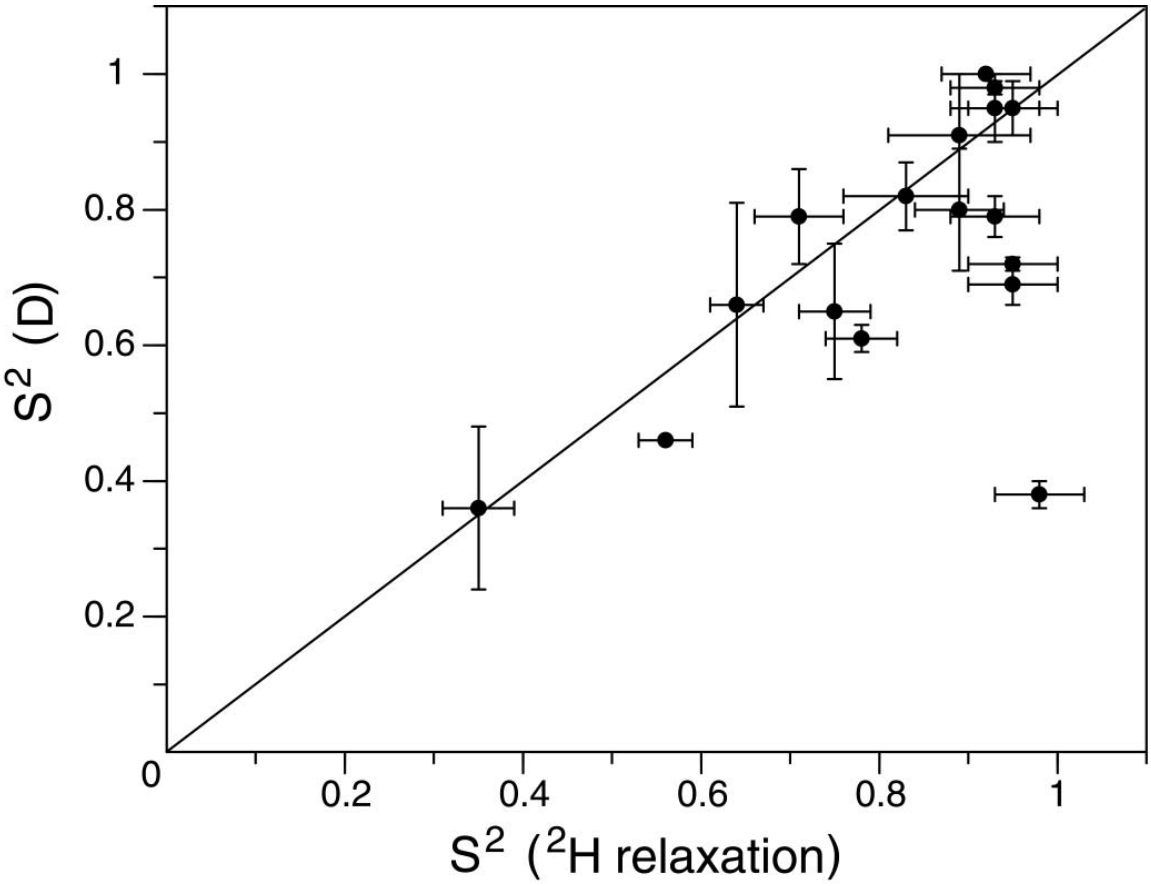
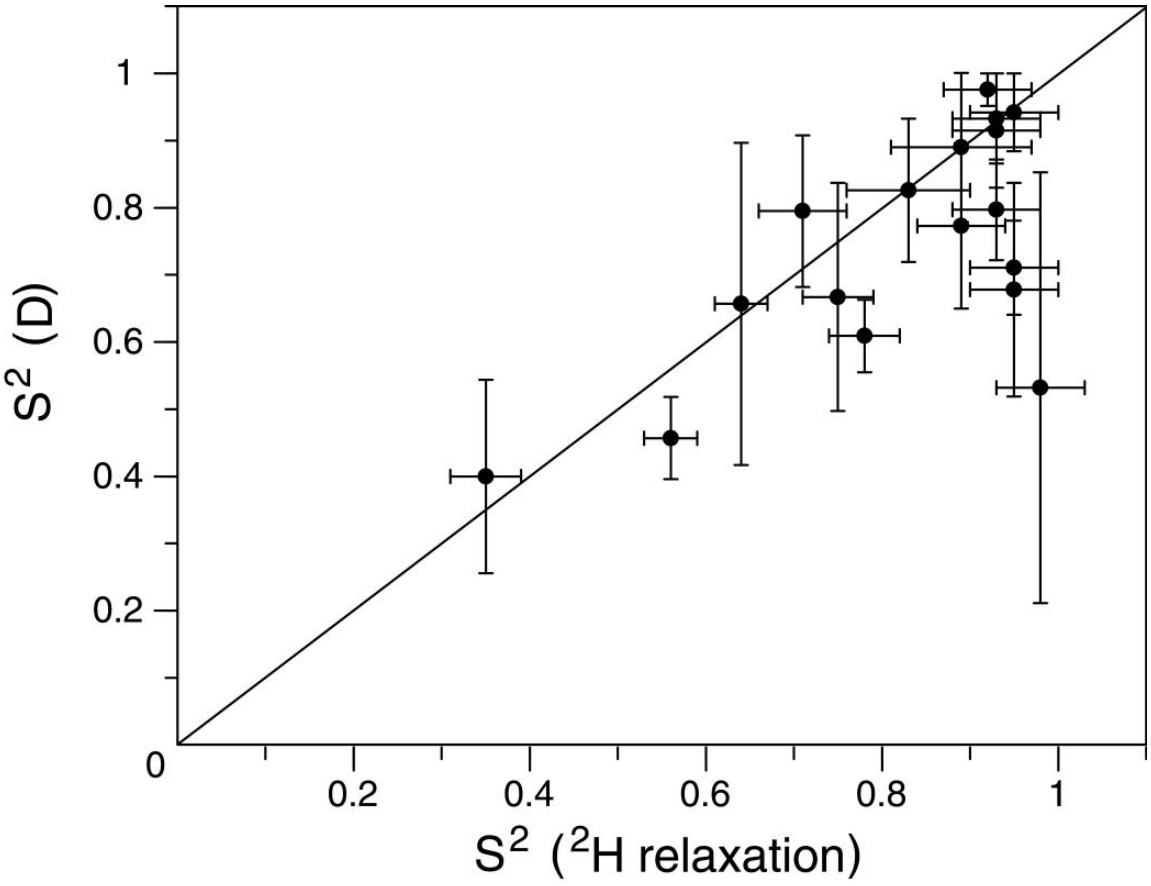
