

Supporting Information for: “Optimization of the additive CHARMM all-atom protein force field targeting improved sampling of the backbone ϕ , ψ and sidechain χ_1 and χ_2 dihedral angles.”

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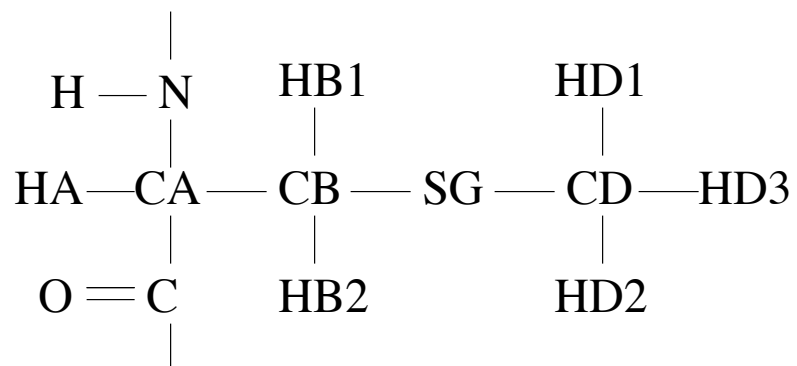


Figure S1) Covalent structure of the modified CME residue (see SI TableS1 for the parameters).

Figure S2) RMS difference of the individual helicies of the dimeric coiled-coil 1u0i as a function of simulation time. Results are for the backbone (N, Ca, C, O) atoms following least squares alignment of the backbone atoms of the individual helicies, with results presented for the helix being aligned to itself (ie. Helix A vs Helix A) or for the second helix based on alignment to the first (ie. Helix B vs Helix A). Results are presented for alignment to helix A (A) or helix B (B). The N- and C-terminal residues were excluded from the analysis.

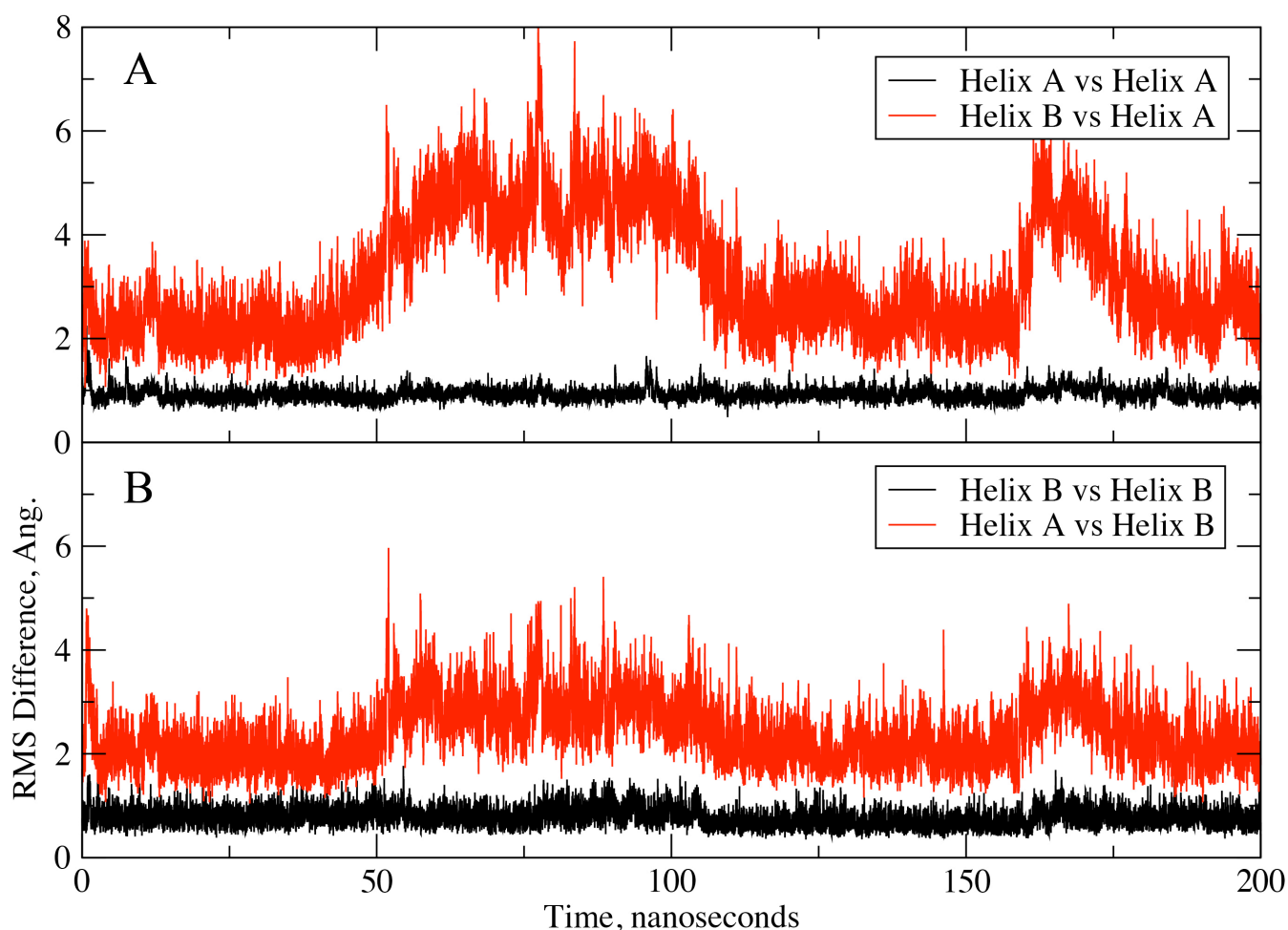


Table S1) Additional parameters for the S-methylated cysteine (CME) residue in HEWL19. Atom types and charges are given in upper part and torsion angle parameters are given in the lower part. The torsion potential has the form: $V_n(\chi) = k_n(1 + \cos[n\chi - \delta_n])$ where k_n is a force constant, δ_n is a phase shift, and n the multiplicity. All other parameter values were taken from the standard C36 force-fields. Figure S1 shows the structure of the residue.

Atom	CHARMM Atom Type	Charge (e)
N	NH1	-0.47
H	H	0.31
CA	CT1	-0.07
HA	HB1	0.09
CB	CT2	-0.11
HB1	HA2	0.09
HB2	HA2	0.09
SG	S	-0.23
CD	CT3	-0.11
HD1	HA3	0.09
HD2	HA3	0.09
HD3	HA3	0.09
C	C	0.51
O	O	-0.51

ATOM 1	ATOM 2	ATOM 3	ATOM 4	n	k_n [kcal/mol]	δ_n
CT3	S	CT2	CT1	1	0.24	180.0°
CT3	S	CT2	CT1	3	0.37	0.0°

Table S2) Distances used for water deletion, simulation temperatures, experimental protein crystal lattice distances and average percent changes for the lattice distances for the full unit-cell crystal simulations.

PDB ID	Water del (Å) ¹	T(K)	Crystallographic			C22/CMAP			C36		
			A	B	C	ΔA (%)	ΔB	ΔC	ΔA	ΔB	ΔC
135L	2.82	298	38.59	32.89	48.37	1.46	0.39	3.58	1.55	1.51	2.47
3EBX	4.00	298	52.19	47.49	21.49	5.10	1.09	0.91	6.00	3.62	-0.70
1EJG	3.20	100	40.83	18.51	22.34	-0.75	0.30	0.17	0.05	-0.19	0.14
1I27	3.50	282	29.42	44.34	49.20	1.72	3.83	1.70	2.82	2.13	1.17
5PTI	3.50	298	71.88	25.14	28.89	-2.05	3.94	-0.19	-0.43	3.41	-0.79
3ICB	2.78	298	53.32	43.94	29.95	-4.15	0.87	2.60	-1.27	0.80	0.43
1BYI	2.85	100	72.53	47.73	61.58	-0.57	0.34	2.40	0.00	0.02	0.77
1BZP	3.10	298	36.68	30.60	68.22	2.54	0.20	7.63	4.13	-1.74	10.58

Lattice parameters (Å) were calculated by averaging over all snapshots at 5ps intervals within the last 35ns of the 40ns crystal simulations. 1) Water O to protein non-hydrogen distance used for the deletion of water molecules during preparation of the crystal for MD simulations.

Table S3) Estimated uncertainty for predictions of scalar couplings from various Karplus equation parametrizations and for predictions of chemical shifts by SPARTA+. In most cases, the RMSD between experimental and predicted observables reported by the original authors was used (since the same data were often used in the parameter fitting, this value of σ should be considered a lower bound). Deviations reported by Hu and Bax were absolute deviations, and have therefore been increased by 30% to approximate mean-square deviations.¹ Deviations from the data of Ding and Gronenborn² and Hennig *et al.*³ were computed directly from the experimental and predicted couplings in those papers. The value of σ for prediction of C' chemical shifts is one case in which the data used in the test were not included in the optimization of the method.⁴

Parameter	σ	Source
Backbone J-Couplings		
³ J _{HNHA}	0.91 Hz	Hu and Bax ¹
³ J _{HNC}	0.59 Hz	Hu and Bax ¹
³ J _{HAC}	0.38 Hz	Hu and Bax ¹
³ J _{CC}	0.22 Hz	Hu and Bax ¹
³ J _{HNCB}	0.39 Hz	Hu and Bax ¹
¹ J _{NCA}	0.59 Hz	Ding and Gronenborn ²
² J _{NCA}	0.50 Hz	Ding and Gronenborn ²
³ J _{NCA}	0.10 Hz	Hennig <i>et al.</i> ³
Side-chain J-Couplings		
³ J _{NCG} (Thr)	0.21 Hz	Chou and Bax ⁵
³ J _{CCG} (Thr)	0.21 Hz	Chou and Bax ⁵
³ J _{NCG} (Ile,Val)	0.25 Hz	Chou and Bax ⁵
³ J _{CCG} (Ile,Val)	0.25 Hz	Chou and Bax ⁵
³ J _{HAHB}	0.31 Hz	Perez <i>et al.</i> ⁶
³ J _{NHB}	0.41 Hz	Perez <i>et al.</i> ⁶
³ J _{CHB}	0.47 Hz	Perez <i>et al.</i> ⁶
³ J _{HACG}	0.33 Hz	Perez <i>et al.</i> ⁶
³ J _{NCG}	0.18 Hz	Perez <i>et al.</i> ⁶
³ J _{CCG}	0.36 Hz	Perez <i>et al.</i> ⁶
Chemical Shifts		
C' Shifts	1.09 p.p.m.	Shen and Bax ⁴

Table S4) Sidechain dihedral parameter definitions.

Residue	χ^1	$\chi^{1'}$	χ^2	$\chi^{2'}$
Ile	NH1/C CT1 CT1 CT2	NH1/C CT1 CT1 CT3	CT1 CT1 CT2 CT3	
Val	NH1/C CT1 CT1 CT3			
Thr	NH1/C CT1 CT1 OH1	NH1/C CT1 CT1 CT3	CT1 CT1 OH1 H	
Leu	NH1/C CT1 CT2 CT1		CT1 CT2 CT1 CT3	
Lys	NH1/C CT1 CT2 CT2		CT1 CT2 CT2 CT2	
Arg	NH1/C CT1 CT2 CT2		CT1 CT2 CT2 CT2	
Gln	NH1/C CT1 CT2 CT2		CT1 CT2 CT2 CC	
Met	NH1/C CT1 CT2 CT2		CT1 CT2 CT2 S	
Phe	NH1/C CT1 CT2 CA		CT1 CT2 CA CA	
Tyr	NH1/C CT1 CT2 CA		CT1 CT2 CA CA	
Asn	NH1/C CT1 CT2 CC		CT1 CT2 CC NH2	CT1 CT2 CC O
Asp	NH1/C CT1 CT2A CC		CT1 CT2A CC OC	
Trp	NH1/C CT1 CT2 CY		CT1 CT2 CY CA	CT1 CT2 CY CP1
Hsd/Hse	NH1/C CT1 CT2 CPH1		CT1 CT2 CPH1 CPH1	CT1 CT2 CPH1 NR
Hsp	NH1/C CT1 CT2A CPH1		CT1 CT2A CPH1 CPH1	CT1 CT2A CPH1 NR
Ser	NH1/C CT1 CT2 OH1		CT1 CT2 OH1 H	
Glu	NH1/C CT1 CT2A CT2		CT1 CT2A CT2 CC	
Cys	NH1/C CT1 CT2 S		CT1 CT2 S HS	
Ala/Gly	- - - -			
Pro	- - - -			

*Boxed parameters are shared by two or more residues; NR1 (HSD), NR2 (HSE)
 Atom type CT2A created for Cb atom of Glu and Hsp to differentiate those parameters from Lys/Arg/Gln/Met and Hsd/Hse sets, respectively

Table S5) Differences in relative energy of local minima between C22/CMAP and QM calculations.

