Supporting Information

Metacridamides A and B, macrocycles from conidia of the entomopathogenic fungus *Metarhizium acridum*

Stuart B. Krasnoff,*[†] Ulrich Englich,[‡] Paula G. Miller,[§] Michael L. Shuler,[§] Raymond P. Glahn,[†] Bruno G. G. Donzelli,[⊥] and Donna M. Gibson[†]

[†]USDA-ARS-Biological IPM Research Unit, Ithaca, New York
[‡]The Cornell High Energy Synchrotron Source, Ithaca, NY
[§]Department of Biomedical Engineering, Cornell University, Ithaca NY
[⊥]Department of Plant Pathology, Cornell University, Ithaca, NY

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Figure S1. ^{1}H NMR of Metacridamide A (**1**) ($CDCl_3$, 600 MHz).

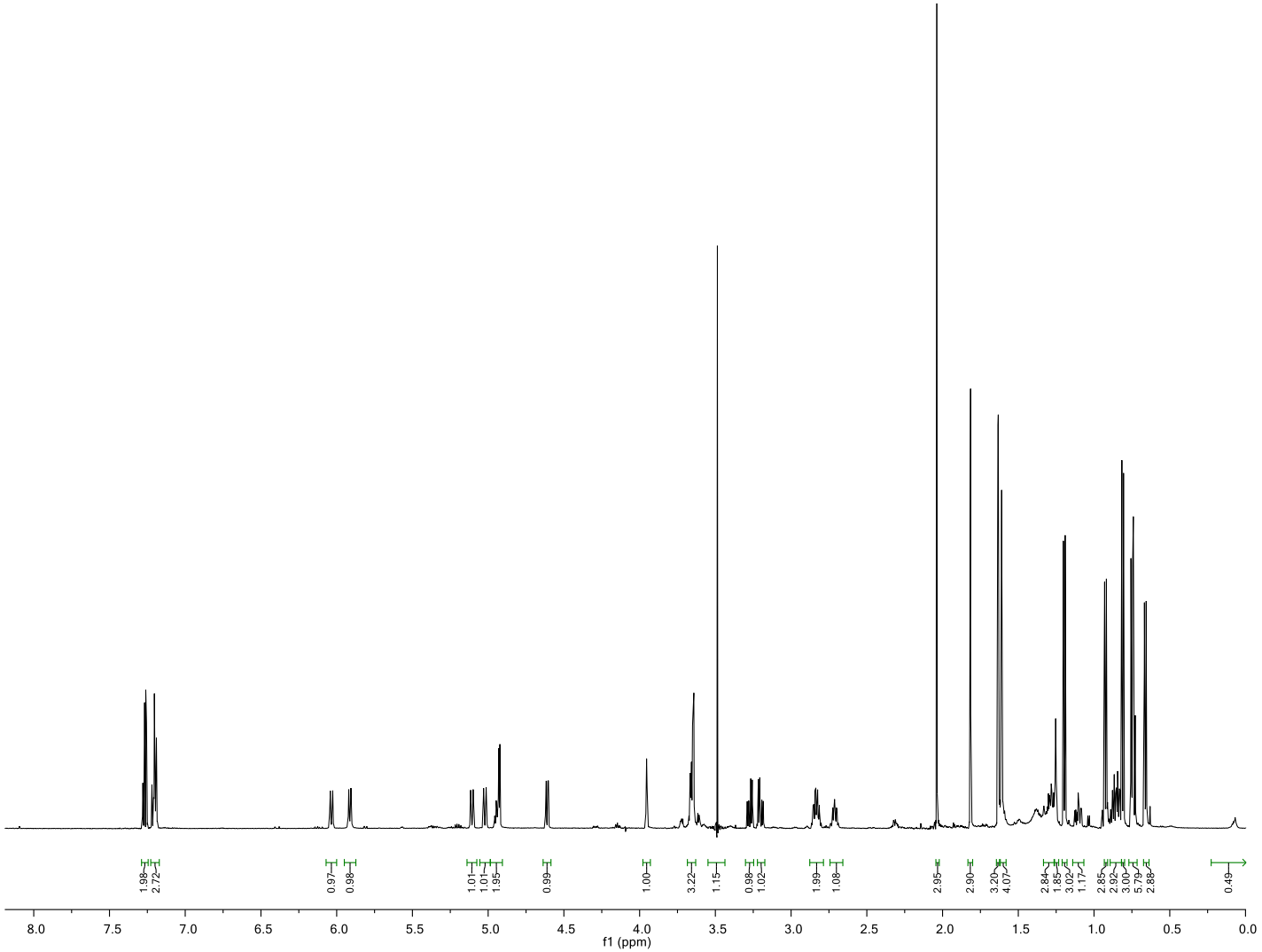

Figure S2 ^{1}H NMR of **1** ($CDCl_3$, 600 MHz), expanded.

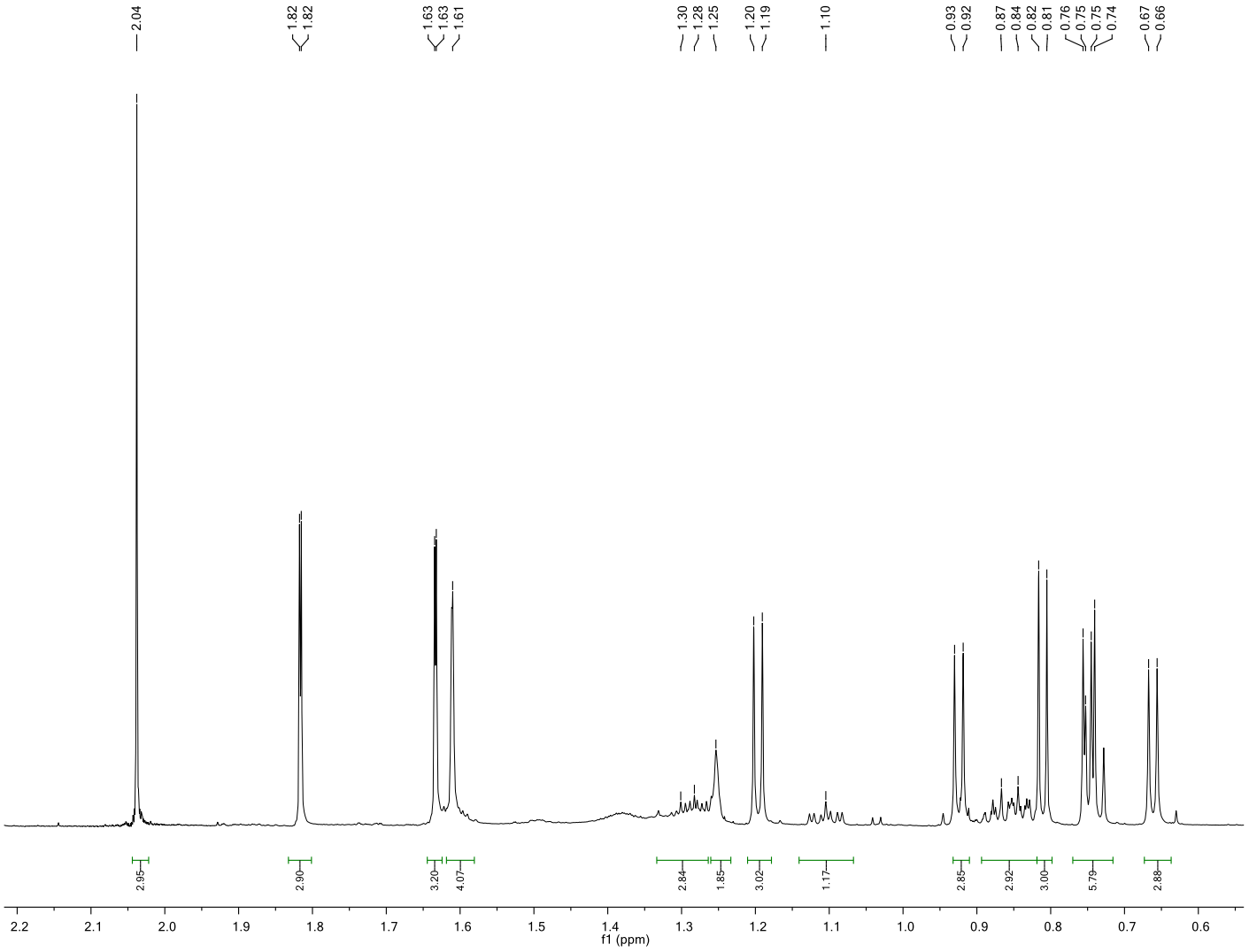

Figure S3. ^{1}H NMR of **1** ($CDCl_3$, 600 MHz), expanded.

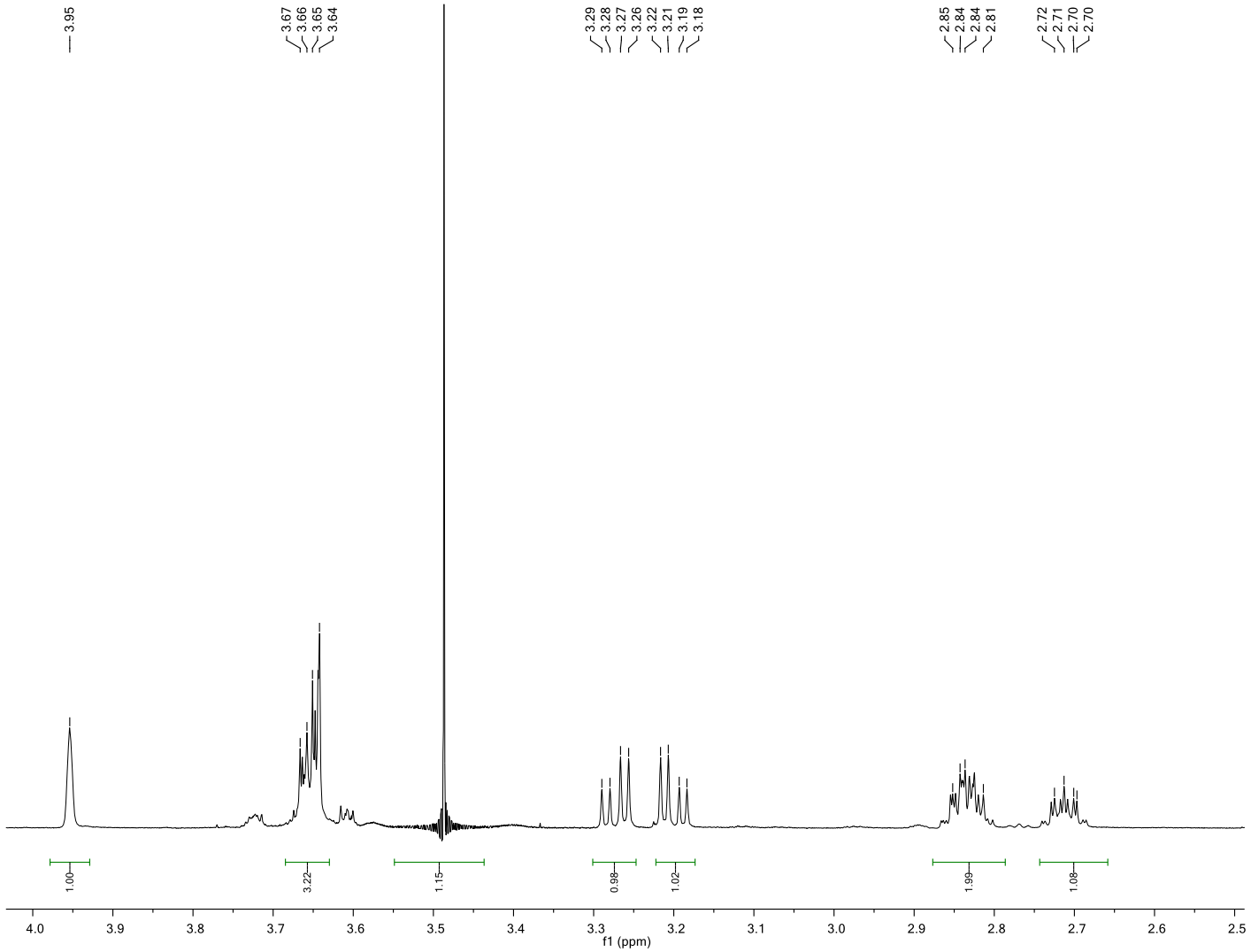

Figure **S4.** ^{1}H NMR of **1** ($CDCl_3$, 600 MHz), expanded.

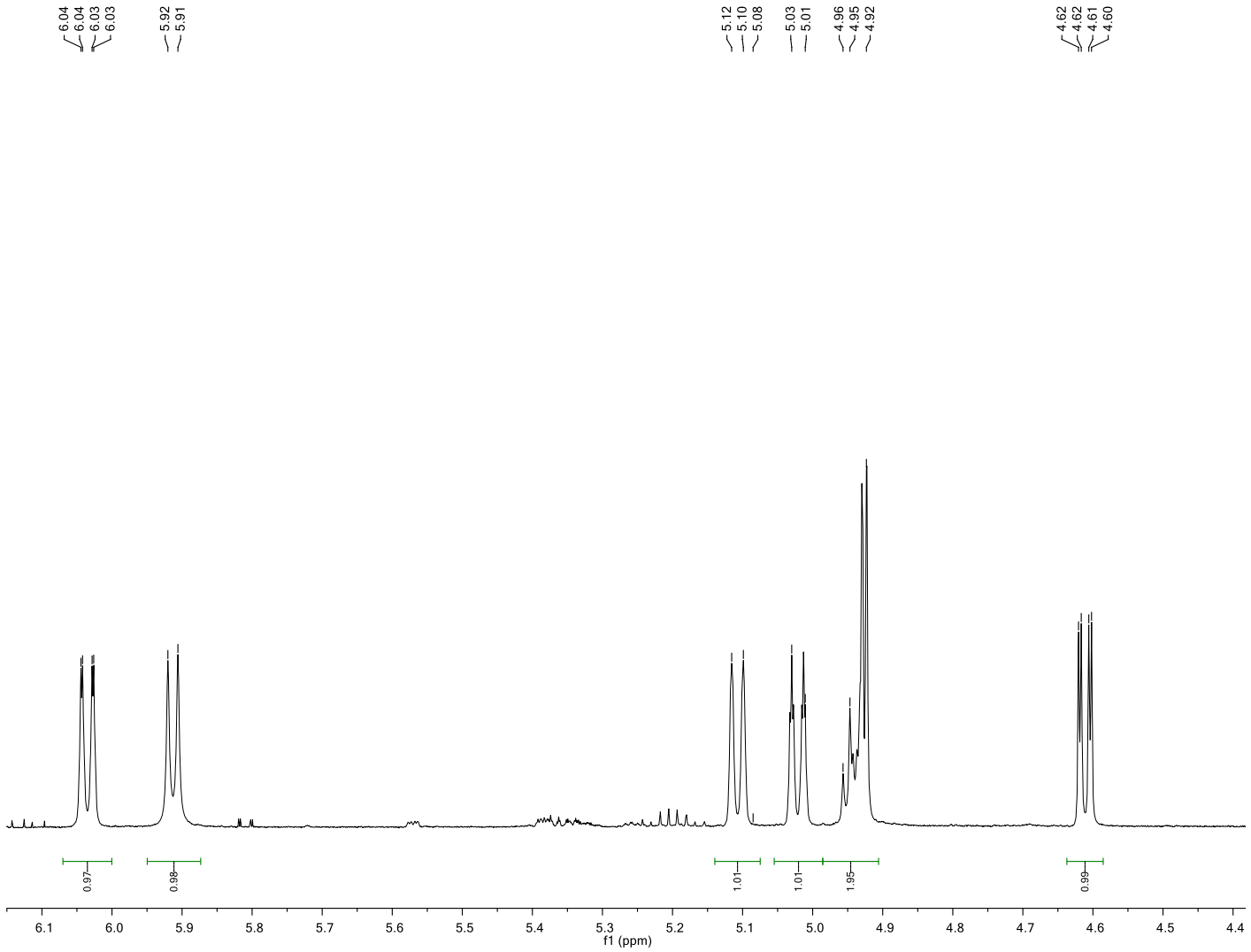

Figure **S5.** ^{1}H NMR of **1** ($CDCl_3$, 600 MHz), expanded.

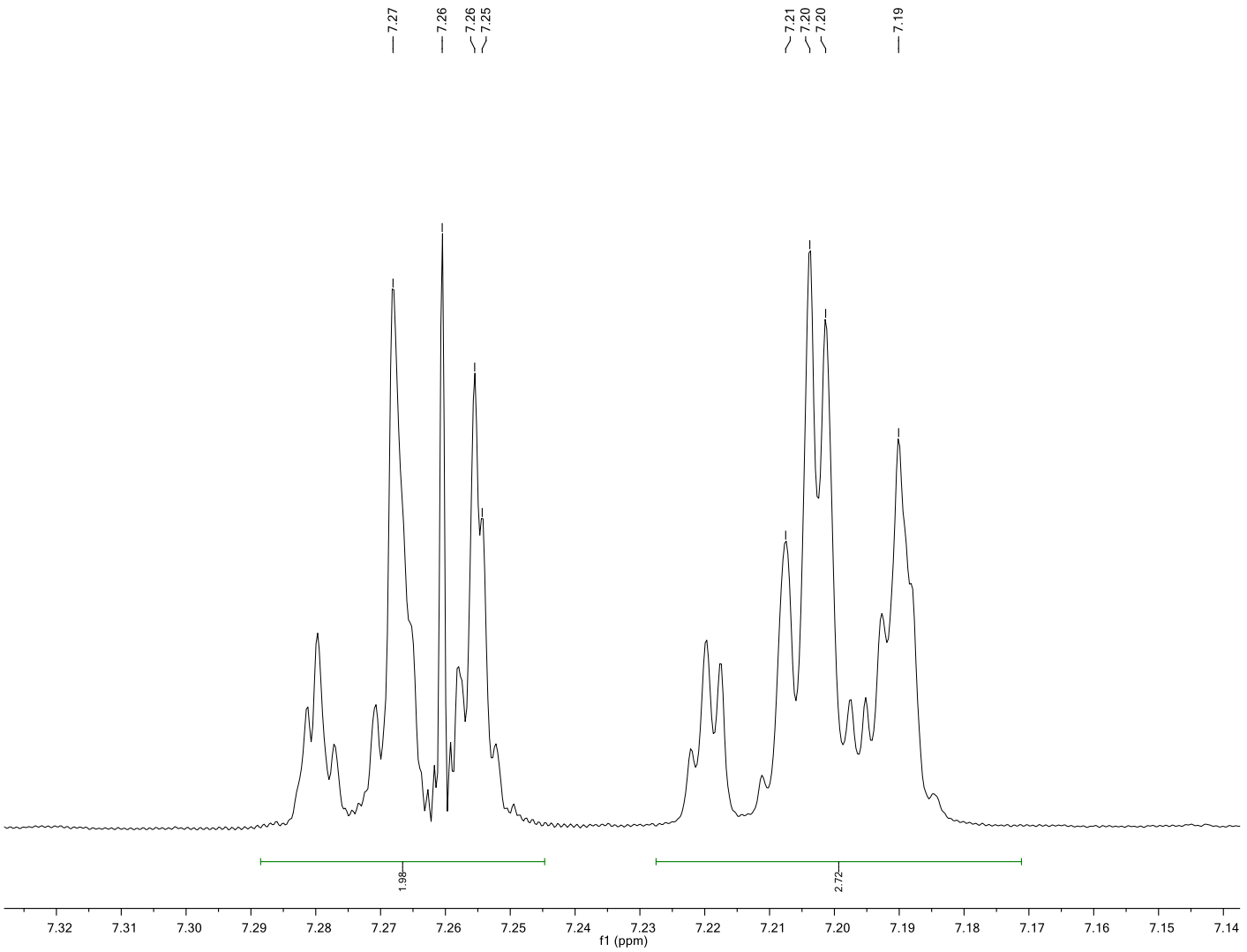

Figure S6. ^{13}C NMR of **1** ($CDCl_3$, 150 MHz).