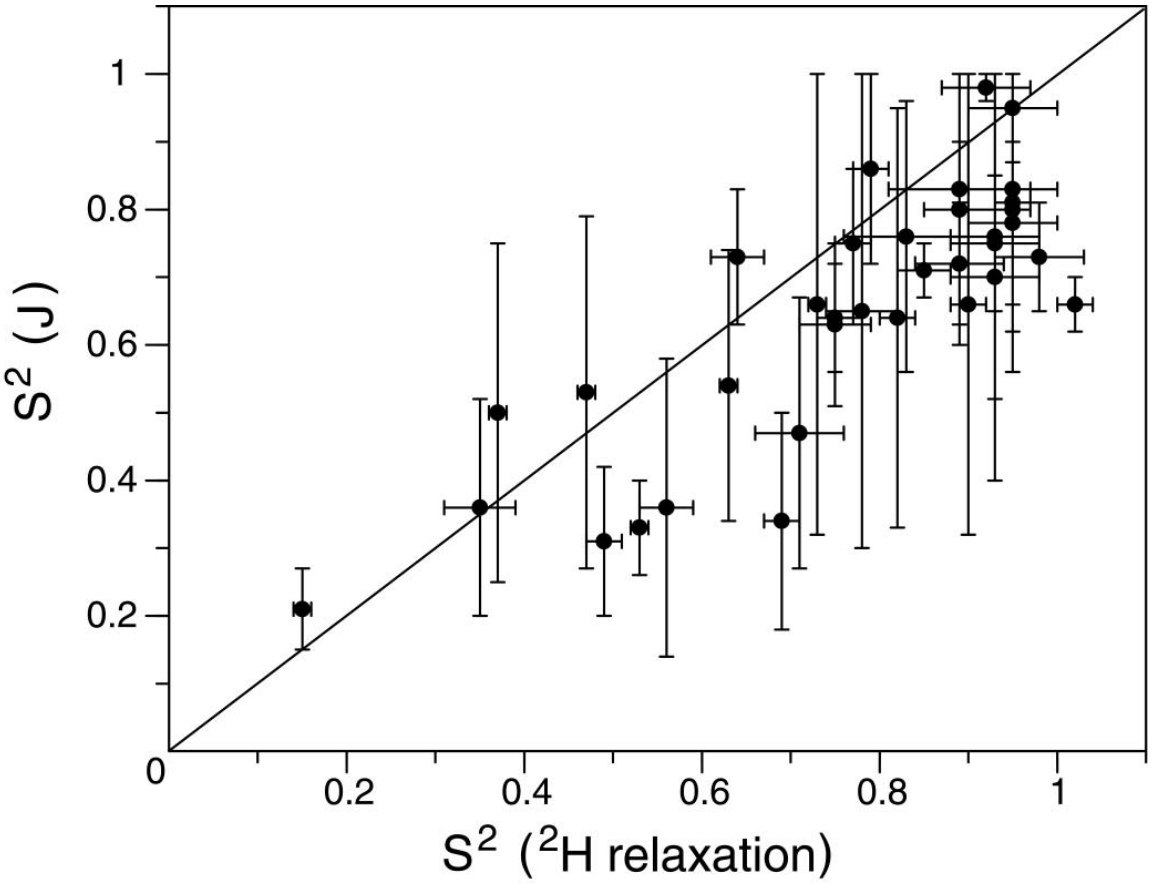