Residue \ Rotamer	tt	tm	tp	mt	mm	mp	pt	pm	pp	RMSD
Alpha										
Arg	2.94	5.12	1.65	2.77	1.54	6.40	5.57	10.70	7.74	5.72
Asn	3.68	1.75	-0.03	2.29	-2.07	1.64	-0.93	3.01	-0.53	2.08
Asp	2.29	2.58	0.84	2.07	-2.66	0.42	0.40	-1.12	-3.40	2.03
Cys	1.23	1.15	0.53	-0.16	0.97	0.19	-2.23	-0.53	0.43	1.03
Gln	1.70	4.27	0.86	-0.04	0.40	2.12	-0.24	4.20	0.92	2.24
Glu	-1.42	12.93	7.33	-2.04	4.51	2.03	-3.11	-1.31	4.51	5.61
Hsd	2.93	2.00	3.26	0.15	1.72	1.87	1.87	0.18	-0.68	1.93
Hse	7.33	5.06	3.81	5.30	1.28	4.09	1.11	2.74	1.06	4.08
Hsp	8.99	2.42	4.46	6.20	4.28	5.61	16.15	10.68	7.43	8.33
Ile	0.80	2.51	1.32	0.79	1.13	1.01	-0.53	-0.72	-0.87	1.21
Leu	3.43	3.14	1.98	0.91	0.28	0.56	0.78	0.12	0.36	1.75
Lys	3.97	6.00	1.71	3.54	1.96	7.35	6.03	11.95	9.38	6.60
Met	0.88	4.03	1.52	-0.51	1.60	1.38	0.24	1.59	-2.68	1.94
Phe	1.96	2.78	1.44	0.17	0.34	-0.01	-1.42	-0.28	0.19	1.33
Ser	1.37	2.16	1.46	-0.33	0.01	0.56	-2.99	-1.45	1.27	1.55
Thr	0.94	1.63	0.94	0.67	1.07	1.13	-3.76	-1.97	0.05	1.68
Trp	1.11	0.83	0.63	1.00	-0.55	-1.16	-1.60	-1.82	-1.79	1.25
Tyr	1.73	3.12	1.80	0.45	0.95	0.06	-0.79	-0.25	0.67	1.42
Val	0.98				-0.08				1.13	0.86
AVG	2.47	3.53	1.97	1.29	0.88	1.96	0.81	1.98	1.33	
RMSD	3.39	4.42	2.61	2.40	1.90	3.02	4.58	4.84	3.65	
AVG(Alpha)					1.80					
RMSD(Alpha)					3.55					
Beta										
Arg	0.95	2.36	1.75	1.15	1.58	3.08	1.39	3.71	2.00	2.17
Asn	0.26	-0.23	-0.37	-0.07	-2.93	-0.73	-0.76	0.45	-2.49	1.35
Asp	4.78	4.49	2.55	4.46	1.08	2.96	2.86	4.29	-0.98	3.45
Cys	-1.79	-0.19	0.56	-1.93	-1.22	-1.23	-2.48	-1.82	-1.38	1.55
Gln	-1.03	1.95	0.56	-1.08	-0.53	2.32	-1.10	1.62	0.23	1.33
Glu	0.33	11.96	3.56	-0.37	3.81	8.45	-0.76	7.62	9.33	6.56
Hsd	0.60	-0.28	0.33	0.55	-0.20	0.06	-0.11	0.56	-1.40	0.59
Hse	3.21	2.53	3.54	4.73	1.85	2.30	3.92	3.19	1.26	3.12
Hsp	6.42	1.42	2.33	5.52	1.22	1.32	5.55	3.03	-0.45	3.69
Ile	-0.25	0.86	-0.92	-0.24	0.00	1.42	-0.63	-0.05	0.42	0.69
Leu	1.39	0.56	-0.38	0.22	0.71	1.10	0.27	0.53	0.46	0.72
Lys	1.43	3.65	2.91	2.13	2.47	4.49	2.18	4.83	2.98	3.19
Met	-1.05	2.16	-0.34	-0.89	0.29	-1.14	-0.79	0.48	-3.12	1.44
Phe	-0.27	0.94	-0.10	0.16	-1.24	0.09	-1.32	0.11	-0.57	0.72
Ser	-2.81	-1.37	-0.18	-2.54	-1.18	-0.85	-2.03	0.20	-0.06	1.58
Thr	-2.40	-1.30	0.05	-2.59	-0.94	-1.11	-1.82	0.21	-0.17	1.48
Trp	-1.50	-1.26	-0.79	0.51	-1.80	-1.23	-0.44	-1.30	-2.39	1.38
Tyr	-0.14	1.09	-0.22	0.05	-1.04	0.16	-1.45	-0.12	-0.20	0.71
Val	0.00				1.91				-0.20	1.11
AVG	0.43	1.63	0.82	0.54	0.20	1.19	0.14	1.53	0.17	
RMSD	2.31	3.39	1.69	2.34	1.65	2.71	2.14	2.81	2.61	
AVG(Beta)					0.74					
RMSD(Beta)					2.46					
AlphaL										
Arg	3.04	4.07	4.42	2.18	4.49	3.72	1.00	4.02	0.00	3.35
Asn	3.77	1.50	5.01	0.79	2.50	0.83	7.06	1.02	1.06	3.35
Asp	8.59	6.46	7.91	5.22	2.10	4.82	15.93	13.53	12.02	9.51

Cys	0.75	0.80	1.62	0.29	2.83	2.02	3.65	1.23	2.42	2.02
Gln	2.56	5.68	4.94	0.67	3.22	3.13	3.78	8.31	3.35	4.45
Glu	6.70		6.82	5.20	3.68	8.23	8.46	14.48		8.29
Hsd	2.73	1.67	3.16	0.62	1.04	1.51	2.24	4.65	3.48	2.64
Hse	5.46	4.00	7.68	4.52	6.24	4.09	11.58	6.43	6.14	6.62
Hsp	4.71	-1.40	2.20	3.67	1.41	1.66	0.68	-4.79	-5.02	3.26
Ile	5.80	7.78	5.47	4.24	3.44	4.69	3.20	5.51	4.42	5.12
Leu	5.88	5.32	3.76	2.56	2.58	3.28	7.05	6.78	5.10	4.97
Lys	3.70	4.94	5.25	2.59	6.10	5.94	2.24	5.72	0.00	4.50
Met	3.11	9.44	4.18	2.17	2.87	2.92	3.73	7.75	4.51	5.08
Phe	3.30	4.76	3.31	2.02	1.90	2.61	5.29	5.19	5.19	3.96
Ser	-0.28	1.36	3.64	-2.05	1.48	-0.33	4.71	2.47	3.86	2.68
Thr	1.44	2.83	4.81	0.52	4.21	1.71	3.45	1.77	2.54	2.90
Trp	3.29	2.21	1.98	2.97	1.66	0.89	4.14	2.39	5.69	3.11
Tyr	2.79	5.16	2.55	2.29	1.61	2.48	4.68	4.82	5.58	3.82
Val	0.23				1.91				-1.76	1.51
AVG	3.56	3.92	4.37	2.25	2.91	3.01	5.16	5.07	3.25	
RMSD	4.18	4.73	4.72	2.92	3.25	3.61	6.34	6.67	4.82	
AVG(AlphaL)					3.72					
RMSD(AlphaL)					4.73					

AVG(all) 2.09

RMSD(all) 3.69

Energy differences in kcal/mol. See Methods for rotamer and secondary structure definitions.
Some values were not successfully calculated due to structural clash.

Table S6) Differences in relative energy of local minima between C22/CMAP with MCSA-fitted sidechain parameters and QM calculations.

Residue \ Rotamer	tt	tm	tp	mt	mm	mp	pt	pm	pp	RMSD
	Alpha									
Arg	2.31	3.90	0.14	1.26	-0.48	2.93	4.07	6.88	5.64	3.75
Asn	2.56	4.26	1.44	2.53	-0.64	3.39	0.23	4.40	3.06	2.86
Asp	-2.53	0.53	-0.96	-0.19	-1.97	1.29	-0.31	1.32	-0.73	1.31
Cys	1.89	1.24	0.44	1.75	2.00	0.99	0.54	1.00	2.04	1.45
Gln	2.97	3.85	-0.20	2.41	0.78	2.08	1.65	3.70	1.42	2.42
Glu	0.67	8.14	1.41	1.28	0.76	0.83	1.25	-1.23	3.62	3.12
Hsd	2.30	0.56	1.15	-0.80	0.72	0.56	3.61	0.14	-0.64	1.56
Hse	4.09	4.10	2.40	3.24	-0.31	2.04	0.35	1.39	1.28	2.53
Hsp	5.04	3.83	5.42	1.66	4.00	5.58	9.60	8.23	4.99	5.81
Ile	1.42	3.18	1.62	0.97	1.13	0.86	0.56	0.22	0.32	1.42
Leu	3.46	3.48	1.80	1.23	0.96	0.78	1.45	1.77	1.60	2.06
Lys	1.92	3.87	-0.47	0.63	-0.93	2.39	3.09	6.32	6.00	3.52
Met	1.43	3.99	1.26	0.84	1.76	2.21	0.92	1.56	-2.87	2.10
Phe	1.43	2.15	0.64	0.86	1.26	1.32	-0.47	0.91	1.47	1.26
Ser	2.20	1.64	0.65	1.79	0.45	-0.08	-1.04	-1.87	1.58	1.43
Thr	2.07	1.08	0.31	2.61	1.08	0.28	-1.28	-2.13	0.56	1.49
Trp	2.79	2.72	1.89	2.27	1.32	2.34	-0.08	1.95	1.33	2.02
Tyr	1.18	2.32	0.85	1.02	1.73	1.42	-0.04	0.93	1.85	1.41
Val	0.92				0.28				1.18	0.88
AVG	2.01	3.05	1.10	1.41	0.73	1.73	1.34	1.97	1.77	
RMSD	2.51	3.52	1.74	1.71	1.46	2.17	2.81	3.44	2.78	
AVG(Alpha)					1.68					
RMSD(Alpha)					2.55					
	Beta									
Arg	-0.06	0.32	-0.56	1.07	0.99	2.05	0.66	1.52	1.28	1.11
Asn	0.21	0.78	0.33	-0.38	-0.64	0.97	-0.20	2.39	0.83	0.98
Asp	0.59	3.08	0.84	0.22	0.14	2.06	-1.14	3.34	-1.73	1.83
Cys	-0.67	-0.15	0.51	-0.25	-0.62	-0.62	0.10	-0.53	0.06	0.45
Gln	0.60	2.03	-0.05	1.18	-0.67	2.61	0.28	1.12	0.39	1.27
Glu	1.26	7.36	-1.46	0.99	-0.91	5.09	1.45	4.54	5.77	3.97
Hsd	-0.80	-2.13	-1.66	-0.38	-1.49	-1.61	0.02	-0.44	-1.10	1.26
Hse	0.80	0.55	1.34	1.99	0.08	0.52	2.20	2.40	1.68	1.51
Hsp	1.03	1.71	2.33	2.48	3.09	2.99	-0.14	1.88	-1.01	2.07
Ile	0.21	1.37	-0.49	-0.22	0.00	1.44	0.12	0.56	1.72	0.92
Leu	1.42	1.07	-0.38	0.34	1.35	1.24	0.57	1.84	1.53	1.19
Lys	-0.64	0.57	-0.67	0.76	1.00	2.63	0.24	1.40	1.65	1.27
Met	-0.49	1.87	-0.34	0.23	0.70	-0.66	-0.38	0.10	-3.24	1.31
Phe	-0.69	0.66	-0.39	0.79	-0.74	0.62	-0.55	0.50	0.28	0.60
Ser	-1.21	-1.70	-0.67	-0.76	-1.29	-0.93	-0.63	-0.24	-0.35	0.97
Thr	-0.77	-1.80	-0.70	-0.84	-1.37	-1.50	-0.02	-0.14	-0.31	1.01
Trp	-0.56	0.25	0.81	1.52	-0.40	0.89	0.79	1.51	0.38	0.90
Tyr	-0.70	0.75	-0.49	0.64	-0.71	0.62	-0.72	0.25	0.45	0.61
Val	0.00				0.47				-1.44	0.87
AVG	-0.02	0.92	-0.09	0.52	-0.05	1.02	0.15	1.22	0.36	
RMSD	0.77	2.24	0.96	1.04	1.10	1.97	0.79	1.81	1.85	
AVG(Beta)					0.45					
RMSD(Beta)					1.49					
	AlphaL									
Arg	2.63	3.71	2.45	1.77	2.14	1.69	1.21	4.44	0.00	2.55
Asn	3.10	3.48	5.56	1.54	3.32	1.39	8.14	2.73	4.04	4.19

Asp	1.12	1.54	2.85	2.53	2.48	5.20	14.25	14.23	11.90	8.15
Cys	1.08	0.68	0.98	2.34	3.41	2.48	5.82	1.91	3.69	2.92
Gln	3.49	5.59	3.26	3.18	3.27	3.85	4.35	7.88	2.97	4.47
Glu	5.76		0.54	6.40	0.28	7.60	9.19	17.63		8.68
Hsd	1.12	0.65	1.31	-0.82	-0.13	0.21	2.87	4.39	2.77	2.09
Hse	2.93	3.86	5.99	2.96	3.93	1.88	10.19	5.44	6.24	5.37
Hsp	1.47	1.01	4.39	-0.56	2.70	3.03	-2.50	-3.23	-3.08	2.70
Ile	5.82	7.63	5.00	4.10	3.16	4.57	3.58	6.97	5.10	5.29
Leu	5.28	5.17	3.13	2.54	3.33	3.50	8.43	8.64	5.43	5.47
Lys	2.37	4.30	2.22	1.33	2.18	2.60	1.40	5.39	0.00	2.85
Met	3.20	8.33	3.48	3.02	2.87	3.84	3.42	8.14	3.56	4.88
Phe	2.07	4.06	2.00	2.40	2.55	3.37	6.58	6.25	6.41	4.37
Ser	0.31	0.70	1.84	0.24	1.21	-0.72	5.85	1.13	3.99	2.53
Thr	2.37	2.29	3.27	2.59	3.44	0.94	5.40	0.74	3.17	3.00
Trp	3.44	4.01	3.42	3.18	3.25	2.90	6.64	4.98	7.08	4.57
Tyr	1.57	4.22	1.27	2.52	2.24	3.24	5.91	5.90	6.48	4.16
Val	5.44				3.91				6.15	5.25
AVG	2.87	3.60	2.94	2.29	2.61	2.87	5.60	5.75	4.22	
RMSD	3.31	4.24	3.31	2.80	2.83	3.41	6.71	7.40	5.28	
AVG(AlphaL)					3.64					
RMSD(AlphaL)					4.64					

AVG(all) 1.92
RMSD(all) 3.17

Energy differences in kcal/mol. See Methods for rotamer and secondary structure definitions.
Some values were not successfully calculated due to structural clash.