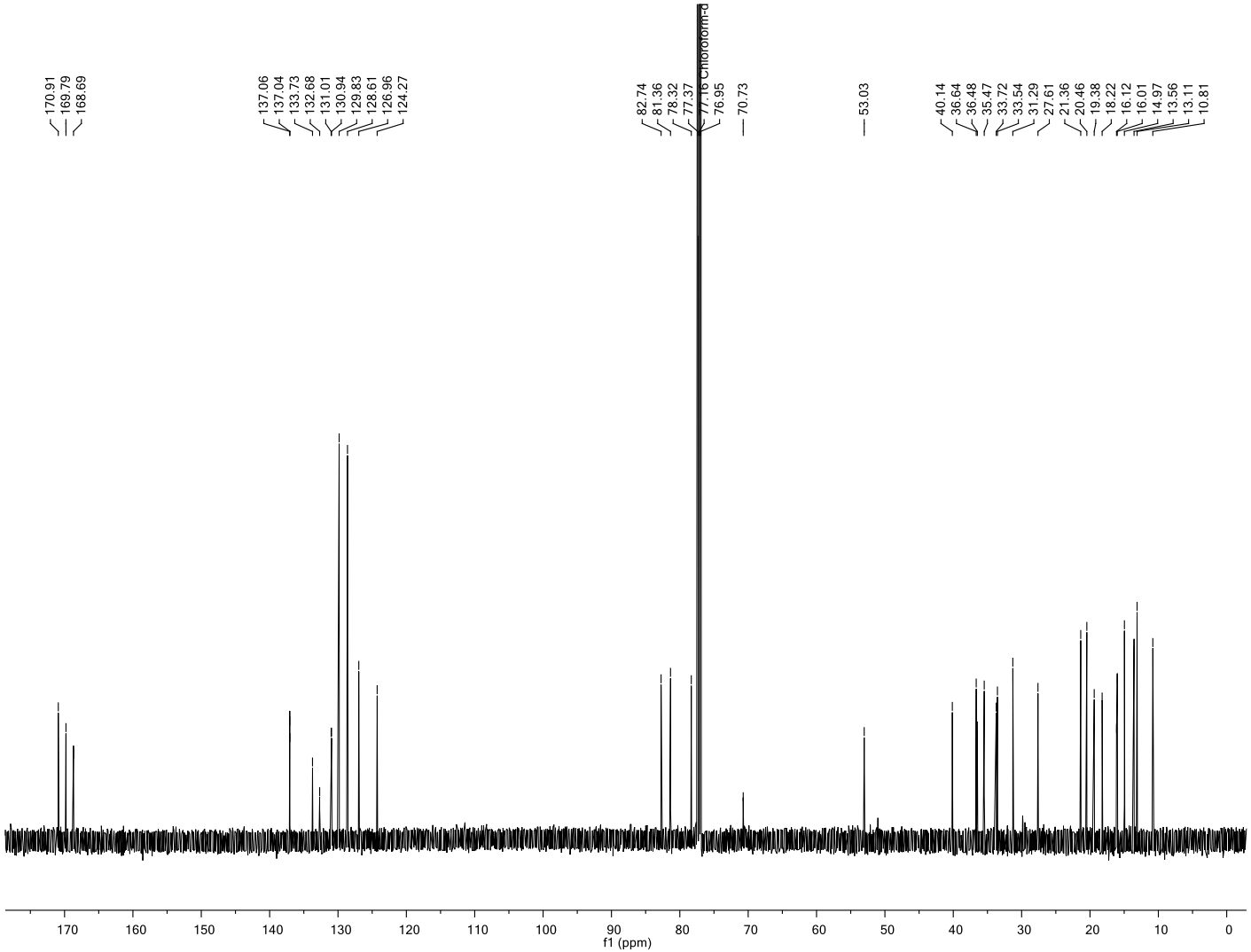

Figure S7. ^{13}C NMR of **1** ($CDCl_3$, 150 MHz), expanded.

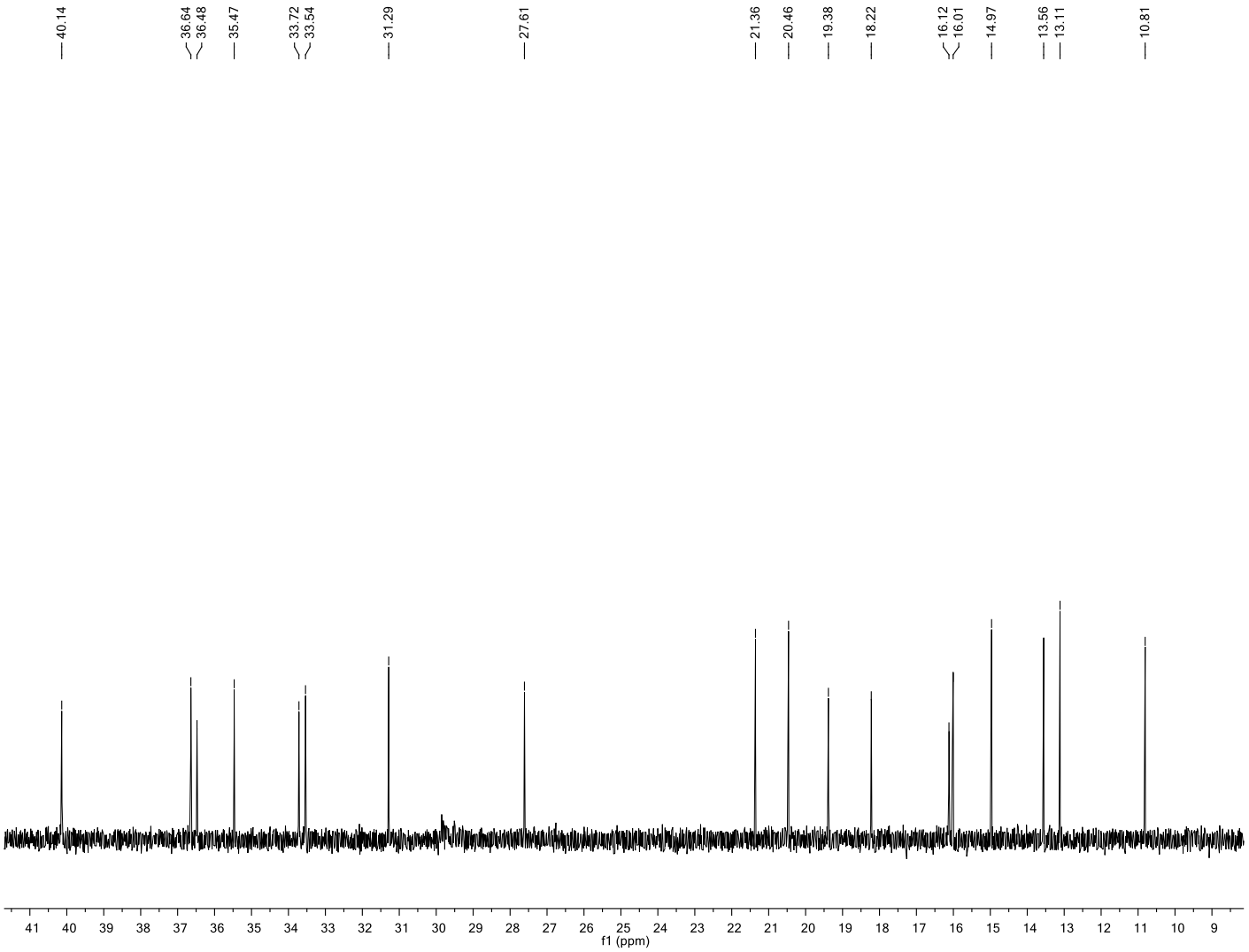

Figure S8. ^{13}C NMR of **1** ($CDCl_3$, 150 MHz), expanded.

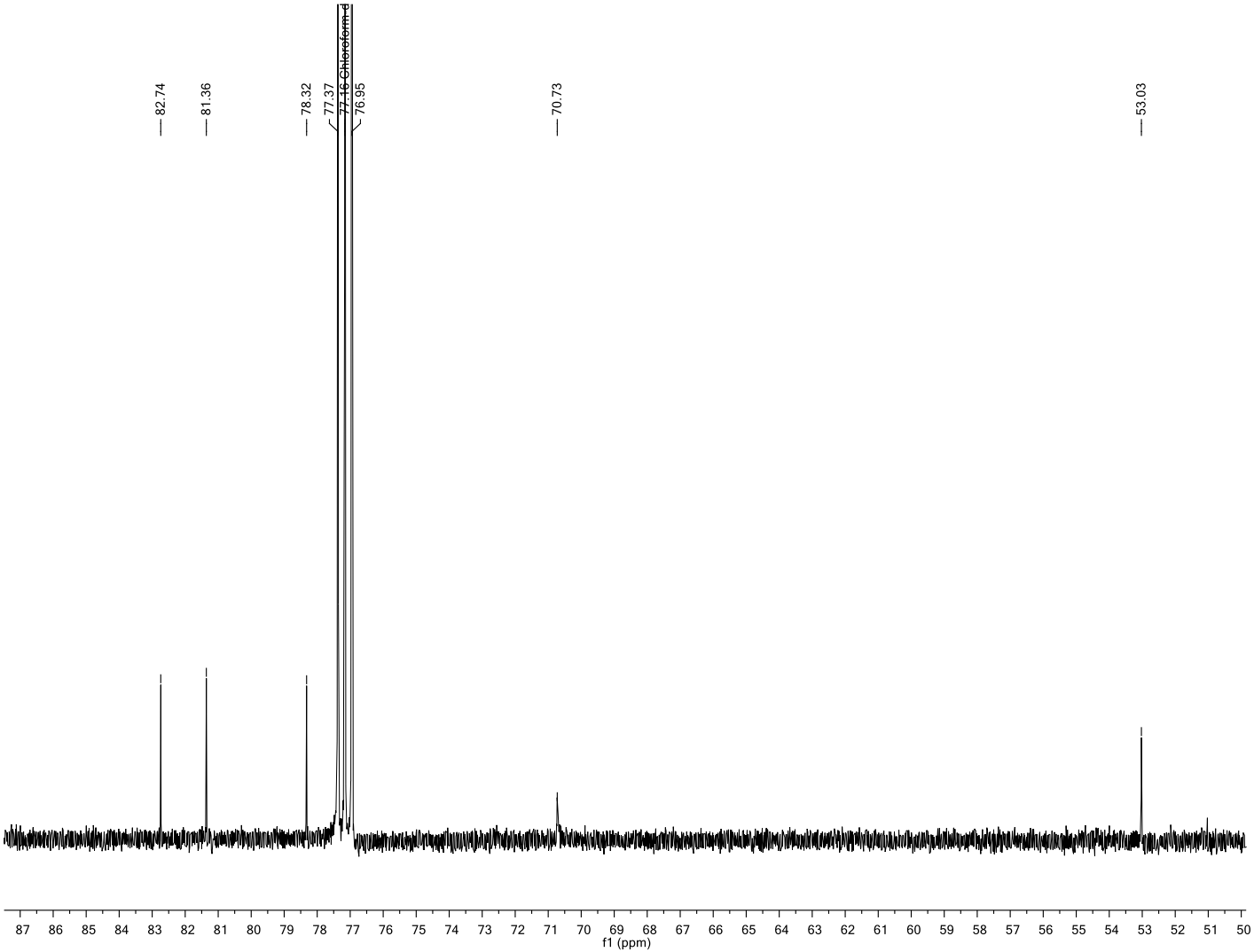

Figure S9. ^{13}C NMR of **1** ($CDCl_3$, 150 MHz), expanded.

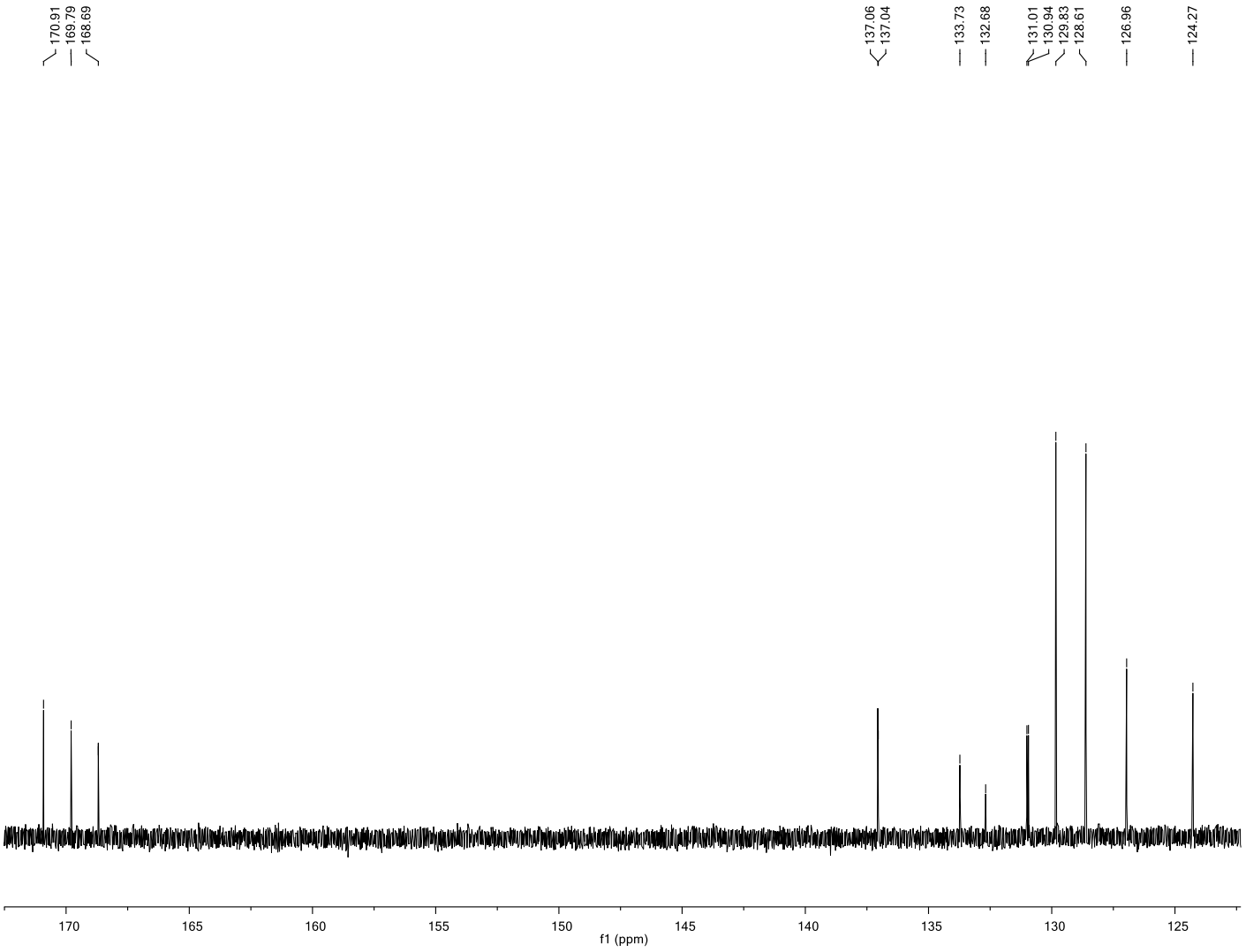

Figure S10. ^{13}C NMR of **1** ($CDCl_3$, 150 MHz), expanded.

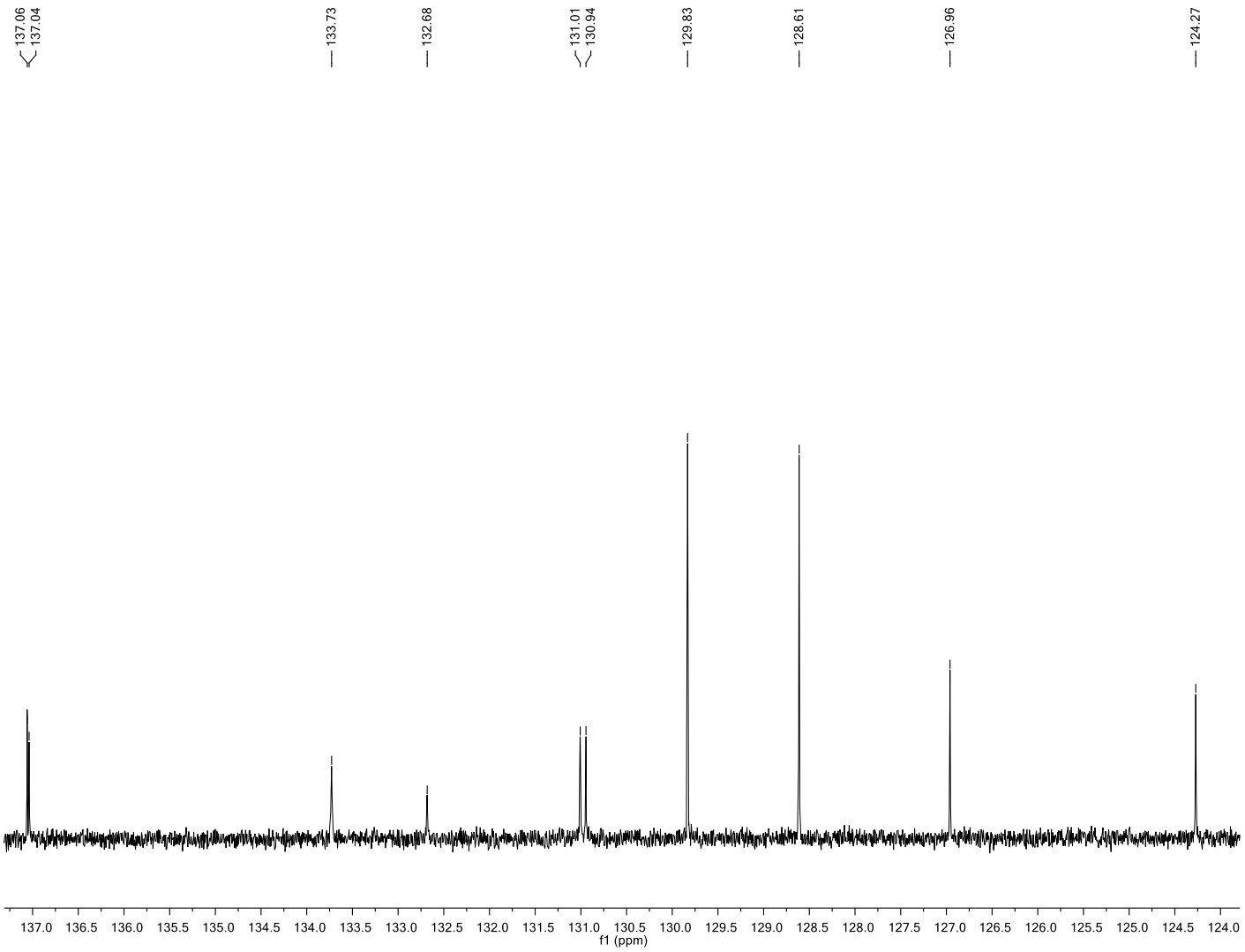

Figure S11. DQF-COSY of **1** ($CDCl_3$, 600 MHz).