Supporting Information Figure 1. Average $\boldsymbol{S}^2$(D) values, derived from the ensembles of rotamer solutions obtained from dipolar coupling, *versus* $\boldsymbol{S}^2$ values from ^{2}H relaxation experiments for C^{γ} methyl groups in ubiquitin. The correlation coefficient is 0.60 (0.82 without the biggest outlier, I3). Vertical error bars represent the standard deviation of each ensemble of solutions; horizontal bars are reported uncertainties in ^{2}H relaxation-derived $\boldsymbol{S}^2$ values.



Supporting Information Figure 2. The full range of $\boldsymbol{S}^2$(D), derived from the ensembles of rotamer solutions obtained from dipolar coupling, *versus* $\boldsymbol{S}^2$ values from ^{2}H relaxation experiments for C^{γ} methyl groups in ubiquitin. The correlation coefficient is 0.60 (0.82 without the biggest outlier, I3). The vertical bars mark the entire range of $\boldsymbol{S}^2$ values for the full ensemble of solutions, whereas the solid circles mark the midpoint ($\boldsymbol{S}^2$(min) + $\boldsymbol{S}^2$(max))/2; horizontal bars mark reported uncertainties in ^{2}H relaxation-derived $\boldsymbol{S}^2$ values. The correlation coefficient is 0.67 (0.81 without the biggest outlier I3).



Supporting Information Figure 3. The full range of $\boldsymbol{S}^2$(J), derived from the ensembles of rotamer solutions obtained from $^3J_{NC\gamma}$, and $^3J_{C'C\gamma}$ coupling, *versus* $\boldsymbol{S}^2$ values from ^{2}H relaxation experiments for C^{γ} methyl groups in ubiquitin and HIV protease. The vertical bars mark the entire range of $\boldsymbol{S}^2$ values for the full ensemble of solutions, whereas the solid circles mark the midpoint ($\boldsymbol{S}^2$(min) + $\boldsymbol{S}^2$(max))/2; horizontal bars mark reported uncertainties in ^{2}H relaxation-derived $\boldsymbol{S}^2$ values. The correlation coefficient is 0.82.

Supporting Information Table 1. Experimental $^3J_{N-C\gamma}$ and $^3J_{C'-C\gamma}$ for Val, Ile, and Thr in ubiquitin, GB3, and HIV-protease, complexed with DMP323.

