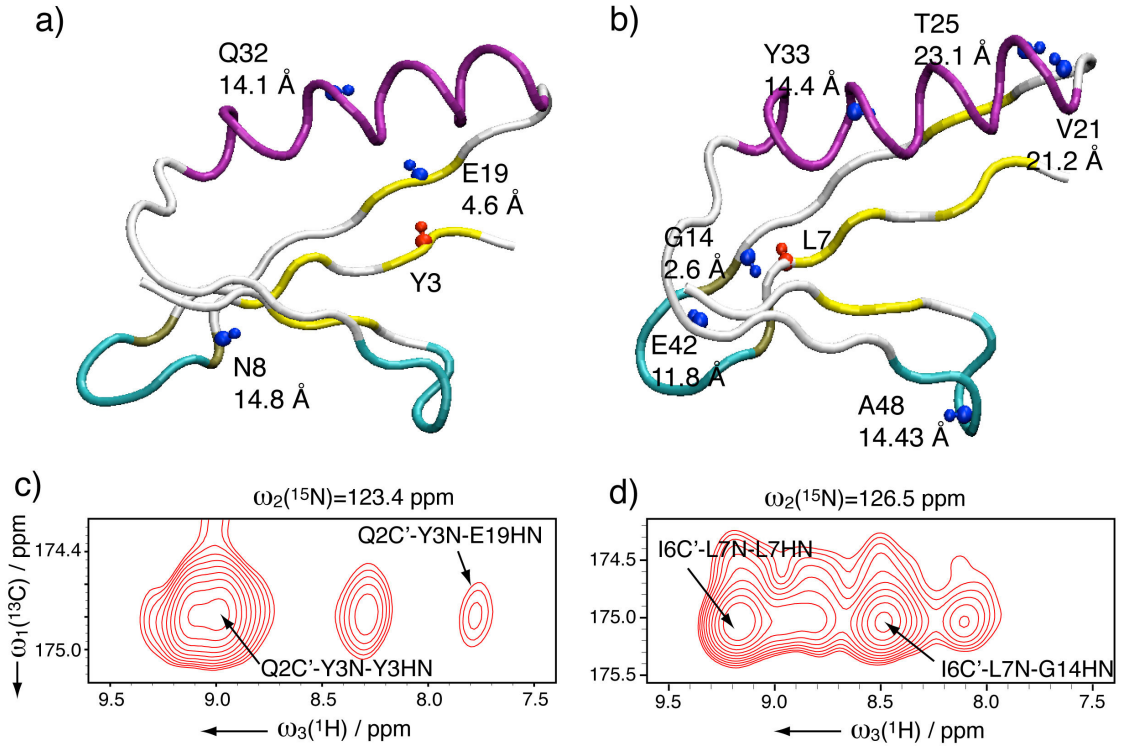

Figure S5. Examples of inter-residue correlation assignments resolved by the assistance of an intermediate structure. (a)-(b) Amide site (red) uniquely resolved by chemical shifts ω_1 (C') and ω_2 (N), corresponding to the origin of spin polarization in the ^{1}H mixing period, and candidate coupling partners that match the HN chemical shift in ω_3 (blue). In each case, only one site with the correct ω_3 chemical shift is within 10 Å. (c)-(d) Two-dimensional plane of CON(H)H 3D showing the inter-residue assignments, which are clarified by the criteria that only pairs within 10 Å give observable correlation peaks at the given 2 ms RFDR mixing. For example, the (174.8, 123.4, 7.78) ppm peak in (c) must arise from Q2C'-Y3N in ω_1 and ω_2, and can be matched in ω_3 to N8HN (7.72), E19HN (7.77), and Q32HN (7.82) within experimental error. However, only E19HN is within 10 Å (a) and therefore this peak is unambiguously assigned to Q2C'-Y3N-E19HN. Similarly, the (175.0, 126.5, 8.49) ppm peak in (d) is assigned to I6C'-L7N-G14HN with the assistance of the intermediate structure despite the presence of several other candidates at similar chemical shifts: G14 (8.50), T25 (8.56), A48 (8.56), V21 (8.57), E42 (8.57), and Y33 (8.59).