Table S7) Differences in relative energy of local minima between C36 and QM calculations.

C36 Residue	Rotamer										RMSD
		tt	tm	tp	mt	mm	mp	pt	pm	pp	
Alpha											
Arg		3.49	5.28	1.71	1.20	-0.60	2.71	3.94	6.84	4.66	3.89
Asn		1.36	1.58	-0.53	2.12	-0.81	1.68	-0.42	3.54	1.05	1.71
Asp		-1.77	1.23	-0.48	0.80	-0.83	2.21	-0.73	0.61	-1.15	1.22
Cys		1.27	0.74	0.03	1.25	1.76	0.60	0.08	0.79	2.06	1.16
Gln		1.62	3.08	-1.06	-0.61	-2.02	-0.31	-0.87	1.73	-1.94	1.68
Glu		-3.85	8.92	2.91	-5.06	0.38	0.52	-4.63	-1.04	3.13	4.23
Hsd		1.76	0.40	1.56	-1.23	0.41	0.89	1.05	0.45	-0.71	1.05
Hse		5.06	4.54	3.22	3.69	1.29	2.78	0.58	2.26	1.96	3.14
Hsp		4.32	1.99	3.99	1.52	2.81	4.52	9.02	6.85	3.11	4.80
Ile		1.46	2.72	1.37	1.31	0.97	0.84	0.69	-0.01	-0.23	1.30
Leu		3.44	3.19	1.88	0.76	0.28	0.46	0.98	0.60	0.69	1.77
Lys		3.34	5.60	1.36	0.79	-0.84	2.45	3.18	6.45	4.95	3.77
Met		1.57	3.69	0.80	-0.73	-0.36	-0.02	-0.29	0.06	-4.55	2.06
Phe		0.94	1.66	0.14	0.06	0.59	0.22	-1.57	-0.09	0.45	0.87
Ser		1.95	1.13	0.30	2.09	0.47	0.29	-1.05	-2.14	1.16	1.37
Thr		0.80	0.65	-0.21	2.55	1.69	1.07	-1.98	-2.08	0.52	1.50
Trp		1.40	1.74	1.33	2.81	2.50	3.30	-1.20	1.86	0.88	2.04
Tyr		0.88	1.96	0.51	0.37	1.20	0.42	-1.00	0.10	0.97	0.98
Val		0.78				4.44				1.15	2.68
AVG		1.57	2.78	1.05	0.76	0.70	1.37	0.32	1.49	0.96	
RMSD		2.51	3.50	1.70	2.03	1.64	1.89	2.82	3.08	2.37	
AVG(Alpha)						1.22					
RMSD(Alpha)						2.46					
Beta											
Arg		1.83	2.19	1.36	0.96	0.87	1.94	1.27	2.13	1.19	1.60
Asn		-0.36	-0.08	-0.47	-0.50	-2.20	-0.11	-0.98	0.84	-1.31	0.99
Asp		1.37	3.83	1.56	1.25	1.02	2.97	-1.53	2.49	-2.44	2.23
Cys		-0.94	-0.10	0.58	-0.52	-0.54	-0.59	-0.43	-0.56	0.08	0.54
Gln		-0.24	1.35	-0.61	-1.58	-3.18	0.02	-1.83	-0.85	-2.27	1.64
Glu		-3.05	9.04	0.12	-5.25	-1.19	4.81	-4.31	4.71	5.21	4.84
Hsd		-0.54	-0.66	0.20	-0.78	-1.63	-1.28	-0.77	-0.07	-2.13	1.10
Hse		2.13	2.22	2.87	2.74	0.97	1.40	2.70	2.67	1.32	2.22
Hsp		0.86	0.13	1.19	3.01	2.24	2.28	-0.24	0.92	-2.59	1.80
Ile		0.62	1.34	-0.57	0.32	0.00	1.48	0.44	0.42	1.00	0.83
Leu		1.69	0.99	-0.14	0.00	0.67	0.95	0.28	0.91	0.77	0.86
Lys		1.44	2.64	1.45	0.86	1.08	2.71	1.02	2.24	1.43	1.78
Met		0.04	1.85	-0.34	-1.16	-1.19	-2.55	-1.15	-1.14	-4.90	2.09
Phe		-1.02	0.56	-0.58	0.22	-1.10	0.28	-1.69	-0.16	-0.55	0.83
Ser		-1.13	-1.94	-0.89	-0.21	-1.04	-0.77	-0.59	-0.59	-0.49	0.97
Thr		-1.43	-1.81	-0.65	-0.63	-0.47	-0.63	-0.63	-0.09	-0.08	0.89
Trp		-1.53	0.05	0.92	2.20	0.91	2.03	-0.32	0.97	-0.59	1.26
Tyr		-0.83	0.79	-0.54	0.26	-0.92	0.43	-1.69	-0.24	-0.22	0.79
Val		0.00				4.44				-0.09	2.56
AVG		-0.06	1.24	0.30	0.07	-0.07	0.85	-0.58	0.81	-0.35	
RMSD		1.34	2.68	1.06	1.79	1.69	1.93	1.57	1.69	2.09	
AVG(Beta)						0.25					
RMSD(Beta)						1.81					
AlphaL											
Arg		4.08	5.50	3.90	1.67	1.96	1.62	1.26	3.25	0.00	3.05
Asn		2.27	1.21	3.07	1.19	2.80	1.17	6.57	1.38	2.44	2.94

Asp	1.33	2.01	2.99	2.89	2.72	5.65	11.24	11.28	10.30	6.85
Cys	0.59	0.16	0.46	1.66	3.13	2.34	4.97	1.81	3.32	2.53
Gln	2.24	4.11	2.15	0.09	0.43	0.41	1.58	3.73	-0.63	2.20
Glu	0.33		1.67	-0.65	-0.48	4.70	2.41	9.53		4.18
Hsd	1.00	-0.12	1.77	-1.38	0.23	0.63	0.90	3.49	1.66	1.57
Hse	4.10	3.46	5.63	3.12	4.76	2.80	9.05	4.96	5.99	5.20
Hsp	1.21	-1.21	2.56	-0.34	2.12	2.03	-3.53	-4.34	-5.06	2.89
Ile	5.30	6.94	4.48	4.31	2.89	4.04	3.52	5.75	4.37	4.76
Leu	5.37	4.92	3.11	1.99	2.21	2.73	6.72	6.44	4.55	4.55
Lys	4.03	6.34	3.83	1.40	2.20	2.73	1.63	4.33	0.00	3.44
Met	3.19	8.34	2.98	1.28	0.61	1.12	1.93	3.62	1.36	3.50
Phe	1.53	2.97	1.42	1.44	1.82	2.52	4.25	4.19	4.41	2.98
Ser	0.34	0.25	1.53	0.51	1.19	-0.56	5.44	0.92	2.93	2.20
Thr	0.92	1.42	2.23	2.40	3.92	1.66	4.04	0.83	2.25	2.44
Trp	2.08	2.25	2.15	3.55	4.41	3.88	4.34	4.16	6.22	3.89
Tyr	1.21	3.33	0.88	1.72	1.69	2.54	3.96	3.97	4.70	2.97
Val	5.10				4.44				5.99	5.21
AVG	2.43	3.05	2.60	1.49	2.27	2.33	3.90	3.85	3.04	
RMSD	2.96	4.02	2.89	2.07	2.69	2.78	5.06	5.07	4.47	
AVG(AlphaL)					2.77					
RMSD(AlphaL)					3.70					
AVG(all)						1.41				
RMSD(all)						2.77				

Energy differences in kcal/mol. See Methods for rotamer and secondary structure definitions. Some values were not successfully calculated due to structural clash.

Table S8) RMS Difference between the QM and MM potential energy surfaces based on regions with relative energies below 2 kcal/mol (Low) and from 2 – 12 kcal/mol (high) above the local minima on each of the three χ_1/χ_2 surfaces for each amino acid.

Residue	LOW (0-2 kcal/mol)			HIGH (2-12 kcal/mol)		
	C22	C36	DIFF	C22	C36	DIFF

Arg	1.16	1.06	-0.10	2.50	2.49	-0.02
Asn	1.11	1.27	0.16	1.99	1.68	-0.31
Asp	1.07	1.10	0.03	2.71	1.93	-0.78
Cys	0.96	0.63	-0.33	1.70	1.34	-0.37
Gln	1.38	1.49	0.11	1.84	1.68	-0.16
Glu	1.05	1.37	0.32	3.16	2.88	-0.28
Hsd	1.12	1.20	0.08	1.41	1.28	-0.13
Hse	1.45	1.35	-0.10	2.19	1.82	-0.37
Hsp	0.72	0.85	0.13	3.57	2.39	-1.17
Ile	0.72	0.51	-0.21	1.32	1.12	-0.20
Leu	0.61	0.64	0.03	1.57	1.46	-0.11
Lys	1.20	1.07	-0.12	2.39	2.23	-0.16
Met	0.68	0.90	0.22	1.29	1.60	0.31
Phe	0.67	0.48	-0.18	1.51	1.09	-0.42
Ser	1.23	0.94	-0.28	2.44	1.71	-0.73
Thr	1.55	1.51	-0.04	2.45	1.80	-0.65
Trp	1.36	0.71	-0.66	1.71	1.16	-0.55
Tyr	0.71	1.11	0.40	1.51	1.26	-0.24
Val	0.61	0.48	-0.13	1.09	0.75	-0.34
Mean signed error			-0.04			-0.35
Mean unsigned error			0.19			0.38

Table S9) NMR J-coupling constants for Ala₃, Ala₅, Ala₇, Val₃, and Gly₃ peptides from experiment⁷ and simulation with new force field. Results with flavodoxin-based⁸ and DFT-based Karplus parameters (in parentheses)⁹ for alanine- and valine-peptides. For Gly₃, only DFT-based parameters were used¹⁰.

	Ala ₃		Ala ₅		Ala ₇		Val ₃		Gly ₃	
	Exp	Sim	Exp	Sim	Exp	Sim	Exp	Sim	Exp	Sim
² J(N,C _α) ψ ₁	9.14	8.60	9.20	8.60	9.17	8.60	8.35	8.58	10.45	8.58
³ J(H _N ,C _α) φ ₃ ,ψ ₁	0.70	0.56	0.67	0.57	0.71	0.57	0.77	0.62	0.78	0.61
³ J(H _N ,H _α) φ ₂	5.68	5.26 (6.19)	5.59	5.40 (6.23)	5.61	5.37 (6.30)	7.94	5.52 (6.64)	5.89	5.82
³ J(H _N ,C') φ ₂	1.13	1.61 (1.05)	1.13	1.62 (1.13)	1.15	1.59 (1.04)	0.58	1.31 (0.66)	1.10	1.10
³ J(H _α ,C') φ ₂	1.84	1.73 (1.74)	1.85	1.97 (2.02)	1.89	1.77 (1.78)	2.42	1.80 (1.84)	4.01	3.73
³ J(C',C') φ ₂	-	0.79 (0.84)	0.19	0.78 (0.83)	-	0.81 (0.86)	0.34	0.62 (0.57)	0.26	0.48
³ J(H _N ,C _β) φ ₂	2.39	1.87 (2.71)	2.30	1.82 (2.61)	2.31	1.84 (2.66)	1.38	1.98 (2.92)	-	-
¹ J(N,C _α) ψ ₂	11.34	11.29	11.36	11.27	11.37	11.29	10.80	10.80	12.17	11.74
² J(N,C _α) ψ ₂	8.45	8.36	8.55	8.33	8.52	8.35	7.80	8.13	9.05	8.50
³ J(H _N ,C _α) φ ₃ ,ψ ₂	0.65	0.60	0.68	0.61	0.66	0.62	0.75	0.56 (0.58)	0.61	0.62
³ J(H _N ,H _α) φ ₃	6.52	5.76 (7.07)	5.74	5.30 (6.19)	5.66	5.38 (6.24)	7.91	5.76 (7.07)	5.87	5.77
³ J(H _N ,C') φ ₃	1.29	1.01 (0.28)	-	1.57 (1.01)	1.20	1.58 (1.05)	1.01	1.03 (0.30)	0.99	1.18
³ J(H _α ,C') φ ₃	2.14	1.79 (1.86)	1.86	1.88 (1.92)	1.85	1.97 (2.01)	2.45	1.79 (1.86)	3.90	3.92
³ J(C',C') φ ₃	-	0.51 (0.38)	-	0.72 (0.74)	-	0.73 (0.76)	-	0.52 (0.39)	-	-
³ J(H _N ,C _β) φ ₃	2.02	2.08 (3.09)	2.24	1.90 (2.75)	2.20	1.87 (2.69)	1.40	2.07 (3.07)	-	-
¹ J(N,C _α) ψ ₃			11.26	11.13	11.27	11.18				
² J(N,C _α) ψ ₃			8.40	8.16	8.29	8.22				
³ J(H _N ,C _α) φ ₃ ,ψ ₃			0.69	0.60	0.56	0.61				
³ J(H _N ,H _α) φ ₃			5.98	5.41 (6.31)	5.77	5.38 (6.25)				
³ J(H _N ,C') φ ₃			1.15	1.57 (1.04)	1.20	1.59 (1.06)				
³ J(H _α ,C') φ ₃			1.89	1.90 (1.94)	1.80	1.95 (1.99)				
³ J(C',C') φ ₃			-	0.77 (0.80)	-	0.75 (0.78)				
³ J(H _N ,C _β) φ ₃			2.14	1.85 (2.66)	2.23	1.86 (2.67)				
¹ J(N,C _α) ψ ₄			11.25	11.14	11.22	11.19				
² J(N,C _α) ψ ₄			8.27	8.15	8.22	8.27				
³ J(H _N ,C _α) φ ₄ ,ψ ₄			0.73	0.59	-	0.62				
³ J(H _N ,H _α) φ ₄			6.54	5.82 (7.13)	5.92	5.45 (6.36)				
³ J(H _N ,C') φ ₄			1.16	1.00 (0.28)	1.19	1.52 (0.98)				
³ J(H _α ,C') φ ₄			2.19	1.81 (1.88)	1.56	1.95 (2.00)				
³ J(C',C') φ ₄			-	0.52 (0.39)	-	0.72 (0.74)				
³ J(H _N ,C _β) φ ₄			1.96	2.06 (3.06)	2.23	1.88 (2.70)				
¹ J(N,C _α) ψ ₅					11.29	11.01				
² J(N,C _α) ψ ₅					8.24	7.96				
³ J(H _N ,C _α) φ ₅ ,ψ ₅					-	0.58				
³ J(H _N ,H _α) φ ₅					6.04	5.53 (6.36)				
³ J(H _N ,C') φ ₅					1.10	1.58 (1.11)				
³ J(H _α ,C') φ ₅					1.67	2.06 (2.13)				
³ J(C',C') φ ₅					-	0.78 (0.82)				
³ J(H _N ,C _β) φ ₅					2.21	1.80 (2.56)				
¹ J(N,C _α) ψ ₆					11.29	11.13				
² J(N,C _α) ψ ₆					8.18	8.14				
³ J(H _N ,C _α) φ ₆ ,ψ ₆					0.59	0.59				
³ J(H _N ,H _α) φ ₆					6.60	5.79 (7.11)				
³ J(H _N ,C') φ ₆					1.25	1.01 (0.28)				
³ J(H _α ,C') φ ₆					2.03	1.80 (1.87)				
³ J(C',C') φ ₆					-	0.52 (0.39)				
³ J(H _N ,C _β) φ ₆					1.99	2.07 (3.07)				