γ-carbon	^3J (N–Cγ)	^3J (C′–Cγ)	χ_1 (X-ray)
ubiquitin			
V5γ1	1.83 (1.81 – 1.85)	0.00 (0.00 – 0.11)	-180
V5γ2	0.46 (0.38 – 0.52)	3.66 (3.65 – 3.67)	
V17γ1	0.25 (0.00 – 0.37)	3.93 (3.92 – 3.94)	-62
V17γ2	0.68 (0.63 – 0.73)	0.96 (0.93 – 0.99)	
V26γ1	2.16 (2.14 – 2.17)	0.82 (0.78 – 0.85)	168
V26γ2	0.62 (0.56 – 0.68)	4.18 (4.17 – 4.19)	
V70γ2	0.50 (0.46 – 0.53)	2.43 (2.42 – 2.44)	177
T7γ2	1.02 (0.98 – 1.05)	2.67 (2.66 – 2.68)	77
T9γ2	0.81 (0.78 – 0.84)	3.00 (2.99 – 3.01)	71
T12γ2	1.61 (1.58 – 1.63)	0.39 (0.29 – 0.46)	-63
T14γ2	1.50 (1.48 – 1.52)	0.76 (0.72 – 0.79)	66
T22γ2	0.75 (0.70 – 0.80)	3.39 (3.38 – 3.40)	61
T55γ2	0.82 (0.77 – 0.86)	3.02 (3.01 – 3.03)	60
I3γ2	0.39 (0.29 – 0.48)	3.68 (3.67 – 3.69)	60
I13γ2	1.44 (1.42 – 1.45)	1.71 (1.70 – 1.72)	126
I23γ2	2.11 (2.09 – 2.13)	0.94 (0.90 – 0.98)	-61
I30γ2	2.10 (2.09 – 2.12)	0.96 (0.92 – 0.99)	-71
I36γ2	2.08 (2.07 – 2.10)	0.71 (0.67 – 0.75)	-54
I44γ2	1.62 (1.60 – 1.64)	0.80 (0.78 – 0.83)	-49
I61γ2	2.15 (2.13 – 2.16)	0.98 (0.95 – 1.01)	-70
GB3			
V6γ1	1.99 (1.97 – 2.00)	0.77 (0.74 – 0.80)	172
V6γ2	0.53 (0.47 – 0.58)	3.68 (3.67 – 3.69)	
V21γ1	0.69 (0.66 – 0.71)	2.52 (2.51 – 2.52)	-66
V21γ2	1.08 (1.06 – 1.10)	1.09 (1.07 – 1.10)	
V39γ1	1.86 (1.84 – 1.87)	0.86 (0.84 – 0.89)	171
V39γ2	0.58 (0.54 – 0.62)	3.27 (3.27 – 3.28)	
V42γ1	1.73 (1.72 – 1.75)	1.27 (1.26 – 1.29)	-62
V42γ2	0.74 (0.71 – 0.76)	3.04 (3.04 – 3.05)	
V54γ1	0.83 (0.78 – 0.87)	0.70 (0.66 – 0.75)	58
V54γ2	1.85 (1.82 – 1.87)	1.01 (0.97 – 1.05)	
I7γ2	1.97 (1.95 – 1.99)	0.58 (0.52 – 0.63)	-47
T11γ2	0.90 (0.87 – 0.92)	2.11 (2.10 – 2.12)	-102
T16γ2	0.21 (0.00 – 0.35)	1.78 (1.76 – 1.80)	-172
T17γ2	0.56 (0.50 – 0.61)	2.80 (2.80 – 2.81)	66
T18γ2	0.00 (0.00 – 0.25)	1.69 (1.67 – 1.71)	-161
T25γ2	1.75 (1.72 – 1.79)	2.60 (2.58 – 2.62)	-59
T44γ2	0.47 (0.40 – 0.53)	2.88 (2.87 – 2.89)	62