Table S1. Interproton distance restraints used in the final round of structure calculations from the CON(H)H 3D with 2 ms ^{1}H-^{1}H mixing.

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
Q2	HN	Q2	HE2	8.5	G14	HN	L7	HN	3.5
Q2	HN	Y3	HN	5.5†	G14	HN	N8	HN	8.5
Q2	HN	T18	HN	8.5	G14	HN	G9	HN	5.5
Q2	HN	A20	HN	5.5	G14	HN	K13	HN	5.5†
Y3	HN	Q2	HN	5.5	E15	HN	L7	HN	8.5
Y3	HN	T18	HN	3.5	E15	HN	G14	HN	5.5†
Y3	HN	E19	HN	8.5	T16	HN	T17	HN	5.5
K4	HN	Q2	HN	8.5	T16	HN	T18	HN	8.5†
K4	HN	Y3	HN	5.5†	T17	HN	T16	HN	5.5
K4	HN	T51	HN	8.5	T17	HN	T18	HN	5.5†
K4	HN	F52	HN	3.5	T17	HN	E19	HN	8.5
L5	HN	G14	HN	8.5	T18	HN	Q2	HE*	8.5
L5	HN	T17	HN	8.5	T18	HN	Y3	HN	3.5
L5	HN	F52	HN	8.5	T18	HN	T17	HN	5.5
L5	HN	V54	HN	8.5	T18	HN	E19	HN	5.5
I6	HN	L5	HN	5.5†	E19	HN	Q2	HN	8.5
I6	HN	F52	HN	3.5	E19	HN	Y3	HN	5.5
I6	HN	V54	HN	5.5†	E19	HN	T18	HN	5.5
L7	HN	I6	HN	5.5†	E19	HN	A20	HN	5.5
L7	HN	G14	HN	3.5	E19	HN	D22	HN	8.5
L7	HN	E15	HN	8.5	A20	HN	Q2	HN	5.5
L7	HN	V54	HN	5.5	A20	HN	Y3	HN	5.5
N8	HN	G9	HN	5.5†	A20	HN	E19	HN	5.5†
N8	HN	K10	HN	8.5	A20	HN	V21	HN	8.5
N8	HN	G14	HN	5.5	A20	HN	D22	HN	8.5
N8	HN	T55	HN	8.5	V21	HN	A20	HN	8.5
N8	HN	E56	HN	5.5	V21	HN	D22	HN	3.5
G9	HN	L7	HN	8.5†	V21	HN	A23	HN	8.5
G9	HN	N8	HN	5.5†	V21	HN	A24	HN	8.5
G9	HN	L12	HN	8.5	D22	HN	Q2	HN	8.5
G9	HN	G14	HN	5.5	D22	HN	A20	HN	8.5
G9	HN	E56	HN	5.5	D22	HN	V21	HN	3.5
K10	HN	G9	HN	5.5	D22	HN	A24	HN	8.5
K10	HN	T11	HN	3.5	A23	HN	V21	HN	5.5
K10	HN	L12	HN	3.5	A23	HN	D22	HN	5.5
K10	HN	E56	HN	3.5	A23	HN	A24	HN	3.5
T11	HN	G9	HN	8.5	A24	HN	D22	HN	8.5
T11	HN	K10	HN	3.5	A24	HN	A23	HN	3.5
T11	HN	L12	HN	3.5	A24	HN	E27	HN	5.5†
T11	HN	E56	HN	8.5	T25	HN	A23	HN	8.5
L12	HN	G9	HN	5.5	T25	HN	A24	HN	5.5
L12	HN	K10	HN	3.5	T25	HN	A26	HN	5.5
L12	HN	T11	HN	3.5	T25	HN	K28	HN	8.5
L12	HN	G14	HN	8.5	T25	HN	V29	HN	8.5
L12	HN	E56	HN	8.5	A26	HN	A23	HN	5.5
K13	HN	L7	HN	8.5†	A26	HN	A24	HN	5.5
K13	HN	G9	HN	8.5	A26	HN	E27	HN	3.5
K13	HN	L12	HN	5.5	A26	HN	K28	HN	5.5
K13	HN	G14	HN	5.5	A26	HN	V29	HN	5.5

