Supporting Information for "Evaluation of a Cyclopentane-Based γ-Amino Acid for the Ability to Promote α/γ-Peptide Secondary Structure"

Michael W. Giuliano,** Stacy J. Maynard, Aaron M. Almeida, Andrew Reidenbach, Li Guo, Emily C. Ulrich, Ilia A. Guzei, and Samuel H. Gellman*

Department of Chemistry, University of Wisconsin-Madison, Madison, Wisconsin 53705, United States.

*corresponding author: gellman@chem.wisc.edu
** current address: Department of Chemistry, Yale University; michael.giuliano@yale.edu

---

Table of Contents

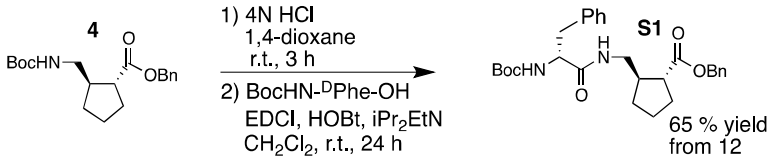
---

note: All structural figures prior to section VII of this supporting information were prepared with Pymol.[1] Statistics and structural ensembles for a/g-peptides **9**, **12**, and **15** were generated using CNS software.[2]

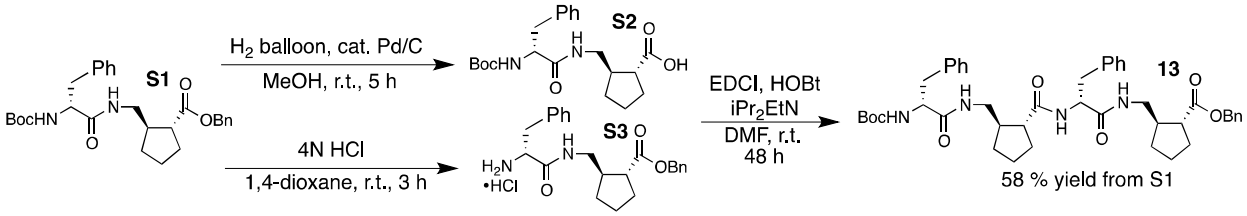
I. Additional Synthetic Procedures

Schemes:

Compound S1: Boc-HN-(^{D}Phe-AMCP)-OBn.



Compound 13: Boc-HN-(^{D}Phe-AMCP)$_2$-OBn.



Ia. Development of an Enantioselective Conjugate Addition.

Previously, we reported on the enantioselective conjugate addition of aldehydes to 1-nitrocyclohexene as a route to enantiopure γ-amino acids.[3] In this study, we sought γ-amino acids that possessed a five-membered ring across the Cα-Cβ bond. We briefly summarize our efforts in the optimization of the conjugate addition of nitromethane to 1-cyclopentene-1-carboxaldehyde.

Reaction screening: Reaction optimization screens were run according conjugate addition procedure detailed for the preparation of nitroalcohol **1** (crude mixtures were analyzed without the borohydride reduction step) in clean, dried 4 mL vials equipped with micro stir bars and Teflon lined caps. In cases where small (<10 μL) volumes of reagents were required, more concentrated solutions of the reagent were prepared in the reaction solvent and added in the appropriate quantity by dilution into the reaction medium. Reactions were run on a scale of 0.5 mmol 1-cyclopentene-1-carboxaldehyde substrate at a concentration of 0.5 M (1 mL total volume).

Determination of conversion and diastereomeric ratio by ^{1}H NMR of crude reaction mixtures: Reaction diastereoselectivity and conversion in the below were determined via integration of the aldehyde resonances in the ^{1}H NMR spectra of crude reaction mixtures. A 60 μL aliquot of reaction mixture was diluted with 600 μL $CDCl_3$ (w/ 0.03 % TMS) in a 5 mm NMR tube. Reliable integration of the aldehyde region required either 32 or 64 scan ^{1}H 1D data collections. A typical analysis is shown below.

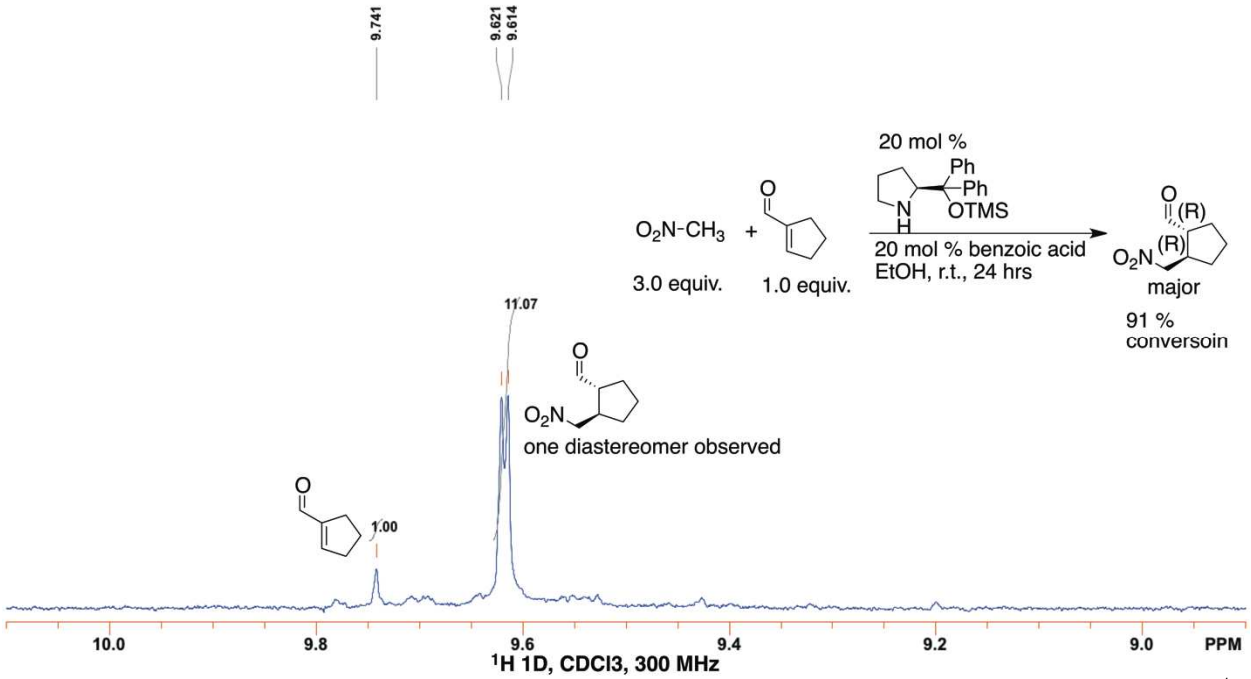
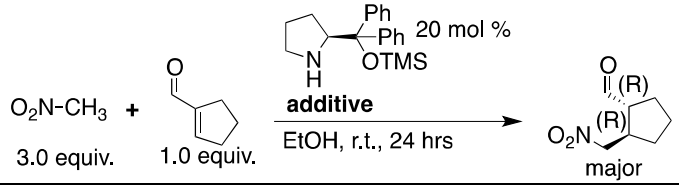


Figure S1. Determination of dr for nitromethane addition to 1-cyclopentene-1-carboxaldehyde from ^{1}H NMR of crude reaction mixture (Table S1, entry 1). Structures indicate aldehyde peaks used for conversion and dr calculation. 1,2-addition products were not observed in this or any other condition. Stereochemical configuration of only observed product was assigned as (R,R) on the basis of the crystal structure of dipeptide **3**.

Acid/Basic Additive Screening: We screened additives for the conjugate addition of nitromethane to 1-cyclopentene-1-carboxaldehyde (Table S1). Following a brief literature survey, we proposed that a mixture of Brønsted acid[4,5] and amine base[6,7] additives may provide a synergistic effect on the conversion and/or reaction time. Following a survey of Brønsted acidic additives, from which we find benzoic acid or acetic acid as equally effective co-catalysts (entries 1 and 3), we arrived at an optimized mixture of 2,4,6-collidine and benzoic acid (entry 7). These conditions yield a single observable diastereomer in the ^{1}H NMR spectrum of the crude reaction and shorten the reaction time from 24 hours to 2 hours at room temperature.

Table S1. Screening of additives for the conjugate addition of nitromethane to 1-cyclopentene-1-carboxaldehyde.

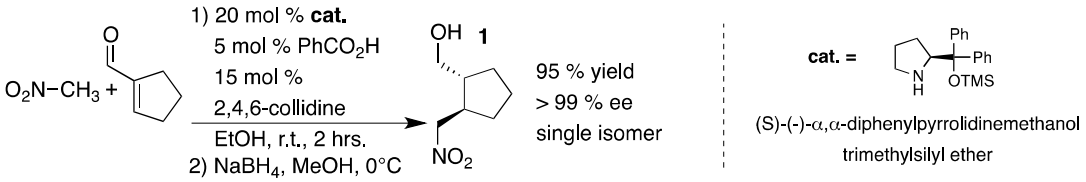


entry	additive 1	additive 2	Conv. (%)[a]	dr (major:minor)[a]
1	20 mol % benzoic acid	none	91	1:0
2	20 mol % *m*-nitro benzoic acid	none	83	9:1
3	20 mol % acetic acid	none	94	1:0
4	20 mol % H_2O	none	90	1:0
5	15 mol % benzoic acid	5 mol % 2,4,6-collidine	90	1:0
6	10 mol % benzoic acid	10 mol % 2,4,6-collidine	92	1:0
7[b]	**5 mol % benzoic acid**	**15 mol % 2,4,6-collidine**	**97[b]**	**1:0**

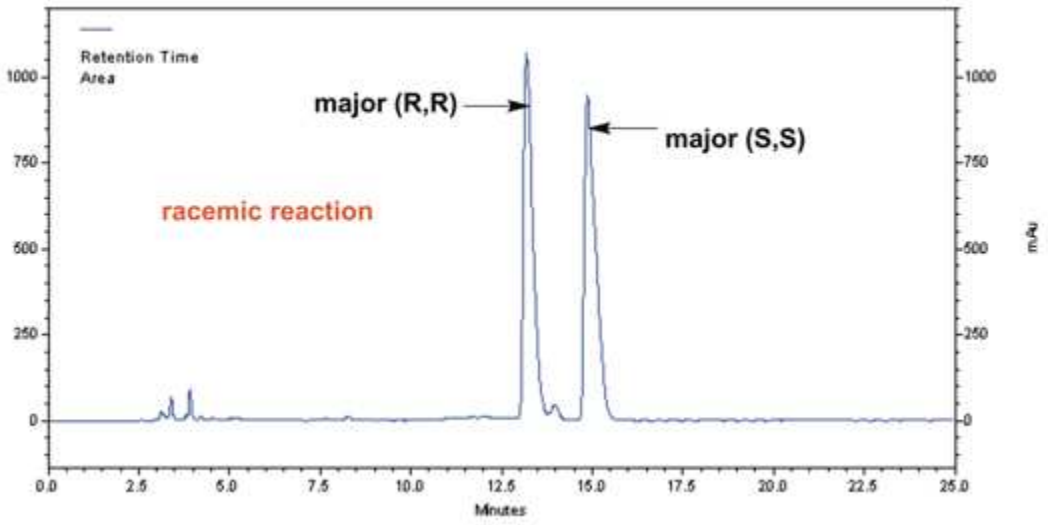
[a]Determined as illustrated above via analysis of the crude reaction mixture by 1H NMR.
[b]Reaction was complete to > 90% conversion in 2 hours.

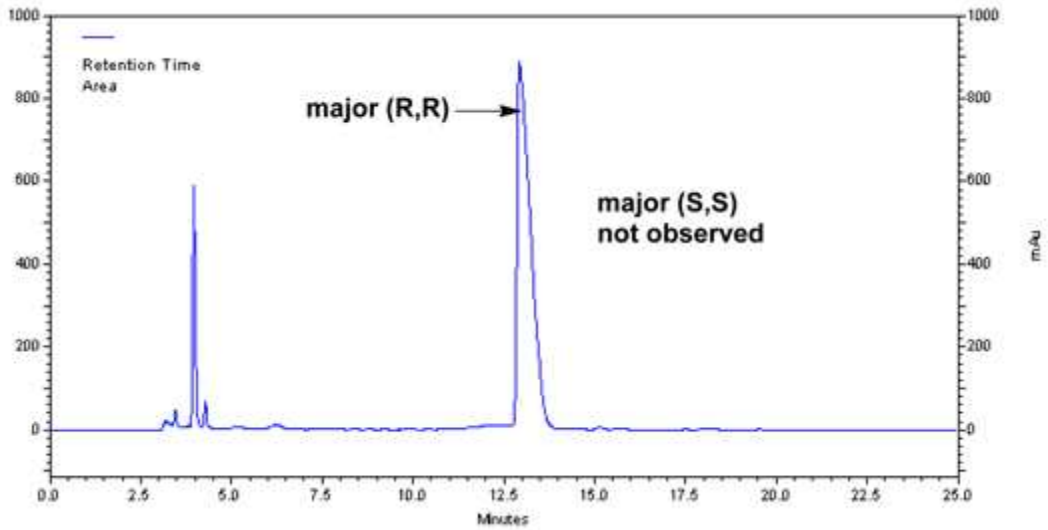
HPLC traces for ee determination of nitroalcohol 1: Samples were dissolved in approximately 5-10% (v/v) iPrOH in hexanes (solvents are Aldrich HPLC grade) and analyzed from 1-5 μL injections. All columns were analytical size – 4.6 mm x 250 mm. Racemic nitroalcohol product was obtained by running conjugate addition with 10 mol % of each enantiomer of the pyrrolidine catalyst using the optimized procedure for the synthesis of nitroalcohol **1**. The HPLC trace of this material is shown above that of the optimized reaction.

optimized reaction:



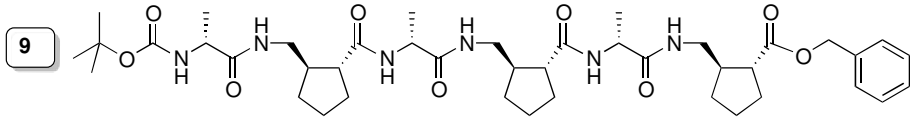
Chromatograms: Chiracel OJ-H column, 40°C, 1 mL/min., isocratic at 5% (v/v) iPrOH in hexanes. Retention time (R,R) configuration of major product = 13.2 min. Retention time (S,S) configuration of major product = 14.8 min. Product observed in > 99% ee for the (R,R) configuration of the major product. No integrable peak for the (S,S) configuration was observed.