T49γ2	0.77 (0.73 – 0.80)	3.05 (3.04 – 3.06)	63
T51γ2	1.61 (1.58 – 1.64)	0.52 (0.43 – 0.60)	-58
T53γ2	1.57 (1.54 – 1.60)	0.45 (0.35 – 0.53)	-53
T55γ2	1.51 (1.48 – 1.53)	0.00 (0.00 – 0.18)	-177
HIV-protease			
V11γ1	0.33 (0.00 – 0.84)	3.71 (3.63 – 3.80)	73
V11γ2	0.18 (0.00 – 0.65)	0.47 (0.00 – 1.01)	
V32γ1	1.53 (1.38 – 1.69)	0.43 (0.03 – 0.84)	36
V56γ1	0.38 (0.00 – 0.80)	3.90 (3.80 – 3.98)	106
V56γ2	0.44 (0.01 – 0.96)	1.12 (0.64 – 1.63)	
V75γ1	1.44 (1.36 – 1.51)	1.75 (1.65 – 1.83)	-40
V75γ2	0.00 (0.00 – 0.46)	2.64 (2.54 – 2.75)	
V77γ1	1.73 (1.63 – 1.87)	1.11 (0.80 – 1.43)	175
V77γ2	0.40 (0.08 – 0.71)	3.54 (3.46 – 3.60)	
V82γ1	0.89 (0.82 – 0.95)	1.73 (1.69 – 1.77)	-68
V82γ2	1.09 (1.04 – 1.14)	1.48 (1.43 – 1.52)	
I13γ2	0.64 (0.19 – 1.12)	3.66 (3.56 – 3.78)	61
I15γ2	1.03 (0.80 – 1.26)	0.55 (0.11 – 0.99)	-16
I33γ2	1.53 (1.39 – 1.68)	1.29 (1.05 – 1.53)	c
I47γ2	0.78 (0.48 – 1.09)	2.86 (2.80 – 2.92)	75
I54γ2	0.60 (0.18 – 1.03)	3.73 (3.65 – 3.81)	62
I62γ2	2.13 (2.04 – 2.21)	0.41 (0.00 – 0.98)	-46
I63γ2	1.86 (1.80 – 1.92)	0.84 (0.66 – 1.03)	c
I64γ2	1.20 (1.00 – 1.40)	0.78 (0.37 – 1.19)	-176
I66γ2	2.26 (2.02 – 2.44)	0.92 (0.22 – 1.59)	-57
I72γ2	1.40 (1.33 – 1.46)	0.67 (0.49 – 0.87)	-155
I84γ2	0.95 (0.61 – 1.26)	0.64 (0.15 – 1.16)	-62
I85γ2	2.11 (1.95 – 2.26)	0.28 (0.00 – 0.91)	-66

[a] The range of couplings compatible with the measurement is shown in parentheses. Note that due to the nature of quantitative J correlation, the range is no symmetric about the center, most probably value, particularly for the smallest couplings.
[b] The X-ray χ_1 angles are extracted from PDB codes 1UBQ for ubiquitin, 1IGD for GB3, and 1QBS for the HIV-protease.
[c] Different residue in X-ray structure.

Supporting Information Table 2. Sidechain rotamer populations (P) and corresponding average χ_1 angles of Val, Ile, and Thr residues in GB3, derived from sidechain dipolar couplings in two liquid crystalline media.[a]

Residue	P^{180}	P^{-60}	P^{+60}	χ_1^{180}	χ_1^{-60}	χ_1^{+60}	χ_1 (Xray) [b]
V6	0.81 (0.06)	0.18 (0.06)	0.01 (0.02)	177 (3)	-56 (16)	60 (18)	172
V21	0.50 (0.02)	0.50 (0.02)	0.00 (0.00)	168 (3)	-86 (3)	60 (18)	-66
V39	0.77 (0.01)	0.13 (0.01)	0.10 (0.01)	176 (3)	-70 (14)	64 (17)	171
V42	0.80 (0.02)	0.08 (0.02)	0.12 (0.02)	175 (4)	-55 (17)	56 (17)	-62
V54	0.01 (0.02)	0.20 (0.06)	0.79 (0.06)	180 (18)	-63 (16)	52 (4)	58
I7	0.07 (0.02)	0.92 (0.02)	0.01 (0.02)	174 (15)	-60 (1)	60 (18)	-47
T11	0.21 (0.02)	0.28 (0.02)	0.51 (0.01)	202 (7)	-86 (4)	73 (2)	-102
T16	0.77 (0.01)	0.01 (0.01)	0.22 (0.02)	187 (1)	-61 (18)	38 (5)	-172
T17	0.11 (0.02)	0.07 (0.01)	0.82 (0.02)	196 (12)	-71 (16)	68 (1)	66
T18	0.92 (0.01)	0.02 (0.02)	0.06 (0.02)	192 (1)	-55 (18)	46 (15)	-161
T25	0.09 (0.07)	0.86 (0.03)	0.05 (0.05)	189 (16)	-64 (6)	54 (17)	-59
T44	0.08 (0.06)	0.11 (0.08)	0.81 (0.05)	182 (17)	-63 (17)	62 (4)	62
T49	0.04 (0.00)	0.01 (0.01)	0.95 (0.01)	185 (17)	-62 (18)	66 (2)	63
T51	0.02 (0.04)	0.98 (0.04)	0.00 (0.00)	177 (19)	-55 (2)	60 (18)	-58
T53	0.03 (0.05)	0.68 (0.02)	0.29 (0.05)	171 (19)	-56 (2)	90 (1)	-53
T55	0.24 (0.04)	0.75 (0.04)	0.01 (0.01)	161 (5)	-63 (2)	59 (18)	-177

[a] Values represent the mean of all possible solutions from the dipolar grid search; standard deviations are shown in parentheses.