Resid.	Atom	Resid.	Atom	d_{max} (Å)
E27	HN	A24	HN	8.5
E27	HN	T25	HN	5.5†
E27	HN	A26	HN	3.5
E27	HN	K28	HN	3.5
E27	HN	V29	HN	5.5
E27	HN	K31	HN	8.5
E27	HN	Q32	HN	8.5
K28	HN	E27	HN	3.5
K28	HN	V29	HN	3.5
K28	HN	F30	HN	8.5
K28	HN	K31	HN	8.5
K28	HN	Q32	HN	8.5
V29	HN	K28	HN	3.5
V29	HN	F30	HN	3.5
V29	HN	K31	HN	5.5
V29	HN	Q32	HE2	8.5
V29	HN	Q32	HN	8.5
F30	HN	K28	HN	5.5
F30	HN	V29	HN	3.5
F30	HN	K31	HN	3.5
F30	HN	Q32	HN	5.5
F30	HN	Q32	HE*	8.5
F30	HN	N35	HN	8.5
K31	HN	K28	HN	8.5
K31	HN	V29	HN	5.5
K31	HN	F30	HN	3.5
K31	HN	Q32	HN	5.5
K31	HN	Q32	HE*	8.5
K31	HN	N35	HN	5.5
Q32	HN	V29	HN	5.5
Q32	HN	Y33	HN	3.5
Y33	HN	K28	HN	8.5
Y33	HN	V29	HN	8.5
Y33	HN	Q32	HN	3.5
Y33	HN	A34	HN	3.5
Y33	HN	N35	HN	5.5
Y33	HN	N35	HD*	8.5
A34	HN	Q32	HN	5.5
A34	HN	Y33	HN	3.5
A34	HN	N35	HN	3.5
A34	HN	N35	HD*	8.5
A34	HN	V39	HN	5.5
N35	HN	Q32	HN	5.5
N35	HN	Q32	HE*	8.5
N35	HN	N35	HD*	8.5
N35	HN	D36	HN	3.5
D36	HN	N35	HN	3.5
D36	HN	N35	HD*	5.5
N37	HN	N35	HN	5.5
N37	HN	N35	HD*	8.5
N37	HN	D36	HN	5.5
N37	HN	G38	HN	3.5
N37	HN	V39	HN	3.5
G38	HN	Y33	HN	8.5
G38	HN	N35	HD*	8.5
G38	HN	N35	HN	8.5
G38	HN	N37	HN	5.5
G38	HN	V39	HN	3.5
G38	HN	D40	HN	8.5†
V39	HN	N35	HN	5.5
V39	HN	N35	HD*	8.5
V39	HN	N37	HN	5.5
V39	HN	G38	HN	3.5
V39	HN	D40	HN	5.5
D40	HN	L12	HN	8.5
D40	HN	N35	HN	8.5
D40	HN	V39	HN	5.5
D40	HN	G41	HN	5.5†
D40	HN	W43	HE1	5.5
G41	HN	D40	HN	5.5†
G41	HN	E42	HN	5.5
G41	HN	W43	HE1	3.5
G41	HN	T55	HN	8.5
E42	HN	D40	HN	8.5†
E42	HN	G41	HN	5.5†
E42	HN	W43	HN	5.5
E42	HN	V54	HN	5.5
E42	HN	T55	HN	3.5
W43	HN	G41	HN	8.5
W43	HN	E42	HN	5.5†
W43	HN	W43	HE1	8.5
W43	HN	T55	HN	5.5
T44	HN	E42	HN	8.5
T44	HN	W43	HN	5.5
D46	HN	T44	HG1	8.5
D46	HN	A48	HN	8.5
D46	HN	F52	HN	8.5
D46	HN	T53	HN	5.5
D47	HN	Y45	HN	8.5
D47	HN	D46	HN	5.5
D47	HN	T49	HN	8.5
D47	HN	K50	HN	8.5
A48	HN	D47	HN	3.5
A48	HN	T49	HN	8.5
A48	HN	K50	HN	8.5
A48	HN	T51	HN	8.5
T49	HN	D47	HN	5.5
T49	HN	A48	HN	8.5
T49	HN	K50	HN	8.5
T49	HN	T51	HN	8.5
K50	HN	D47	HN	5.5
K50	HN	A48	HN	8.5
K50	HN	T49	HN	8.5
K50	HN	T51	HN	5.5