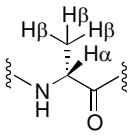




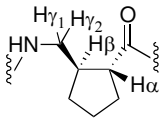
II. Tabulated 2D NMR Data for α/γ-peptides 9, 12, and 15

Table S2. Assigned ^{1}H chemical shifts for α/γ-peptide hexamer **9**
(chemical shift error = ± 0.02 ppm)





^{D}Alanine

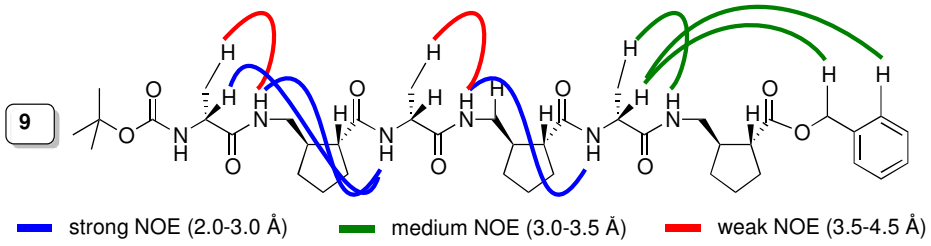


AMCP

	Hα	Hβ	Hγ1	Hγ2	NH	CH2	HAr
^{D}Ala(1)	4.12	1.35	-	-	5.09	-	-
AMCP(2)	2.31	-	322	3.53	7.45	-	-
^{D}Ala(3)	4.31	1.32	-	-	7.96	-	-
AMCP(4)	2.29	-	3.10	3.54	7.67	-	-
^{D}Ala(5)	4.26	1.22	-	-	8.28	-	-
AMCP(6)	2.55	2.34	3.10	3.38	6.64	-	-
Benzyl	-	-	-	-	-	5.14	7.36

A note on unassigned resonances: The non-backbone ring protons of AMCP were overlapped with each other such that their chemical shifts could not be uniquely assigned. This was also the case of the β-protons of most AMCP residues. Unassigned crosspeaks are indicated on the 2D spectra for **9** in section V of this supporting information.

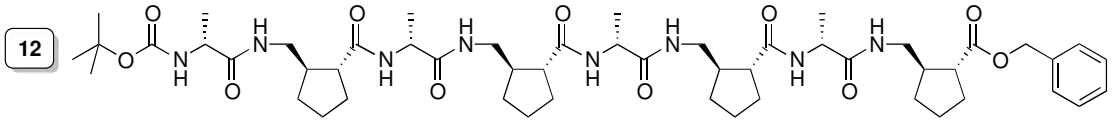
Table S3. Structural NOEs for α/γ-peptide hexamer **9**
(shown for two protons bewteen given residues, *i* and *j*)

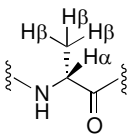


very strong NOE: 2.0-2.5 Å
strong NOE: 2.0-3.0 Å
medium NOE: 3.0-3.5 Å
weak NOE: 3.5-4.5 Å

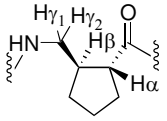
Residue (i)	Resiude (j)	Integrated Distance (Å)	Designation
^{D}Ala(1) Hα	^{D}Ala(3) NH	2.9	strong
^{D}Ala(1) Hβ	AMCP(2) NH	4.3	weak
AMCP(2) NH	^{D}Ala(3) NH	2.9	strong
^{D}Ala(3) Hβ	AMCP(4) NH	4.5	weak
AMCP(4) NH	^{D}Ala(5) NH	2.9	strong
^{D}Ala(5) Hα	Benzyl HAr	3.2	medium
^{D}Ala(5) Hα	Benzyl CH_2	3.2	medium
^{D}Ala(5) Hβ	AMCP(6) NH	3.6	weak

Table S4. Assigned ^{1}H chemical shifts for α/γ-peptide octamer **12**
(chemical shift error = ± 0.02 ppm)





^{D}Alanine

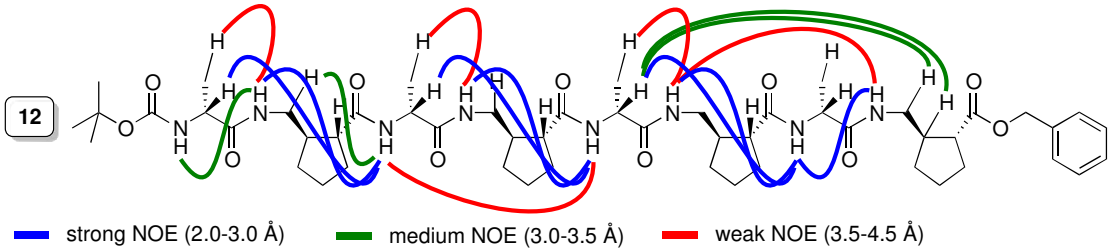


AMCP

	Hα	**Hβ**	**Hγı**	**Hγ2**	**NH**	**CH2**	**HAr**
^{D}Ala(1)	4.20	1.36	-	-	5.11	-	-
AMCP(2)	2.33	-	3.20	3.54	7.47	-	-
^{D}Ala(3)	4.42	1.36	-	-	7.95	-	-
AMCP(4)	2.33	-	3.12	3.58	7.71	-	-
^{D}Ala(5)	4.30	1.27	-	-	8.72	-	-
AMCP(6)	2.31	-	3.07	3.55	7.76	-	-
^{D}Ala(7)	4.26	1.22	-		8.36		
AMCP(8)	2.35	2.54	3.09	3.44	6.61		
Benzyl	-	-	-	-	-	5.14	7.36

A note on unassigned resonances: The non-backbone ring protons of AMCP were overlapped with each other such that their chemical shifts could not be uniquely assigned. This was also the case of the β-protons of most AMCP residues. Unassigned crosspeaks are indicated on the 2D spectra for **12** in section V of this supporting information.

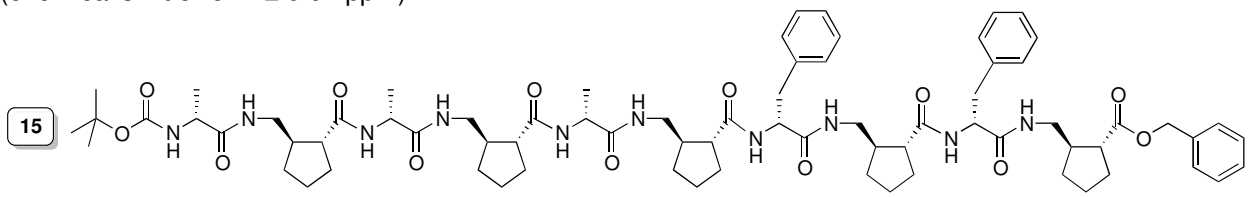
Table S5. Structural NOEs for α/γ-peptide octamer **12**
(shown for two protons bewteen given residues, *i* and *j*)

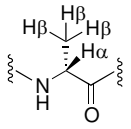


very strong NOE: 2.0-2.5 Å
strong NOE: 2.5-3.0 Å
medium NOE: 3.0-3.5 Å
weak NOE: 3.5-4.5 Å

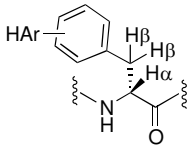
Residue (i)	Resiude (j)	Integrated Distance (Å)	Designation
^{D}Ala(1) Hα	^{D}Ala(3) NH	2.6	strong
^{D}Ala(1) Hβ	AMCP(2) NH	4.1	weak
^{D}Ala(1) NH	AMCP(2) NH	3.4	medium
AMCP(2) NH	^{D}Ala(3) NH	2.5	strong
AMCP(2) Hγ	^{D}Ala(3) NH	3.2	medium
^{D}Ala(3) Hα	^{D}Ala(5) NH	2.4	very strong
^{D}Ala(3) Hβ	AMCP(4) NH	4.3	weak
^{D}Ala(3) NH	^{D}Ala(5) NH	3.9	weak
AMCP(4) NH	^{D}Ala(5) NH	2.4	very strong
^{D}Ala(5) Hα	^{D}Ala(7) NH	2.1	very strong
^{D}Ala(5) Hα	AMCP(8) Hγ	3.0	medium
^{D}Ala(5) Hα	AMCP(8) Hβ	3.1	medium
^{D}Ala(5) Hβ	AMCP(6) NH	3.5	weak
AMCP(6) NH	^{D}Ala(7) NH	2.4	very strong
AMCP(6) NH	AMCP(8) NH	3.6	weak
^{D}Ala(7) NH	AMCP(8) NH	2.8	strong

Table S6. Assigned ^{1}H chemical shifts for α/γ-peptide decamer **15**
(chemical shift error = ± 0.02 ppm)

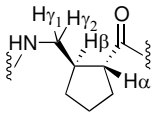




^{D}Alanine



^{D}Phenylalanine

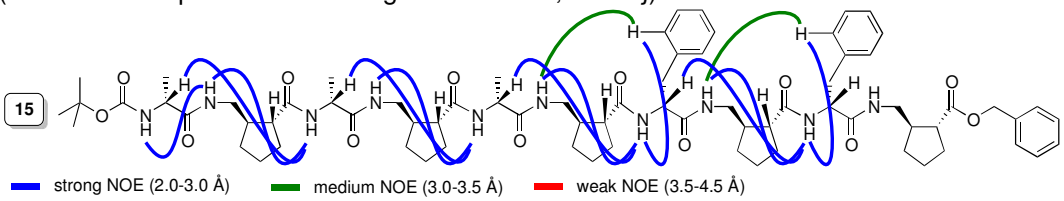


AMCP

	Hα	Hβ*	Hγ1	Hγ2	NH	CH2	HAr
^{D}Ala(1)	4.18	1.35	-	-	5.59	-	-
AMCP(2)	2.31	-	3.19	3.44	7.84	-	-
^{D}Ala(3)	4.33	1.38	-	-	7.98	-	-
AMCP(4)	2.37	-	3.12	3.51	8.10	-	-
^{D}Ala (5)	4.45	1.33	-	-	8.59	-	-
AMCP (6)	2.34	-	3.10	3.48	8.08	-	-
^{D}Phe (7)	4.60	2.97	-		8.48	-	7.35
AMCP (8)	2.18		2.98	3.40	7.74	-	-
^{D}Phe (9)	4.46	2.92	-		8.14	-	7.19
AMCP (10)	2.23		3.10	3.23	6.96	-	-
Benzyl	-	-	-	-	-	5.09	7.33

A note on unassigned resonances: The non-backbone ring protons of AMCP were overlapped with each other such that their chemical shifts could not be uniquely assigned. This was also the case of the β-protons of AMCP residues. Unassigned crosspeaks are indicated on the 2D spectra for **15** in section V of this supporting information. * Diastereotopic β-protons of ^{D}Phe residues were not resolved, thus a single chemical shift for each methylene unit is reported.