Table S10: NMR J-coupling constants for Ala₅ from experiment⁷ and simulations with different force fields. Flavodoxin-based Karplus parameters⁸ were used in all cases.

		<i>NMR</i>	<i>C36</i>	<i>C22/CMAP</i>	<i>C22/MP2</i>	<i>Amber 99SB</i>	<i>OPLS</i>	<i>Gromos 53A6</i>
² J(N,C _α)	ψ ₁	9.20	8.60	8.59	8.60	8.54	8.64	8.61
³ J(H _N ,C _α)	φ ₁ ,ψ ₁	0.67	0.57	0.61	0.49	0.70	0.68	0.71
³ J(H _N ,H _α)	φ ₁	5.59	5.40	5.85	3.79	6.26	7.07	6.90
³ J(H _N ,C') _β	φ ₂	1.13	1.62	1.60	2.30	1.35	0.90	1.17
³ J(H _α ,C')	φ ₂	1.85	1.97	1.96	1.72	1.97	2.21	2.23
³ J(C',C')	φ ₂	0.19	0.78	1.04	0.52	1.01	0.91	1.00
³ J(H _N ,C _β)	φ ₂	2.30	1.82	1.60	2.12	1.58	1.56	1.46
¹ J(N,C _α)	ψ ₁	11.36	11.27	11.10	11.18	11.40	11.33	10.74
² J(N,C _α)	ψ ₁	8.55	8.33	7.95	8.21	8.28	8.33	8.21
³ J(H _N ,C _α)	φ ₁ ,ψ ₂	0.68	0.61	0.58	0.55	0.64	0.64	0.65
³ J(H _N ,H _α)	φ ₁	5.74	5.30	5.97	3.91	6.41	7.12	6.81
³ J(H _N ,C')	φ ₁	-	1.57	1.51	2.21	1.39	0.88	1.17
³ J(H _α ,C')	φ ₁	1.86	1.88	2.23	1.74	2.37	2.23	2.26
³ J(C',C')	φ ₁	-	0.72	0.90	0.52	0.90	0.90	0.94
³ J(H _N ,C _β)	φ ₁	2.24	1.90	1.65	2.12	1.56	1.56	1.51
¹ J(N,C _α)	ψ ₂	11.26	11.13	10.74	11.03	11.05	11.17	10.59
² J(N,C _α)	ψ ₂	8.40	8.16	7.42	8.06	7.75	8.20	8.11
³ J(H _N ,C _α)	φ ₂ ,ψ ₃	0.69	0.60	0.52	0.54	0.59	0.63	0.65
³ J(H _N ,H _α)	φ ₂	5.98	5.41	6.20	4.35	6.62	7.14	6.98
³ J(H _N ,C')	φ ₂	1.15	1.57	1.46	2.13	1.23	0.89	1.15
³ J(H _α ,C')	φ ₂	1.89	1.90	2.11	2.08	2.07	2.23	2.32
³ J(C',C')	φ ₂	-	0.77	1.03	0.55	1.04	0.91	0.99
³ J(H _N ,C _β)	φ ₂	2.14	1.85	1.55	2.01	1.51	1.54	1.44
¹ J(N,C _α)	ψ ₁	11.25	11.14	10.88	10.89	11.20	11.06	10.58
² J(N,C _α)	ψ ₁	8.27	8.15	7.58	7.82	7.98	8.10	8.12
³ J(H _N ,C _α)	φ ₂ ,ψ ₁	0.73	0.59	0.49	0.55	0.58	0.63	0.68
³ J(H _N ,H _α)	φ ₂	6.54	5.82	5.83	5.82	6.06	7.52	7.66
³ J(H _N ,C')	φ ₂	1.16	1.00	0.99	1.00	1.75	0.90	1.04
³ J(H _α ,C')	φ ₂	2.19	1.81	1.81	1.81	2.52	2.40	2.47
³ J(C',C')	φ ₂	-	0.52	0.52	0.52	0.84	1.03	1.19
³ J(H _N ,C _β)	φ ₂	1.96	2.06	2.06	2.06	1.52	1.37	1.20

Table S11. Old and new dihedral parameters for Glycine termini. Torsion potentials are of the form $V_n(\theta) = k_n(1 + \cos[n\theta - \theta_0])$, where θ is the torsion angle as defined, θ_0 is a phase offset and k_n is the force constant, which was optimized, and the multiplicity $n=1$.

Atom types	Backbone torsion	Old k_θ [kcal/mol]	Old θ_0	New k_θ [kcal/mol]	New θ_0
NH3-CT2-C-NH1	N-ter, ψ	0.4	0°	1.0	0°
CC-CT2-NH1-C	C-ter, ϕ	0.2	180°	2.0	180°

Table S12. Scalar couplings of GPGG

Residue	J -coupling type	Torsion probed	J (expt)	J (ff99SB)	J (C22/CMAP)	J (C36)
Pro 2	$^3J_{\text{HaC}}$	ϕ_2	1.3	1.22	1.12	1.00
Gly 3	$^3J_{\text{HaC}}$	ϕ_3	4.1	4.27	5.01	3.96
Gly 4	$^3J_{\text{HaC}}$	ϕ_4	3.7	2.49	1.04	2.43
Gly 4	$^3J_{\text{HNC}}$	ϕ_4	1.1	1.68	2.55	1.59
Gly 3	$^3J_{\text{HNHa}}$	ϕ_3	6.3	5.92	6.58	6.32
Gly 4	$^3J_{\text{HNHa}}$	ϕ_4	6.0	4.49	2.03	4.18

Table S13) Scalar couplings of central Ala residues in the HEWL19 peptide.

		Expt		Amber ff99SB	Amber ff99SB*	C22/CMAP	C36
A9	$^1\text{JNC}\alpha$ (ψ_9)	10.54	0.59	10.84	10.53	9.90	10.40
A10	$^1\text{JNC}\alpha$ (ψ_{10})	10.58	0.59	10.84	10.27	9.79	10.35
A11	$^1\text{JNC}\alpha$ (ψ_{11})	10.57	0.59	10.64	10.21	9.78	10.40
A10	$^2\text{JNC}\alpha$ (ψ_9)	7.24	0.50	7.50	7.06	6.49	7.02
A11	$^2\text{JNC}\alpha$ (ψ_{10})	7.02	0.50	7.54	6.64	6.37	6.91
M12	$^2\text{JNC}\alpha$ (ψ_{11})	7.17	0.50	7.01	6.57	6.33	7.06
A9	$^3\text{JH}\alpha$ C(ϕ_9)	2.06	0.38	2.47	1.76	1.15	1.93
A10	$^3\text{JH}\alpha$ C(ϕ_{10})	1.72	0.38	2.55	1.82	1.18	2.10
A11	$^3\text{JH}\alpha$ C(ϕ_{11})	2.20	0.38	2.87	2.16	1.09	2.32
A9	$^3\text{JHNC}$ (ϕ_9)	1.39	0.59	1.05	0.65	0.76	1.03
A10	$^3\text{JHNC}$ (ϕ_{10})	1.33	0.59	1.10	0.65	0.77	0.88
A11	$^3\text{JHNC}$ (ϕ_{11})	1.09	0.59	1.22	0.77	0.85	0.97
A9	$^3\text{JHNC}\beta$ (ϕ_9)	2.26	0.39	2.03	2.74	3.68	2.77
A10	$^3\text{JHNC}\beta$ (ϕ_{10})	2.19	0.39	2.23	3.01	3.73	2.86
A11	$^3\text{JHNC}\beta$ (ϕ_{11})	2.21	0.39	2.31	2.37	3.75	2.73
A9	$^3\text{JHNH}\alpha$ (ϕ_9)	5.18	0.91	7.49	6.22	4.94	6.15
A10	$^3\text{JHNH}\alpha$ (ϕ_{10})	5.10	0.91	7.08	6.46	4.83	6.19
A11	$^3\text{JHNH}\alpha$ (ϕ_{11})	5.67	0.91	6.67	7.45	4.78	6.23
A10	$^3\text{JHNC}\alpha$ (ϕ_{10} , ψ_9)	0.46	0.10	0.52	0.39	0.19	0.37
A11	$^3\text{JHNC}\alpha$ (ϕ_{11} , ψ_{10})	0.43	0.10	0.49	0.38	0.16	0.38
M12	$^3\text{JHNC}\alpha$ (ϕ_{12} , ψ_{11})	0.43	0.10	0.49	0.38	0.16	0.41
$\chi^2(\text{J})$				1.2	1.0	4.7	0.6