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
T51	HN	F52	HN	8.5	V54	HN	T55	HN	5.5
F52	HN	K4	HN	5.5	V54	HN	E56	HN	8.5†
F52	HN	L5	HN	5.5	T55	HN	L7	HN	8.5
F52	HN	I6	HN	3.5	T55	HN	N8	HN	5.5
F52	HN	T51	HN	5.5	T55	HN	E42	HN	5.5
T53	HN	I6	HN	8.5	T55	HN	V54	HN	5.5
T53	HN	T44	HN	3.5	T55	HN	E56	HN	5.5
T53	HN	T53	HG1	5.5	E56	HN	G9	HN	5.5
T53	HN	V54	HN	8.5	E56	HN	K10	HN	3.5
V54	HN	L7	HN	5.5	E56	HN	D40	HN	5.5
V54	HN	N8	HN	3.5	E56	HN	E42	HN	5.5
V54	HN	E42	HN	8.5	E56	HN	T55	HN	8.5
V54	HN	T53	HG1	8.5					

* These restraints were defined as ambiguous, to both HD1 and HD2 of Asn residues or HE1 and HE2 of Gln residues.
† These restraints were identified as violations and the allowed distance ranges increased to the values listed here.

Table S2. Proton distance restraints used in the final round of structure calculation from the HN(H)H 3D with 2 ms ^{1}H-^{1}H mixing.

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
Q2	HN	Q2	HE*	8.5	G9	HN	E56	HN	5.5
Q2	HN	Y3	HN	5.5†	K10	HN	G9	HN	5.5
Q2	HN	T18	HN	8.5†	K10	HN	T11	HN	3.5
Q2	HN	A20	HN	5.5	K10	HN	L12	HN	3.5
Y3	HN	Q2	HN	5.5	K10	HN	E56	HN	3.5
Y3	HN	T18	HN	3.5	T11	HN	G9	HN	8.5
Y3	HN	E19	HN	8.5	T11	HN	K10	HN	3.5
K4	HN	Q2	HN	8.5	T11	HN	L12	HN	3.5
K4	HN	Y3	HN	5.5†	T11	HN	E56	HN	8.5
K4	HN	T51	HN	8.5	L12	HN	G9	HN	8.5
K4	HN	F52	HN	3.5	L12	HN	K10	HN	3.5
L5	HN	I6	HN	5.5†	L12	HN	T11	HN	3.5
L5	HN	T16	HN	3.5	L12	HN	E56	HN	8.5
L5	HN	F52	HN	8.5	K13	HN	L7	HN	8.5†
I6	HN	L5	HN	5.5†	K13	HN	G9	HN	5.5
I6	HN	F52	HN	3.5	K13	HN	L12	HN	5.5
I6	HN	V54	HN	5.5†	K13	HN	G14	HN	5.5
L7	HN	G14	HN	3.5	G14	HN	L7	HN	3.5
L7	HN	V54	HN	5.5	G14	HN	N8	HN	8.5
N8	HN	G9	HN	5.5†	G14	HN	G9	HN	5.5
N8	HN	K10	HN	8.5	G14	HN	K13	HN	5.5†
N8	HN	G14	HN	8.5	E15	HN	L7	HN	8.5
N8	HN	T55	HN	5.5	E15	HN	G14	HN	5.5
N8	HN	E56	HN	5.5	T16	HN	L5	HN	3.5
G9	HN	L7	HN	8.5†	T16	HN	G14	HN	8.5
G9	HN	N8	HN	5.5†	T16	HN	T17	HN	5.5
G9	HN	K10	HN	5.5	T16	HN	F52	HN	8.5
G9	HN	L12	HN	5.5	T17	HN	T16	HN	5.5
G9	HN	G14	HN	5.5	T17	HN	T18	HN	5.5