Table S7. Structural NOEs for α/γ-peptide decamer **15**
(shown for two protons bewteen given residues, *i* and *j*)



very strong NOE: 2.0-2.5 Å
strong NOE: 2.5-3.0 Å
medium NOE: 3.0-3.5 Å
weak NOE: 3.5-4.5 Å

Residue (i)	Resiude (j)	Integrated Distance (Å)	Designation
^{D}Ala(1) Hα	^{D}Ala(3) NH	2.4	very strong
^{D}Ala(1) NH	AMCP(2) NH	2.6	strong
AMCP(2) NH	^{D}Ala(3) NH	2.8	strong
^{D}Ala(3) Hα	^{D}Ala(5) NH	2.2	very strong
AMCP(4) NH	^{D}Ala(5) NH	2.2	very strong
^{D}Ala(5) Hα	^{D}Phe(7) NH	2.2	very strong
AMCP(6) NH	^{D}Phe(7) NH	2.1	very strong
^{D}Phe(7) Hα	^{D}Phe(9) NH	2.4	very strong
AMCP(8) NH	^{D}Phe(9) NH	2.4	very strong
^{D}Phe(9) NH	AMCP(10) NH	2.9	strong
^{D}Phe(7) NH	^{D}Phe(7) HAr	2.9	strong
AMCP(6) NH	^{D}Phe(7) HAr	3.2	medium
^{D}Phe(9) NH	^{D}Phe(9) HAr	3.4	medium

IIa. Aggregation Control Experiment for α/γ-peptide 15

The solubility of α/γ-peptides composed of hydrophobic residues tends to decrease with peptide length. Therefore, if we conclude that **15** is not aggregated in solution, we suspect that **9** and **12** which show very similar spectral characteristics to **15** (albeit in CDCl3 solution; dissolution of **15** required 5 % CD_3OH by volume to prevent gelation of the sample)**,** are also not aggregated in solution. We subjected α/γ-peptide decamer **15** to a dilution experiment, in which ^1H 1D spectra were taken at each concentration. If **15** aggregates in solution under the conditions of our experiments, then we would expect that as concentration decreases, the dispersion of proton resonances in the 1H 1D spectrum of **15** would decrease as the local environment around each proton becomes less anisotropic due to the break up and dissolution of aggregates at lower concentrations. However, if **15** is not aggregated, we would expect there to be little to no change in the chemical shifts of the proton resonances in the ^1H 1D NMR spectrum across all measured concentrations. We feel that decamer **15** is representative of the peptides in the present work as it is the longest of the sequence and exhibited the lowest solubility. This study is summarized below.

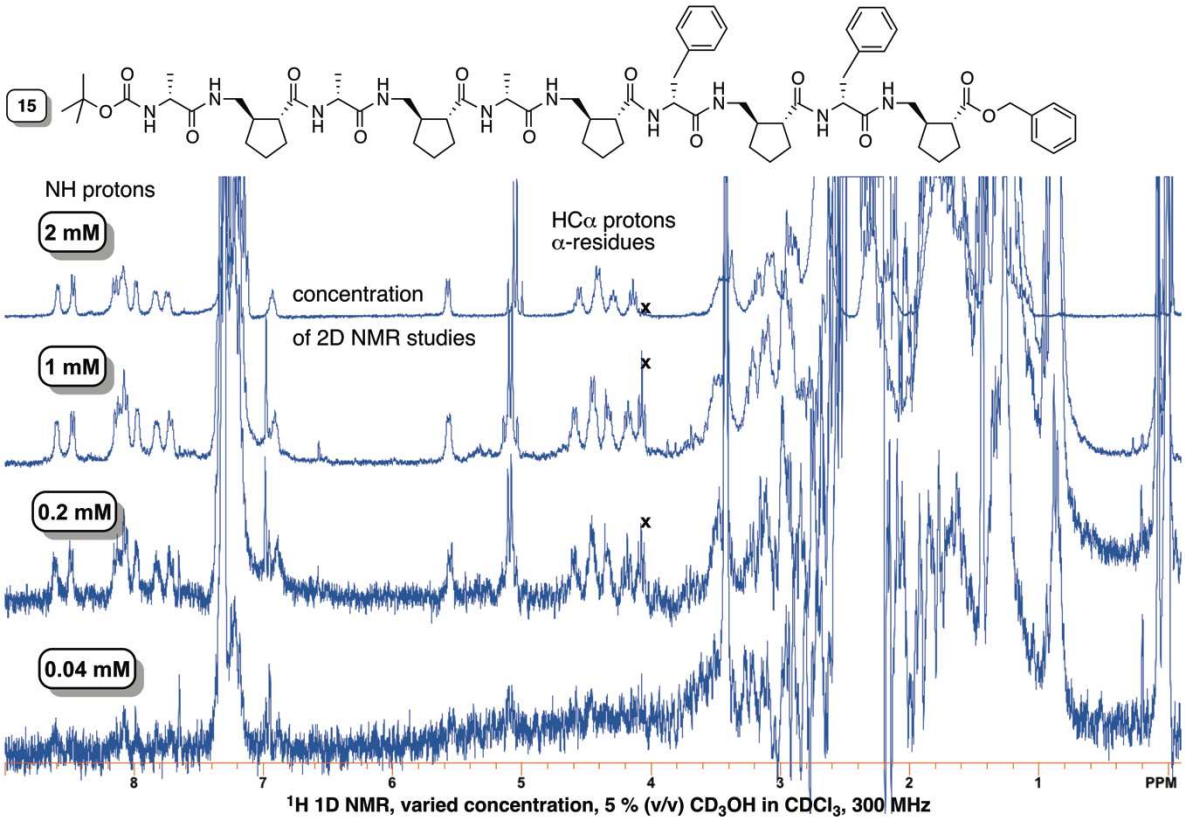


Figure S2. Variable concentration ^1H 1D NMR spectra of α/γ-peptide decamer **15** in 5 % CD_3OH in $CDCl_3$ (0.03 % TMS). The concentration of each trace is indicated above.

We *do not* observe changes in the chemical shifts of the NH proton or α-resiude HCα proton resonances of α/γ-peptide decamer **15** over a 50-fold range of concentration; overlap of other resonances with each other and the solvent peak of CD_3OH precluded meaningful observation in this experiment. We are therefore confident that **15** is not aggregated in our NMR studies. All three samples remained in solution (**9** and **12** in neat $CDCl3_3$; **15** with the addition of 5 % CD_3OH co-solvent) for more than one week without observation of gelation or precipitation. The latter only occurred for **15**, and only after $CDCl_3$ had evaporated from the co-solvent mixture over the course of more than two weeks. We therefore believe that the NMR observations reported for these α/γ-peptides arise from the folding preferences of individual peptide molecules and not from the influence of some type of aggregation induced conformation.

IIb. DMSO titration of NMR sample of α/γ-peptide 15

In an effort to gain more information about the nature of the structure of AMCP-containing α/γ-peptides **9**, **12**, and **15** that leads to the observed repeated NOE pattern, we subjected the NMR sample of decamer **15**, for which we observe the longest chain of this pattern, to a d_6-DMSO titration. Protons that are exposed to solvent will interact with the oxygen of d_6-DMSO solvent molecules and exhibit downfield shifting of their resonances with increasing volumes of added d_6-DMSO. By contrast, protons that are not exposed to solvent due to intramolecular hydrogen bonding will shift to a much lesser degree, often in the upfield direction. The data for α/γ-peptide **15** is depicted in a bar graph and discussed in detail in the manuscript. Below we present the stack plot of the NH proton region of the 1D ^{1}H NMR spectrum of **15** with volume of added DMSO indicated for each trace. Tables of the measured chemical shifts and calculated chemical shift changes for each proton at each concentration (used to generate the graph in the manuscript) are also included.

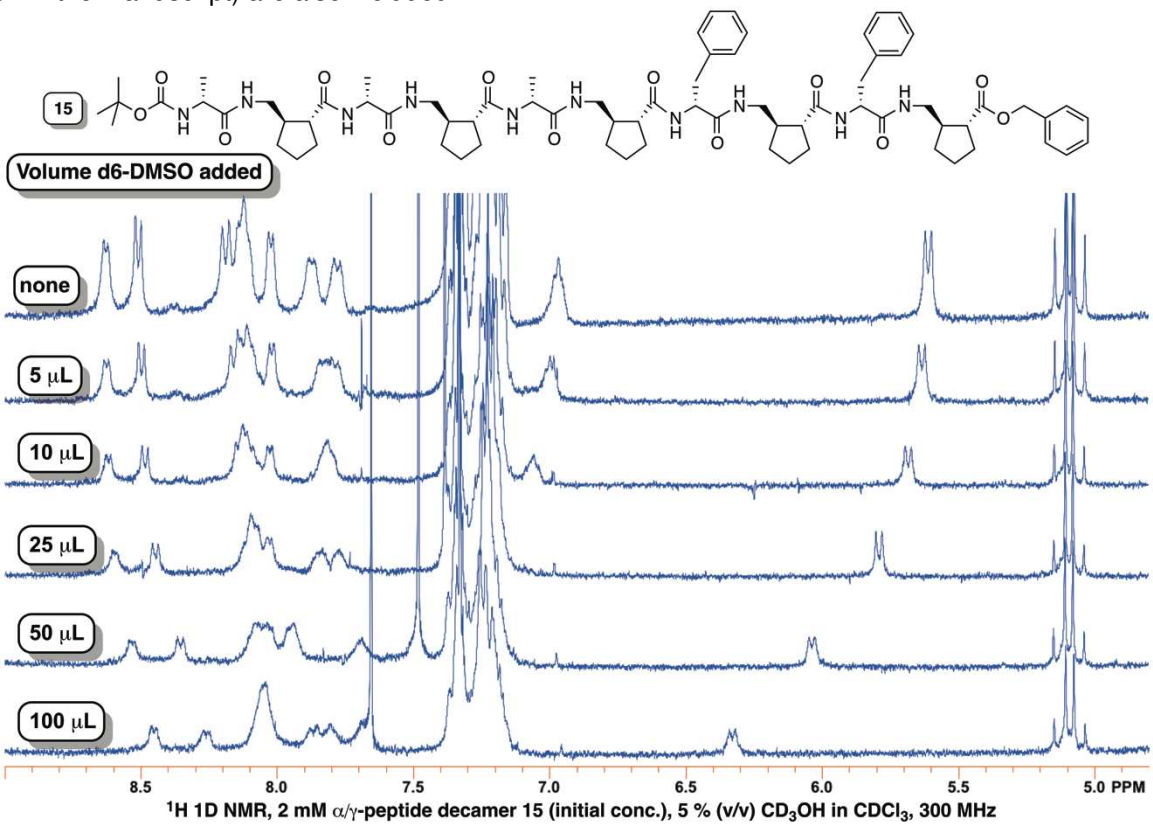


Figure S3. Stacked amide regions of 1D ^{1}H NMR spectra of titrated α/γ-peptide decamer **15** (300 MHz, $CDCl_3$ with 5% (v/v) CD_3OH) Volume of added d_6-DMSO is indicated with each trace.

Table S8. Measured Chemical shifts of amide NH protons of α/γ-peptide decamer **15** during DMSO titration experiment.

Vol. d_6-DMSO (μL)	**0**	**5**	**10**	**25**	**50**	**100**
Amide NH	**δ (ppm)**	**δ (ppm)**	**δ (ppm)**	**δ (ppm)**	**δ (ppm)**	**δ (ppm)**
^{D}Ala(1)	5.59	5.64	5.68	5.78	6.04	6.32
AMCP(2)	7.87	7.84	7.82	7.77	7.69	-
^{D}Ala(3)	8.02	8.02	8.02	8.03	7.94	7.86
AMCP(4)	8.14	8.11	-	-	-	-
^{D}Ala(5)	8.64	8.63	8.62	8.59	8.53	8.45
AMCP(6)	8.11	8.11	-	-	-	-
^{D}Phe(7)	8.52	8.50	8.48	8.44	8.35	8.25
AMCP(8)	7.77	7.79	7.82	7.84	7.94	8.04
^{D}Phe(9)	8.19	8.16	8.14	8.09	-	-
AMCP(10)	6.95	6.99	7.06	-	7.49	7.66

note: dashed entries indicate resonances that were overlapped and thus unable to be assigned unambiguously.

Table S9. Calculated chemical shift changes relative to zero DMSO added of amide NH protons of α/γ-peptide decamer **15** during DMSO titration experiment.

Vol. d_6-DMSO (μL)	**5**	**10**	**25**	**50**	**100**
Amide NH	**Δδ (ppm)**	**Δδ (ppm)**	**Δδ (ppm)**	**Δδ (ppm)**	**Δδ (ppm)**
^{D}Ala(1)	0.05	0.09	0.19	0.45	0.73
AMCP(2)	-0.03	-0.05	-0.10	-0.18	-
^{D}Ala(3)	0.00	0.00	0.01	-0.08	-0.16
AMCP(4)	-0.03	-	-	-	-
^{D}Ala(5)	-0.01	-0.02	-0.05	-0.11	-0.19
AMCP(6)	0.00	-	-	-	-
^{D}Phe(7)	-0.02	-0.04	-0.08	-0.17	-0.27
AMCP(8)	0.02	0.05	0.07	0.17	0.27
^{D}Phe(9)	-0.03	0.05	-0.10	-	-
AMCP(10)	0.04	0.11	-	0.54	0.71

note: dashed entries indicate resonances that were overlapped and thus unable to be assigned unambiguously.

III. NMR Structure Statistics and Ensembles for α/γ-peptides 9, 12, and 15

Table S10. Structure statistics for α/γ-peptides **9**, **12**, and **15**.