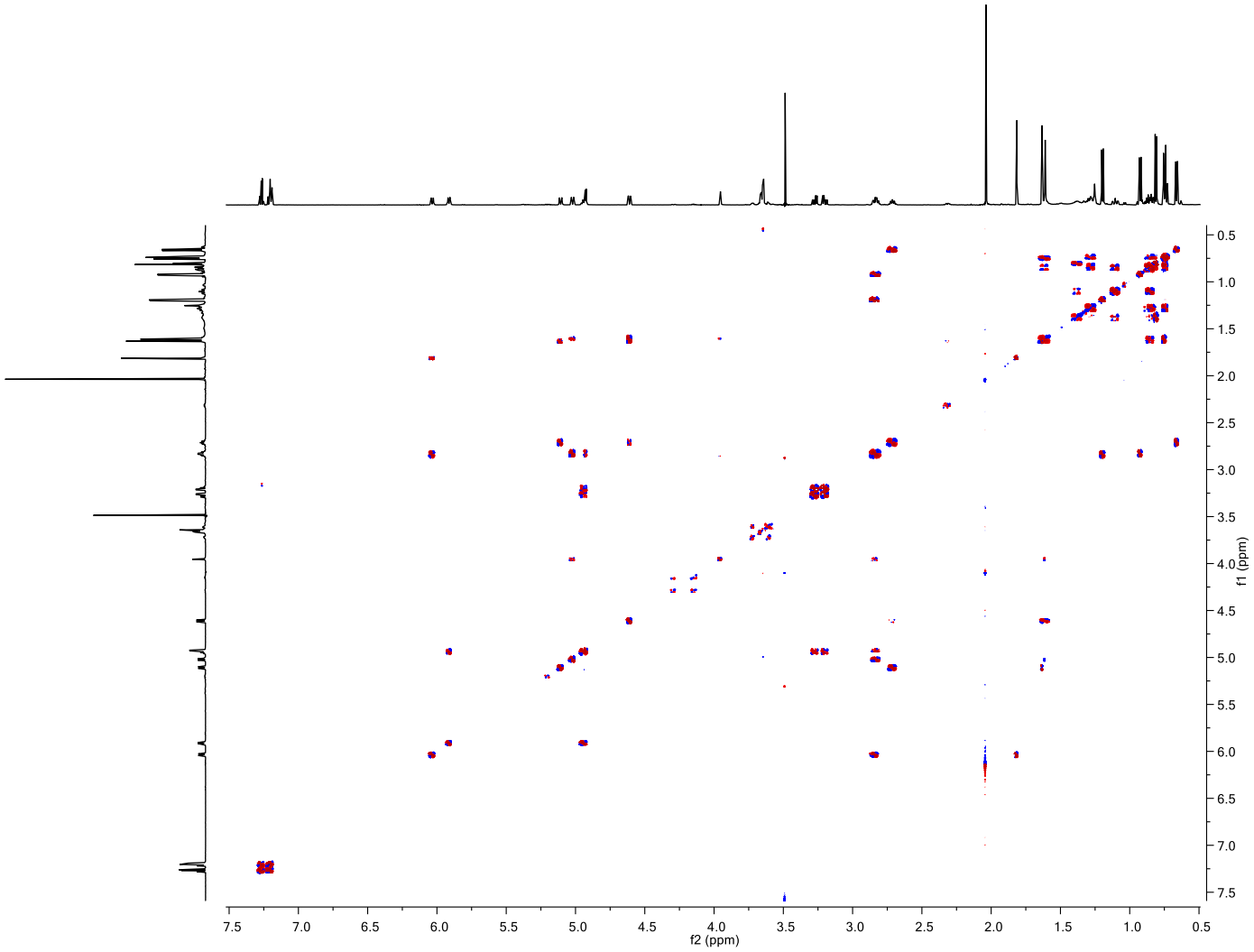

Figure S12. DQF-COSY of **1** ($CDCl_3$, 600 MHz) detail showing crosspeaks for three similar structural units. Clusters of analogous crosspeaks correspond to couplings as indicated. Color coded envelopes identify crosspeaks from same unit.

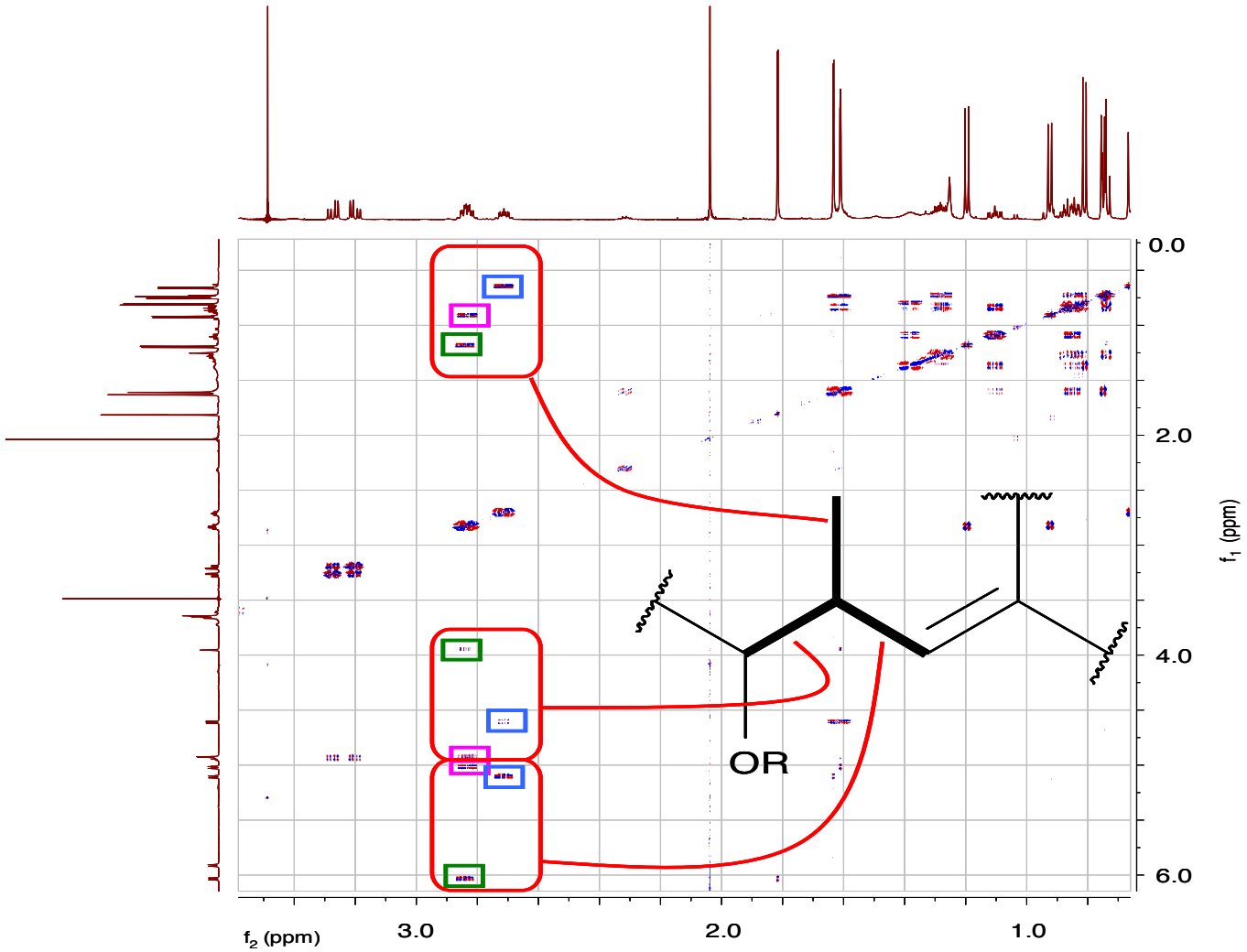

Figure S13. HSQC of **1** ($CDCl_3$, 600 MHz).

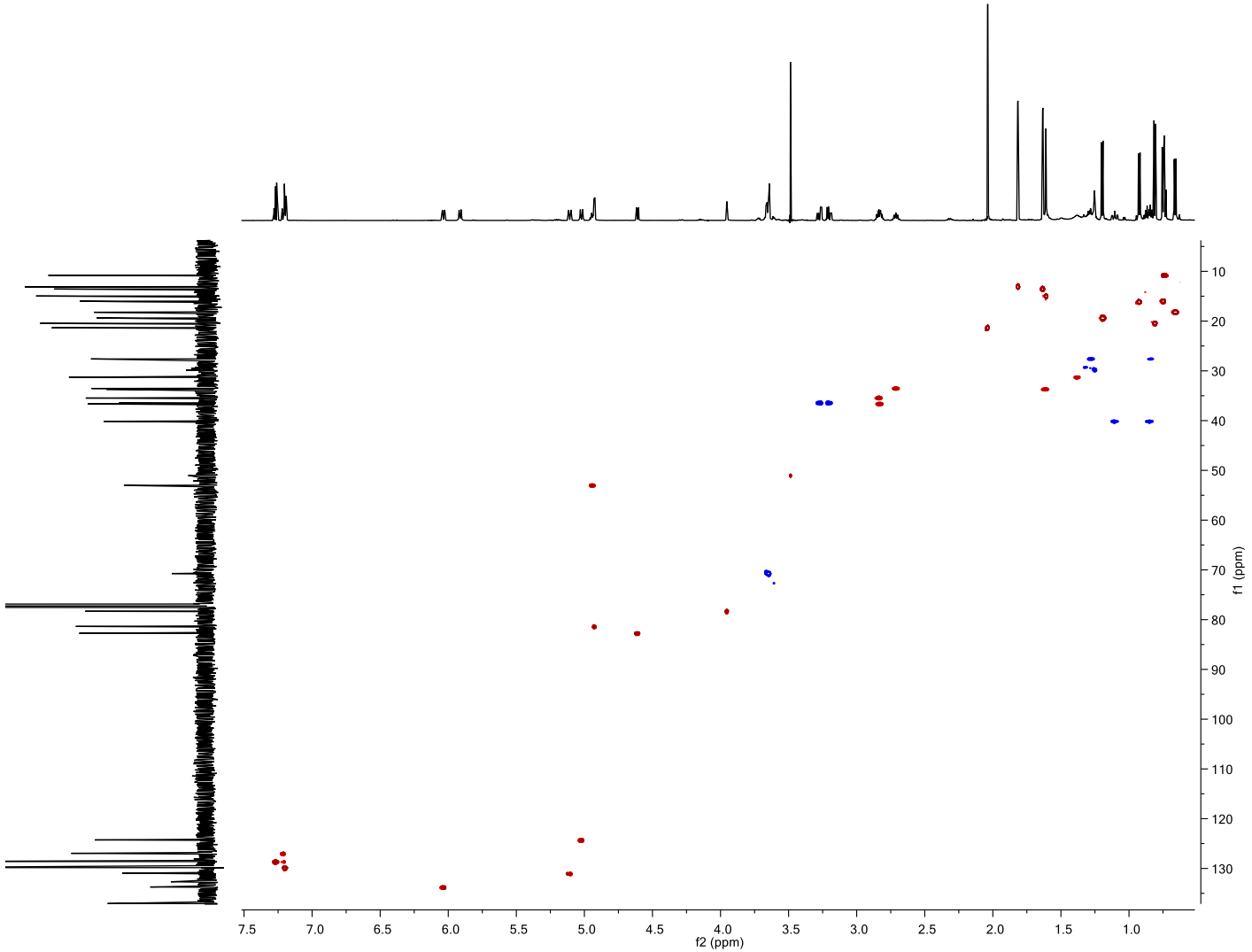

Figure S14. HSQC of **1** (CDCl3, 600 MHz) detail showing crosspeaks for alkenyl, oxymethine, methine, and methyl carbons in three similar structural units color coded as in Figure S12. Bolded bonds in structure indicate COSY network.

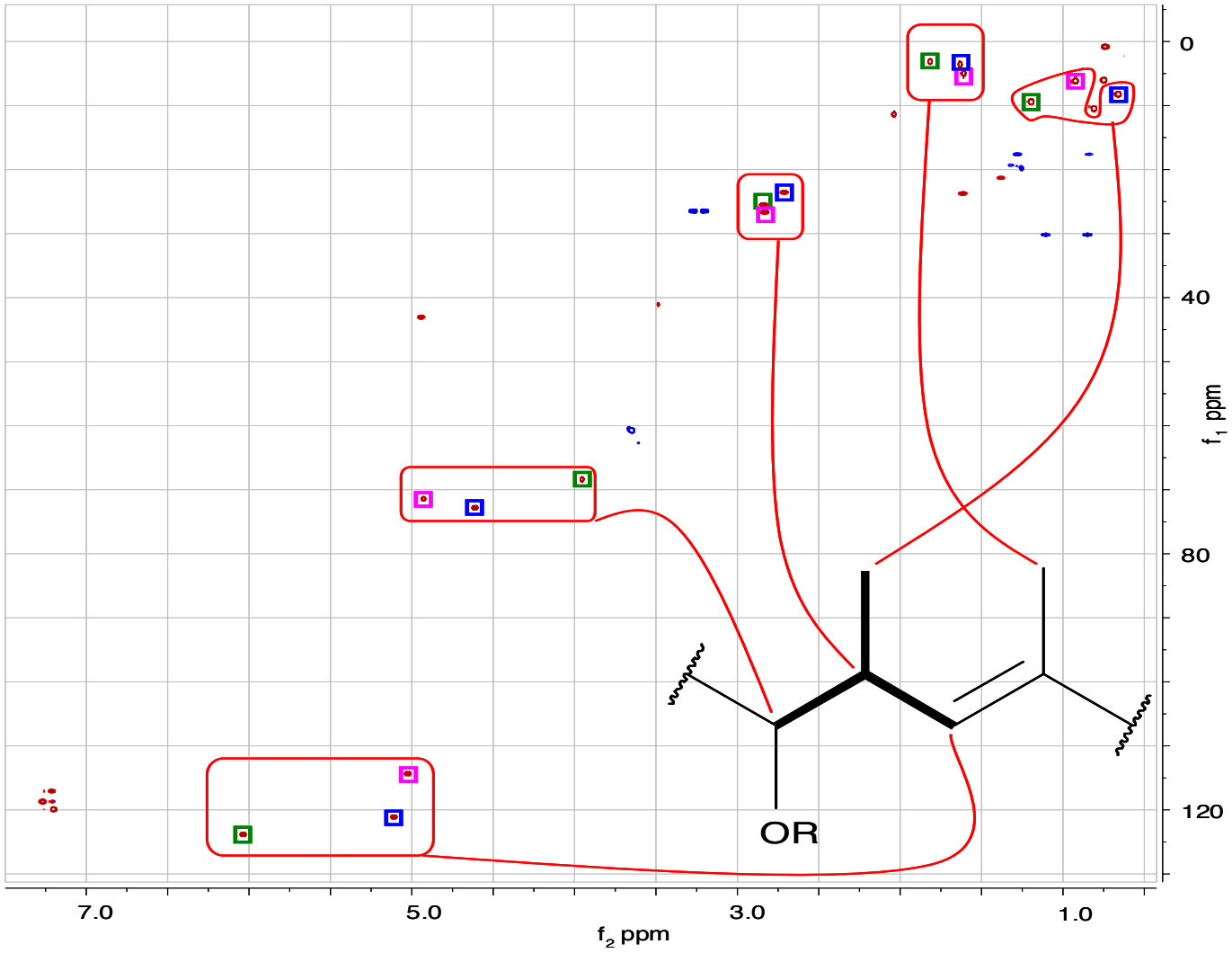

Figure S15. HMBC of **1** ($CDCl_3$, 600 MHz).

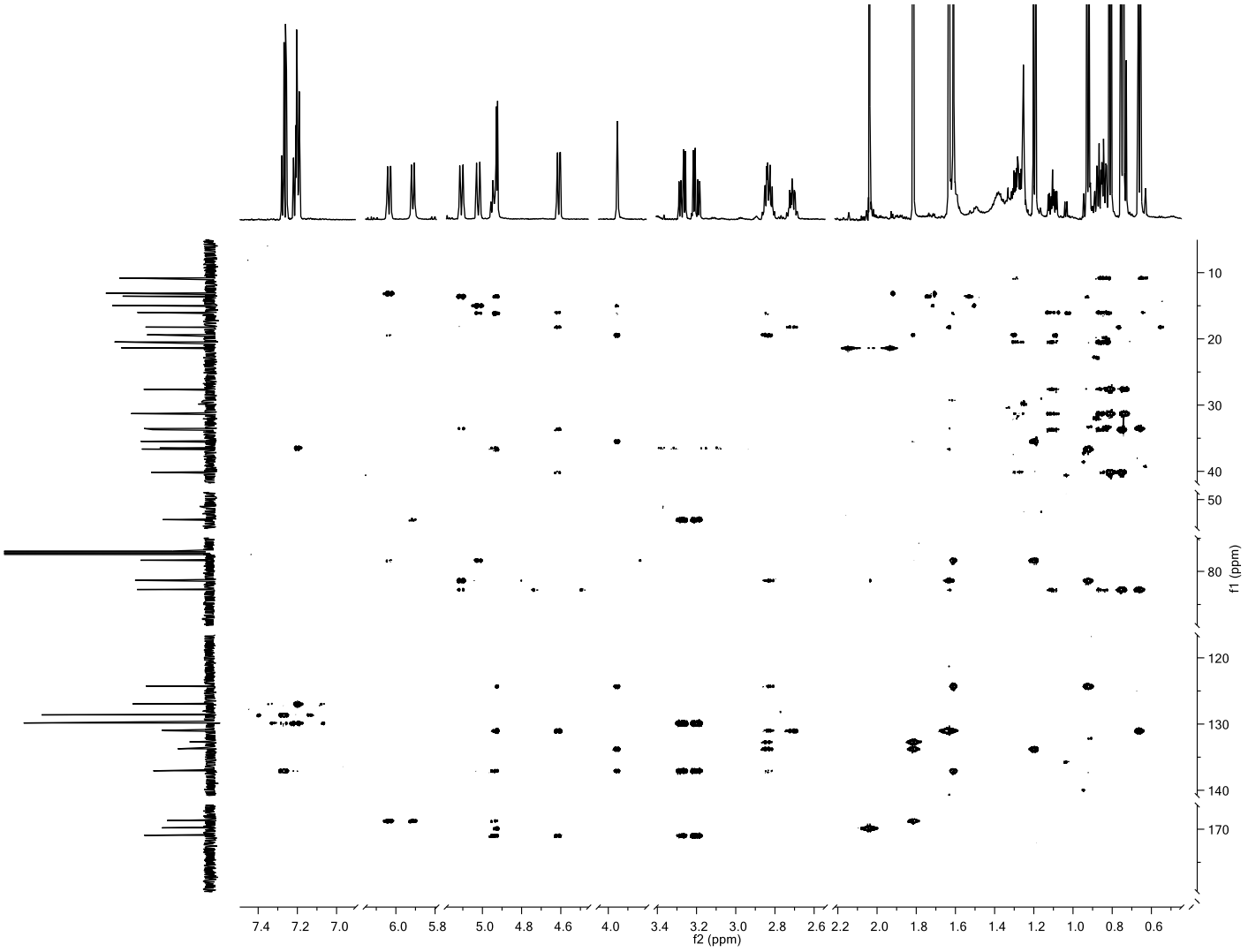

Figure S16. HMBC ($CDCl_3$, 600 MHz) of **1** showing 5-bond correlations.