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
T18	HN	Q2	HN	8.5†	K31	HN	Q32	HN	5.5
T18	HN	Y3	HN	3.5	K31	HN	N35	HN	8.5
T18	HN	E19	HN	5.5	Q32	HN	K28	HN	8.5
E19	HN	Y3	HN	5.5	Q32	HN	V29	HN	8.5
E19	HN	T17	HN	8.5	Q32	HN	K31	HN	3.5
E19	HN	T18	HN	5.5†	Q32	HN	Y33	HN	3.5
E19	HN	A20	HN	5.5	Q32	HN	N35	HN	8.5
A20	HN	Q2	HN	5.5	Y33	HN	Q32	HN	3.5
A20	HN	Y3	HN	5.5	Y33	HN	A34	HN	3.5
A20	HN	E19	HN	5.5	Y33	HN	N35	HN	5.5
A20	HN	V21	HN	8.5	A34	HN	Q32	HN	5.5
A20	HN	D22	HN	8.5	A34	HN	Y33	HN	3.5
V21	HN	A20	HN	8.5	A34	HN	N35	HN	5.5
V21	HN	D22	HN	3.5	A34	HN	N35	HN	8.5
V21	HN	A24	HN	8.5	N35	HN	Q32	HN	5.5
D22	HN	V21	HN	8.5	N35	HN	Y33	HN	5.5
D22	HN	A23	HN	8.5	N35	HN	N35	HD*	8.5
D22	HN	A24	HN	8.5	N35	HN	D36	HN	3.5
A23	HN	T25	HN	5.5	D36	HN	N35	HD*	5.5
A23	HN	A26	HN	8.5	D36	HN	N35	HN	5.5
A24	HN	A23	HN	3.5	D36	HN	N35	HD*	8.5
A24	HN	A26	HN	5.5	D36	HN	N37	HN	8.5
A24	HN	E27	HN	5.5	D36	HN	G38	HN	5.5
A24	HN	K28	HN	8.5	D36	HN	V39	HN	5.5
A26	HN	A23	HN	8.5	N37	HN	D36	HN	5.5
A26	HN	A24	HN	8.5	N37	HN	V39	HN	5.5
A26	HN	E27	HN	3.5	G38	HN	V39	HN	3.5
A26	HN	K28	HN	5.5	V39	HN	N35	HD*	8.5
A26	HN	V29	HN	8.5	V39	HN	N35	HN	8.5
E27	HN	A23	HN	5.5	V39	HN	N37	HN	5.5
E27	HN	A24	HN	8.5	V39	HN	G38	HN	8.5
E27	HN	A26	HN	3.5	D40	HN	N35	HN	8.5
E27	HN	K28	HN	3.5	D40	HN	V39	HN	5.5
E27	HN	V29	HN	5.5	D40	HN	G41	HN	5.5†
E27	HN	Q32	HN	8.5	D40	HN	W43	HE1	5.5†
K28	HN	E27	HN	3.5	G41	HN	K10	HN	8.5
K28	HN	V29	HN	3.5	G41	HN	V39	HN	8.5†
K28	HN	K31	HN	8.5	G41	HN	D40	HN	5.5†
K28	HN	Q32	HE*	8.5	G41	HN	E42	HN	5.5
K28	HN	Q32	HN	8.5	G41	HN	W43	HE1	3.5
V29	HN	K28	HN	3.5	G41	HN	T55	HN	5.5
V29	HN	F30	HN	3.5	E42	HN	D40	HN	8.5
V29	HN	K31	HN	8.5	E42	HN	G41	HN	5.5†
V29	HN	Q32	HN	8.5	E42	HN	W43	HE1	8.5
V29	HN	Q32	HE*	8.5	E42	HN	W43	HN	8.5
F30	HN	K28	HN	5.5	E42	HN	V54	HN	8.5
F30	HN	V29	HN	5.5	E42	HN	T55	HN	3.5
F30	HN	K31	HN	5.5	W43	HN	W43	HE1	8.5
F30	HN	Q32	HN	5.5	T44	HN	E42	HN	8.5
K31	HN	K28	HN	8.5	T44	HN	Y45	HN	5.5
K31	HN	V29	HN	8.5	T44	HN	V54	HN	8.5
K31	HN	F30	HN	3.5	Y45	HN	T44	HG1	8.5