NMR constraints	**9**	**12**	**15**
Distance constraints			
Total NOE	9	16	13
Intra-residue	0	0	0
Inter-residue	9	16	13
Sequential ($\|i-j\| = 1$) (not across γ-residue)	0	0	0
Medium-range ($\|i-j\| < 4$) (includes NOEs across γ-residues to nearest neighbor)	9	16	13
Long-range ($\|i-j\| > 5$)	0	0	0
Intermolecular	0	0	0
Hydrogen bonds	0	0	0
Total dihedral angle restraints			
ϕ	0	0	0
ψ	0	0	0
Structure statistics			
Violations (mean and s.d.)	1.00 ± 0.0**	0	0
Distance constraints (Å)	0.01 ± 0.001	0.02 ± 0.01	0.02 ± 0.01
Dihedral angle constraints (º)	0	0	0
Max. dihedral angle violation (º)	55.6**	0	0
Max. distance constraint violation (Å)	0	0	0
Deviations from idealized geometry			
Bond lengths (Å)	± 0.0047	± 0.0047	± 0.0052
Bond angles (º)	± 0.77	± 0.78	± 0.63
Impropers (º)	± 0.62	± 0.66	± 0.70
Average pairwise r.m.s. deviation (Å) (10 Structures)			
Heavy	1.2 ± 0.2	3.0 ± 1.1	3.6 ± 1.0
Backbone	0.8 ± 0.1	2.0 ± 1.0	2.4 ± 0.4

** We occasionally observe violation of the cyclopentyl ring dihedral restraints we manually put into CNS.

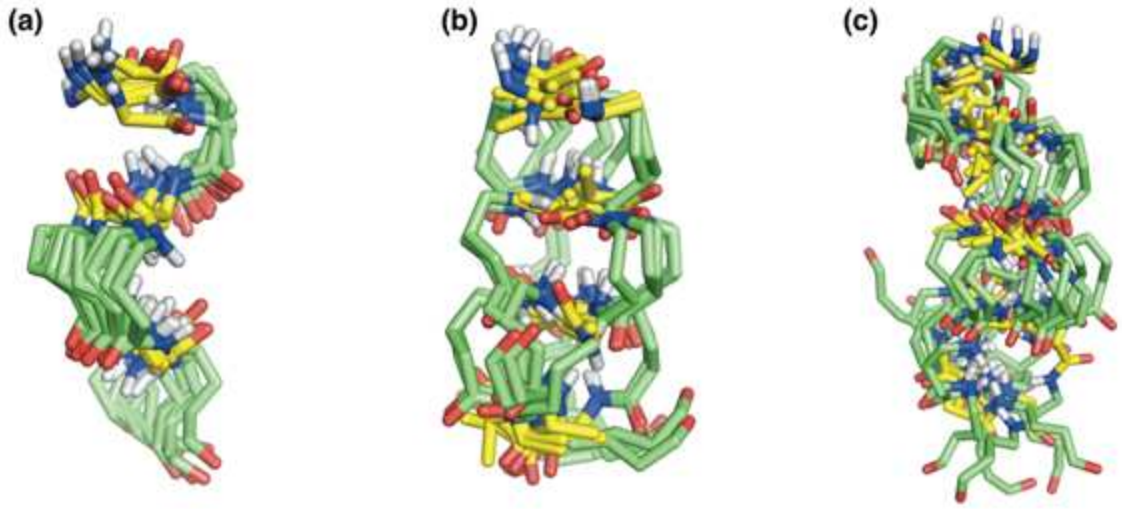


Figure S4. (a) Ten lowest-energy structures of α/γ-peptide hexamer **9**. (b) Ten lowest-energy structures of α/γ-peptide octamer **12**. (c) Ten lowest-energy structure of α/γ-peptide decamer **15**. AMCP residues are shown in green, α-residues and protecting groups are shown in yellow.

IV. References

1) The PyMOL Molecular Graphics System, Version 1.5.0.4 Schrödinger, LLC.

2) (a) Brunger, A. T.; Adams, P. D.; Clore, G. M.; DeLano, W. L.; Gros, P.; Grosse-Kunstleve, R. W.; Jiang, J. S.; Kuszewski, J.; Nilges, M.; Pannu, N. S.; Read, R. J.; Rice, L. M.; Simonson, T.; Warren, G. L. *Acta Crystallogr., Sect. D: Biol. Crystallogr.*. **1998**, *54*, 905. (b) Brunger, A. T. *Nat. Protoc.* **2007**, *2*, 2728.

3) Guo, L.; Chi, Y. G.; Almeida, A. M.; Guzei, I. A.; Parker, B. K.; Gellman, S. H. *J. Am. Chem. Soc.* **2009**, *131*, 16018.

4) Zu, L.; Xie, H.; Li, H.; Wang, H.; Wang, W. *Adv. Synth. Catal.* **2007**, *349*, 2660.

5) Palomo, C.; Landa, A.; Mielgo, A.; Oiarbide, M.; Puente, A.; Vera, S. *Angew. Chem. Int. Ed.* **2007**, *46*, 8431.

6) Hanessian, S.; Pham, V. *Org. Lett.* **2000**, *2*, 2975.

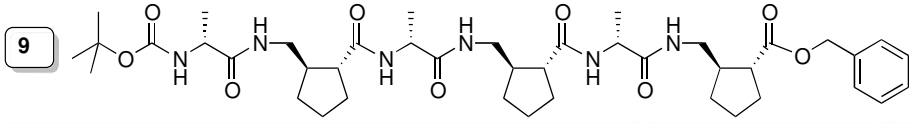
7) Hanessian, S.; Shao, Z. H.; Warrier, J. S. *Org. Lett.* **2006**, *8*, 4787.

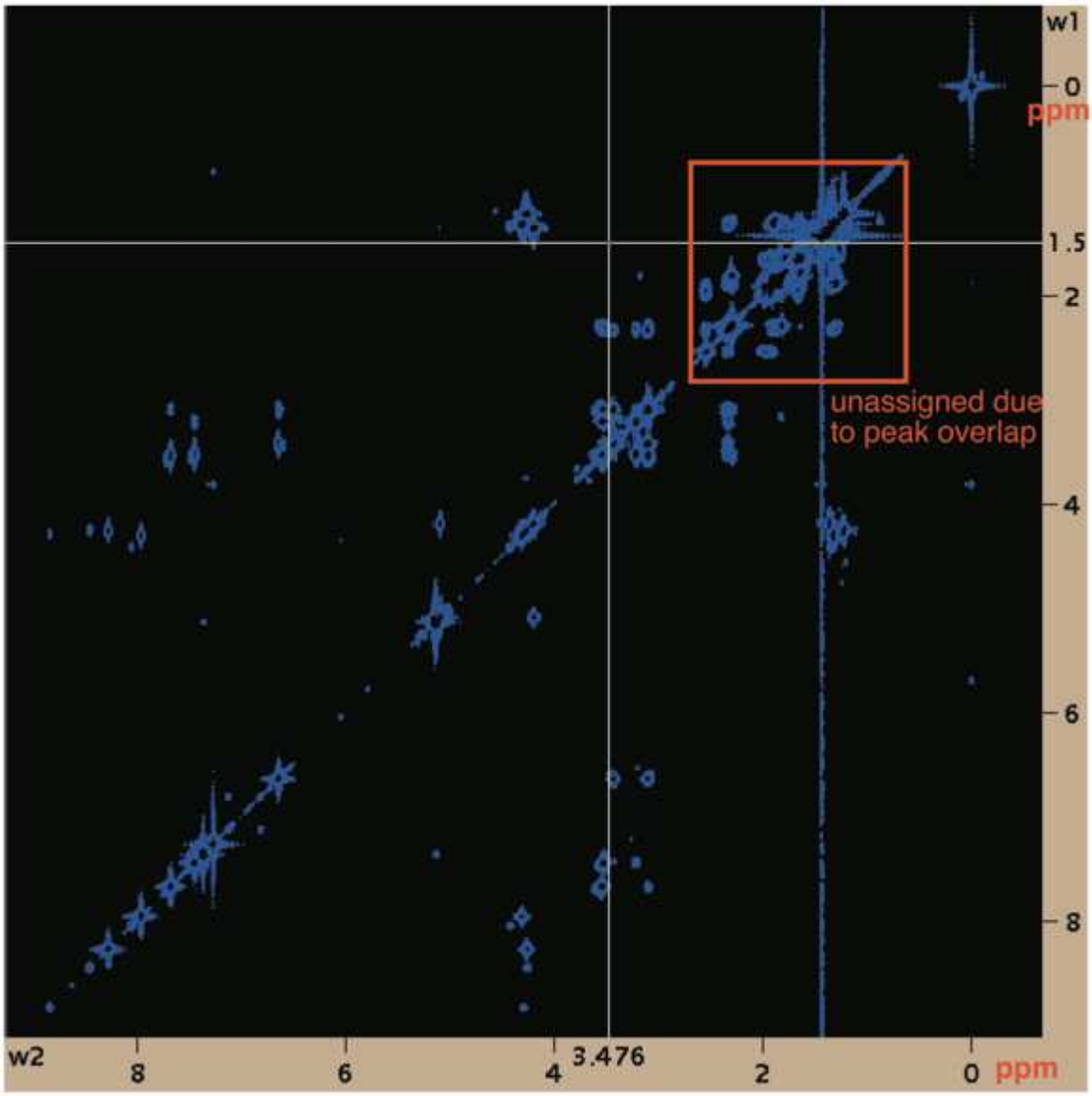
8) Goddard, D. T.; Kneller, D. G. SPARKY 3, University of California, San Francisco.

V. 2D NMR Spectra for α/γ-peptides 9, 12 and 15

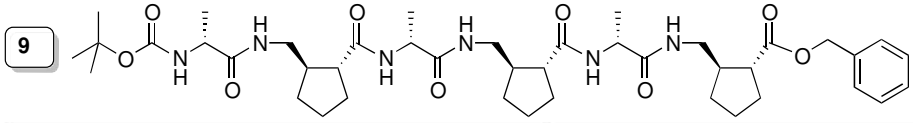
Spectra plots were generated in SPARKY,[8] which was used for assignment and integration of all data.

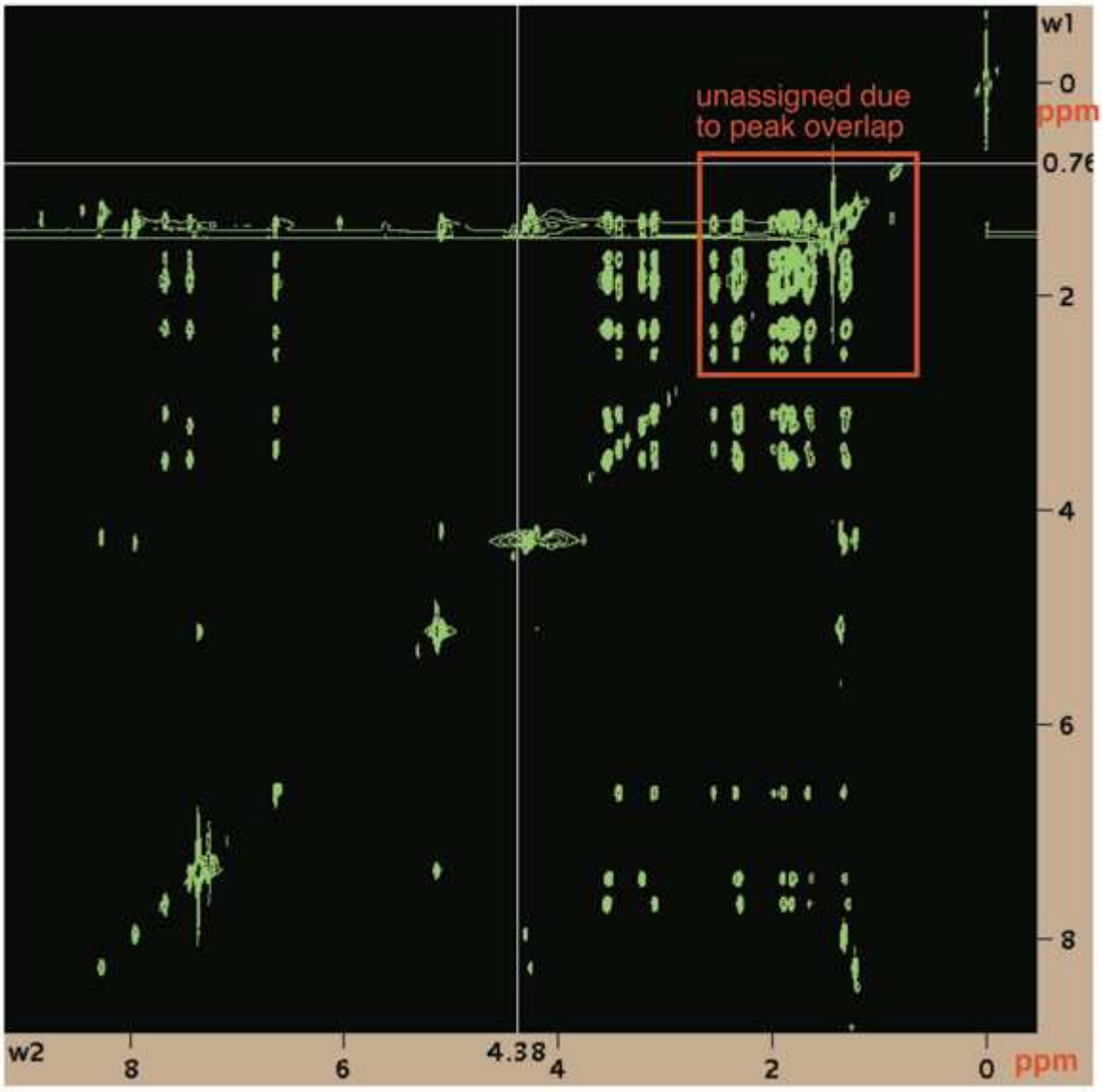
gCOSY: 2 mM α/γ-peptide hexamer **9** in $CDCl_3$ solution.