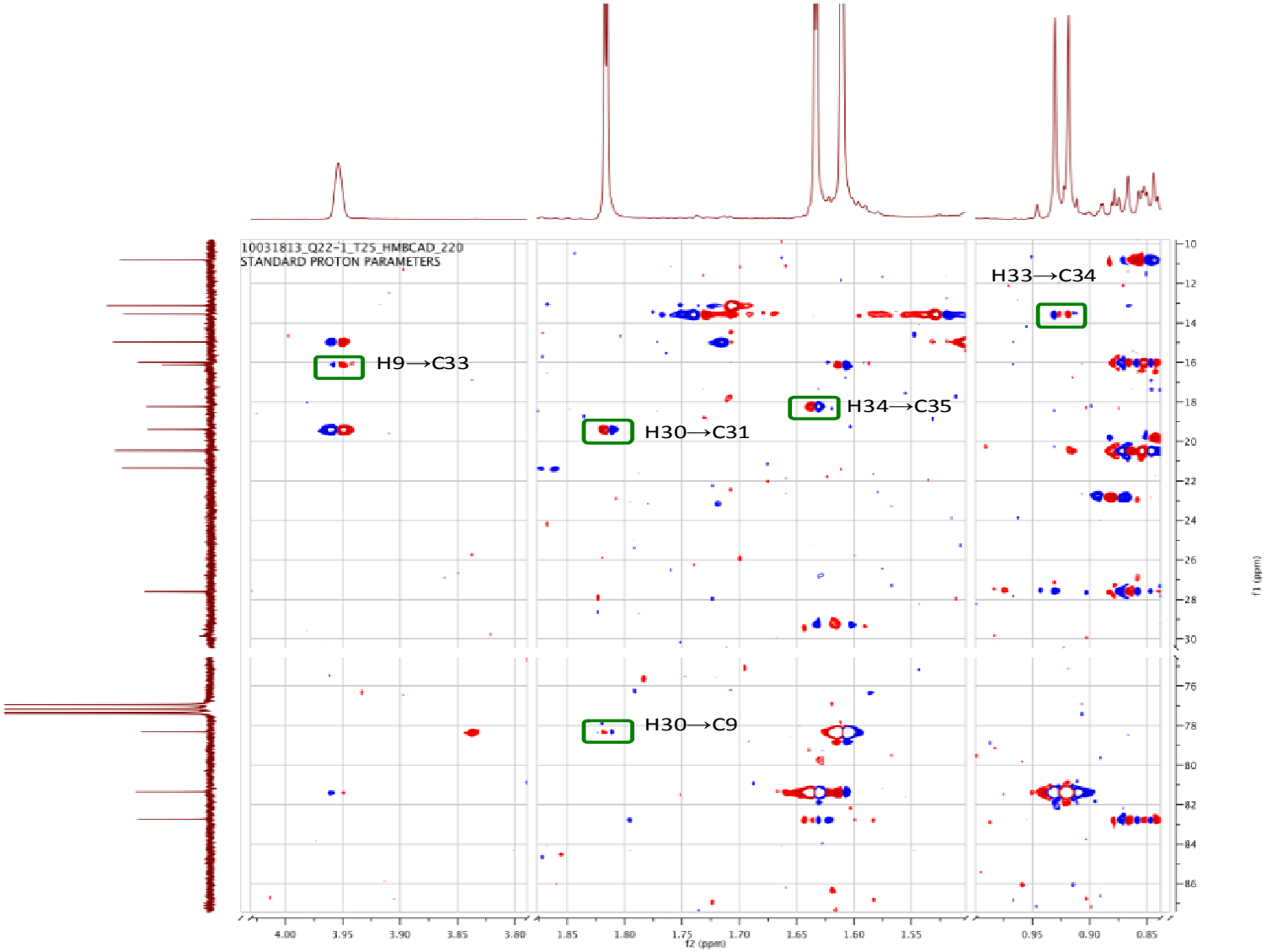

Figure S17. ROESY of **1** ($CDCl_3$, 600 MHz).

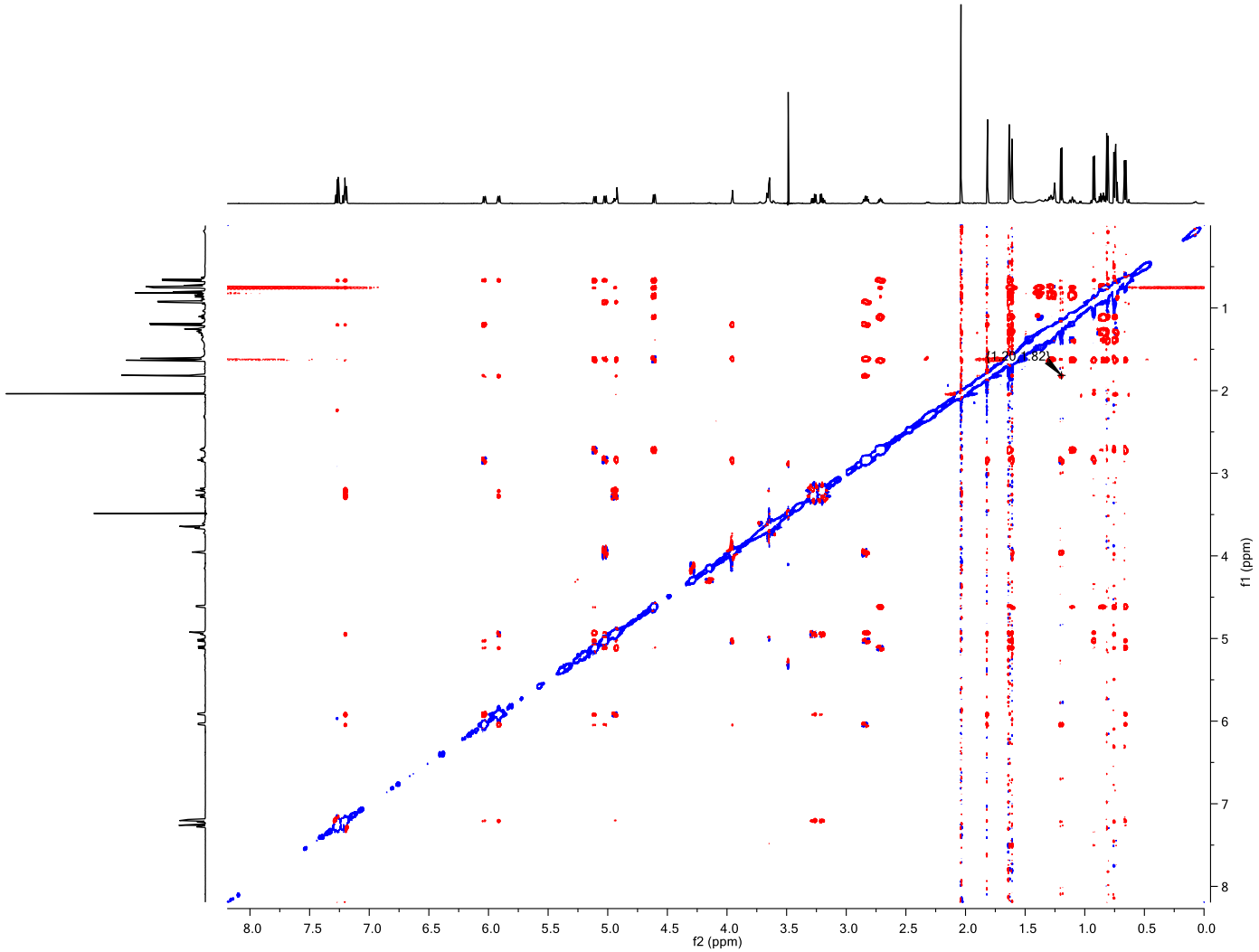

Figure S18. ^{1}H NMR of Metacridamide B (**2**) (CD_3OD, 600 MHz).

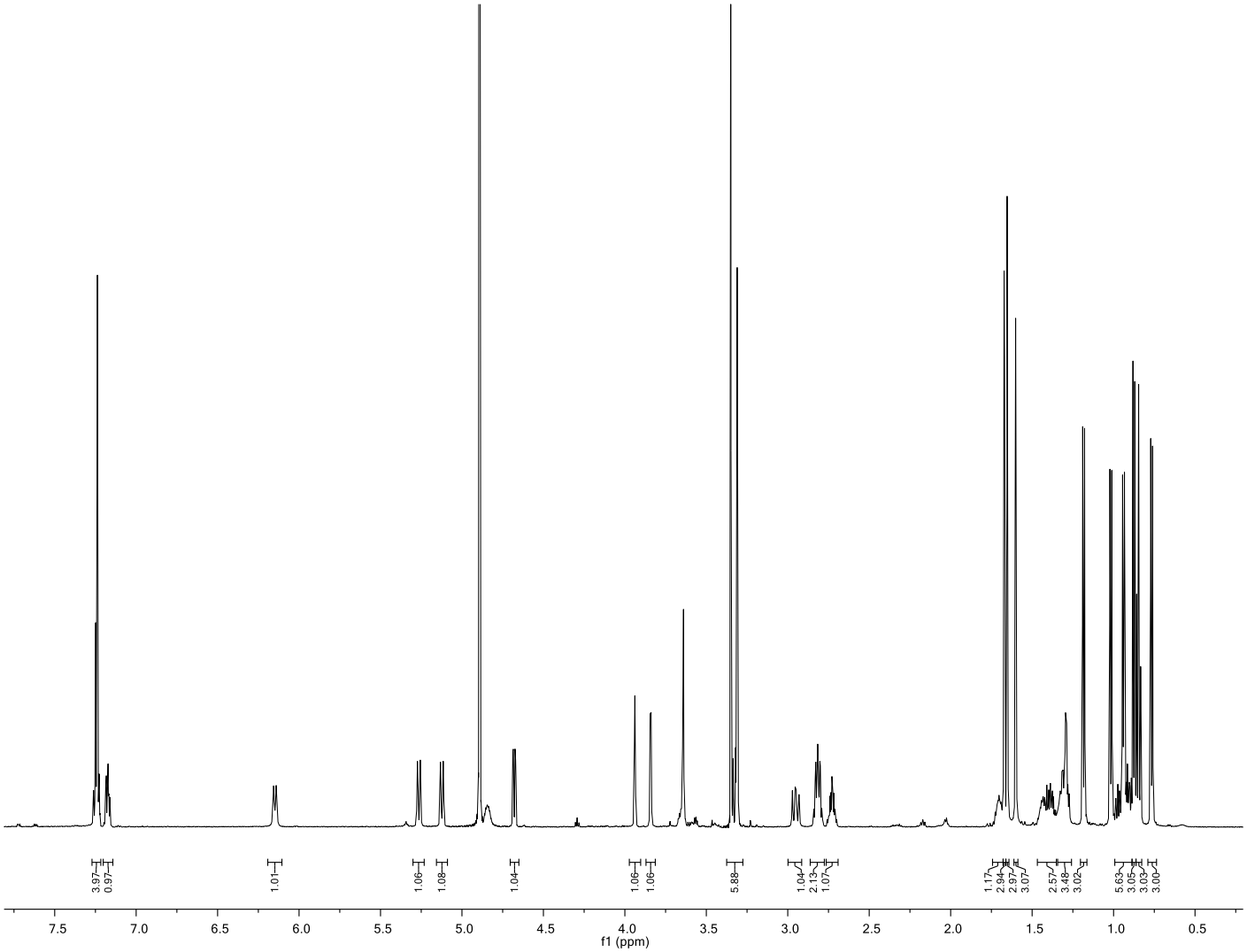

Figure S19. ^{1}H NMR of **2** (CD_3OD, 600 MHz), expanded.

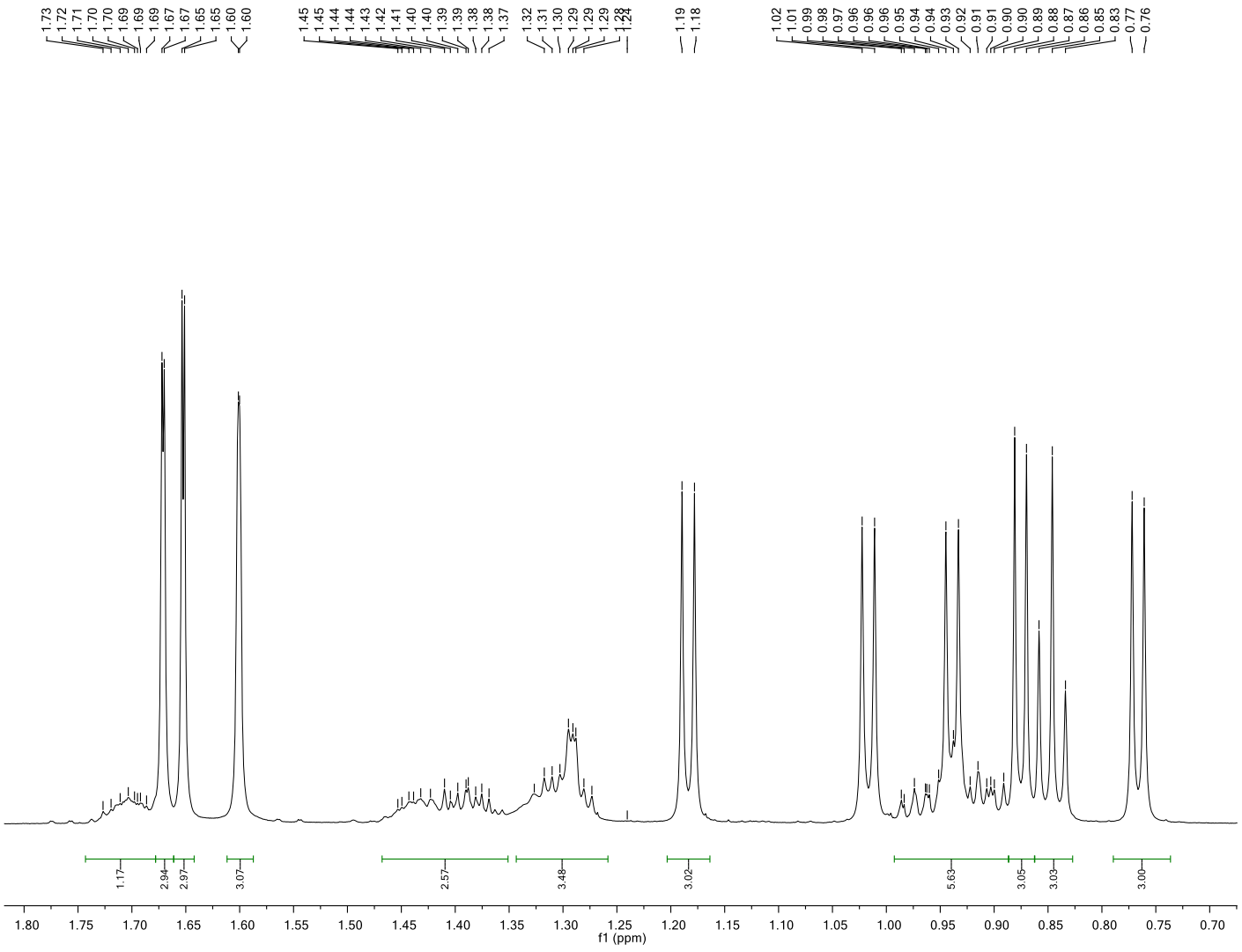

Figure S20. ^{1}H NMR of **2** (CD_3OD, 600 MHz), expanded.