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
Y45	HN	T44	HN	5.5†	T53	HN	T53	HG1	5.5
Y45	HN	D46	HN	8.5	T53	HN	V54	HN	8.5
Y45	HN	D47	HN	8.5	V54	HN	L7	HN	5.5
D46	HN	D47	HN	8.5	V54	HN	N8	HN	5.5
D46	HN	F52	HN	5.5	V54	HN	E42	HN	5.5
D46	HN	T53	HN	5.5	V54	HN	F52	HN	8.5
D47	HN	D46	HN	8.5	V54	HN	T53	HG1	8.5
D47	HN	T49	HN	8.5	V54	HN	T55	HN	5.5
T49	HN	D47	HN	8.5	V54	HN	E56	HN	8.5
T49	HN	K50	HN	8.5	T55	HN	L7	HN	8.5
T49	HN	T51	HN	8.5	T55	HN	N8	HN	8.5
T51	HN	K4	HN	8.5	T55	HN	E42	HN	8.5
T51	HN	D47	HN	8.5	T55	HN	V54	HN	8.5
T51	HN	K50	HN	8.5	T55	HN	E56	HN	5.5
T51	HN	F52	HN	8.5	E56	HN	N8	HN	5.5
F52	HN	K4	HN	3.5	E56	HN	G9	HN	5.5
F52	HN	I6	HN	3.5	E56	HN	K10	HN	3.5
F52	HN	T51	HN	5.5	E56	HN	E42	HN	5.5
F52	HN	V54	HN	8.5	E56	HN	W43	HE1	8.5
T53	HN	T44	HN	3.5	E56	HN	W43	HN	8.5
T53	HN	F52	HN	5.5†	E56	HN	T55	HN	5.5

* These restraints were defined as ambiguous, to both HD1 and HD2 of Asn residues or HE1 and HE2 of Gln residues.
† These restraints were identified as violations and the allowed distance ranges increased to the values listed here.

Table S3. Proton distance restraints used in the final round of structure calculation from the NH 2D with 3 ms ^{1}H-^{1}H mixing.

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
K4	HN	T51	HN	6	L12	HN	T11	HN	6
K4	HN	F52	HN	6	L12	HN	E56	HN	9
L5	HN	T16	HN	4	K13	HN	K10	HN	9
L5	HN	F52	HN	9	G14	HN	L7	HN	4
I6	HN	F52	HN	6	G14	HN	G9	HN	6
N8	HN	G9	HN	6†	G14	HN	K13	HN	6
N8	HN	K10	HN	9	T16	HN	L5	HN	4
N8	HN	E56	HN	6	T16	HN	F52	HN	9
G9	HN	L7	HN	6	D22	HN	V21	HN	4
G9	HN	N8	HN	6	A23	HN	D22	HN	6
G9	HN	K10	HN	6	K28	HN	E27	HN	4
G9	HN	L12	HN	9	K28	HN	V29	HN	6
G9	HN	G14	HN	6	F30	HN	V29	HN	4
G9	HN	T55	HG1	9	K31	HN	W43	HE1	9
G9	HN	E56	HN	6	Q32	HN	W43	HE1	9
T11	HN	G9	HN	9	N35	HD*	D36	HN	9
T11	HN	K10	HN	6	N35	HD*	V39	HN	6
T11	HN	L12	HN	6	N35	HN	W43	HE1	9
T11	HN	E56	HN	9	G38	HN	N37	HN	6
L12	HN	G9	HN	9	G38	HN	V39	HN	6
L12	HN	K10	HN	6	V39	HN	D40	HN	6