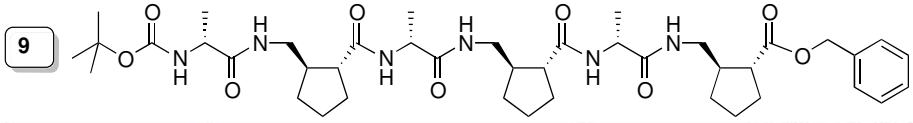


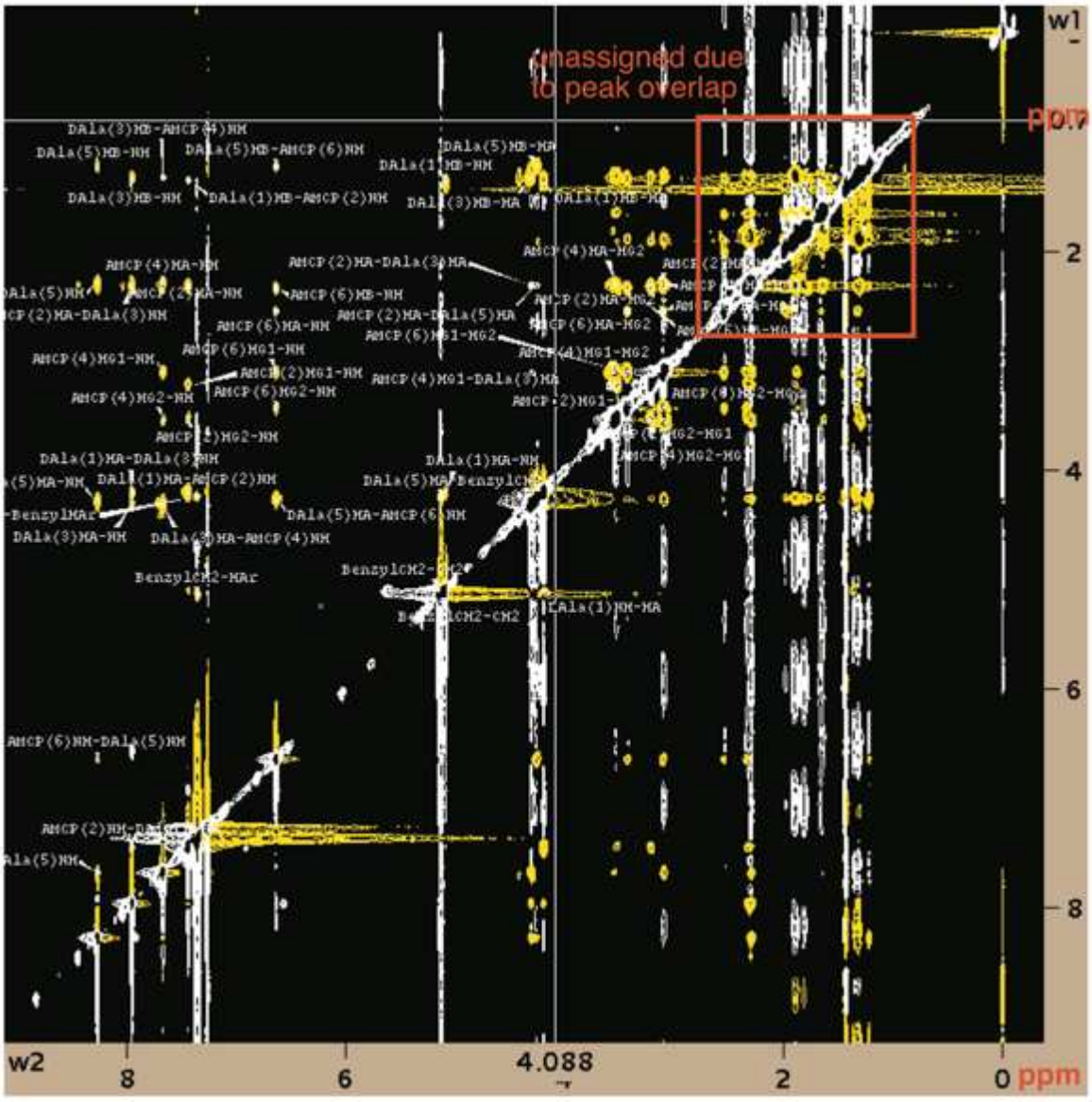
TOCSY: 2 mM α/γ-peptide hexamer **9** in $CDCl_3$ solution.



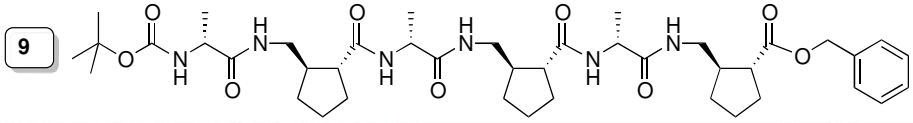


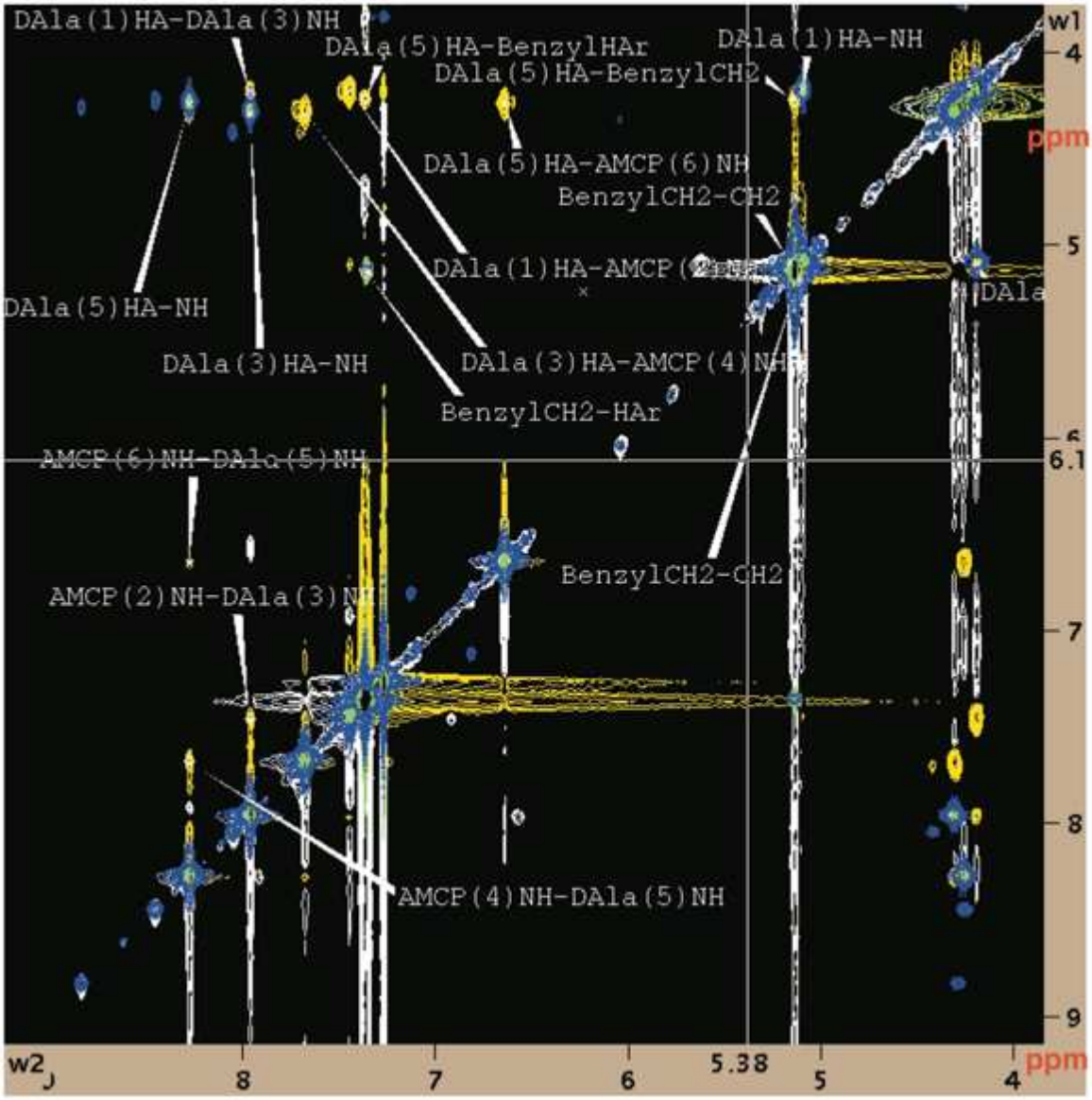
ROESY: 2 mM α/γ-peptide hexamer **9** in $CDCl_3$ solution. Positive peaks in gold, negative peaks in white.



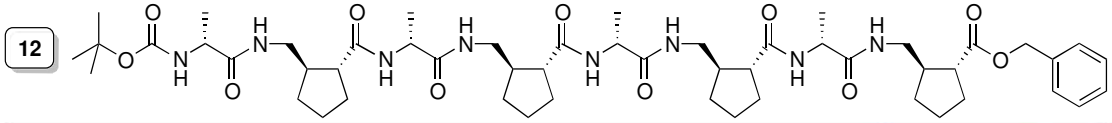


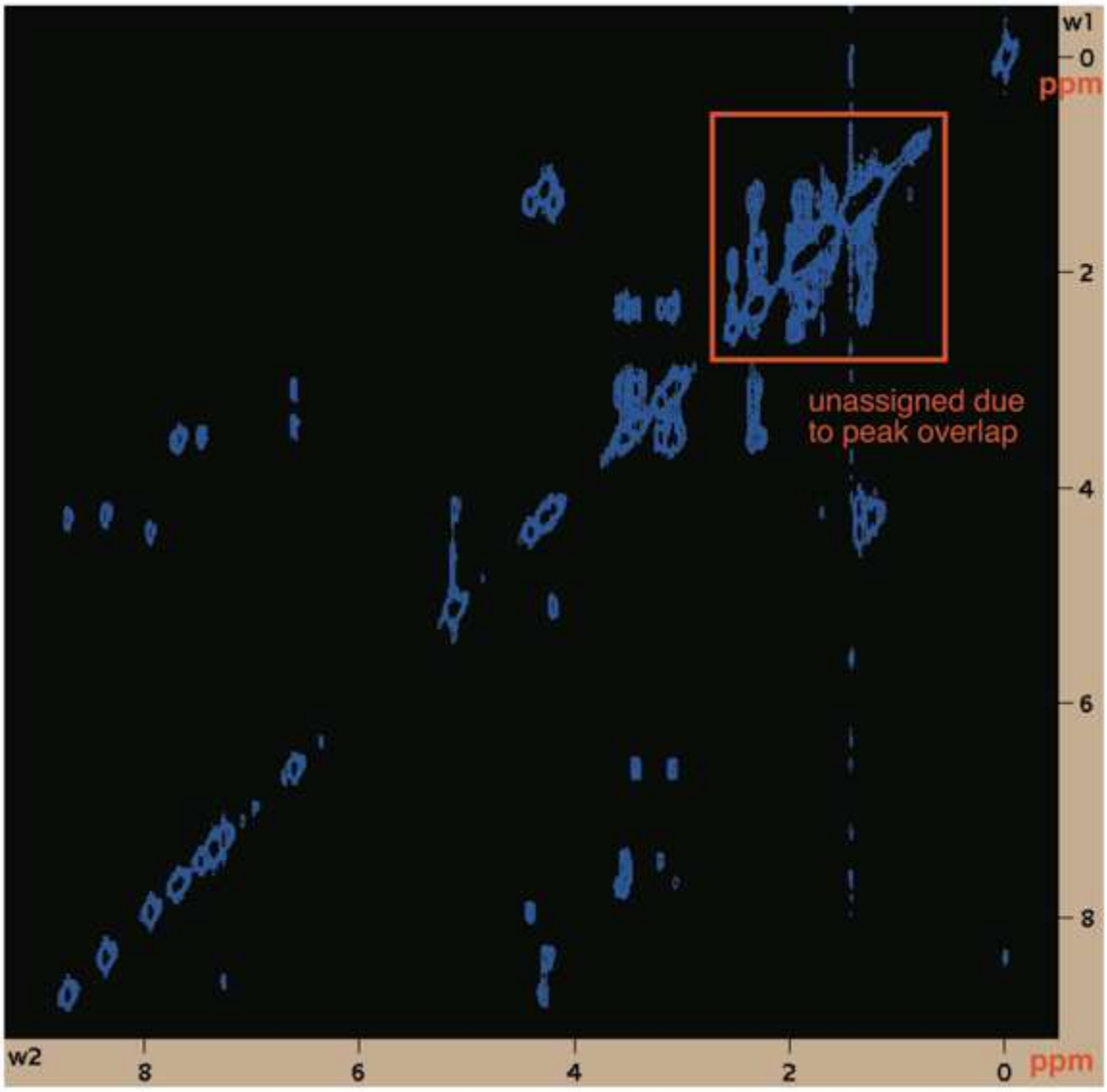
Partial overlay of gCOSY, TOCSY, ROESY used for assignment: 2 mM α/γ-peptide hexamer **9** in $CDCl_3$ solution. Positive ROESY peaks in gold, negative ROESY peaks in white. TOCSY peaks are in green. gCOSY peaks are in blue.