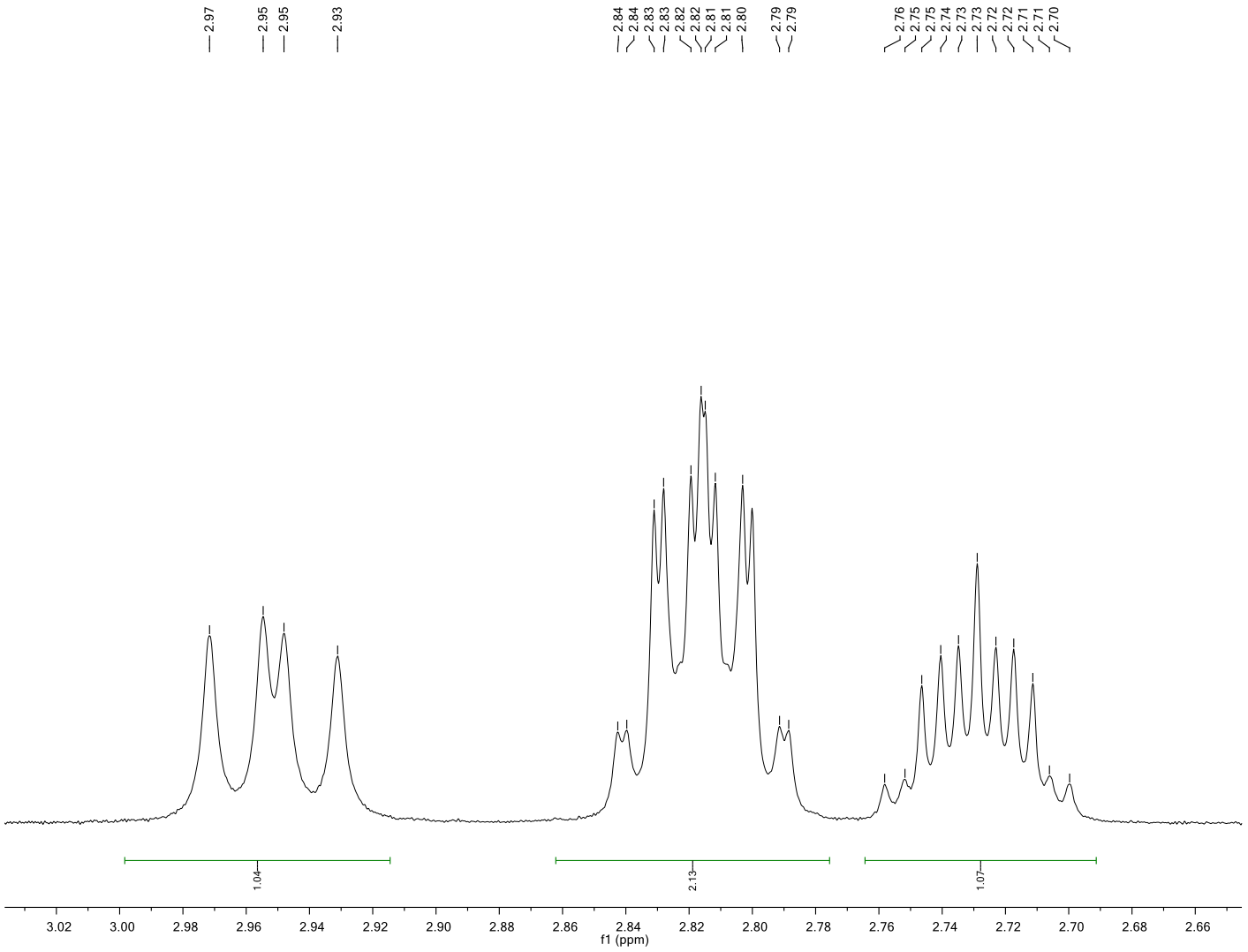

Figure S21. ^{1}H NMR of **2** (CD_3OD, 600 MHz), expanded.

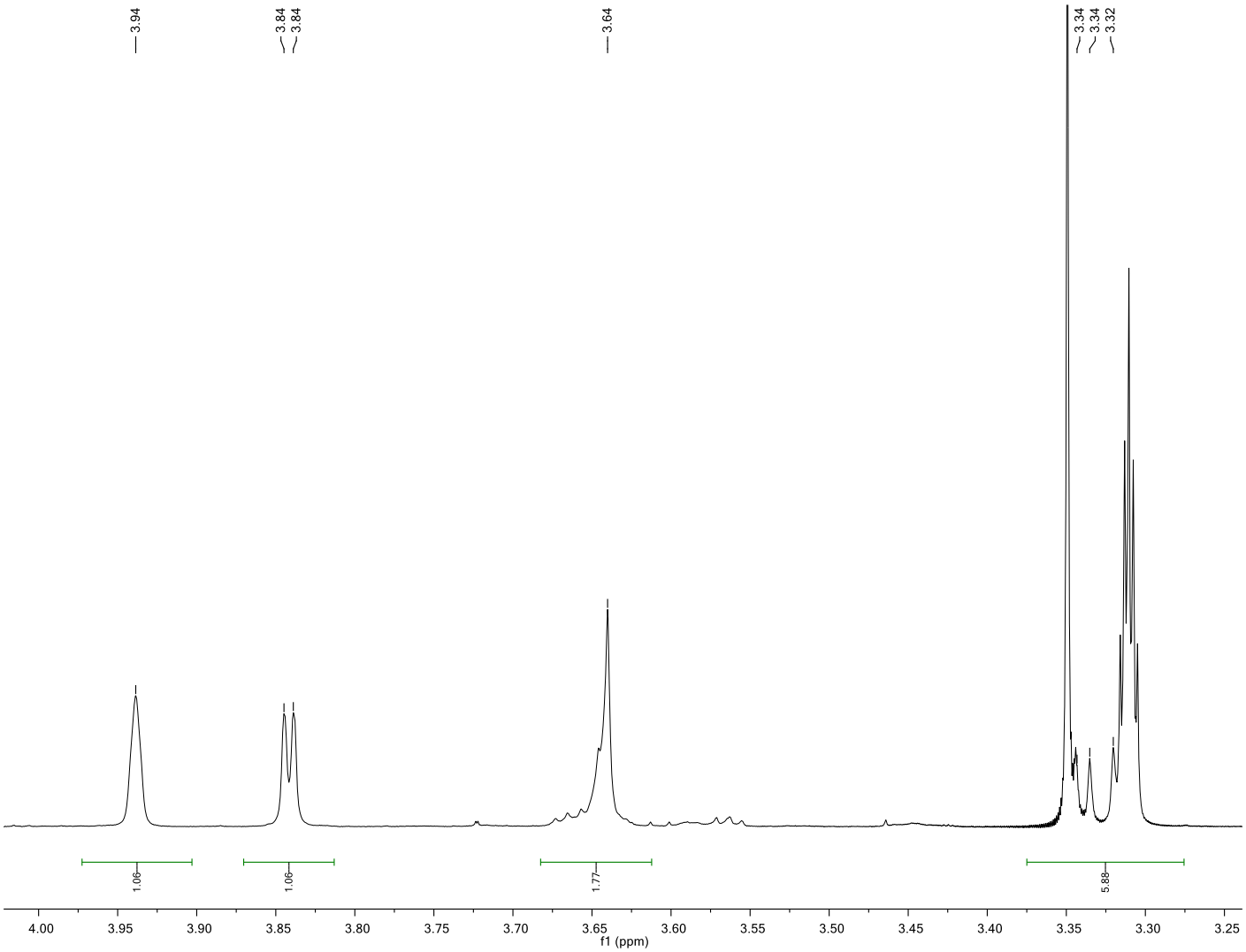

Figure S22. ^{1}H NMR of **2** (CD_3OD, 600 MHz), expanded.

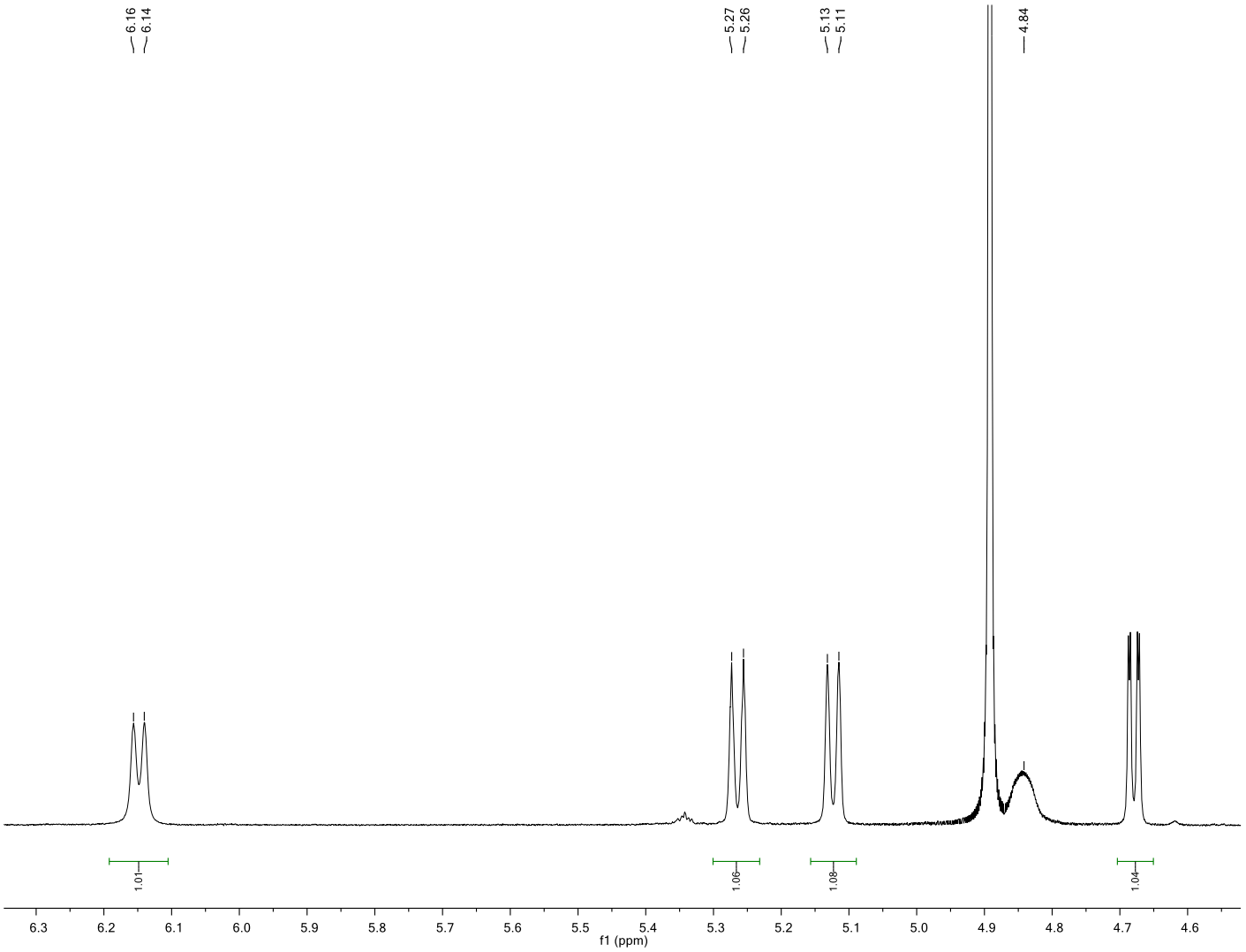

Figure S23. ^{1}H NMR of **2** (CD_3OD, 600 MHz), expanded.

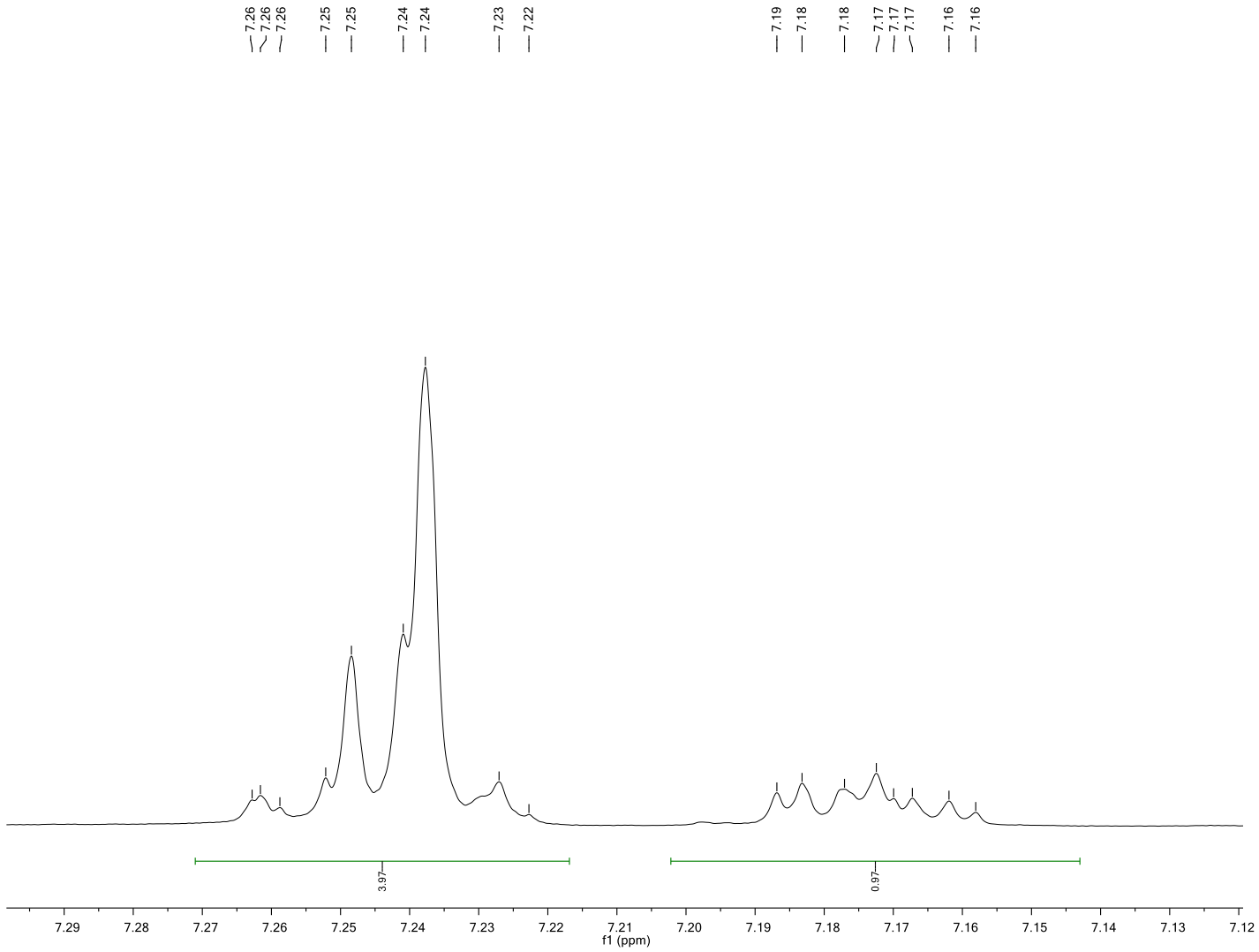

Figure S24. ^{13}C NMR of **2** (CD_3OD, 125 MHz).

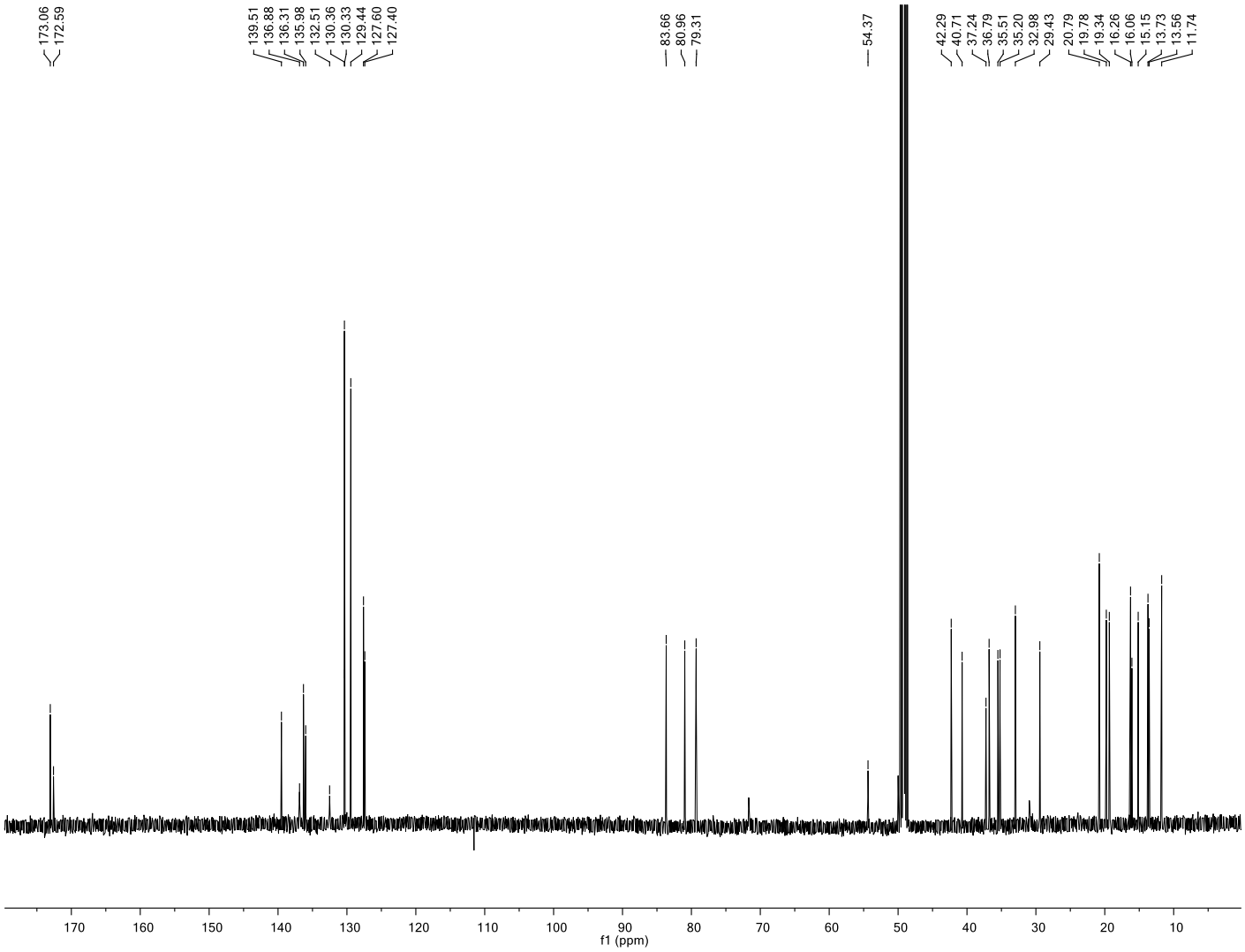

Figure S25. ^{13}C NMR of **2** (CD_3OD, 125 MHz), expanded.