[b] The X-ray χ_1 angles are taken from the 1.1-Å X-ray structure of GB3 (PDB code 1IGD).

Supporting Information Table 3. Generalized order parameters derived from experimental $^3J_{N-C\gamma}$ and $^3J_{C'-C\gamma}$ ($\boldsymbol{S}_J^2$), dipolar couplings ($\boldsymbol{S}_D^2$), and ^{2}H relaxation rates ($\boldsymbol{S}_{rel}^2$) in GB3 and HIV protease.[a]

γ-carbon	$\boldsymbol{S}_J^2$ Mean (Std)	$\boldsymbol{S}_J^2$ Min - Max	$\boldsymbol{S}_D^2$ Mean (Std)	$\boldsymbol{S}_D^2$ Min - Max	$\boldsymbol{S}_{rel}^2$ [b]
GB3					
V6γ	0.67 (0.02)	0.62 – 0.73	0.64 (0.08)	0.52 – 0.74	-
V21γ	0.24 (0.02)	0.20 – 0.29	0.26 (0.01)	0.24 – 0.28	-
V39γ	0.46 (0.02)	0.42 – 0.51	0.49 (0.01)	0.43 – 0.57	-
V42γ	0.35 (0.01)	0.32 – 0.40	0.59 (0.07)	0.48 – 0.73	-
V54γ	0.62 (0.06)	0.48 – 0.76	0.56 (0.06)	0.45 – 0.65	-
I7γ2	0.73 (0.11)	0.43 – 0.95	0.81 (0.01)	0.76 – 0.85	-
T11γ2	0.27 (0.05)	0.18 – 0.51	0.40 (0.04)	0.36 – 0.45	-
T16γ2	0.47 (0.16)	0.18 – 1.00	0.68 (0.04)	0.63 – 0.76	-
T17γ2	0.47 (0.03)	0.41 – 0.59	0.65 (0.02)	0.57 – 0.78	-
T18γ2	0.32 (0.16)	0.11 – 1.00	0.86 (0.01)	0.81 – 0.91	-
T25γ2	0.97 (0.02)	0.92 – 1.00	0.66 (0.17)	0.49 – 0.80	-
T44γ2	0.50 (0.03)	0.45 – 0.62	0.61 (0.05)	0.52 – 0.69	-
T49γ2	0.73 (0.04)	0.64 – 0.84	0.89 (0.04)	0.84 – 0.93	-
T51γ2	0.77 (0.12)	0.39 – 1.00	0.97 (0.03)	0.76 – 1.00	-
T53γ2	0.73 (0.12)	0.37 – 1.00	0.58 (0.01)	0.55 – 0.63	-
T55γ2	0.57 (0.15)	0.29 – 1.00	0.59 (0.02)	0.53 – 0.66	-
HIV-protease					
V11γ	0.72 (0.05)	0.63 – 0.86	-	-	0.77 ± 0.02
V32γ	0.59 (0.14)	0.32 – 1.00	-	-	0.73 ± 0.01
V56γ	0.81 (0.03)	0.73 – 0.88	-	-	0.95 ± 0.02
V75γ	0.27 (0.04)	0.20 – 0.41	-	-	0.49 ± 0.02
V77γ	0.62 (0.03)	0.56 – 0.72	-	-	0.75 ± 0.02
V82γ	0.20 (0.02)	0.15 – 0.27	-	-	0.15 ± 0.01
I13γ2	0.66 (0.02)	0.62 – 0.70	-	-	1.02 ± 0.02
I15γ2	0.58 (0.13)	0.33 – 1.00	-	-	0.90 ± 0.02
I33γ2	0.29 (0.07)	0.18 – 0.50	-	-	0.69 ± 0.02
I47γ2	0.32 (0.03)	0.26 – 0.41	-	-	0.53 ± 0.01
I54γ2	0.71 (0.02)	0.66 – 0.75	-	-	0.85 ± 0.03
I62γ2	0.94 (0.06)	0.71 – 1.00	-	-	0.79 ± 0.02
I63γ2	0.53 (0.10)	0.34 – 0.74	-	-	0.63 ± 0.01
I64γ2	0.43 (0.10)	0.25 – 0.75	-	-	0.37 ± 0.01
I66γ2	0.90 (0.11)	0.62 – 1.00	-	-	0.95 ± 0.02
I72γ2	0.47 (0.10)	0.27 – 0.78	-	-	0.47 ± 0.01
I84γ2	0.56 (0.13)	0.33 – 0.95	-	-	0.82 ± 0.02
I85γ2	0.91 (0.07)	0.60 – 1.00	-	-	0.89 ± 0.04