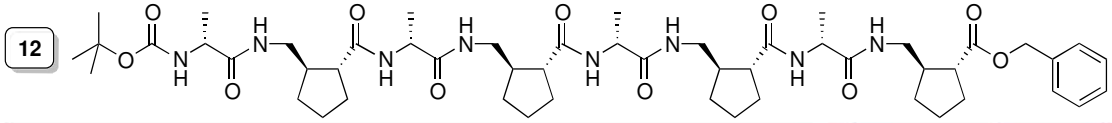


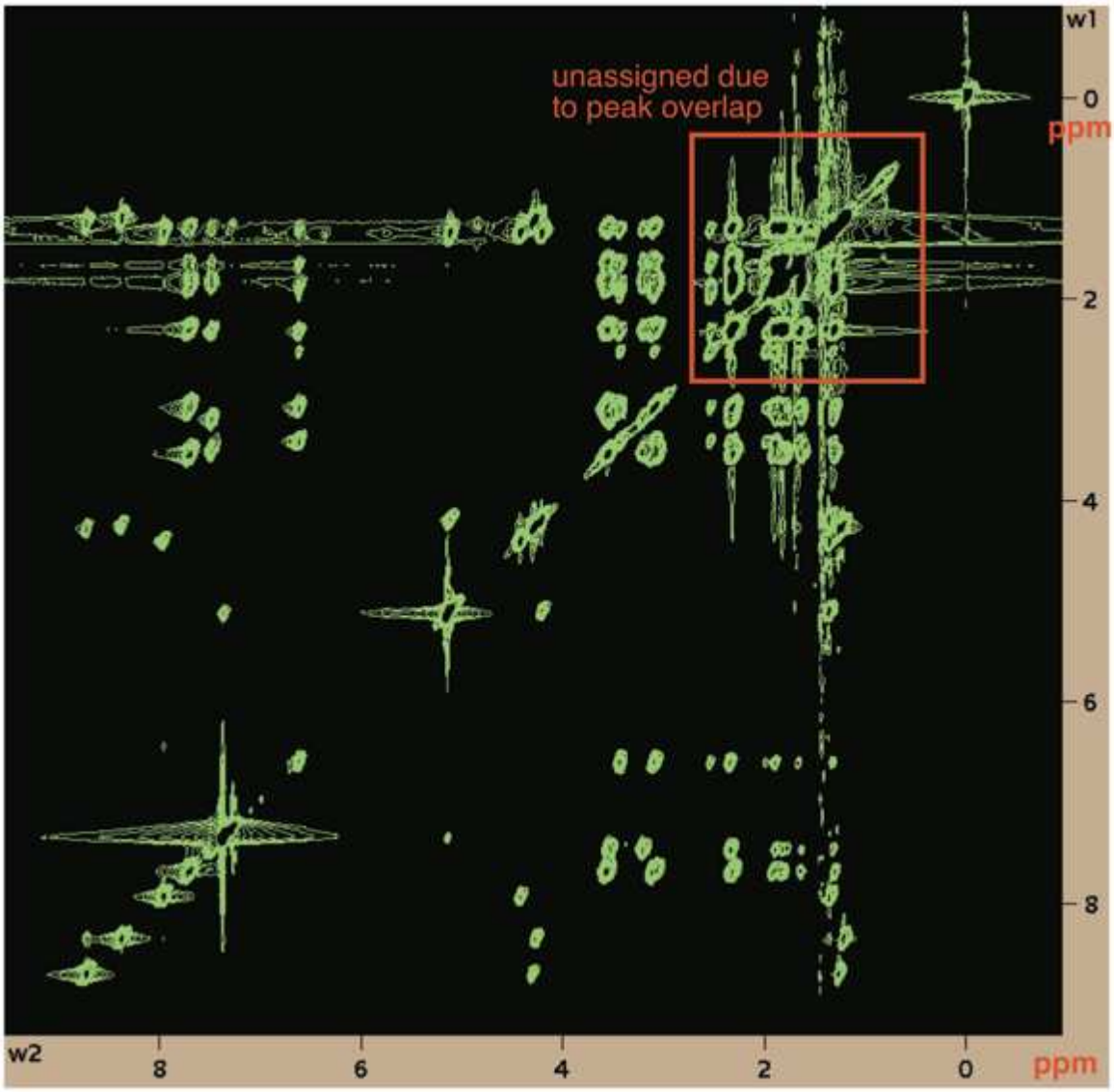
gCOSY: 2 mM α/γ-peptide octamer **12** in $CDCl_3$ solution.



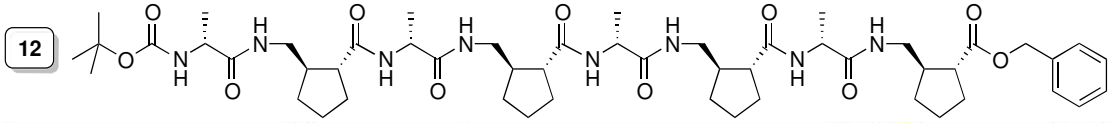


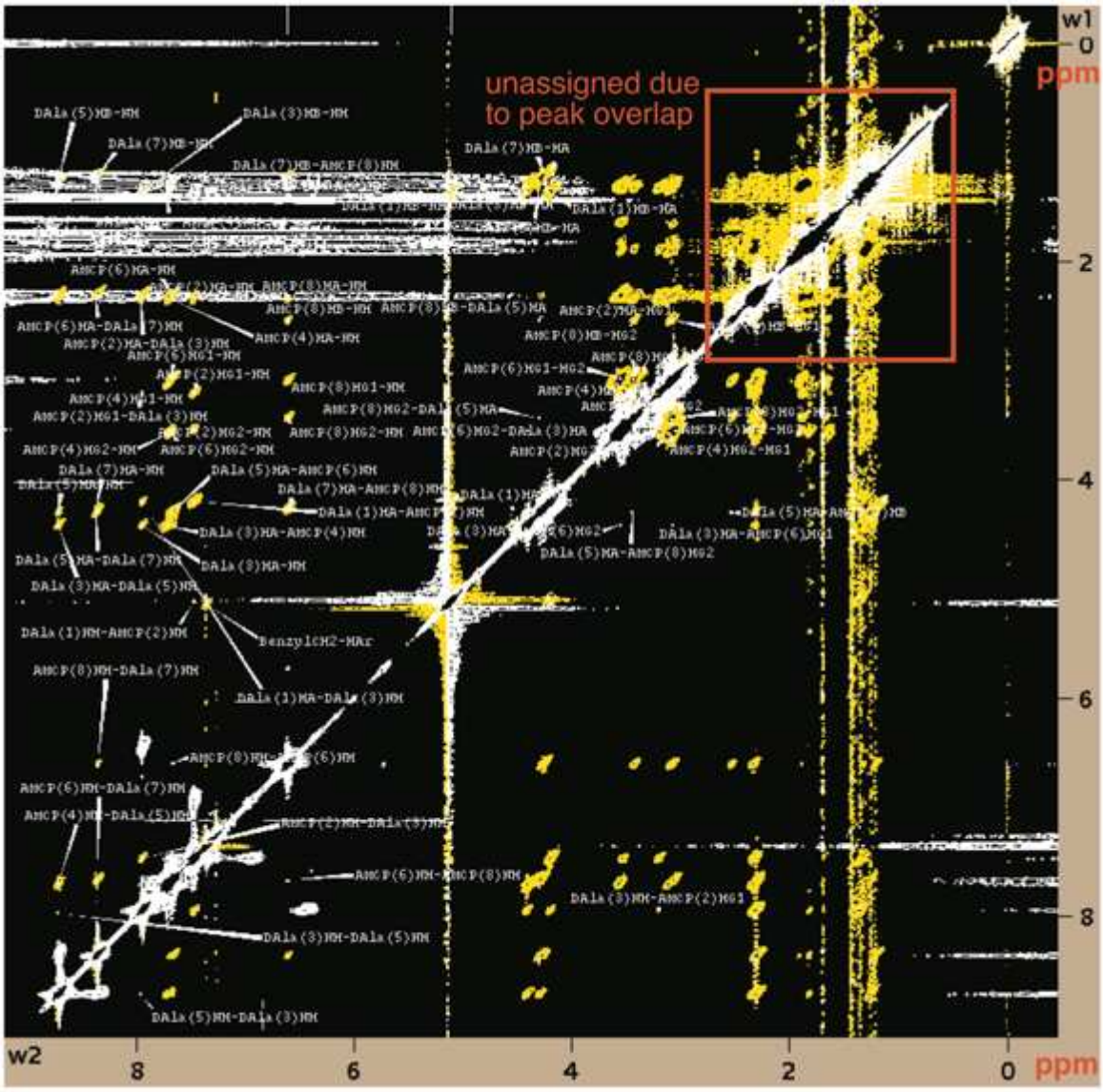
TOCSY: 2 mM α/γ-peptide octamer **12** in $CDCl_3$ solution.



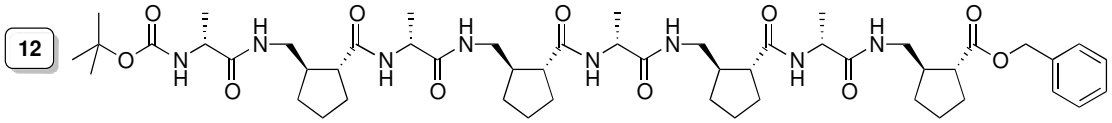


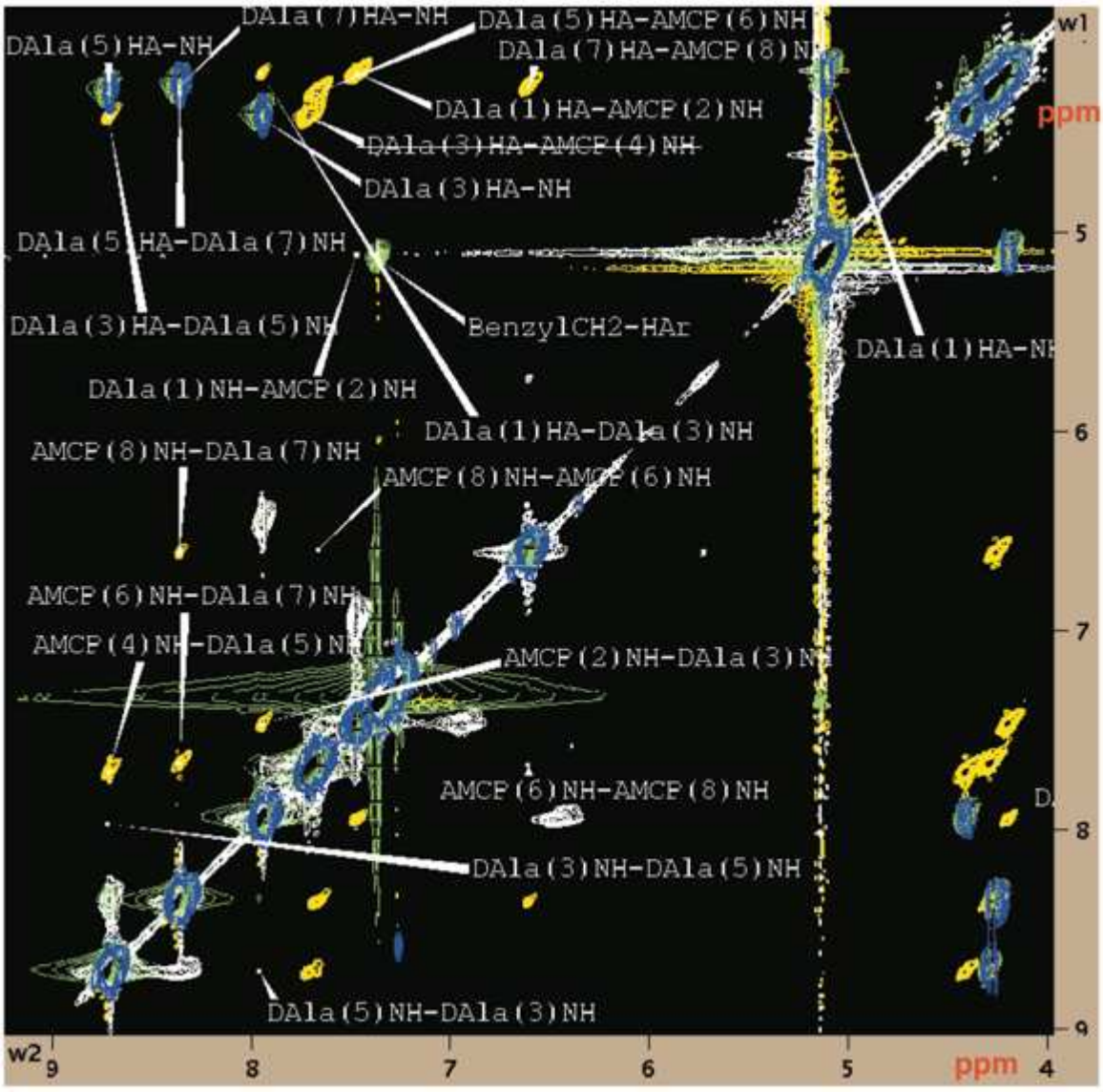
ROESY: 2 mM α/γ-peptide octamer **12** in $CDCl_3$ solution.