Table S14) New atom types and parameters in the C36 force field.

```

MASS      51 CT2A  12.01100

BONDS
CT2A CT1   222.500    1.5380
CT2  CT2A  222.500    1.5300
CT2A HA2   309.000    1.1110
CT2A CPH1  229.630    1.5000
CT2A CC    200.000    1.5220

ANGLES
CT2A CT1  CC      52.000   108.0000
CT2A CT2  CD      52.000   108.0000
NH1  CT1  CT2A    70.000   113.5000
HB1  CT1  CT2A    35.000   111.0000
CT2A CT1  C       52.000   108.0000
CT1  CT2A HA2     26.500   110.1000   22.53   2.17900
CT1  CT2A CT2     58.350   113.5000   11.16   2.56100
HA2  CT2A HA2     35.500   109.0000    5.40   1.80200
HA2  CT2A CT2     26.500   110.1000   22.53   2.17900
CT2A CT2  HA2     26.500   110.1000   22.53   2.17900
CT2A CT2  CC      52.000   108.0000
CT1  CT2A CPH1    58.350   113.0000
HA2  CT2A CPH1    33.430   109.5000
CT2A CPH1 CPH1    45.800   130.0000
CT2A CPH1 NR3     45.800   122.0000
CT1  CT2A CC      52.000   108.0000
HA2  CT2A CC      33.000   109.5000   30.00   2.16300
OC   CC   CT2A    40.000   118.0000   50.00   2.38800
NH3  CT1  CT2A    67.700   110.0000
CT2A CT1  CD      52.000   108.0000

DIHEDRALS
!Glu/Hsp, CT2A terms
NH1  CT1  CT2A HA2      0.2000  3      0.00
CT1  CT2A CT2  HA2      0.1900  3      0.00
HB1  CT1  CT2A HA2      0.2000  3      0.00
HB1  CT1  CT2A CT2      0.2000  3      0.00
HA2  CT2A CT1  C        0.2000  3      0.00
HA2  CT2A CT1  CC       0.2000  3      0.00
HA2  CT2A CT2  HA2      0.1900  3      0.00
HA2  CT2A CT2  CC       0.1900  3      0.00
HB1  CT1  CT2A CPH1     0.2000  3      0.00
C    NH1  CT1  CT2A     1.8000  1      0.00
H    NH1  CT1  CT2A     0.0000  1      0.00
CT2A CT1  C    O        1.4000  1      0.00
CT2A CT1  C    NH1     0.0000  1      0.00
CT2A CT1  C    N        0.0000  1      0.00
! Glup
CT1  CT2A CT2  CD      0.1900  3      0.00
HA2  CT2A CT2  CD      0.1900  3      0.00
CT2A CPH1 CPH1 HR1     1.0000  2     180.00
CT2A CPH1 CPH1 NR3     2.5000  2     180.00
CT2A CPH1 NR3  H       3.0000  2     180.00
CT2A CPH1 NR3  CPH2    2.5000  2     180.00
HA2  CT2A CPH1 CPH1    0.0000  3      0.00
HA2  CT2A CPH1 NR3     0.1900  3      0.00
! Fit dihedrals

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! Group-fitted for Lys/Arg/Gln/Met
C   CT1  CT2  CT2      0.3500  1  180.00
C   CT1  CT2  CT2      0.4200  2  180.00
C   CT1  CT2  CT2      1.9100  3  180.00
CT2 CT2  CT1  NH1      0.8800  1  180.00
CT2 CT2  CT1  NH1      0.0000  2  180.00
CT2 CT2  CT1  NH1      1.9000  3    0.00
CC  CT2  CT2  CT1      1.8400  1  180.00
CC  CT2  CT2  CT1      0.8400  2  180.00
CC  CT2  CT2  CT1      0.3900  3  180.00
CT1 CT2  CT2  CT2      0.6300  1  180.00
CT1 CT2  CT2  CT2      0.0100  2    0.00
CT1 CT2  CT2  CT2      0.1500  3    0.00
CT1 CT2  CT2  S       0.1400  1  180.00
CT1 CT2  CT2  S       0.5400  2    0.00
CT1 CT2  CT2  S       0.6900  3    0.00
! Fitted Asn
C   CT1  CT2  CC       1.4100  1  180.00
C   CT1  CT2  CC       1.2900  2  180.00
C   CT1  CT2  CC       0.5900  3  180.00
CC  CT2  CT1  NH1      0.2800  1  180.00
CC  CT2  CT1  NH1      0.5000  2  180.00
CC  CT2  CT1  NH1      0.3800  3    0.00
CT1 CT2  CC   NH2      0.6200  1  180.00
CT1 CT2  CC   NH2      0.6600  2  180.00
CT1 CT2  CC   NH2      0.7200  3  180.00
CT1 CT2  CC   O       0.4200  1  180.00
CT1 CT2  CC   O       0.1500  2  180.00
CT1 CT2  CC   O       0.9500  3  180.00
! Fitted Asp
C   CT1  CT2A  CC      1.6100  1  180.00
C   CT1  CT2A  CC      1.2900  2  180.00
C   CT1  CT2A  CC      0.5900  3  180.00
CC  CT2A  CT1  NH1      0.6800  1  180.00
CC  CT2A  CT1  NH1      0.1000  2  180.00
CC  CT2A  CT1  NH1      0.3800  3    0.00
CT1 CT2A  CC   OC      0.8400  1    0.00
CT1 CT2A  CC   OC      0.9800  2  180.00
CT1 CT2A  CC   OC      1.4600  3    0.00
! Fitted Cys
CT1 CT2  S    HS       0.2000  1    0.00
CT1 CT2  S    HS       0.6500  2    0.00
CT1 CT2  S    HS       0.2200  3    0.00
C   CT1  CT2  S       0.2400  1  180.00
C   CT1  CT2  S       0.7500  2  180.00
C   CT1  CT2  S       1.3500  3  180.00
NH1 CT1  CT2  S       0.3400  1    0.00
NH1 CT1  CT2  S       0.5000  2  180.00
NH1 CT1  CT2  S       1.4300  3    0.00
! Fitted Glu
CC  CT2  CT2A  CT1      0.0000  1  180.00
CC  CT2  CT2A  CT1      0.3800  2  180.00
CC  CT2  CT2A  CT1      0.5900  3  180.00
C   CT1  CT2A  CT2      0.1100  1    0.00
C   CT1  CT2A  CT2      0.9800  2  180.00
C   CT1  CT2A  CT2      1.6000  3  180.00
CC  CT1  CT2A  CT2      1.6000  3  180.00
CT2 CT2A  CT1  NH1      0.3000  1    0.00
CT2 CT2A  CT1  NH1      0.3500  2    0.00
CT2 CT2A  CT1  NH1      1.7600  3    0.00
! Group-fitted for Hsd/Hse

```

CPH1	CPH1	CT2	CT1	1.7400	1	0.00
CPH1	CPH1	CT2	CT1	0.1500	2	0.00
CPH1	CPH1	CT2	CT1	0.7700	3	180.00
CT1	CT2	CPH1	NR1	1.4900	1	0.00
CT1	CT2	CPH1	NR1	0.0900	2	180.00
CT1	CT2	CPH1	NR1	0.7900	3	180.00
CT1	CT2	CPH1	NR2	1.0900	1	0.00
CT1	CT2	CPH1	NR2	0.0900	2	0.00
CT1	CT2	CPH1	NR2	0.6700	3	180.00
C	CT1	CT2	CPH1	0.1800	1	180.00
C	CT1	CT2	CPH1	0.6400	2	180.00
C	CT1	CT2	CPH1	0.8700	3	180.00
CPH1	CT2	CT1	NH1	0.0000	1	0.00
CPH1	CT2	CT1	NH1	0.0000	2	180.00
CPH1	CT2	CT1	NH1	0.9000	3	0.00
! Group-fitted for Hsp						
CPH1	CPH1	CT2A	CT1	2.0400	1	0.00
CPH1	CPH1	CT2A	CT1	0.4400	2	0.00
CPH1	CPH1	CT2A	CT1	0.1300	3	180.00
CT1	CT2A	CPH1	NR3	0.5300	1	180.00
CT1	CT2A	CPH1	NR3	0.4200	2	180.00
CT1	CT2A	CPH1	NR3	0.3000	3	180.00
C	CT1	CT2A	CPH1	1.7500	1	180.00
C	CT1	CT2A	CPH1	0.1300	2	0.00
C	CT1	CT2A	CPH1	1.8600	3	180.00
CPH1	CT2A	CT1	NH1	1.0900	1	180.00
CPH1	CT2A	CT1	NH1	0.2200	2	180.00
CPH1	CT2A	CT1	NH1	2.3200	3	0.00
! Group-fitted for Ile/Thr						
CT1	CT1	CT2	CT3	0.3800	1	180.00
CT1	CT1	CT2	CT3	0.1300	2	180.00
CT1	CT1	CT2	CT3	0.2900	3	180.00
C	CT1	CT1	CT2	0.1000	1	180.00
C	CT1	CT1	CT2	0.5200	2	180.00
C	CT1	CT1	CT2	0.2900	3	180.00
CT2	CT1	CT1	NH1	0.1200	1	180.00
CT2	CT1	CT1	NH1	0.3600	2	180.00
CT2	CT1	CT1	NH1	0.4100	3	0.00
! Fitted Leu						
CT1	CT2	CT1	CT3	0.0500	1	0.00
CT1	CT2	CT1	CT3	0.1000	2	180.00
CT1	CT2	CT1	CT3	0.0100	3	180.00
C	CT1	CT2	CT1	0.3200	1	180.00
C	CT1	CT2	CT1	0.6100	2	180.00
C	CT1	CT2	CT1	0.7200	3	180.00
CT1	CT2	CT1	NH1	0.4800	1	180.00
CT1	CT2	CT1	NH1	0.4200	2	180.00
CT1	CT2	CT1	NH1	0.6500	3	0.00
! Group-fitted for Phe/Tyr						
CA	CA	CT2	CT1	1.0700	1	0.00
CA	CA	CT2	CT1	0.2400	2	180.00
CA	CA	CT2	CT1	0.1700	3	180.00
C	CT1	CT2	CA	1.2800	1	180.00
C	CT1	CT2	CA	0.9400	2	180.00
C	CT1	CT2	CA	1.5700	3	180.00
CA	CT2	CT1	NH1	0.5200	1	180.00
CA	CT2	CT1	NH1	0.6200	2	180.00
CA	CT2	CT1	NH1	1.5800	3	0.00
! Fitted Ser						
CT1	CT2	OH1	H	0.0200	1	0.00
CT1	CT2	OH1	H	0.5600	2	0.00

CT1	CT2	OH1	H	0.4900	3	0.00
C	CT1	CT2	OH1	0.6500	1	180.00
C	CT1	CT2	OH1	0.2500	2	180.00
C	CT1	CT2	OH1	1.1700	3	180.00
NH1	CT1	CT2	OH1	0.1800	1	180.00
NH1	CT1	CT2	OH1	0.1900	2	180.00
NH1	CT1	CT2	OH1	1.4600	3	0.00
! Group-fitted for Ile/Thr						
CT1	CT1	OH1	H	0.1800	1	0.00
CT1	CT1	OH1	H	0.0600	2	0.00
CT1	CT1	OH1	H	0.2500	3	0.00
C	CT1	CT1	OH1	0.7900	1	180.00
C	CT1	CT1	OH1	0.3900	2	180.00
C	CT1	CT1	OH1	0.9900	3	180.00
NH1	CT1	CT1	OH1	0.0900	1	0.00
NH1	CT1	CT1	OH1	0.1900	2	180.00
NH1	CT1	CT1	OH1	0.1700	3	0.00
! Fitted Trp side-chain						
CA	CY	CT2	CT1	0.0300	1	0.00
CA	CY	CT2	CT1	0.5500	2	0.00
CA	CY	CT2	CT1	0.3900	3	180.00
CPT	CY	CT2	CT1	0.3600	1	180.00
CPT	CY	CT2	CT1	0.0500	2	0.00
CPT	CY	CT2	CT1	0.1900	3	180.00
C	CT1	CT2	CY	1.0900	1	180.00
C	CT1	CT2	CY	0.5000	2	180.00
C	CT1	CT2	CY	1.1700	3	180.00
CY	CT2	CT1	NH1	0.2900	1	180.00
CY	CT2	CT1	NH1	0.6600	2	180.00
CY	CT2	CT1	NH1	1.1700	3	0.00
! Fitted Val						
C	CT1	CT1	CT3	0.1400	1	180.00
C	CT1	CT1	CT3	0.2600	2	180.00
C	CT1	CT1	CT3	0.3300	3	180.00
CT3	CT1	CT1	NH1	0.1800	1	0.00
CT3	CT1	CT1	NH1	0.0600	2	0.00
CT3	CT1	CT1	NH1	0.5900	3	0.00

Lennard-Jones parameters

CT1	0.0	-0.0320	2.000	0.0	-0.01	1.9
CT2	0.0	-0.0560	2.010	0.0	-0.01	1.9
CT2A	0.0	-0.0560	2.010	0.0	-0.01	1.9
CT3	0.0	-0.0780	2.040	0.0	-0.01	1.9
HA1	0.0	-0.045	1.3400			
HA2	0.0	-0.034	1.3400			
HA3	0.0	-0.024	1.3400			

CMAP

! 2D grid correction data.

! alanine map

C	NH1	CT1	C	NH1	CT1	C	NH1	24
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! phi = -180.0

0.126790	0.768700	0.971260	1.250970	2.121010
2.720430	2.089440	1.789790	0.780870	-0.688474
1.001130	-2.200520	-4.827670	-4.821447	-4.913223
-3.591106	-2.766446	-2.784200	-2.454589	-2.346991
-2.335350	-1.522656	-0.951542	-0.036650	