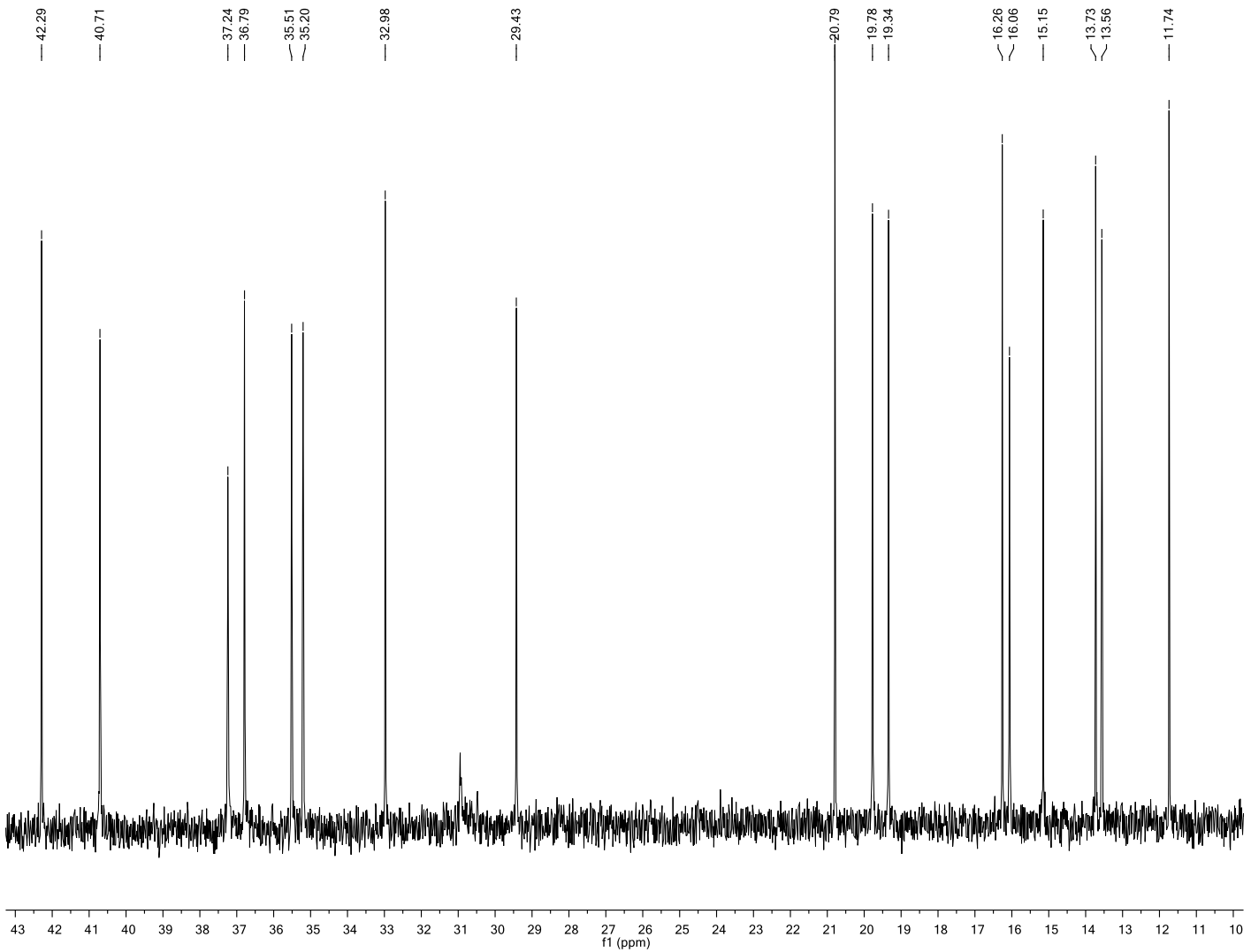

Figure S26. ^{13}C NMR of **2** (CD_3OD, 125 MHz), expanded.

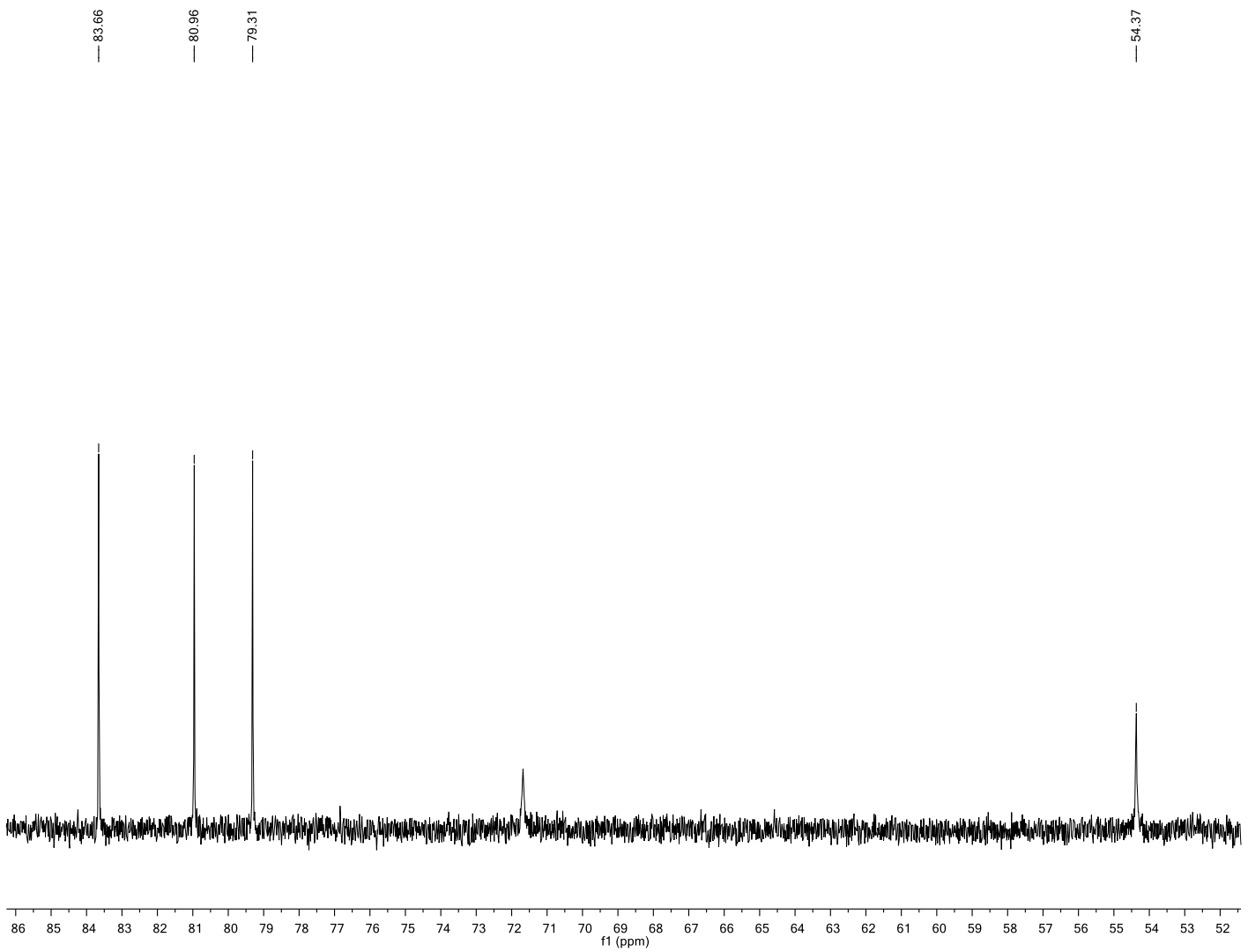

Figure S27. ^{13}C NMR of **2** (CD_3OD, 125 MHz), expanded.

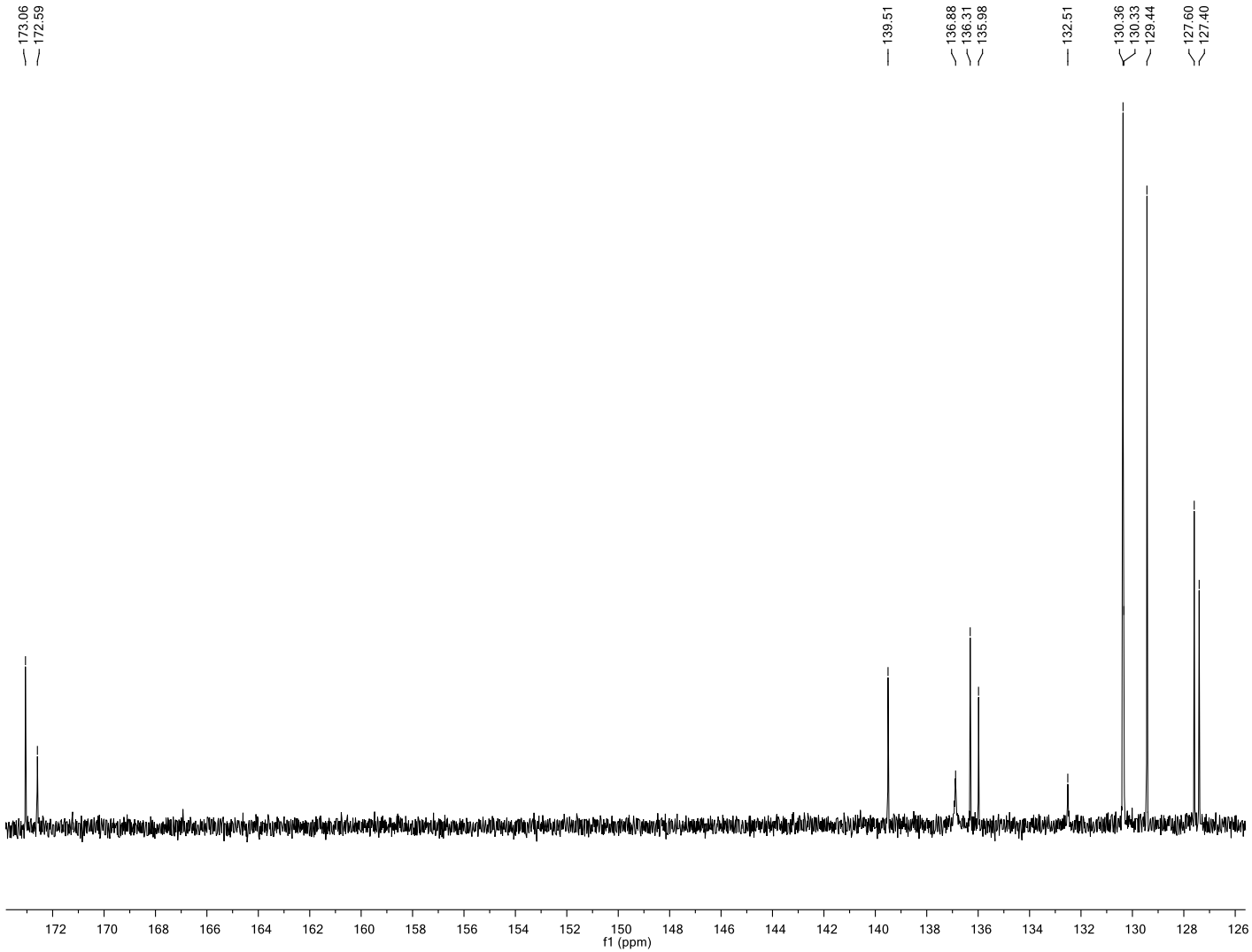

Figure S28. COSY of **2** (CD_3OD, 600 MHz).

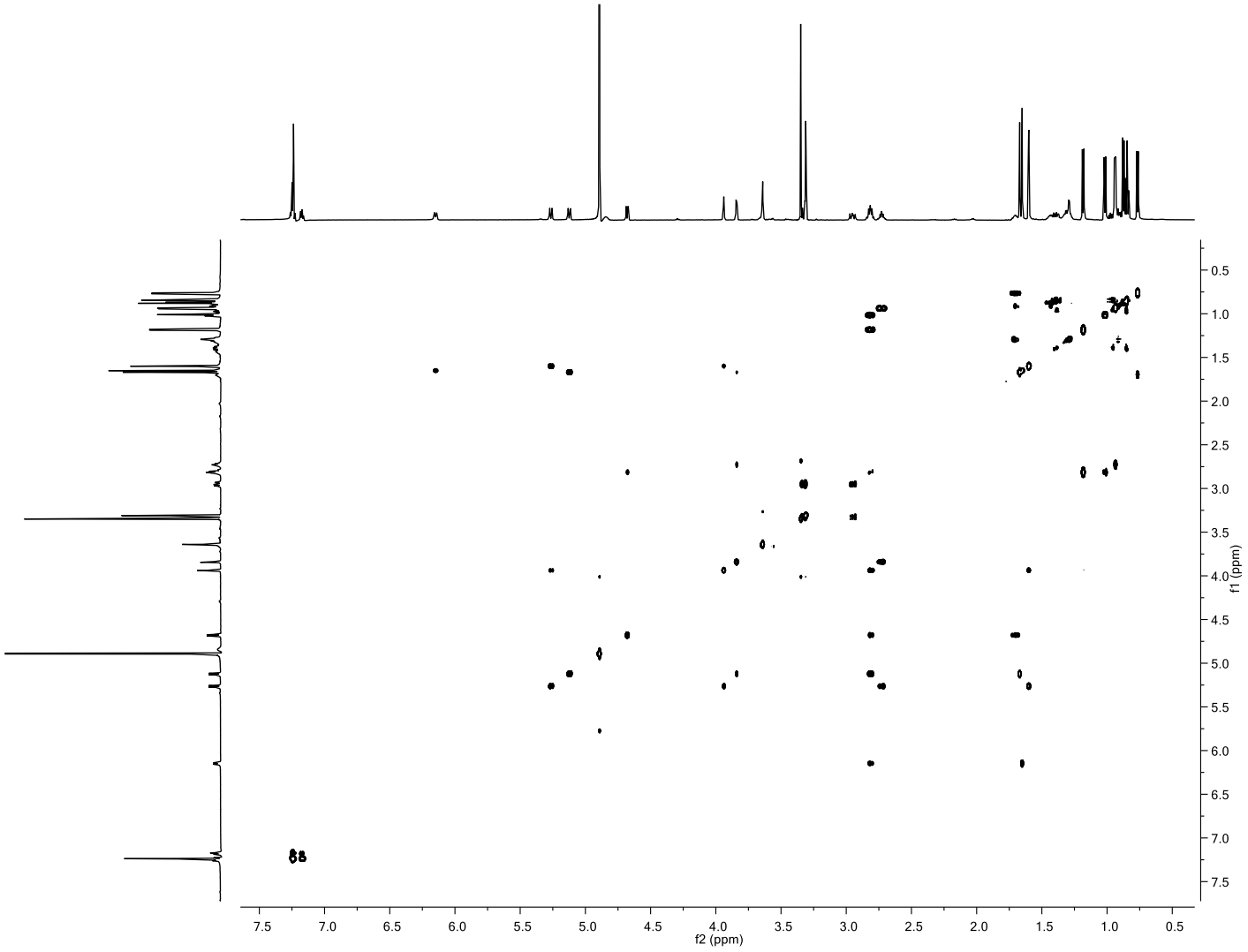

Figure S29. COSY of **2** (CD_3OH, 600 MHz) detail showing amide proton correlations.

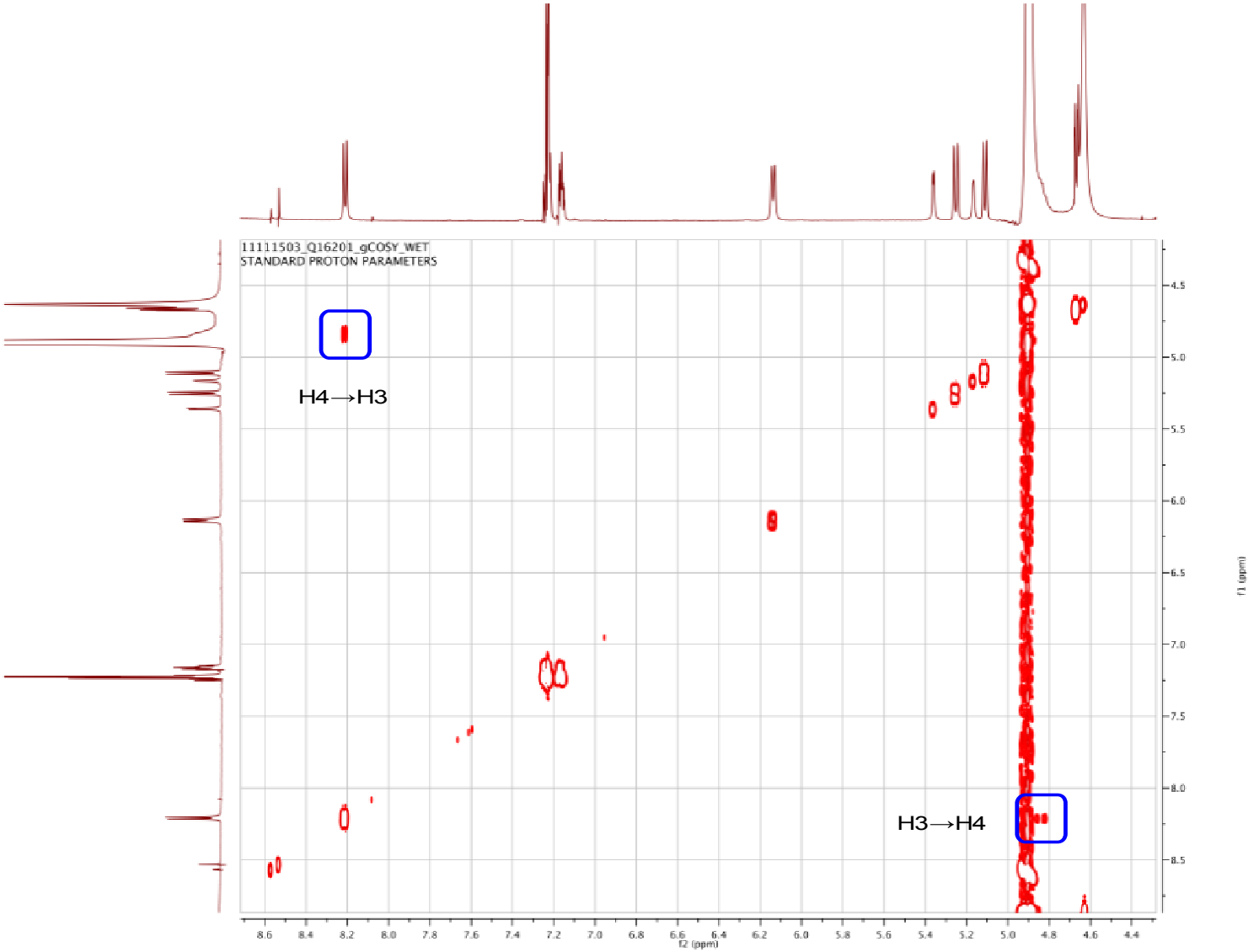

Figure S30. HSQC of **2** (CD_3OD, 600 MHz).