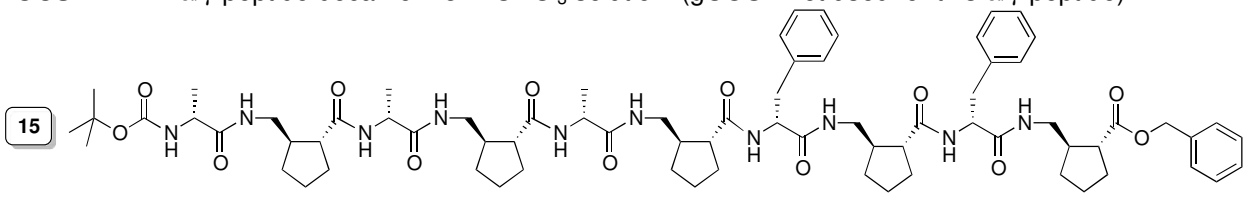


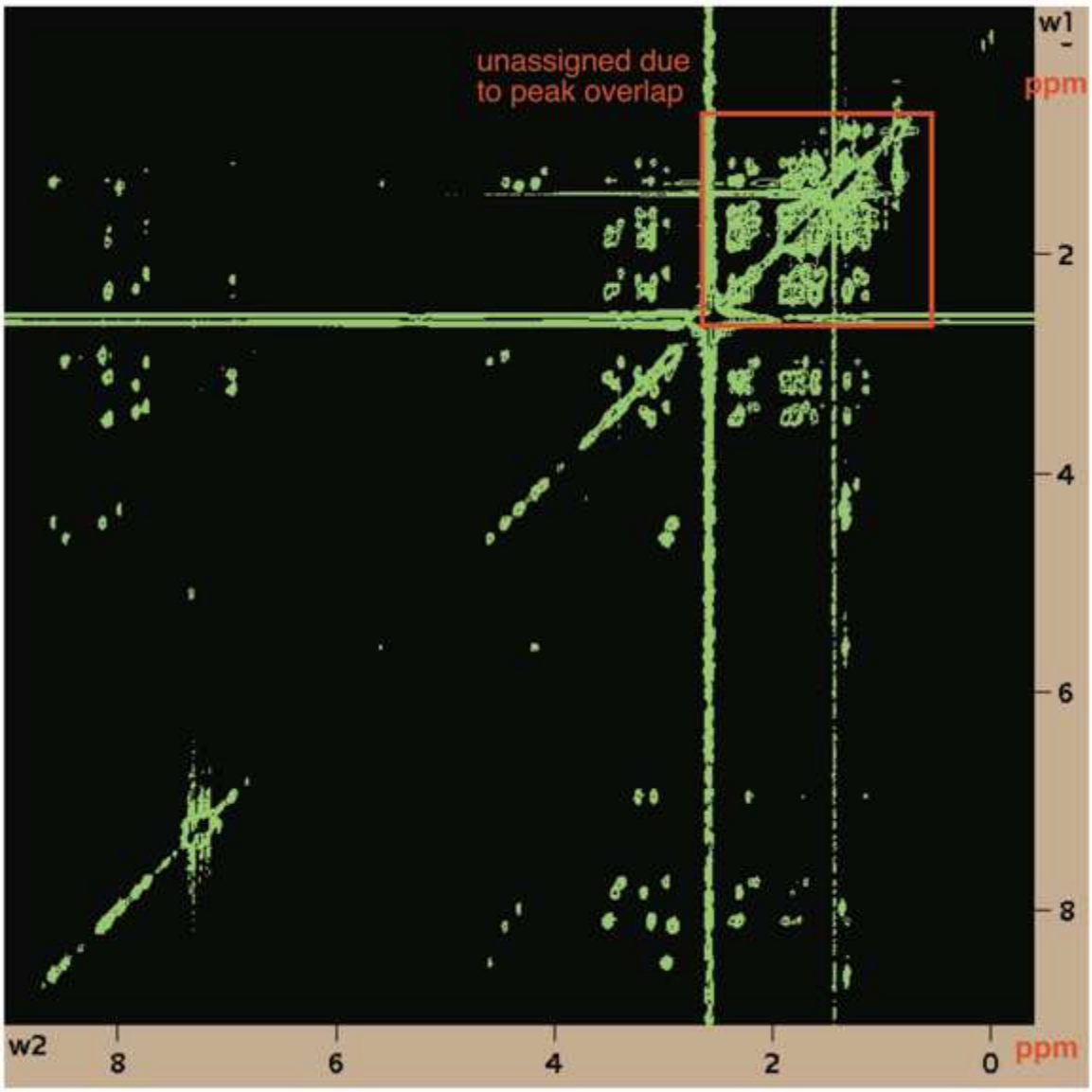
Partial overlay of gCOSY, TOCSY, and ROESY used for assignment: 2 mM α/γ-peptide octamer **12** in $CDCl_3$ solution. Positive ROESY peaks in gold, negative ROESY peaks in white. TOCSY peaks are in green.



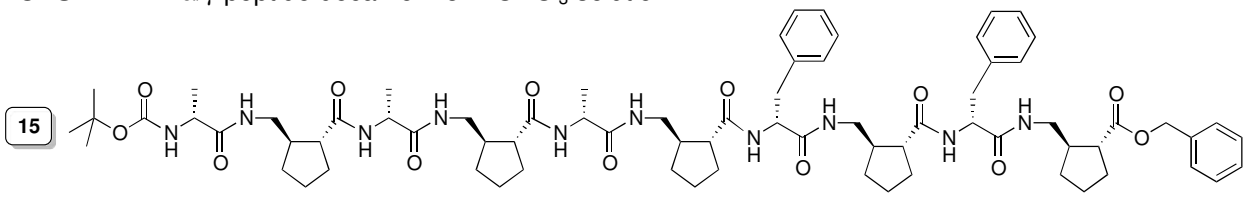


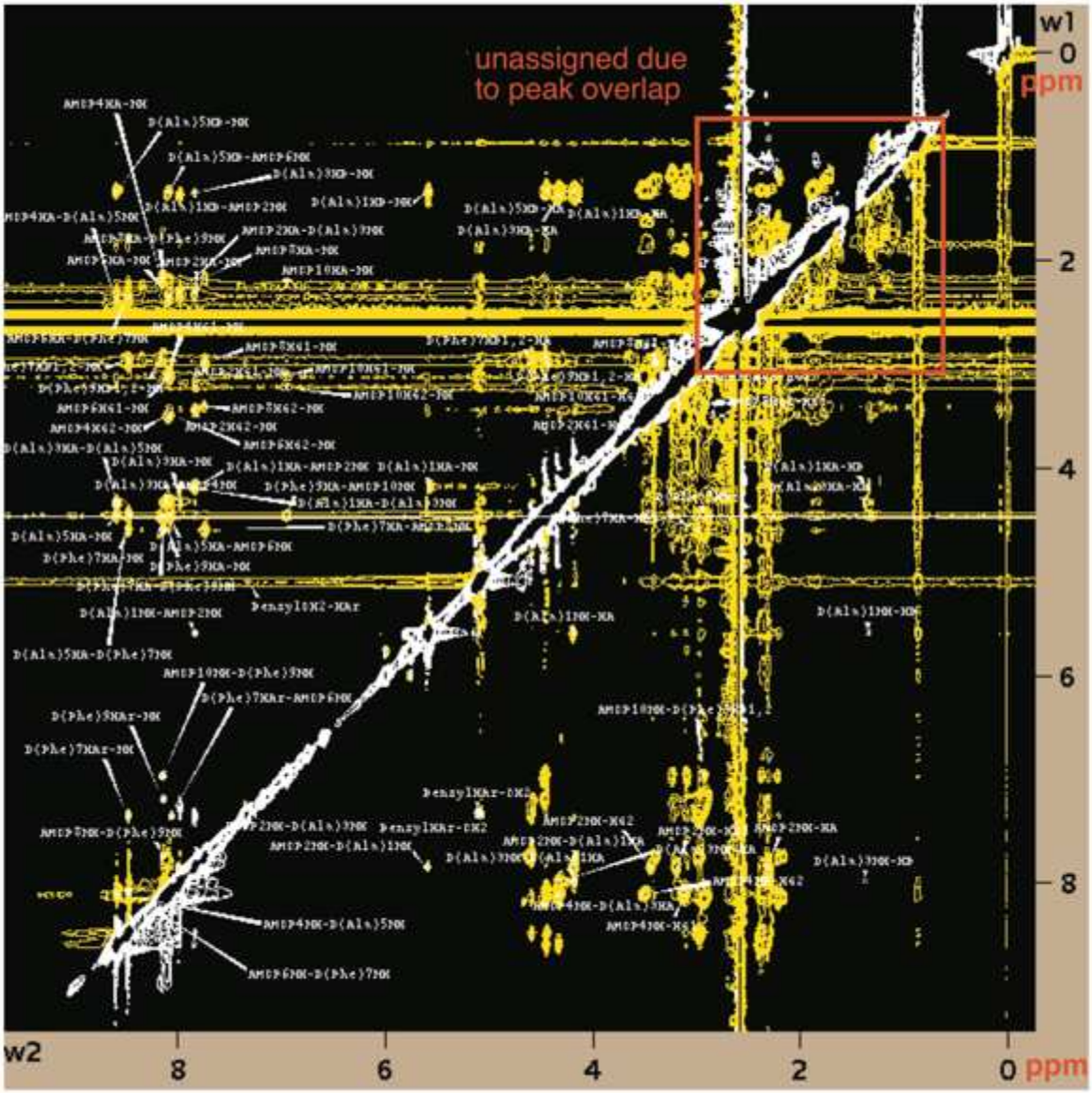
TOCSY: 2 mM α/γ-peptide decamer **15** in $CDCl_3$ solution. (gCOSY not used for this α/γ-peptide)



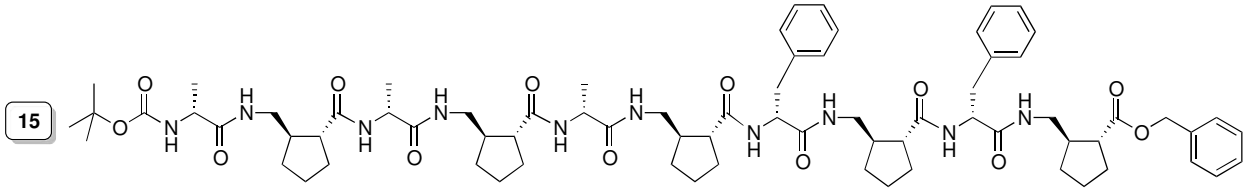


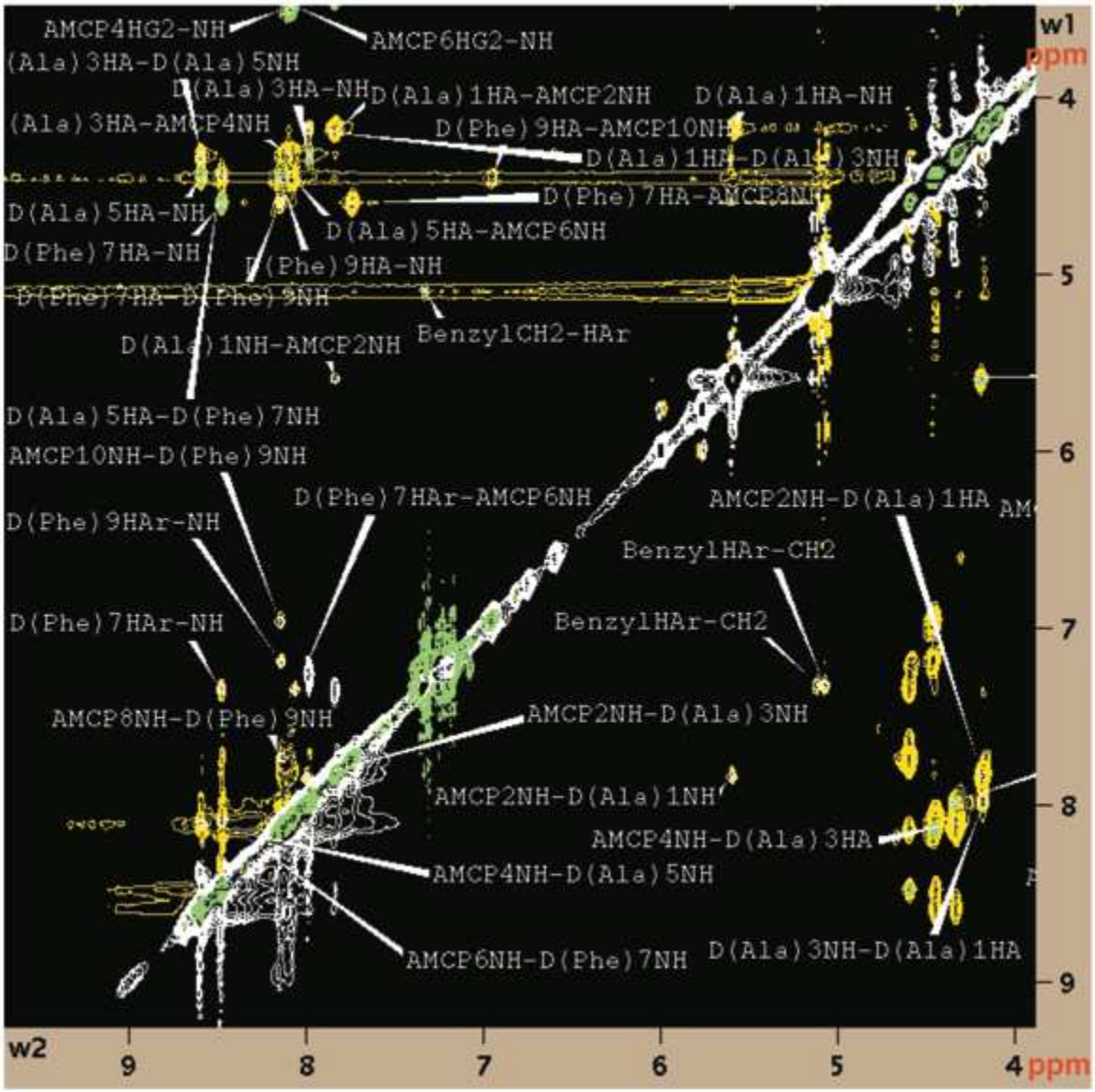
ROESY: 2 mM α/γ-peptide decamer **15** in $CDCl_3$ solution.