! phi = -165.0

-0.127133	1.377090	1.577020	1.872290	2.398990
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2.486630	2.436754	1.929070	1.086456	0.643400
0.258676	-2.800440	-4.009477	-4.135306	-3.420090
-2.602140	-2.299128	-1.501241	-1.101780	-0.861434
-0.640168	-0.207701	-1.076344	-1.122030	
! phi = -150.0				
0.084069	1.420317	1.624350	2.047200	2.653910
2.716410	2.321416	1.985454	1.557466	2.463293
-0.225720	-1.815886	-2.583256	-3.006154	-2.551995
-1.890683	-1.354215	-0.727243	0.068512	-0.225016
-0.765479	-1.283444	-1.293226	-0.816303	
! phi = -135.0				
0.927992	1.521370	2.242218	2.546305	3.111384
2.918410	2.460813	2.187970	2.058314	1.852278
0.115935	-1.183897	-1.995479	-2.278329	-1.959136
-1.340467	-0.932949	0.021790	0.313725	-0.517358
-1.152891	-0.983285	-0.566518	-0.442565	
! phi = -120.0				
1.357468	1.959160	2.698894	3.037857	3.698960
3.558453	2.639296	2.773853	2.719664	1.627997
0.705667	-0.785637	-2.118268	-2.628489	-1.803113
-0.425969	-0.062320	0.439040	0.910952	-0.546994
-0.968118	-0.856791	-0.250116	0.449309	
! phi = -105.0				
2.045006	2.544424	2.818030	3.088582	3.370620
3.551568	3.073520	2.903794	2.956634	2.124759
0.906487	-0.823628	-2.090819	-2.241579	-1.456524
0.206160	0.082195	0.771710	1.040241	-0.124647
-0.316550	-0.164333	0.314474	0.733747	
! phi = -90.0				
1.451735	2.748481	2.738185	3.156796	3.450028
3.344157	3.180200	3.898724	3.335030	2.440579
0.912671	-0.606502	-1.511772	-1.620864	-0.962798
-0.020653	0.415153	0.908250	0.459433	0.145910
-0.071054	0.017622	0.280839	0.748823	
! phi = -75.0				
1.378160	3.345958	2.352424	3.063543	3.814070
3.700796	3.580310	4.212293	3.536425	1.693809
0.095172	-0.682452	-0.123614	-0.427765	-0.598368
0.226352	0.423308	0.301999	0.551890	0.191719
-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0				
0.237754	1.229980	1.716960	3.168570	4.208190
4.391860	4.276080	3.673107	2.272295	-0.482789
-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
0.139806	0.267796	0.322420	0.309664	-0.666399
-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0				
-1.184837	0.078060	2.347410	4.211350	5.376000
5.389940	4.380200	2.461506	1.123713	0.107016
0.007574	-0.149443	-0.797230	-0.582210	0.082910
0.271580	-0.045570	0.379430	0.247770	-0.890956
-1.582430	-1.954532	-1.980965	-2.000433	

```

! phi = -30.0
-1.174720      1.067030      4.180460      6.741610      6.070770
 4.806470      2.783340      1.320806      0.765978     -0.008448
 0.276860     -0.707140      1.314360      1.522590      1.915550
 2.223490      0.194290      0.534000      0.331780     -1.595147
-2.849141     -3.550465     -3.277369     -2.655135

! phi = -15.0
 0.293590      5.588070      3.732620      3.217620      3.272450
 2.517320      1.588700      1.381760      0.856410      0.655170
 1.616970      0.846920      0.511070      0.740760      1.021020
 1.616580     -0.342400      0.181770     -0.613920     -2.558037
-3.786839     -3.807325     -3.155346     -1.749204

! phi =  0.0
 2.832310      0.787990      0.323280      0.479230      0.628600
 0.976330      1.238750      1.671950      1.645480      2.520340
 1.606970      0.776350      0.119780      0.070390      0.121170
-1.569230     -1.213010     -1.846360     -2.744510     -3.792530
-3.934880     -3.615930     -2.675750     -0.924170

! phi =  15.0
-0.778340     -1.912680     -2.052140     -1.846280     -1.047430
 0.183400      1.682950      2.223500      1.358370      2.448660
 1.436920      0.678570     -0.237060     -0.535320     -0.790380
-2.182580     -3.251140     -4.195110     -4.269270     -3.908210
-3.455620     -2.773970      1.755370      0.313410

! phi =  30.0
-2.963810     -3.483730     -3.441809     -2.400349     -1.125083
 0.336200      1.428450      1.394630      0.970370      2.462720
 1.522430      0.553620     -0.407380     -1.482950     -3.613920
-4.159810     -4.709721     -4.496271     -3.764540     -2.959140
-1.963850     -1.071260     -1.599580     -2.445320

! phi =  45.0
-4.021496     -3.836549     -3.365327     -2.334377     -0.984725
 0.362000      0.814380      0.754110      0.502370      1.903420
 0.770220     -0.416420     -3.286310     -3.875270     -4.611550
-5.287977     -5.146239     -4.038627     -2.865450     -2.368170
-2.860490     -3.416560     -3.666490     -3.595217

! phi =  60.0
-3.353683     -2.984416     -2.317412     -1.240143     -0.257890
 0.722610      0.668070      0.438130      2.395330      1.632470
-2.041450     -3.218100     -3.915080     -4.568574     -5.096776
-5.526955     -5.005312     -3.777879     -2.840678     -3.508820
-3.756430     -3.640810     -3.451845     -3.342810

! phi =  75.0
-2.248733     -1.641080     -1.010583      0.039656      0.636063
 0.823710      0.517140     -0.013120     -0.370910     -1.192809
-2.305650     -3.420580     -4.484960     -5.597237     -5.601264
-5.727739     -4.740525     -3.819378     -3.685150     -4.151360
-4.170739     -3.725589     -3.736732     -2.620673

! phi =  90.0
-1.720840     -1.177830     -0.428430      0.277730      0.807900
 0.803260      0.482510     -0.336900     -0.786270     -1.774070
-2.793220     -3.828560     -5.211800     -6.294328     -6.617221
-5.763953     -5.072995     -3.911450     -4.158306     -4.473413

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-4.099325    -3.769822    -3.157300    -2.651694

! phi = 105.0
-1.850640    -1.092420    -0.445020     0.128490     1.005520
 0.884820     0.485850    -0.218470    -0.857670    -1.682330
-3.014400    -4.481110    -6.053510    -6.865400    -6.871130
-5.728240    -3.912230    -4.802110    -5.034640    -4.715990
-4.600554    -4.086721    -3.274630    -2.410940

! phi = 120.0
-1.969230    -1.116650    -0.540250    -0.150330     0.763520
 1.038890     0.758480     0.313530    -0.333050    -1.872770
-3.366270    -5.008260    -6.124810    -7.034830    -6.724320
-3.700200    -4.510620    -5.185650    -5.361620    -4.847490
-4.444320    -4.004260    -3.415720    -2.751230

! phi = 135.0
-2.111250    -1.168960    -0.322790    -0.006920     0.316660
 1.086270     0.939170     0.625340    -0.166360    -1.830310
-3.469470    -4.946030    -6.112560    -1.915580    -4.047310
-4.996740    -4.996730    -4.842690    -4.886620    -4.300540
-4.494620    -4.442210    -4.163570    -3.183510

! phi = 150.0
-1.757590    -0.403620     0.023920     0.362390     0.634520
 1.264920     1.361360     0.948420    -0.073680    -1.483560
-3.152820     1.835120    -1.762860    -5.093660    -5.744830
-5.390070    -4.783930    -4.190630    -4.115420    -4.042280
-4.125570    -4.028550    -4.026100    -2.937910

! phi = 165.0
-0.810590    -0.071500     0.378890     0.543310     1.277880
 1.641310     1.698840     1.519950     0.631950    -1.088670
-2.736530    -0.735240    -4.563830    -6.408350    -5.889450
-5.141750    -4.194970    -3.666490    -3.843450    -3.555000
-3.548722    -3.246995    -2.751289    -1.814368

! alanine before proline map
C   NH1  CT1  C   NH1  CT1  C   N   24
! phi = -180.0
 0.126790     0.768700     0.971260     1.250970     2.121010
 2.720430     2.089440     1.789790     0.780870    -0.688474
 1.001130    -2.200520    -4.827670    -4.821447    -4.913223
-3.591106    -2.766446    -2.784200    -2.454589    -2.346991
-2.335350    -1.522656    -0.951542    -0.036650

! phi = -165.0
-0.127133     1.377090     1.577020     1.872290     2.398990
 2.486630     2.436754     1.929070     1.086456     0.643400
 0.258676    -2.800440    -4.009477    -4.135306    -3.420090
-2.602140    -2.299128    -1.501241    -1.101780    -0.861434
-0.640168    -0.207701    -1.076344    -1.122030

! phi = -150.0
 0.084069     1.420317     1.624350     2.047200     2.653910
 2.716410     2.321416     1.985454     1.557466     2.463293
-0.225720    -1.815886    -2.583256    -3.006154    -2.551995
-1.890683    -1.354215    -0.727243     0.068512    -0.225016

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	-0.765479	-1.283444	-1.293226	-0.816303	
! phi = -135.0	0.927992	1.521370	2.242218	2.546305	3.111384
	2.918410	2.460813	2.187970	2.058314	1.852278
	0.115935	-1.183897	-1.995479	-2.278329	-1.959136
	-1.340467	-0.932949	0.021790	0.313725	-0.517358
	-1.152891	-0.983285	-0.566518	-0.442565	
! phi = -120.0	1.357468	1.959160	2.698894	3.037857	3.698960
	3.558453	2.639296	2.773853	2.719664	1.627997
	0.705667	-0.785637	-2.118268	-2.628489	-1.803113
	-0.425969	-0.062320	0.439040	0.910952	-0.546994
	-0.968118	-0.856791	-0.250116	0.449309	
! phi = -105.0	2.045006	2.544424	2.818030	3.088582	3.370620
	3.551568	3.073520	2.903794	2.956634	2.124759
	0.906487	-0.823628	-2.090819	-2.241579	-1.456524
	0.206160	0.082195	0.771710	1.040241	-0.124647
	-0.316550	-0.164333	0.314474	0.733747	
! phi = -90.0	1.451735	2.748481	2.738185	3.156796	3.450028
	3.344157	3.180200	3.898724	3.335030	2.440579
	0.912671	-0.606502	-1.511772	-1.620864	-0.962798
	-0.020653	0.415153	0.908250	0.459433	0.145910
	-0.071054	0.017622	0.280839	0.748823	
! phi = -75.0	1.378160	3.345958	2.352424	3.063543	3.814070
	3.700796	3.580310	4.212293	3.536425	1.693809
	0.095172	-0.682452	-0.123614	-0.427765	-0.598368
	0.226352	0.423308	0.301999	0.551890	0.191719
	-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0	0.237754	1.229980	1.716960	3.168570	4.208190
	4.391860	4.276080	3.673107	2.272295	-0.482789
	-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
	0.139806	0.267796	0.322420	0.309664	-0.666399
	-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0	-1.184837	0.078060	2.347410	4.211350	5.376000
	5.389940	4.380200	2.461506	1.123713	0.107016
	0.007574	-0.149443	-0.797230	-0.582210	0.082910
	0.271580	-0.045570	0.379430	0.247770	-0.890956
	-1.582430	-1.954532	-1.980965	-2.000433	
! phi = -30.0	-1.174720	1.067030	4.180460	6.741610	6.070770
	4.806470	2.783340	1.320806	0.765978	-0.008448
	0.276860	-0.707140	1.314360	1.522590	1.915550
	2.223490	0.194290	0.534000	0.331780	-1.595147
	-2.849141	-3.550465	-3.277369	-2.655135	
! phi = -15.0	0.293590	5.588070	3.732620	3.217620	3.272450
	2.517320	1.588700	1.381760	0.856410	0.655170

1.616970	0.846920	0.511070	0.740760	1.021020
1.616580	-0.342400	0.181770	-0.613920	-2.558037
-3.786839	-3.807325	-3.155346	-1.749204	
! phi = 0.0				
2.832310	0.787990	0.323280	0.479230	0.628600
0.976330	1.238750	1.671950	1.645480	2.520340
1.606970	0.776350	0.119780	0.070390	0.121170
-1.569230	-1.213010	-1.846360	-2.744510	-3.792530
-3.934880	-3.615930	-2.675750	-0.924170	
! phi = 15.0				
-0.778340	-1.912680	-2.052140	-1.846280	-1.047430
0.183400	1.682950	2.223500	1.358370	2.448660
1.436920	0.678570	-0.237060	-0.535320	-0.790380
-2.182580	-3.251140	-4.195110	-4.269270	-3.908210
-3.455620	-2.773970	1.755370	0.313410	
! phi = 30.0				
-2.963810	-3.483730	-3.441809	-2.400349	-1.125083
0.336200	1.428450	1.394630	0.970370	2.462720
1.522430	0.553620	-0.407380	-1.482950	-3.613920
-4.159810	-4.709721	-4.496271	-3.764540	-2.959140
-1.963850	-1.071260	-1.599580	-2.445320	
! phi = 45.0				
-4.021496	-3.836549	-3.365327	-2.334377	-0.984725
0.362000	0.814380	0.754110	0.502370	1.903420
0.770220	-0.416420	-3.286310	-3.875270	-4.611550
-5.287977	-5.146239	-4.038627	-2.865450	-2.368170
-2.860490	-3.416560	-3.666490	-3.595217	
! phi = 60.0				
-3.353683	-2.984416	-2.317412	-1.240143	-0.257890
0.722610	0.668070	0.438130	2.395330	1.632470
-2.041450	-3.218100	-3.915080	-4.568574	-5.096776
-5.526955	-5.005312	-3.777879	-2.840678	-3.508820
-3.756430	-3.640810	-3.451845	-3.342810	
! phi = 75.0				
-2.248733	-1.641080	-1.010583	0.039656	0.636063
0.823710	0.517140	-0.013120	-0.370910	-1.192809
-2.305650	-3.420580	-4.484960	-5.597237	-5.601264
-5.727739	-4.740525	-3.819378	-3.685150	-4.151360
-4.170739	-3.725589	-3.736732	-2.620673	
! phi = 90.0				
-1.720840	-1.177830	-0.428430	0.277730	0.807900
0.803260	0.482510	-0.336900	-0.786270	-1.774070
-2.793220	-3.828560	-5.211800	-6.294328	-6.617221
-5.763953	-5.072995	-3.911450	-4.158306	-4.473413
-4.099325	-3.769822	-3.157300	-2.651694	
! phi = 105.0				
-1.850640	-1.092420	-0.445020	0.128490	1.005520
0.884820	0.485850	-0.218470	-0.857670	-1.682330
-3.014400	-4.481110	-6.053510	-6.865400	-6.871130
-5.728240	-3.912230	-4.802110	-5.034640	-4.715990
-4.600554	-4.086721	-3.274630	-2.410940	
! phi = 120.0				

-1.969230	-1.116650	-0.540250	-0.150330	0.763520				
1.038890	0.758480	0.313530	-0.333050	-1.872770				
-3.366270	-5.008260	-6.124810	-7.034830	-6.724320				
-3.700200	-4.510620	-5.185650	-5.361620	-4.847490				
-4.444320	-4.004260	-3.415720	-2.751230					
! phi = 135.0								
-2.111250	-1.168960	-0.322790	-0.006920	0.316660				
1.086270	0.939170	0.625340	-0.166360	-1.830310				
-3.469470	-4.946030	-6.112560	-1.915580	-4.047310				
-4.996740	-4.996730	-4.842690	-4.886620	-4.300540				
-4.494620	-4.442210	-4.163570	-3.183510					
! phi = 150.0								
-1.757590	-0.403620	0.023920	0.362390	0.634520				
1.264920	1.361360	0.948420	-0.073680	-1.483560				
-3.152820	1.835120	-1.762860	-5.093660	-5.744830				
-5.390070	-4.783930	-4.190630	-4.115420	-4.042280				
-4.125570	-4.028550	-4.026100	-2.937910					
! phi = 165.0								
-0.810590	-0.071500	0.378890	0.543310	1.277880				
1.641310	1.698840	1.519950	0.631950	-1.088670				
-2.736530	-0.735240	-4.563830	-6.408350	-5.889450				
-5.141750	-4.194970	-3.666490	-3.843450	-3.555000				
-3.548722	-3.246995	-2.751289	-1.814368					
! proline								
! VTZ CBS map								
C	N	CP1	C	N	CP1	C	NH1	24
! phi = -180								
2.973500	3.348200	3.062900	2.113400	1.040500				
0.770600	0.785200	0.263300	-0.479000	-0.583000				
-0.463800	-0.292600	0.000000	0.259100	0.177100				
-0.151200	-0.173500	0.211700	0.348900	-0.135600				
-0.950000	-1.256600	-0.292800	1.560000					
! phi = -165								
5.674100	6.011400	5.562700	4.467300	3.390800				
3.008800	2.848600	2.311200	1.661400	1.468400				
1.142700	1.437400	2.113200	2.799500	2.989100				
2.869000	3.016100	3.328500	3.232900	2.547600				
1.647200	1.422700	2.517100	4.339800					
! phi = -150								
6.752800	6.973200	6.444300	5.389800	4.438600				
4.046000	3.832800	3.442400	3.303500	3.010000				
2.838100	3.162200	3.778300	4.362800	4.603600				
4.546200	4.702100	4.837200	4.549500	3.849600				
3.099200	3.031800	4.060200	5.624800					
! phi = -135								
7.627800	8.153400	7.342500	5.893500	4.799200				
4.433400	4.551500	4.442800	2.222200	0.776300				
0.790000	2.152300	3.932900	5.274900	5.830800				
5.988600	5.588500	5.211000	4.918000	4.292100				
3.495500	3.449800	4.617700	6.311700					
! phi = -120								

8.115600	8.477200	7.754300	6.585000	5.537900
4.964300	4.929000	4.421200	2.336100	1.257800
1.769300	3.359900	5.018000	6.055500	6.217600
5.726100	5.512200	5.820200	5.716700	4.872300
4.066800	4.094600	5.284900	6.931500	
! phi = -105				
9.249700	9.483000	8.668500	7.525300	7.003200
6.834600	6.822100	5.287600	3.320600	2.640300
3.464800	5.100300	6.537600	6.885600	5.842000
5.248700	5.540200	6.652400	7.196700	6.625400
5.710100	5.581700	6.651500	8.192800	
! phi = -90				
9.335600	9.208000	8.564600	8.010200	7.885100
8.212200	8.737100	8.429100	7.306500	6.474200
6.651300	7.484700	8.195300	8.295000	7.407200
6.529900	6.242000	6.227500	6.347300	6.449700
6.404700	6.579300	7.391700	8.570700	
! phi = -75				
10.955200	11.455400	11.173300	10.428700	10.062400
10.044500	9.279600	6.965100	5.361500	5.102700
6.267600	7.871600	8.009800	7.104500	6.616400
6.733700	7.504000	8.664700	9.282800	8.795900
7.872500	7.612400	8.498100	9.894000	
! phi = -60				
8.422900	8.529200	8.608500	9.306400	10.239400
11.025900	11.510800	9.283500	7.566000	6.624600
7.038700	8.222400	8.786400	8.512000	8.103500
7.988200	8.192900	8.291000	8.055600	7.436800
6.651800	6.317000	6.802500	7.746300	
! phi = -45				
6.913200	7.937400	8.610800	9.316600	9.388500
9.408400	8.828800	7.297900	5.456400	4.742700
5.793100	7.118800	7.565400	7.598500	7.438700
7.512500	7.878100	8.082200	7.642700	6.320500
4.680400	3.830500	4.215800	5.435200	
! phi = -30				
5.466700	7.116000	8.908800	8.347200	7.413500
7.047000	6.031600	4.193100	2.674800	3.023700
4.485300	5.451700	6.214900	6.422600	6.229300
6.191100	6.488900	6.646400	5.833400	3.751300
1.719800	1.064900	1.955800	3.860800	
! phi = -15				
3.061500	5.603800	12.179500	6.295200	5.323400
4.826500	3.705600	2.461500	2.291600	3.145900
3.562100	4.443600	5.337500	5.728800	5.694800
5.641600	5.943300	6.169000	4.759500	2.569400
1.357100	1.669800	3.212300	5.031900	
! phi = 0				
8.085900	8.051100	5.023600	3.450800	2.836100
2.192500	1.566200	1.456300	2.039300	1.945200
2.188400	2.921300	3.467500	3.543500	3.374500
3.472300	4.069900	3.615600	2.082200	0.958600
0.792600	1.494200	2.794900	4.853100	