Resid.	Atom	Resid.	Atom	d_{max} (Å)	Resid.	Atom	Resid.	Atom	d_{max} (Å)
V39	HN	W43	HE1	9	T51	HN	A48	HN	6
D40	HN	G41	HN	6†	T51	HN	F52	HN	6
G41	HN	K10	HN	9	F52	HN	K4	HN	4
G41	HN	D40	HN	6†	F52	HN	I6	HN	6
G41	HN	E42	HN	6	F52	HN	T51	HN	9
G41	HN	W43	HE1	4	F52	HN	T53	HG1	9
G41	HN	T55	HG1	9	F52	HN	V54	HN	9
E42	HN	W43	HE1	6	T53	HN	T44	HN	6
E42	HN	T55	HG1	6	T53	HN	T53	HG1	6
W43	HE2	N35	HD*	9	T53	HN	T55	HG1	9
W43	HN	W43	HE1	6	T53	HN	T55	HN	9
W43	HN	T44	HG1	9	V54	HN	N8	HN	4
W43	HN	T55	HG1	9	V54	HN	W43	HE1	9
T44	HN	T44	HG1	6	V54	HN	F52	HN	9
D46	HN	T44	HG1	9	V54	HN	T55	HG1	9
D47	HN	T49	HN	6	T55	HN	W43	HE1	9
A48	HN	F52	HN	9††	T55	HN	T55	HG1	6
T49	HN	D47	HN	6	E56	HN	G9	HN	6
T49	HN	K50	HN	9	E56	HN	K10	HN	6
T49	HN	T51	HN	6	E56	HN	L12	HN	9
T49	HN	F52	HN	9	E56	HN	E42	HN	6
K50	HN	T51	HN	6	E56	HN	T55	HN	6
T51	HN	K4	HN	6	E56	HN	T55	HG1	9

* These restraints were defined as ambiguous, to both HD1 and HD2 of Asn residues or HE1 and HE2 of Gln residues.

† These restraints were identified as violations and the allowed distance ranges increased to the values listed here.

†† This restraint persistently violated and therefore were removed from the final rounds of calculations. The distance between A48 and F52 in the final structure is 9.6 Å. Spin diffusion might have helped to establish this very long distance correlation.

***Table S4*.** XPLOR calculation Statistics.

Restraints	
Total NOE Restraints	517
Intra-Residue	12
Sequential |i-j| = 1	190
Medium Range 1 < |i-j| <= 4	173
Long Range |i-j| > 4	142
2 ms Mixing:	
Strong (1.0 Å to 3.5 Å)	91
Medium (1.0 Å to 5.5 Å)	168
Weak (1.0 Å to 8.5 Å)	179
3 ms Mixing:	
Strong (1.0 Å to 4.0 Å)	9
Medium (1.0 Å to 6.0 Å)	44
Weak (1.0 Å to 9.0 Å)	34
Dihedral restraints (TALOS)	94
Energies (kcal/mol)	
Total	49.0 ± 4.0
Bond lengths	1.2 ± 0.3
Bond angles	33.0 ± 2.0
Van der Waals	1.6 ± 0.8
NOE	8.0 ± 2.0
Dihedral	3.0 ± 1.0
Impropers	3.3 ± 0.5
R.M.S.D.	
Ensemble Backbone	0.82 ± 0.14
Ensemble All	1.71 ± 0.17
Beta Sheet Backbone, Aligned	0.68 ± 0.13
Beta Sheet All, Aligned	1.65 ± 0.17
Helical Backbone, Aligned	0.52 ± 0.13
Helical All, Aligned	1.47 ± 0.13
Average to 2GI9	1.91
Average to 2GI9, Beta Sheet	1.52
Average to 2GI9, Helical	2.42
Average to 2GI9, Helical Aligned	0.57