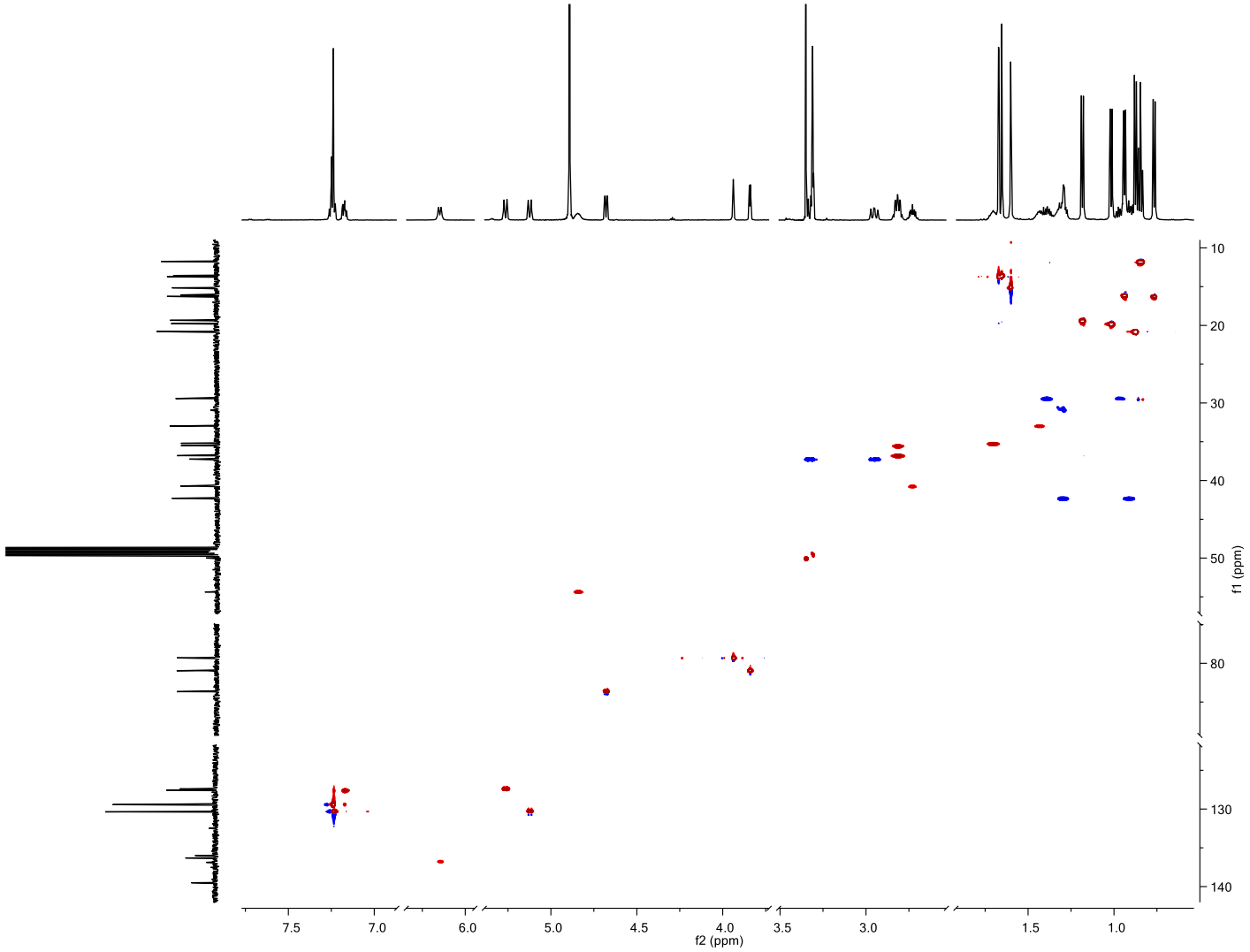

Figure S31. HMBC of **2** (CD_3OD, 600 MHz).

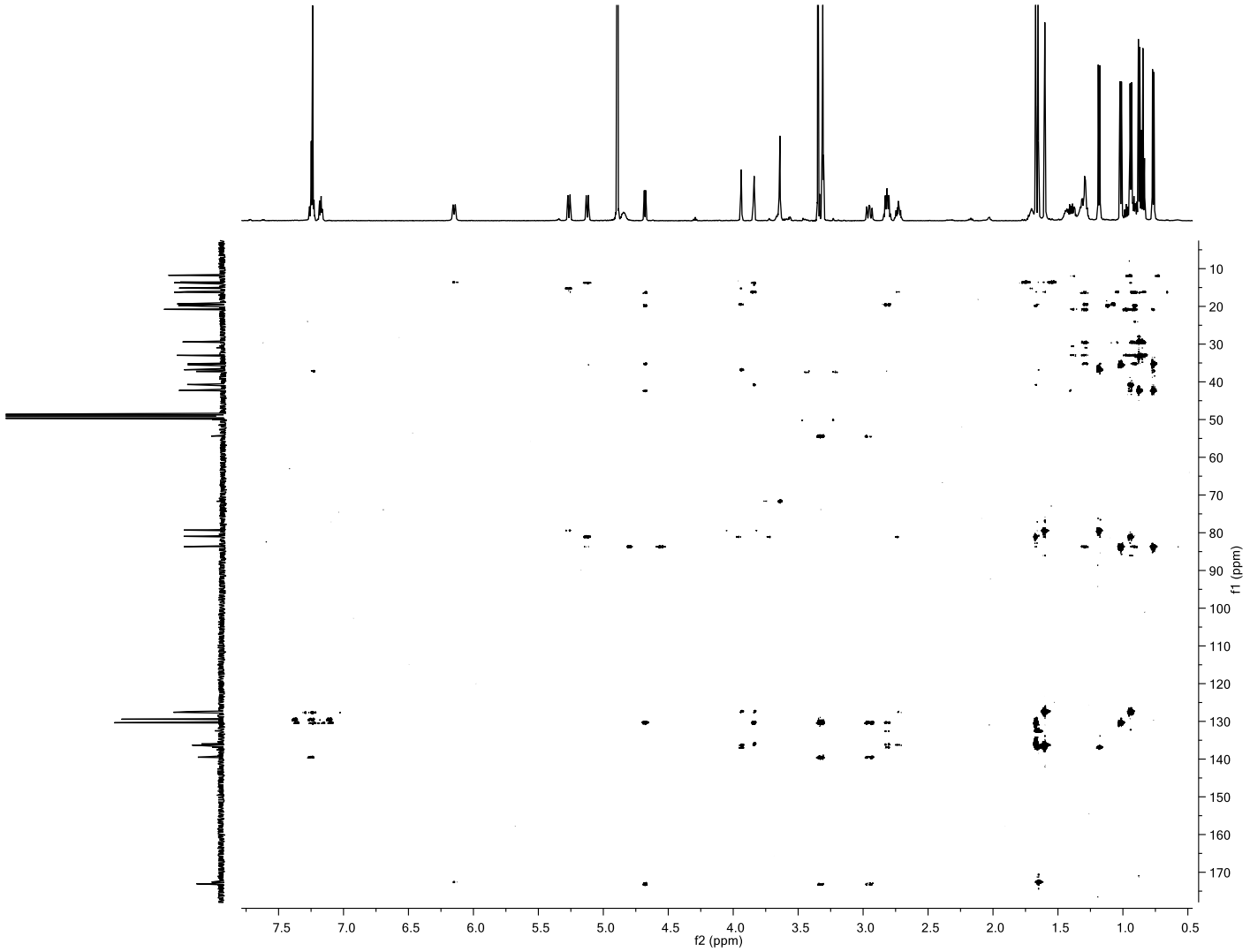

Figure S32 HMBC of **2** (CD_3OD, 600 MHz) detail showing 5-bond correlations.

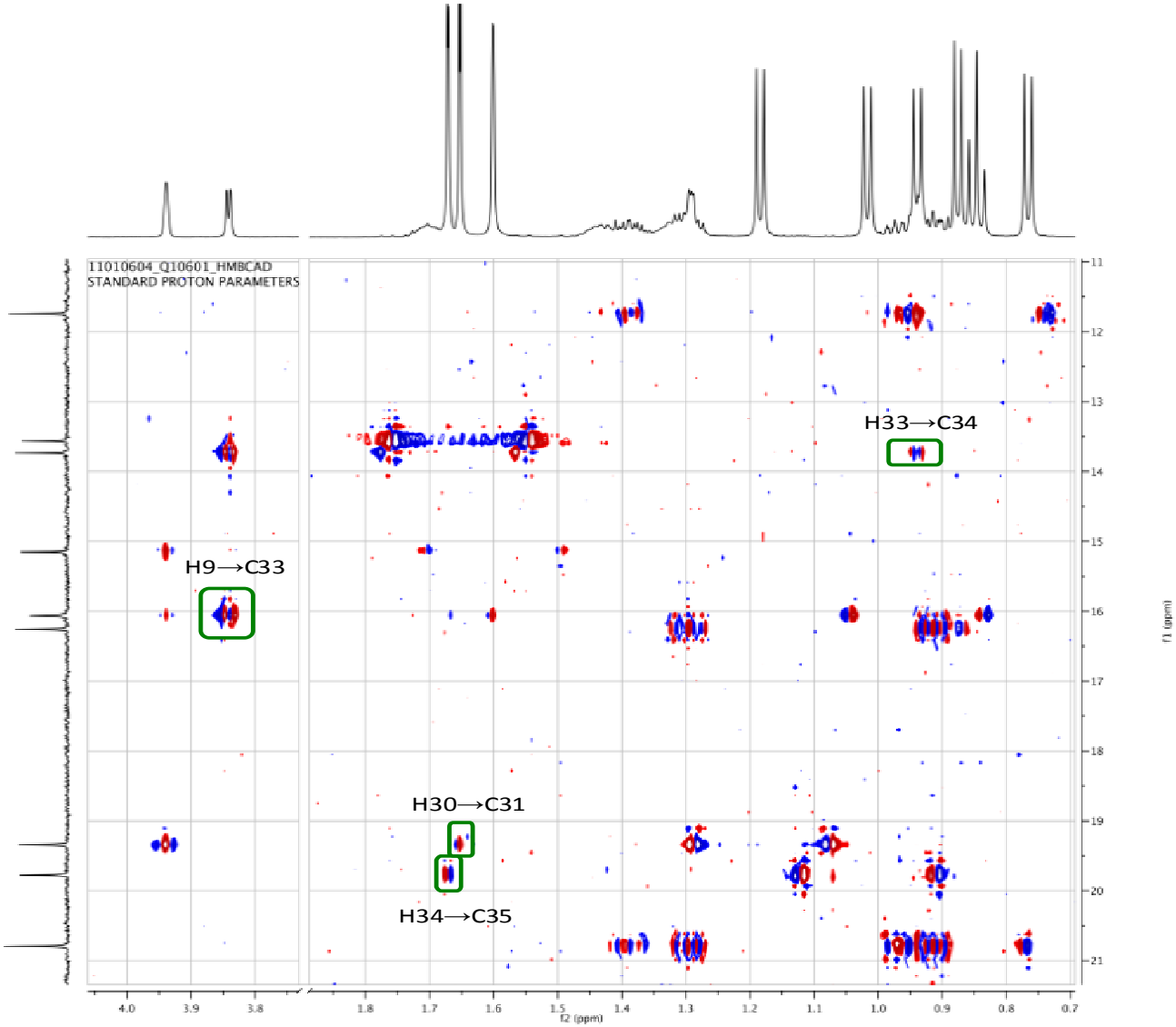

Figure S33. HMBC of **2** (CD_3OH, 600 MHz) detail showing amide proton correlations in blue envelopes. Other correlations shown for reference.

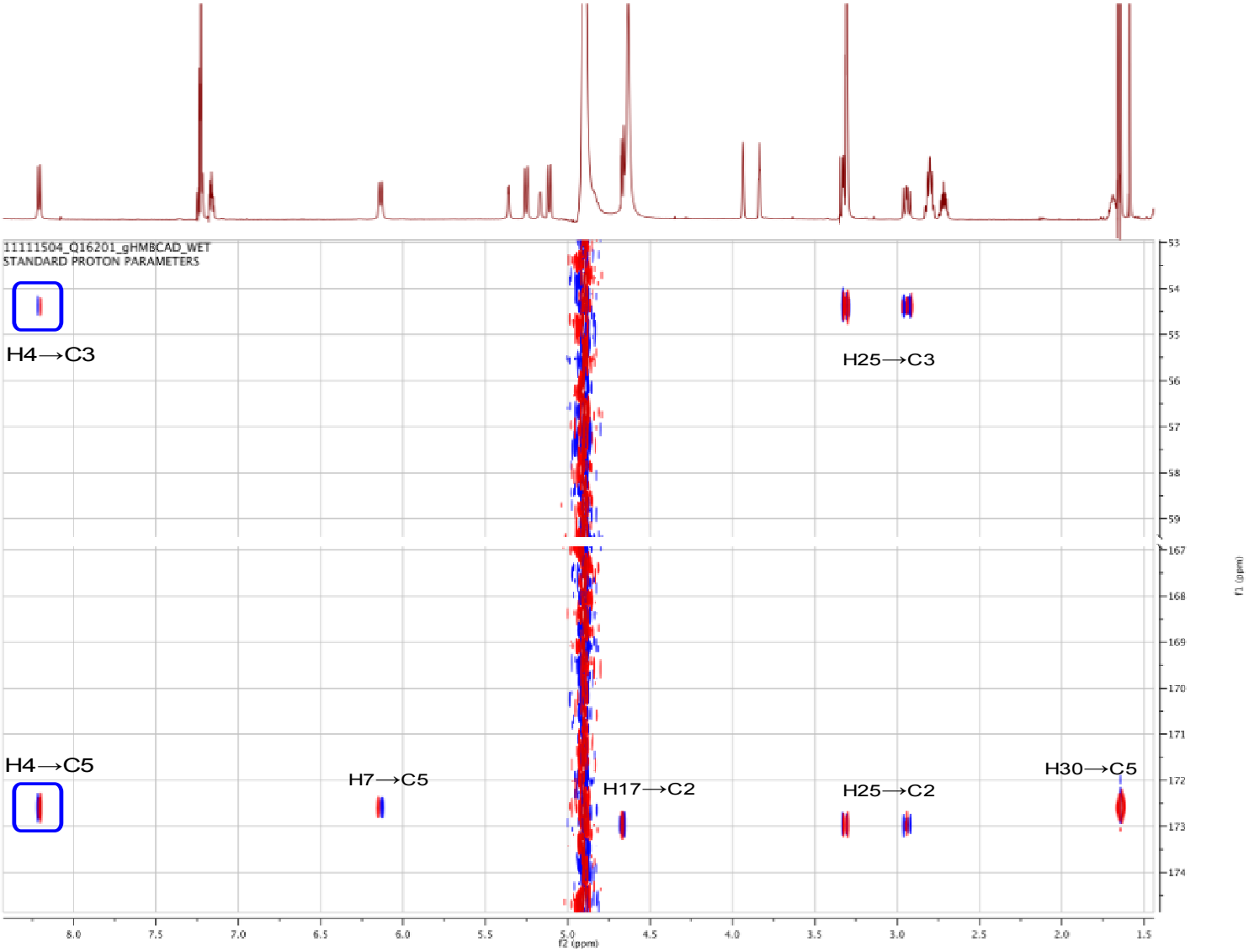

Figure S34. ROESY of **2** (CD_3OD, 600 MHz).

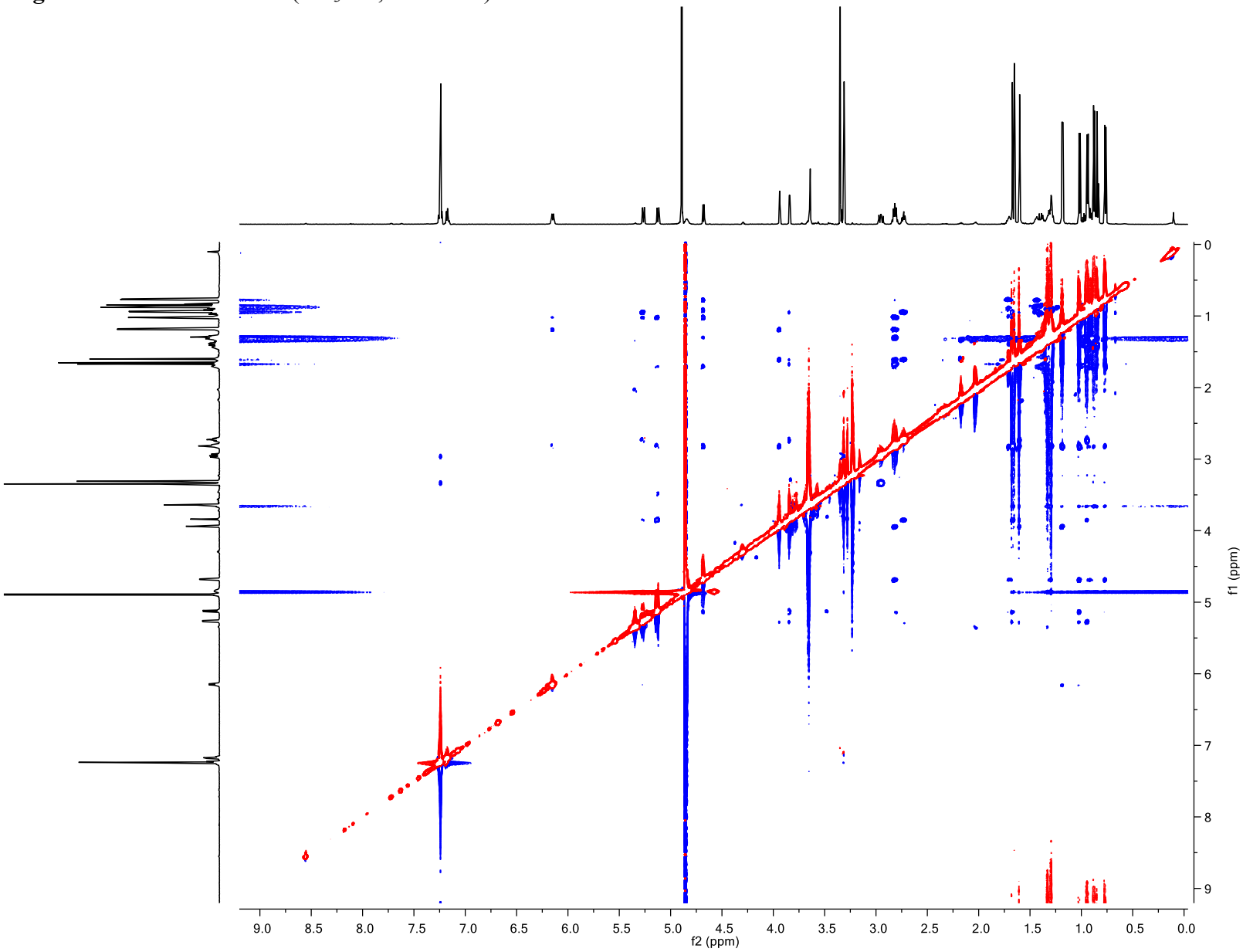

Figure **S35.** Chiral HPLC amino acid analysis of metacridamide A (**1**). **A**. The hydrolyzate of (**1**). **B**. Standard equimolar mixture of L-Phe (t_R: 22.2 min) and D-Phe (t_R: 24.4 min). **C.** Co-chromatography of hydrolysate and standard. **A** shows evidence of racemization (5-10%). See text for details of hydrolysis and chiral chromatography.