```

! phi = 15
  6.639500    5.177400    3.252300    1.952700    1.078400
  0.888300    1.505400    2.442300    2.178600    1.578600
  1.777400    2.395400    2.820200    2.795200    2.662400
  2.917100    2.562100    1.557900    1.322300    1.631400
  2.051200    2.555600    3.039100    4.915000

! phi = 30
  7.548800    5.095500    2.747000    0.955200    0.444500
  1.318700    2.733300    3.223200    2.565500    2.150900
  2.394400    2.939300    3.266000    3.210000    3.113400
  2.491300    0.978300    0.815300    1.522700    2.055600
  2.199900    2.327600    3.474200    7.977800

! phi = 45
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 60
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 75
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 90
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 105
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 120
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

! phi = 135
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000

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0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000

! phi = 150
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000

! phi = 165
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000
0.000000    0.000000    0.000000    0.000000    0.000000

!2 adjacent prolines
! VTZ CBS map
C      N      CP1  C      N      CP1      C      N 24
! phi = -180
2.973500    3.348200    3.062900    2.113400    1.040500
0.770600    0.785200    0.263300   -0.479000   -0.583000
-0.463800   -0.292600    0.000000    0.259100    0.177100
-0.151200   -0.173500    0.211700    0.348900   -0.135600
-0.950000   -1.256600   -0.292800    1.560000

! phi = -165
5.674100    6.011400    5.562700    4.467300    3.390800
3.008800    2.848600    2.311200    1.661400    1.468400
1.142700    1.437400    2.113200    2.799500    2.989100
2.869000    3.016100    3.328500    3.232900    2.547600
1.647200    1.422700    2.517100    4.339800

! phi = -150
6.752800    6.973200    6.444300    5.389800    4.438600
4.046000    3.832800    3.442400    3.303500    3.010000
2.838100    3.162200    3.778300    4.362800    4.603600
4.546200    4.702100    4.837200    4.549500    3.849600
3.099200    3.031800    4.060200    5.624800

! phi = -135
7.627800    8.153400    7.342500    5.893500    4.799200
4.433400    4.551500    4.442800    2.222200    0.776300
0.790000    2.152300    3.932900    5.274900    5.830800
5.988600    5.588500    5.211000    4.918000    4.292100
3.495500    3.449800    4.617700    6.311700

! phi = -120
8.115600    8.477200    7.754300    6.585000    5.537900
4.964300    4.929000    4.421200    2.336100    1.257800
1.769300    3.359900    5.018000    6.055500    6.217600
5.726100    5.512200    5.820200    5.716700    4.872300
4.066800    4.094600    5.284900    6.931500

! phi = -105
9.249700    9.483000    8.668500    7.525300    7.003200
6.834600    6.822100    5.287600    3.320600    2.640300

```

3.464800	5.100300	6.537600	6.885600	5.842000
5.248700	5.540200	6.652400	7.196700	6.625400
5.710100	5.581700	6.651500	8.192800	
! phi = -90				
9.335600	9.208000	8.564600	8.010200	7.885100
8.212200	8.737100	8.429100	7.306500	6.474200
6.651300	7.484700	8.195300	8.295000	7.407200
6.529900	6.242000	6.227500	6.347300	6.449700
6.404700	6.579300	7.391700	8.570700	
! phi = -75				
10.955200	11.455400	11.173300	10.428700	10.062400
10.044500	9.279600	6.965100	5.361500	5.102700
6.267600	7.871600	8.009800	7.104500	6.616400
6.733700	7.504000	8.664700	9.282800	8.795900
7.872500	7.612400	8.498100	9.894000	
! phi = -60				
8.422900	8.529200	8.608500	9.306400	10.239400
11.025900	11.510800	9.283500	7.566000	6.624600
7.038700	8.222400	8.786400	8.512000	8.103500
7.988200	8.192900	8.291000	8.055600	7.436800
6.651800	6.317000	6.802500	7.746300	
! phi = -45				
6.913200	7.937400	8.610800	9.316600	9.388500
9.408400	8.828800	7.297900	5.456400	4.742700
5.793100	7.118800	7.565400	7.598500	7.438700
7.512500	7.878100	8.082200	7.642700	6.320500
4.680400	3.830500	4.215800	5.435200	
! phi = -30				
5.466700	7.116000	8.908800	8.347200	7.413500
7.047000	6.031600	4.193100	2.674800	3.023700
4.485300	5.451700	6.214900	6.422600	6.229300
6.191100	6.488900	6.646400	5.833400	3.751300
1.719800	1.064900	1.955800	3.860800	
! phi = -15				
3.061500	5.603800	12.179500	6.295200	5.323400
4.826500	3.705600	2.461500	2.291600	3.145900
3.562100	4.443600	5.337500	5.728800	5.694800
5.641600	5.943300	6.169000	4.759500	2.569400
1.357100	1.669800	3.212300	5.031900	
! phi = 0				
8.085900	8.051100	5.023600	3.450800	2.836100
2.192500	1.566200	1.456300	2.039300	1.945200
2.188400	2.921300	3.467500	3.543500	3.374500
3.472300	4.069900	3.615600	2.082200	0.958600
0.792600	1.494200	2.794900	4.853100	
! phi = 15				
6.639500	5.177400	3.252300	1.952700	1.078400
0.888300	1.505400	2.442300	2.178600	1.578600
1.777400	2.395400	2.820200	2.795200	2.662400
2.917100	2.562100	1.557900	1.322300	1.631400
2.051200	2.555600	3.039100	4.915000	
! phi = 30				

7.548800	5.095500	2.747000	0.955200	0.444500
1.318700	2.733300	3.223200	2.565500	2.150900
2.394400	2.939300	3.266000	3.210000	3.113400
2.491300	0.978300	0.815300	1.522700	2.055600
2.199900	2.327600	3.474200	7.977800	

! phi = 45

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 60

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 75

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 90

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 105

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 120

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 135

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

! phi = 150

0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000

```

! phi = 165
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000
  0.000000    0.000000    0.000000    0.000000    0.000000

```

```

! glycine map
! VTZ CBS map

```

```

C      NH1  CT2  C      NH1  CT2  C      NH1  24

```

```

! phi = -180
  0.235350    0.182300    0.177200    0.396800    0.859400
  1.489700    2.092500    2.297700    1.808600    0.696200
 -0.563300   -1.432700   -1.015100    1.426300   -0.564300
  0.696200    1.808200    2.301700    2.092600    1.489100
  0.859500    0.396900    0.176900    0.182400

```

```

! phi = -165
  0.020100   -0.203800   -0.269700    0.014200    0.620800
  1.392400    2.046200    2.188200    1.683900    0.688500
 -0.373700   -0.703500    0.837800    3.704000   -0.730100
  0.594100    1.713100    2.205800    2.026400    1.529800
  1.027400    0.623800    0.348400    0.182800

```

```

! phi = -150
 -0.533600   -0.807400   -0.804600   -0.379800    0.365300
  1.168000    1.641000    1.618100    1.302200    0.615100
  0.065700    0.738500    2.959500   -2.036600   -0.934600
  0.407900    1.517000    1.984800    1.833100    1.435200
  0.995600    0.562200    0.150600   -0.209000

```

```

! phi = -135
 -1.208500   -1.429400   -1.319200   -0.817500   -0.112400
  0.454400    0.737600    0.879300    0.850100    0.670300
  0.943500   -2.651200   -2.829400   -2.199100   -1.065700
  0.279600    1.322000    1.668300    1.521300    1.193900
  0.765300    0.246000   -0.315500   -0.823200

```

```

! phi = -120
 -1.789100   -1.965500   -1.860700   -1.447900   -0.896500
 -0.401000   -0.015100    0.321300    0.634600    0.976300
 -1.977500   -2.883200   -2.848500   -2.137900   -0.960300
  0.308700    1.098100    1.245300    1.133600    0.881800
  0.448200   -0.153900   -0.823700   -1.404300

```

```

! phi = -105
 -2.246700   -2.487000   -2.473700   -2.135600   -1.577700
 -0.980600   -0.429100    0.144700    0.734000   -0.918300
 -2.299200   -2.882200   -2.668600   -1.847100   -0.719800
  0.107000    0.496000    0.553500    0.584300    0.494000
  0.098300   -0.529800   -1.237900   -1.840100

```