[a] The mean $\boldsymbol{S}^2$ with corresponding standard deviation (in parentheses) of solution ensembles, derived from ^3J and dipolar couplings are shown respectively in columns 2 and 4; columns 3 and 5 present the full $\boldsymbol{S}^2$ ranges compatible with the experimental data.
[b] Values reported in: Ishima, R.; Petkova, A. P.; Louis, J. M.; Torchia, D. A. *J. Am. Chem. Soc.* **2001**, *123*, 6164-6171.

Supporting Information Table 4. DFT results for $^{3}J_{N-C\gamma}$ and $^{3}J_{C'-C\gamma}$ for Val and Thr.

a. Valine, backbone sheet configuration

τ(Cγ1-C)	τ(Cγ2-C)	^{3}J(Cγ1-C)	^{3}J(Cγ2-C)
-169.7	-45.8	3.47	0.99
-154.9	-30.4	2.35	1.60
-138.7	-12.7	1.13	2.41
-121.3	6.4	0.24	2.71
-104.4	24.5	-0.08	2.58
-89.6	38.9	0.11	2.08
-76.3	50.9	0.35	1.38
-62.9	62.9	0.74	0.47
-48.9	75.8	1.27	-0.07
-34.3	89.7	1.74	-0.01
-18.5	105.9	1.93	0.70
-1.6	124.0	2.05	2.00
15.4	142.0	1.73	3.14
31.7	157.9	1.45	3.72
46.6	171.2	1.01	3.77
60.6	-176.4	0.51	3.51
74.2	-164.0	0.13	3.12
88.0	-150.5	0.09	2.35
103.0	-134.3	0.73	1.46
119.3	-115.7	2.07	0.59
135.2	-98.2	3.53	0.01
149.4	-84.3	4.40	-0.03
162.7	-72.2	4.63	0.03
176.2	-59.5	4.29	0.45

b. Valine, backbone helix configuration

τ(Cγ1-C)	τ(Cγ2-C)	^{3}J(Cγ1-C)	^{3}J(Cγ2-C)
-176.6	-51.6	3.35	1.18
-161.8	-36.4	2.34	2.04
-145.7	-19.3	1.31	2.79
-127.9	-0.2	0.50	2.94
-110.6	18.4	0.06	2.64
-95.0	33.8	-0.11	1.93
-81.3	46.5	0.20	0.98
-67.8	58.8	0.60	0.34
-54.2	71.0	1.22	-0.09
-40.2	83.8	1.82	0.09
-25.0	98.8	2.27	0.67
-8.4	116.6	2.31	1.64
8.7	134.8	2.12	2.62
24.9	150.5	1.69	3.32
40.0	163.4	1.12	3.64
54.4	176.0	0.43	3.78
69.1	-169.5	0.02	3.53
83.2	-154.7	0.18	3.23
97.7	-138.5	0.89	1.89
113.4	-120.6	2.17	0.91
129.1	-103.2	3.44	0.22
143.4	-88.9	4.27	-0.11
156.8	-76.5	4.42	0.00
169.8	-64.5	4.09	0.46

c. Valine, backbone sheet configuration

τ(Cγ1-N)	τ(Cγ2-N)	^{3}J(Cγ1-N)	^{3}J(Cγ2-N)
-180	-57.0	-1.90	-0.46
-165	-43.2	-1.79	-0.89
-150	-28.5	-1.48	-1.43
-135	-12.3	-1.01	-1.94
-120	5.0	-0.47	-2.16
-105	21.7	-0.07	-1.96
-90	36.3	0.10	-1.61
-75	50.1	0.00	-0.99
-60	64.3	-0.39	-0.36
-45	79.0	-0.91	0.01
-30	94.5	-1.49	0.11
-15	111.0	-1.98	-0.03
0	127.9	-2.21	-0.34
15	143.9	-2.03	-0.76
30	158.4	-1.59	-1.22
45	172.2	-0.97	-1.64
60	-174.1	-0.36	-1.99
75	-160.2	0.10	-2.17
90	-146.0	0.12	-2.05
105	-130.6	-0.16	-1.61
120	-114.4	-0.68	-0.91
135	-98.4	-1.25	-0.26
150	-83.8	-1.67	0.06
165	-70.4	-1.86	-0.04
180	-57.0	-1.90	-0.46