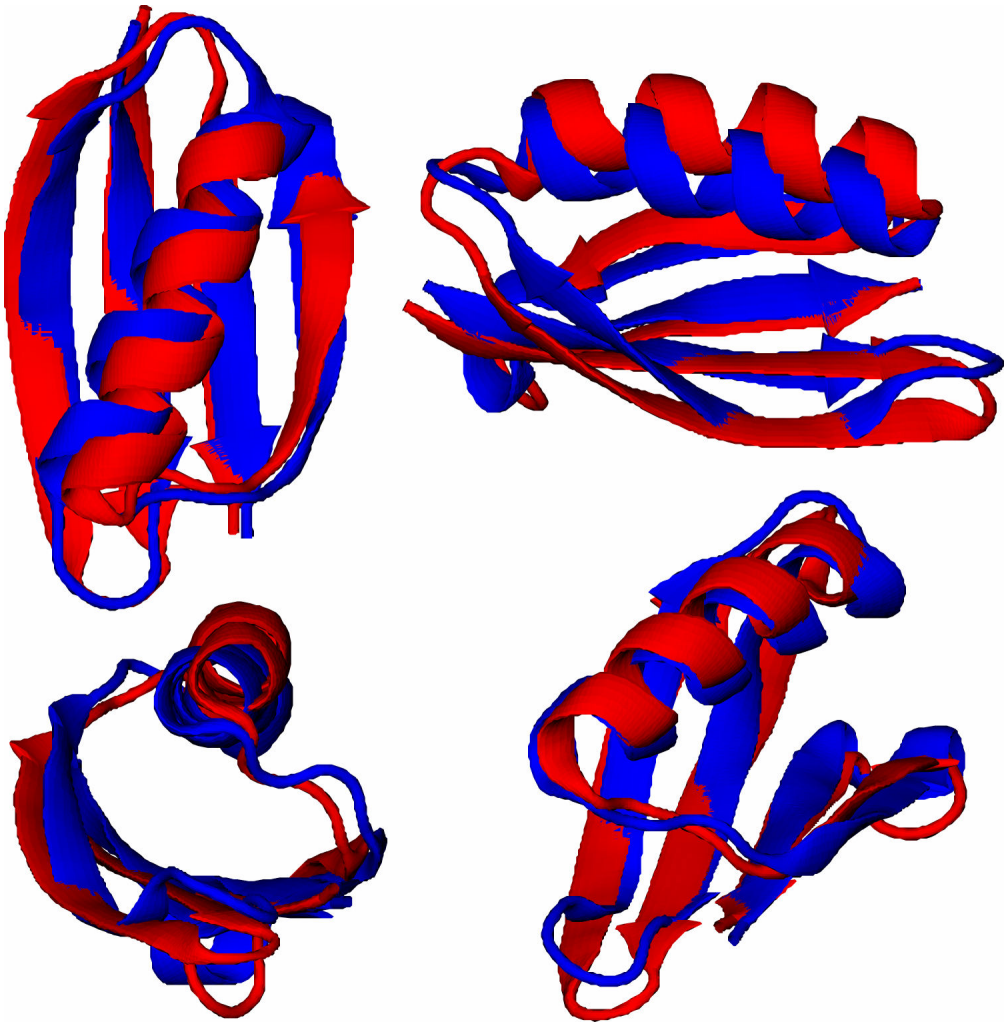

Figure S6. Average SSNMR structure (red) aligned with the crystal structure, PDB entry 2GI9 (blue).

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