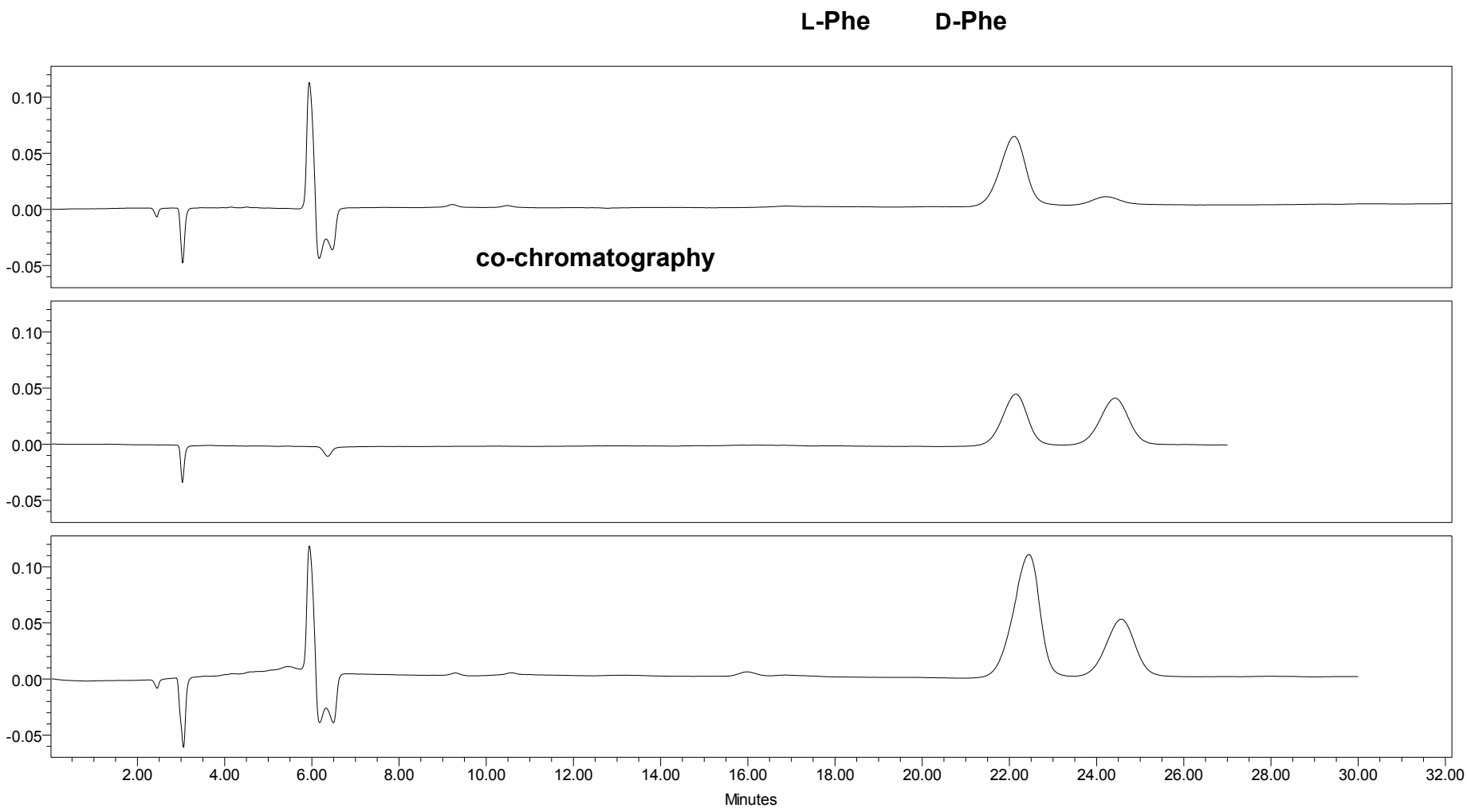

Figure **S36.** Selected correlations from ROESY of metacridamide A (1) shown in Figure S17.

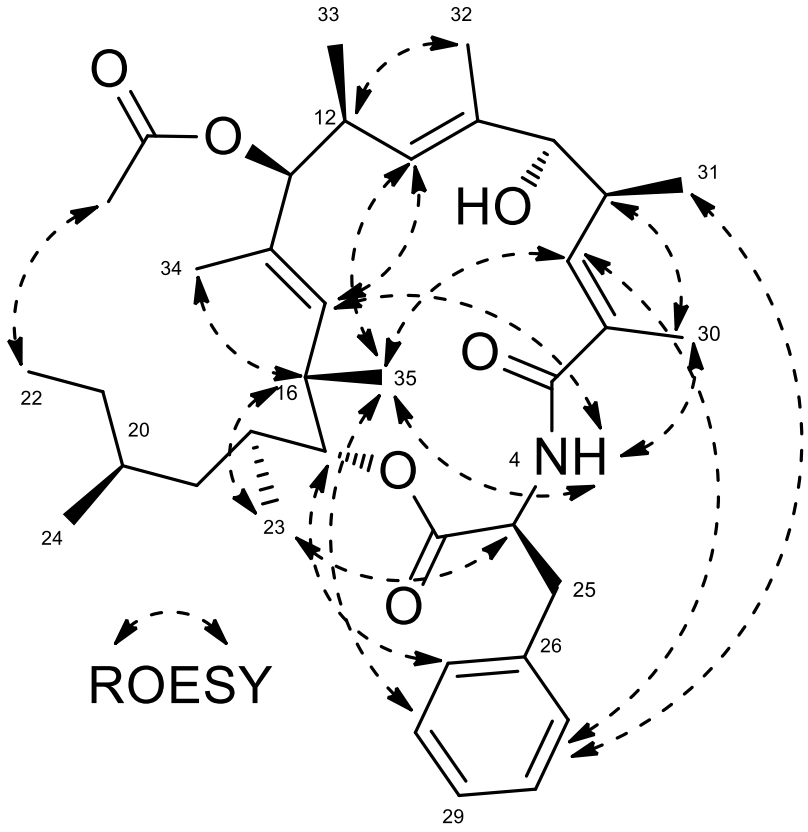

Figure S37. Interatomic distances (Å) from a model (Chem 3D Pro®) of the crystal structure of metacridamide A (**1**) for selected proton pairs that exhibited ROESY correlations. Chemically equivalent pairs of carbons (C27, C27'; C28 C28') proved to be magnetically equivalent (proton and carbon resonances were indiscernible). ROESY crosspeaks are unlikely for the distances shown, so alternate conformations that brought the indicated distances within 4 Å for all pairs were generated by rotations around both the α–β and β–γ bonds of the Phe unit (see Figure S38 and Table S3).

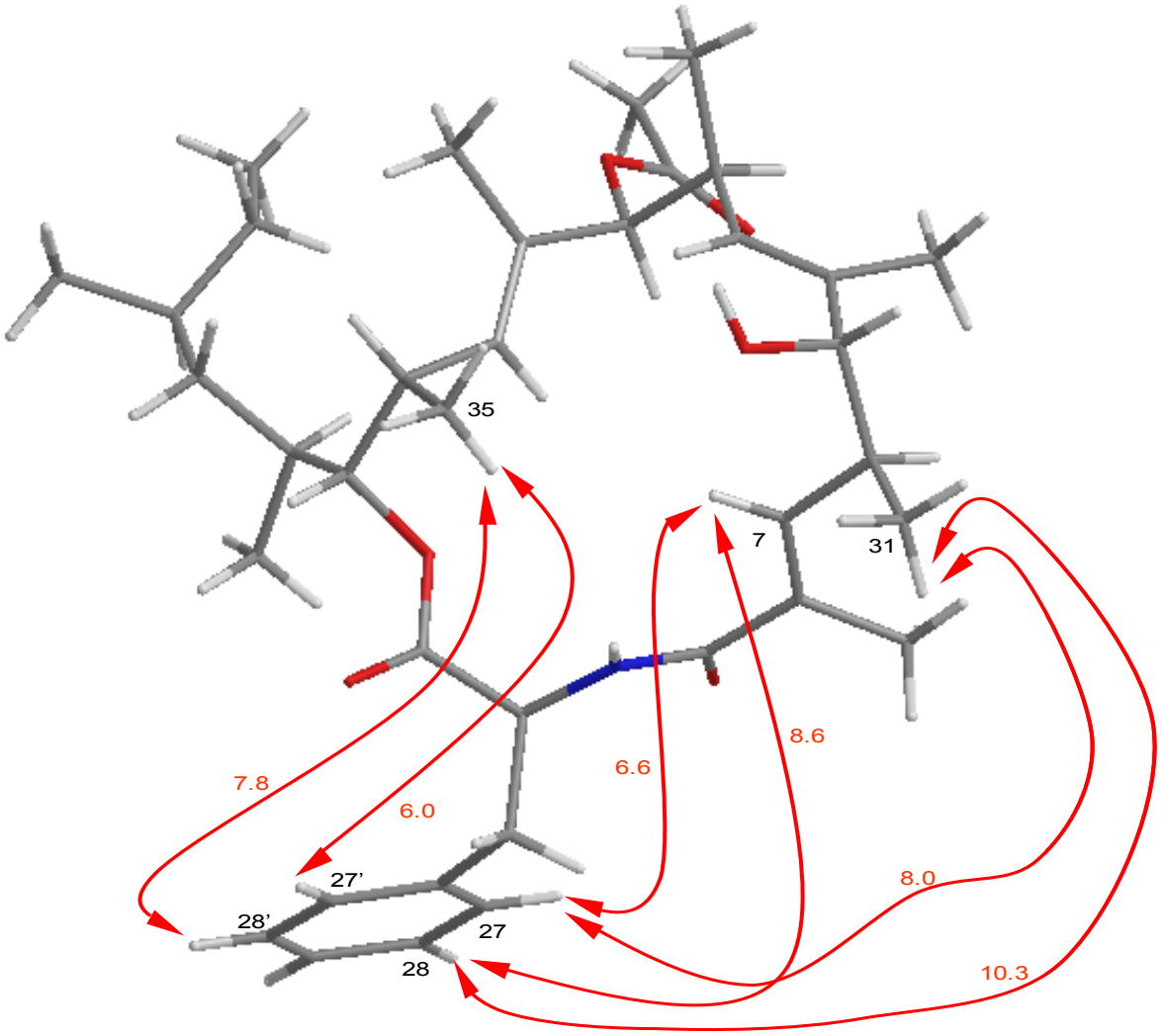

Figure S38. Conformers (A-C) generated by rotating the α–β and β–γ bonds of the Phe unit in the crystal structure model (Figure S37) of metacridamide A (**1**).

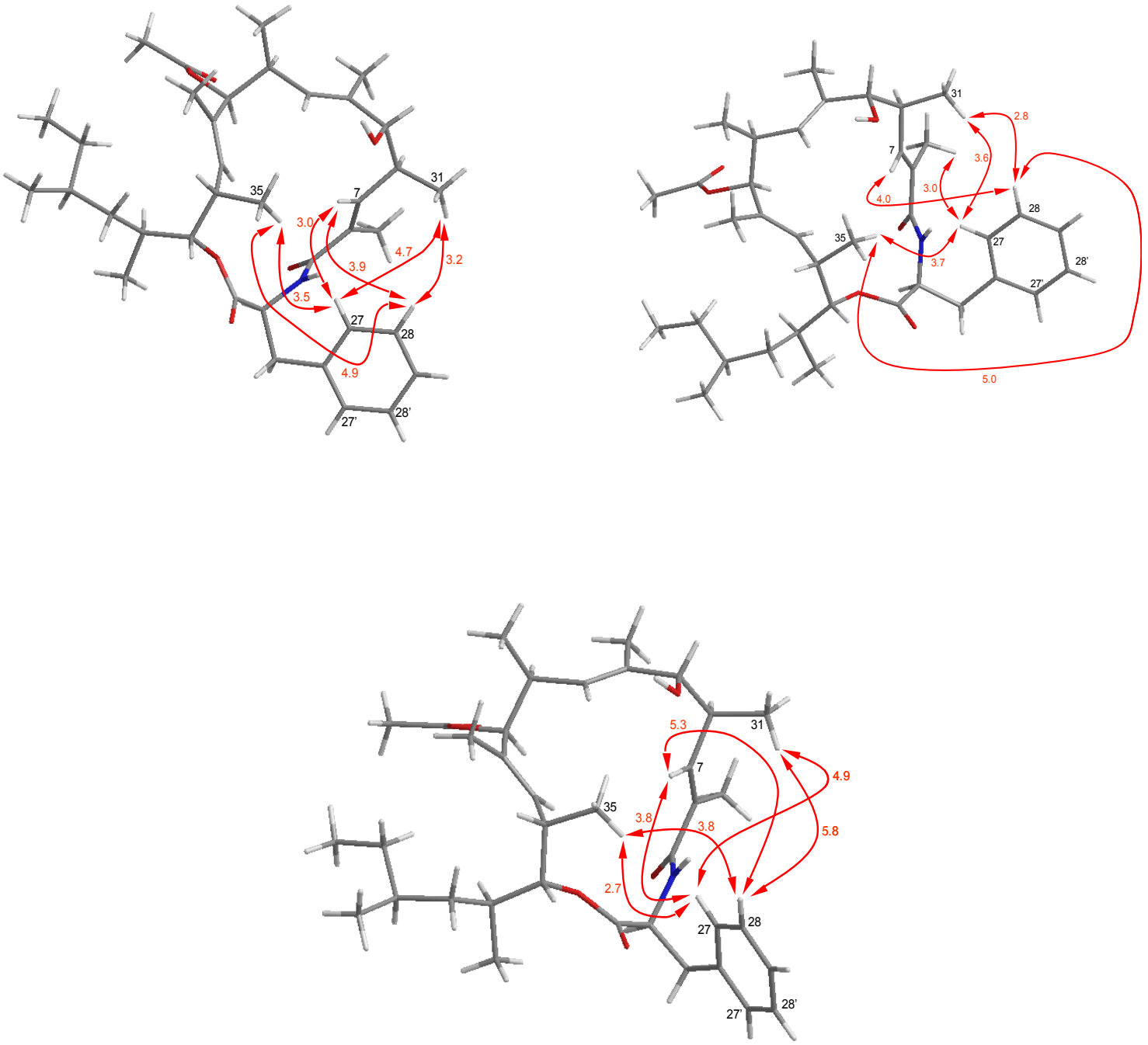

Table S1. Crystal data and structure refinement for metacridamide A.

Identification code	MetaA
Empirical formula	C_{37} H_{55} N O_6
Formula weight	609.82
Temperature	100(2) K
Wavelength	0.91770 A
Crystal system, space group	Orthorhombic, P 2_1 2_1 2_1
Unit cell dimensions	a = 12.480(3) Å alpha = 90° b = 13.140(3) Å beta = 90° c = 21.920(4) Å gamma = 90°
Volume	3594.6(12) $Å^3$
Z, Calculated density	4, 1.127 Mg/m^3
Absorption coefficient	0.075 mm^{-1}
F(000)	1328
Crystal size	0.10 x 0.01 x 0.01 mm^3
Theta range for data collection	2.40 to 30.64°
Limiting indices	-13<=h<=13, -14<=k<=14, -22<=l<=22
Reflections collected / unique	15222 / 4991 [$R_{(int)}$ = 0.0432]
Completeness to theta = 30.64	96.4 %
Max. and min. transmission	0.9996 and 0.9925
Refinement method	Full-matrix least-squares on F^2
Data / restraints / parameters	4991 / 0 / 398
Goodness-of-fit on F^2	1.056
Final R indices [I>2σ(I)]	R1 = 0.0497, wR2 = 0.1287
R indices (all data)	R1 = 0.0531, wR2 = 0.1315
Absolute structure parameter	0.0(12)
Extinction coefficient	0.034(3)
Largest diff. peak and hole	0.236 and -0.198 $e^-/Å^3$

Table S2. Atomic coordinates (x 10^4) and equivalent isotropic displacement parameters (Å^2 x 10^3) for metacridamide A (**1**). U(eq) is defined as one third of the trace of the orthogonalized Uij tensor.

	x	y	z	U(eq)
O(1)	1286(2)	8356(1)	8485(1)	32(1)
C(2)	1009(2)	7633(2)	8087(1)	33(1)
O(2)	412(2)	7744(2)	7669(1)	47(1)
C(3)	1581(2)	6651(2)	8263(1)	31(1)
C(25)	1551(2)	5866(2)	7746(1)	36(1)
C(26)	2349(2)	6165(2)	7256(1)	34(1)
C(27)	2044(2)	6693(2)	6741(1)	38(1)
C(28)	2795(3)	7045(2)	6332(2)	45(1)
C(29)	3867(3)	6872(3)	6429(2)	48(1)
C(28')	4188(3)	6332(3)	6940(2)	53(1)
C(27')	3427(3)	5986(3)	7350(2)	46(1)
N(4)	1171(2)	6268(2)	8839(1)	30(1)
C(5)	1861(2)	5946(2)	9273(1)	32(1)
O(3)	2835(2)	5932(2)	9190(1)	38(1)
C(6)	1395(2)	5595(2)	9867(1)	32(1)
C(30)	1973(3)	4716(2)	10158(2)	45(1)
C(7)	570(2)	6070(2)	10122(1)	35(1)
C(8)	50(2)	5783(2)	10717(1)	35(1)
C(31)	-768(2)	4933(2)	10619(2)	41(1)
C(9)	-458(2)	6705(2)	11034(1)	38(1)
O(4)	-1221(2)	7105(2)	10622(1)	40(1)
C(10)	382(2)	7466(2)	11246(1)	37(1)
C(32)	1089(3)	7082(3)	11758(2)	59(1)
C(11)	466(2)	8382(2)	11009(1)	37(1)
C(12)	1251(2)	9210(2)	11168(1)	36(1)
C(33)	679(3)	10061(3)	11522(2)	45(1)
C(13)	1838(2)	9553(2)	10588(1)	33(1)
O(5)	2606(1)	10360(1)	10744(1)	33(1)
C(131)	3563(2)	10069(2)	10962(1)	35(1)
O(132)	3812(2)	9202(2)	11059(1)	39(1)
C(132)	4283(2)	10968(2)	11074(2)	47(1)
C(14)	1146(2)	9948(2)	10079(1)	32(1)
C(34)	575(3)	10943(3)	10159(2)	50(1)
C(15)	1000(2)	9362(2)	9590(1)	34(1)
C(16)	243(2)	9518(2)	9064(1)	34(1)
C(35)	-715(2)	8802(3)	9124(2)	45(1)
C(17)	808(2)	9370(2)	8450(1)	32(1)
C(18)	1717(2)	10103(2)	8305(1)	33(1)
C(19)	1310(2)	11193(2)	8203(2)	39(1)
C(20)	2172(2)	12004(2)	8339(2)	46(1)
C(21)	2293(3)	12178(2)	9022(2)	55(1)
C(22)	3255(3)	12809(3)	9212(3)	79(1)
C(23)	2357(3)	9761(2)	7752(2)	44(1)
C(24)	1920(3)	12992(2)	8003(2)	63(1)

Table S3. Summary of interatomic distances (Å) for indicated proton pairs in the crystal structure of metacridamide A(**1**) and in models of conformers A-C (Figures S37-38). The last column shows the minimum distance achieved for the indicated proton pair among the three conformers.

	XTAL	A	B	C	MIN
Proton Pairs					
27↔35	6.0	3.5	3.7	2.7	2.7
27↔7	6.6	3.0	3.0	3.8	3.0
27↔31	8.0	4.7	3.6	4.9	3.6
28↔35	7.8	4.9	5.0	3.8	3.8
28↔7	8.6	3.9	4.0	5.3	3.9
28↔31	10.3	3.2	2.8	5.8	2.8