d. Valine, backbone helix configuration

τ(Cγ1-N)	τ(Cγ2-N)	^{3}J(Cγ1-N)	^{3}J(Cγ2-N)
-180	-58.4	-1.81	-0.57
-165	-43.7	-1.54	-1.39
-150	-27.9	-1.15	-2.09
-135	-11.2	-0.74	-2.51
-120	6.0	-0.37	-2.68
-105	22.7	-0.08	-2.45
-90	37.7	0.01	-1.74
-75	51.7	-0.11	-1.09
-60	65.6	-0.61	-0.41
-45	80.0	-1.37	-0.01
-30	95.5	-2.05	-0.10
-15	111.4	-2.45	-0.05
0	127.8	-2.63	-0.35
15	144.2	-2.41	-0.76
30	158.9	-1.93	-1.17
45	172.9	-1.19	-1.54
60	-173.3	-0.44	-1.86
75	-159.7	0.02	-2.01
90	-146.0	0.10	-1.86
105	-131.2	-0.21	-1.45
120	-115.0	-0.77	-0.81
135	-98.8	-1.35	-0.18
150	-84.4	-1.75	0.12
165	-71.5	-1.87	0.04
180	-58.4	-1.81	-0.57

e. Threonine, backbone sheet configuration

τ(Oγ1-N)	τ(Cγ2-C)	^{3}J(Cγ2-C)	τ(Cγ2-N)	^{3}J(Cγ2-N)
-165	-50.6	1.33	73.7	0.18
-150	-36.1	1.71	88.7	0.14
-135	-20.4	1.76	103.7	-0.24
-120	-3.5	1.60	118.7	-0.83
-105	13.6	1.29	133.7	-1.34
-90	30.1	0.83	148.7	-1.62
-75	45.0	0.46	163.7	-1.65
-60	59.1	0.26	178.7	-1.52
-45	72.9	0.03	-166.3	-1.25
-30	87.0	0.12	-151.3	-0.82
-15	102.0	1.01	-136.3	-0.37
0	118.0	2.36	-121.3	-0.06
15	137.3	3.68	-106.3	0.00
30	152.3	4.21	-91.3	-0.05
45	165.1	4.00	-76.3	-0.14
60	174.8	3.63	-61.3	-0.46
75	-171.7	2.95	-46.3	-0.94
90	-157.2	1.96	-31.3	-1.47
105	-140.7	0.89	-16.3	-1.92
120	-122.6	0.09	-1.3	-1.96
135	-105.0	-0.07	13.7	-1.71
150	-90.0	0.19	28.7	-1.30
165	-76.9	0.51	43.7	-0.71
180	-64.0	0.89	58.7	-0.12

f. Threonine, backbone helix configuration

τ(Oγ1-N)	τ(Cγ2-C)	^{3}J(Cγ2-C)	τ(Cγ2-N)	^{3}J(Cγ2-N)
-165	-57.2	1.07	70.5	0.09
-150	-43.4	1.58	85.1	0.09
-120	-9.7	1.97	117.6	-1.00
-105	8.8	1.71	134.2	-1.57
-90	26.3	1.30	150.1	-1.84
-75	41.5	0.66	164.9	-1.74
-60	55.2	0.21	179.2	-1.42
-45	68.3	0.02	-166.7	-1.01
-30	80.9	0.16	-152.6	-0.70
-15	94.3	1.01	-138.2	-0.45
0	109.8	2.20	-122.8	-0.19
15	126.4	3.45	-106.8	-0.01
30	142.0	4.13	-91.3	0.09
45	155.3	4.09	-76.8	-0.15
60	167.3	3.44	-63.1	-0.87
75	178.4	2.63	-49.8	-1.64
90	-169.3	1.79	-36.0	-2.36
105	-154.4	0.89	-20.8	-2.82
120	-136.5	0.18	-4.5	-2.71
135	-113.2	0.03	15.0	-1.61
150	-101.2	0.12	28.1	-1.10
165	-83.6	0.32	45.0	-0.61
180	-69.6	0.65	57.1	-0.11