```

! phi = -90
 -2.851100   -3.181100   -3.199500   -2.785300   -2.054300
 -1.242900   -0.476500    0.288100   -0.045300   -1.470600
 -2.558800   -2.869400   -2.450300   -1.582200   -0.930800
 -0.426400   -0.022700    0.000000   -0.097400   -0.136100

```

	-0.439600	-1.038600	-1.741000	-2.373200	
! phi = -75					
	-3.961800	-4.268200	-4.109000	-3.364700	-2.252200
	-1.140400	-0.209800	0.487300	-0.746200	-2.127700
	-2.932100	-2.898500	-2.247900	-1.730400	-1.177200
	-0.448200	0.034900	-0.073300	-0.531600	-0.933300
	-1.360700	-2.009200	-2.745700	-3.424900	
! phi = -60					
	-5.408000	-5.355100	-4.640100	-3.283200	-1.710200
	-0.423800	0.354400	-0.103700	-1.577700	-2.828300
	-3.151200	-2.649200	-2.183000	-1.761200	-0.981700
	-0.174700	0.262600	0.039200	-0.663000	-1.530700
	-2.478200	-3.465600	-4.334200	-5.011200	
! phi = -45					
	-6.093200	-5.298400	-3.816620	-1.922530	-0.196160
	0.768200	0.568500	-0.831300	-2.343900	-3.037100
	-2.663700	-2.191100	-2.022900	-1.438500	-0.649000
	0.077000	0.441500	0.257500	-0.491100	-1.820600
	-3.473100	-4.895200	-5.790700	-6.205900	
! phi = -30					
	-5.258225	-3.675795	-1.631110	0.430085	1.496470
	0.318200	-0.555100	-1.695500	-2.434200	-2.192600
	-1.691300	-1.890000	-1.708500	-1.206300	-0.567400
	0.054300	0.497200	0.599600	-0.171000	-2.137600
	-4.237000	-5.584100	-6.135100	-6.067000	
! phi = -15					
	-3.161820	-0.902080	1.432450	-1.452885	-1.560780
	-1.665600	-1.783100	-1.755100	-1.329300	-0.731100
	-1.317000	-1.662800	-1.601200	-1.294900	-0.817300
	-0.197100	0.549500	0.850400	-0.689700	-2.819900
	-4.393000	-5.111500	-5.205690	-4.654785	
! phi = 0					
	0.034035	-2.349860	-3.412065	-3.620070	-3.450950
	-2.875650	-1.787800	-0.541250	0.410450	-0.372500
	-1.126850	-1.498450	-1.608700	-1.498450	-1.126850
	-0.372500	0.410450	-0.541250	-1.787800	-2.875650
	-3.450950	-3.620070	-3.412065	-2.349860	
! phi = 15					
	-3.162345	-4.654785	-5.205690	-5.111500	-4.393000
	-2.819900	-0.689700	0.850400	0.549500	-0.197100
	-0.817300	-1.294900	-1.601200	-1.662800	-1.317000
	-0.731100	-1.329300	-1.755100	-1.783100	-1.665600
	-1.560780	-1.452885	1.432450	-0.902080	
! phi = 30					
	-5.258220	-6.067000	-6.135100	-5.584100	-4.237000
	-2.137600	-0.171000	0.599600	0.497200	0.054300
	-0.567400	-1.206300	-1.708500	-1.890000	-1.691300
	-2.192600	-2.434200	-1.695500	-0.555100	0.318200
	1.496470	0.430085	-1.631110	-3.675795	
! phi = 45					
	-6.093300	-6.205900	-5.790700	-4.895200	-3.473100
	-1.820600	-0.491100	0.257500	0.441500	0.077000

-0.649000	-1.438500	-2.022900	-2.191100	-2.663700
-3.037100	-2.343900	-0.831300	0.568500	0.768200
-0.196160	-1.922530	-3.816620	-5.298400	
! phi = 60				
-5.407500	-5.011200	-4.334200	-3.465600	-2.478200
-1.530700	-0.663000	0.039200	0.262600	-0.174700
-0.981700	-1.761200	-2.183000	-2.649200	-3.151200
-2.828300	-1.577700	-0.103700	0.354400	-0.423800
-1.710200	-3.283200	-4.640100	-5.355100	
! phi = 75				
-3.961900	-3.424900	-2.745700	-2.009200	-1.360700
-0.933300	-0.531600	-0.073300	0.034900	-0.448200
-1.177200	-1.730400	-2.247900	-2.898500	-2.932100
-2.127700	-0.746200	0.487300	-0.209800	-1.140400
-2.252200	-3.364700	-4.109000	-4.268200	
! phi = 90				
-2.854500	-2.373200	-1.741000	-1.038600	-0.439600
-0.136100	-0.097400	0.000000	-0.022700	-0.426400
-0.930800	-1.582200	-2.450300	-2.869400	-2.558800
-1.470600	-0.045300	0.288100	-0.476500	-1.242900
-2.054300	-2.785300	-3.199500	-3.181100	
! phi = 105				
-2.246400	-1.840100	-1.237900	-0.529800	0.098300
0.494000	0.584300	0.553500	0.496000	0.107000
-0.719800	-1.847100	-2.668600	-2.882200	-2.299200
-0.918300	0.734000	0.144700	-0.429100	-0.980600
-1.577700	-2.135600	-2.473700	-2.487000	
! phi = 120				
-1.788800	-1.404300	-0.823700	-0.153900	0.448200
0.881800	1.133600	1.245300	1.098100	0.308700
-0.960300	-2.137900	-2.848500	-2.883200	-1.977500
0.976300	0.634600	0.321300	-0.015100	-0.401000
-0.896500	-1.447900	-1.860700	-1.965500	
! phi = 135				
-1.208900	-0.823200	-0.315500	0.246000	0.765300
1.193900	1.521300	1.668300	1.322000	0.279600
-1.065700	-2.199100	-2.829400	-2.651200	0.943500
0.670300	0.850100	0.879300	0.737600	0.454400
-0.112400	-0.817500	-1.319200	-1.429400	
! phi = 150				
-0.533400	-0.209000	0.150600	0.562200	0.995600
1.435200	1.833100	1.984800	1.517000	0.407900
-0.934600	-2.036600	2.959500	0.738500	0.065700
0.615100	1.302200	1.618100	1.641000	1.168000
0.365300	-0.379800	-0.804600	-0.807400	
! phi = 165				
0.019900	0.182800	0.348400	0.623800	1.027400
1.529800	2.026400	2.205800	1.713100	0.594100
-0.730100	3.704000	0.837800	-0.703500	-0.373700
0.688500	1.683900	2.188200	2.046200	1.392400
0.620800	0.014200	-0.269700	-0.203800	

! glycine before proline map: use glycine map

```

! VTZ CBS map
C   NH1  CT2  C   NH1  CT2  C   N   24

! phi = -180
  0.235350    0.182300    0.177200    0.396800    0.859400
  1.489700    2.092500    2.297700    1.808600    0.696200
 -0.563300   -1.432700   -1.015100    1.426300   -0.564300
  0.696200    1.808200    2.301700    2.092600    1.489100
  0.859500    0.396900    0.176900    0.182400

! phi = -165
  0.020100   -0.203800   -0.269700    0.014200    0.620800
  1.392400    2.046200    2.188200    1.683900    0.688500
 -0.373700   -0.703500    0.837800    3.704000   -0.730100
  0.594100    1.713100    2.205800    2.026400    1.529800
  1.027400    0.623800    0.348400    0.182800

! phi = -150
 -0.533600   -0.807400   -0.804600   -0.379800    0.365300
  1.168000    1.641000    1.618100    1.302200    0.615100
  0.065700    0.738500    2.959500   -2.036600   -0.934600
  0.407900    1.517000    1.984800    1.833100    1.435200
  0.995600    0.562200    0.150600   -0.209000

! phi = -135
 -1.208500   -1.429400   -1.319200   -0.817500   -0.112400
  0.454400    0.737600    0.879300    0.850100    0.670300
  0.943500   -2.651200   -2.829400   -2.199100   -1.065700
  0.279600    1.322000    1.668300    1.521300    1.193900
  0.765300    0.246000   -0.315500   -0.823200

! phi = -120
 -1.789100   -1.965500   -1.860700   -1.447900   -0.896500
 -0.401000   -0.015100    0.321300    0.634600    0.976300
 -1.977500   -2.883200   -2.848500   -2.137900   -0.960300
  0.308700    1.098100    1.245300    1.133600    0.881800
  0.448200   -0.153900   -0.823700   -1.404300

! phi = -105
 -2.246700   -2.487000   -2.473700   -2.135600   -1.577700
 -0.980600   -0.429100    0.144700    0.734000   -0.918300
 -2.299200   -2.882200   -2.668600   -1.847100   -0.719800
  0.107000    0.496000    0.553500    0.584300    0.494000
  0.098300   -0.529800   -1.237900   -1.840100

! phi = -90
 -2.851100   -3.181100   -3.199500   -2.785300   -2.054300
 -1.242900   -0.476500    0.288100   -0.045300   -1.470600
 -2.558800   -2.869400   -2.450300   -1.582200   -0.930800
 -0.426400   -0.022700    0.000000   -0.097400   -0.136100
 -0.439600   -1.038600   -1.741000   -2.373200

! phi = -75
 -3.961800   -4.268200   -4.109000   -3.364700   -2.252200
 -1.140400   -0.209800    0.487300   -0.746200   -2.127700
 -2.932100   -2.898500   -2.247900   -1.730400   -1.177200
 -0.448200    0.034900   -0.073300   -0.531600   -0.933300
 -1.360700   -2.009200   -2.745700   -3.424900

! phi = -60
 -5.408000   -5.355100   -4.640100   -3.283200   -1.710200

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-0.423800	0.354400	-0.103700	-1.577700	-2.828300
-3.151200	-2.649200	-2.183000	-1.761200	-0.981700
-0.174700	0.262600	0.039200	-0.663000	-1.530700
-2.478200	-3.465600	-4.334200	-5.011200	
! phi = -45				
-6.093200	-5.298400	-3.816620	-1.922530	-0.196160
0.768200	0.568500	-0.831300	-2.343900	-3.037100
-2.663700	-2.191100	-2.022900	-1.438500	-0.649000
0.077000	0.441500	0.257500	-0.491100	-1.820600
-3.473100	-4.895200	-5.790700	-6.205900	
! phi = -30				
-5.258225	-3.675795	-1.631110	0.430085	1.496470
0.318200	-0.555100	-1.695500	-2.434200	-2.192600
-1.691300	-1.890000	-1.708500	-1.206300	-0.567400
0.054300	0.497200	0.599600	-0.171000	-2.137600
-4.237000	-5.584100	-6.135100	-6.067000	
! phi = -15				
-3.161820	-0.902080	1.432450	-1.452885	-1.560780
-1.665600	-1.783100	-1.755100	-1.329300	-0.731100
-1.317000	-1.662800	-1.601200	-1.294900	-0.817300
-0.197100	0.549500	0.850400	-0.689700	-2.819900
-4.393000	-5.111500	-5.205690	-4.654785	
! phi = 0				
0.034035	-2.349860	-3.412065	-3.620070	-3.450950
-2.875650	-1.787800	-0.541250	0.410450	-0.372500
-1.126850	-1.498450	-1.608700	-1.498450	-1.126850
-0.372500	0.410450	-0.541250	-1.787800	-2.875650
-3.450950	-3.620070	-3.412065	-2.349860	
! phi = 15				
-3.162345	-4.654785	-5.205690	-5.111500	-4.393000
-2.819900	-0.689700	0.850400	0.549500	-0.197100
-0.817300	-1.294900	-1.601200	-1.662800	-1.317000
-0.731100	-1.329300	-1.755100	-1.783100	-1.665600
-1.560780	-1.452885	1.432450	-0.902080	
! phi = 30				
-5.258220	-6.067000	-6.135100	-5.584100	-4.237000
-2.137600	-0.171000	0.599600	0.497200	0.054300
-0.567400	-1.206300	-1.708500	-1.890000	-1.691300
-2.192600	-2.434200	-1.695500	-0.555100	0.318200
1.496470	0.430085	-1.631110	-3.675795	
! phi = 45				
-6.093300	-6.205900	-5.790700	-4.895200	-3.473100
-1.820600	-0.491100	0.257500	0.441500	0.077000
-0.649000	-1.438500	-2.022900	-2.191100	-2.663700
-3.037100	-2.343900	-0.831300	0.568500	0.768200
-0.196160	-1.922530	-3.816620	-5.298400	
! phi = 60				
-5.407500	-5.011200	-4.334200	-3.465600	-2.478200
-1.530700	-0.663000	0.039200	0.262600	-0.174700
-0.981700	-1.761200	-2.183000	-2.649200	-3.151200
-2.828300	-1.577700	-0.103700	0.354400	-0.423800
-1.710200	-3.283200	-4.640100	-5.355100	

! phi = 75				
-3.961900	-3.424900	-2.745700	-2.009200	-1.360700
-0.933300	-0.531600	-0.073300	0.034900	-0.448200
-1.177200	-1.730400	-2.247900	-2.898500	-2.932100
-2.127700	-0.746200	0.487300	-0.209800	-1.140400
-2.252200	-3.364700	-4.109000	-4.268200	
! phi = 90				
-2.854500	-2.373200	-1.741000	-1.038600	-0.439600
-0.136100	-0.097400	0.000000	-0.022700	-0.426400
-0.930800	-1.582200	-2.450300	-2.869400	-2.558800
-1.470600	-0.045300	0.288100	-0.476500	-1.242900
-2.054300	-2.785300	-3.199500	-3.181100	
! phi = 105				
-2.246400	-1.840100	-1.237900	-0.529800	0.098300
0.494000	0.584300	0.553500	0.496000	0.107000
-0.719800	-1.847100	-2.668600	-2.882200	-2.299200
-0.918300	0.734000	0.144700	-0.429100	-0.980600
-1.577700	-2.135600	-2.473700	-2.487000	
! phi = 120				
-1.788800	-1.404300	-0.823700	-0.153900	0.448200
0.881800	1.133600	1.245300	1.098100	0.308700
-0.960300	-2.137900	-2.848500	-2.883200	-1.977500
0.976300	0.634600	0.321300	-0.015100	-0.401000
-0.896500	-1.447900	-1.860700	-1.965500	
! phi = 135				
-1.208900	-0.823200	-0.315500	0.246000	0.765300
1.193900	1.521300	1.668300	1.322000	0.279600
-1.065700	-2.199100	-2.829400	-2.651200	0.943500
0.670300	0.850100	0.879300	0.737600	0.454400
-0.112400	-0.817500	-1.319200	-1.429400	
! phi = 150				
-0.533400	-0.209000	0.150600	0.562200	0.995600
1.435200	1.833100	1.984800	1.517000	0.407900
-0.934600	-2.036600	2.959500	0.738500	0.065700
0.615100	1.302200	1.618100	1.641000	1.168000
0.365300	-0.379800	-0.804600	-0.807400	
! phi = 165				
0.019900	0.182800	0.348400	0.623800	1.027400
1.529800	2.026400	2.205800	1.713100	0.594100
-0.730100	3.704000	0.837800	-0.703500	-0.373700
0.688500	1.683900	2.188200	2.046200	1.392400
0.620800	0.014200	-0.269700	-0.203800	

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