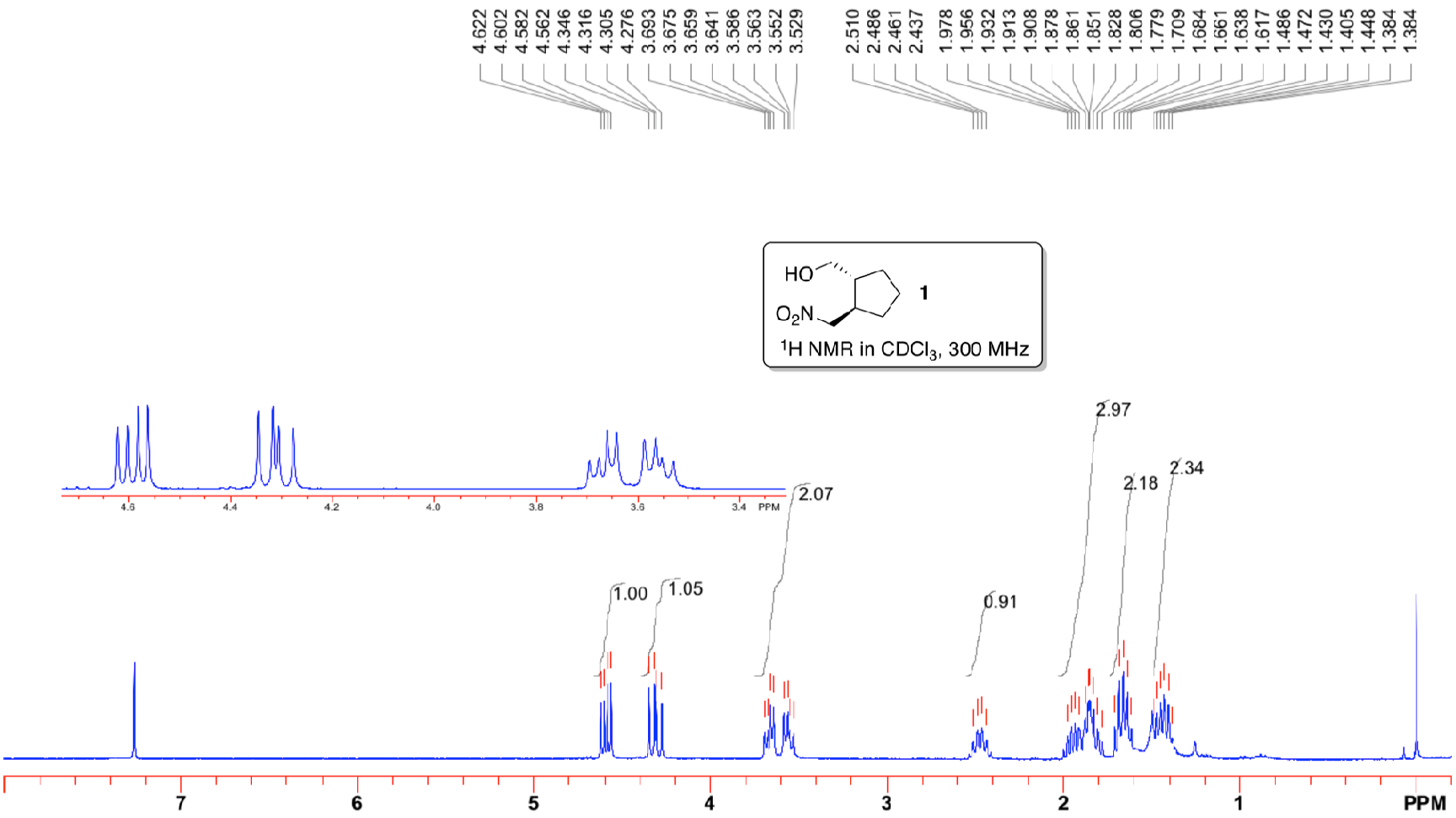


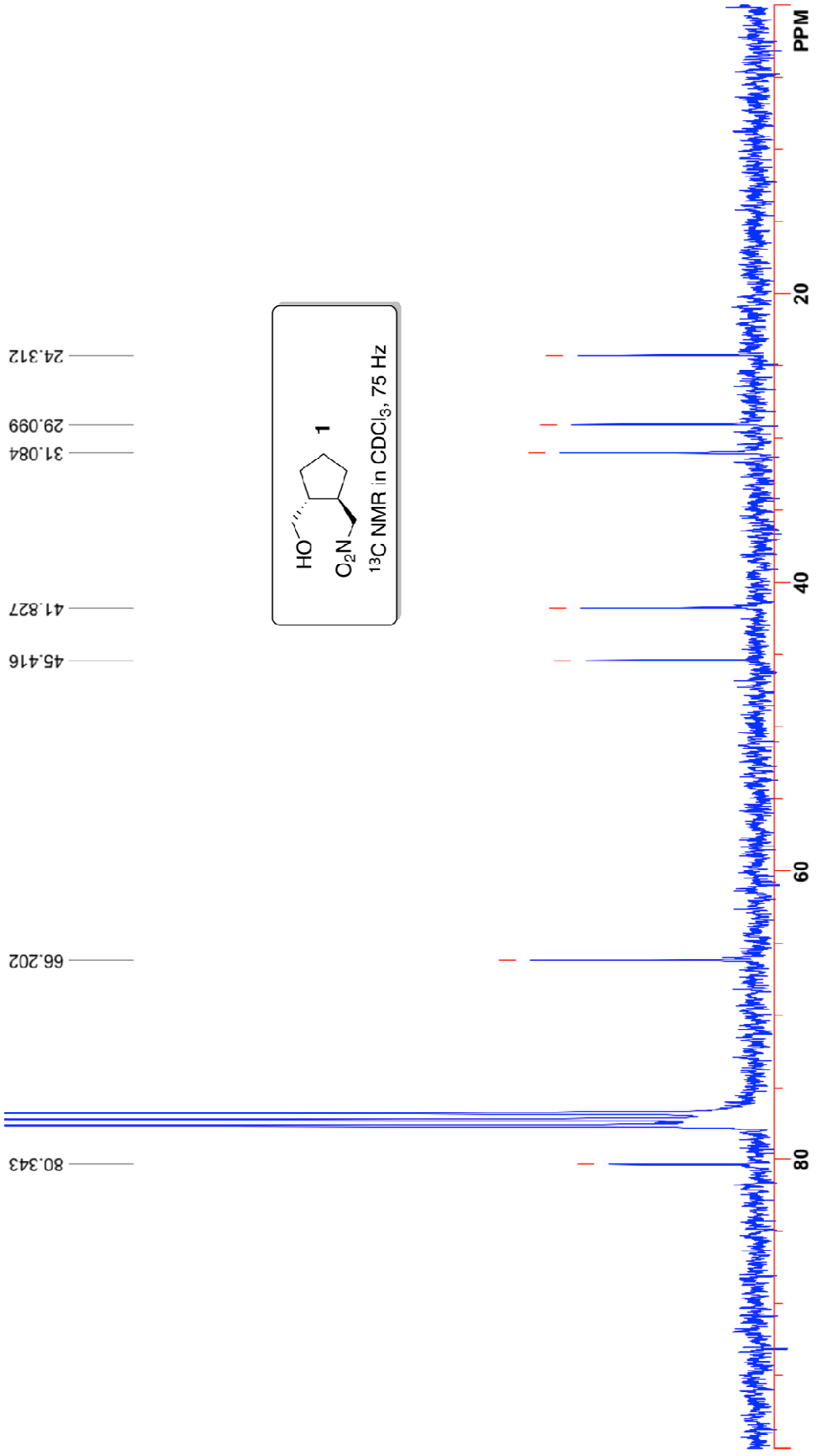
Partial overlay of TOCSY and ROESY used for assignment: 2 mM α/γ-peptide decamer **15** in $CDCl_3$ solution. Positive ROESY peaks in gold, negative ROESY peaks in white. TOCSY peaks are in green.

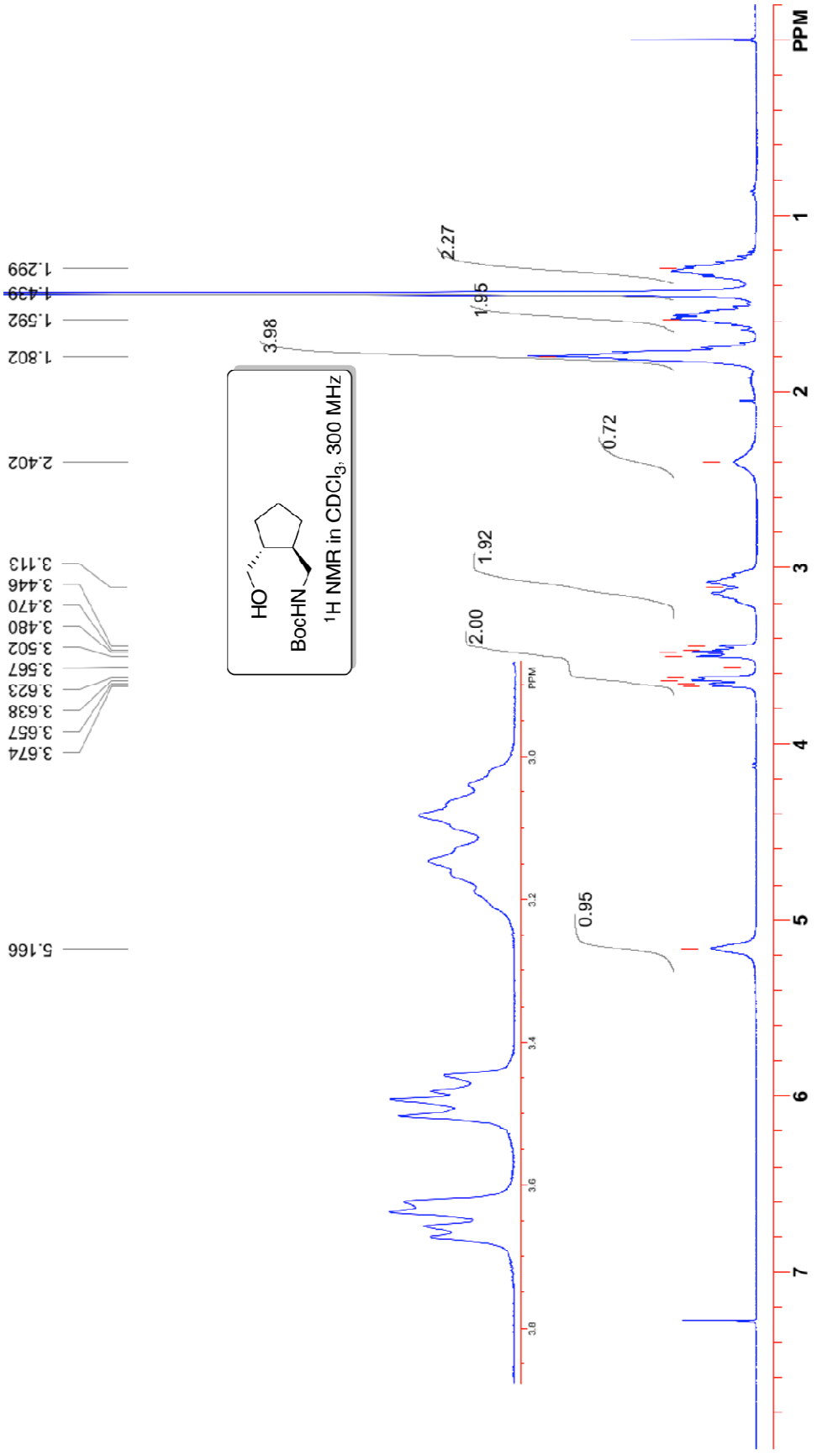


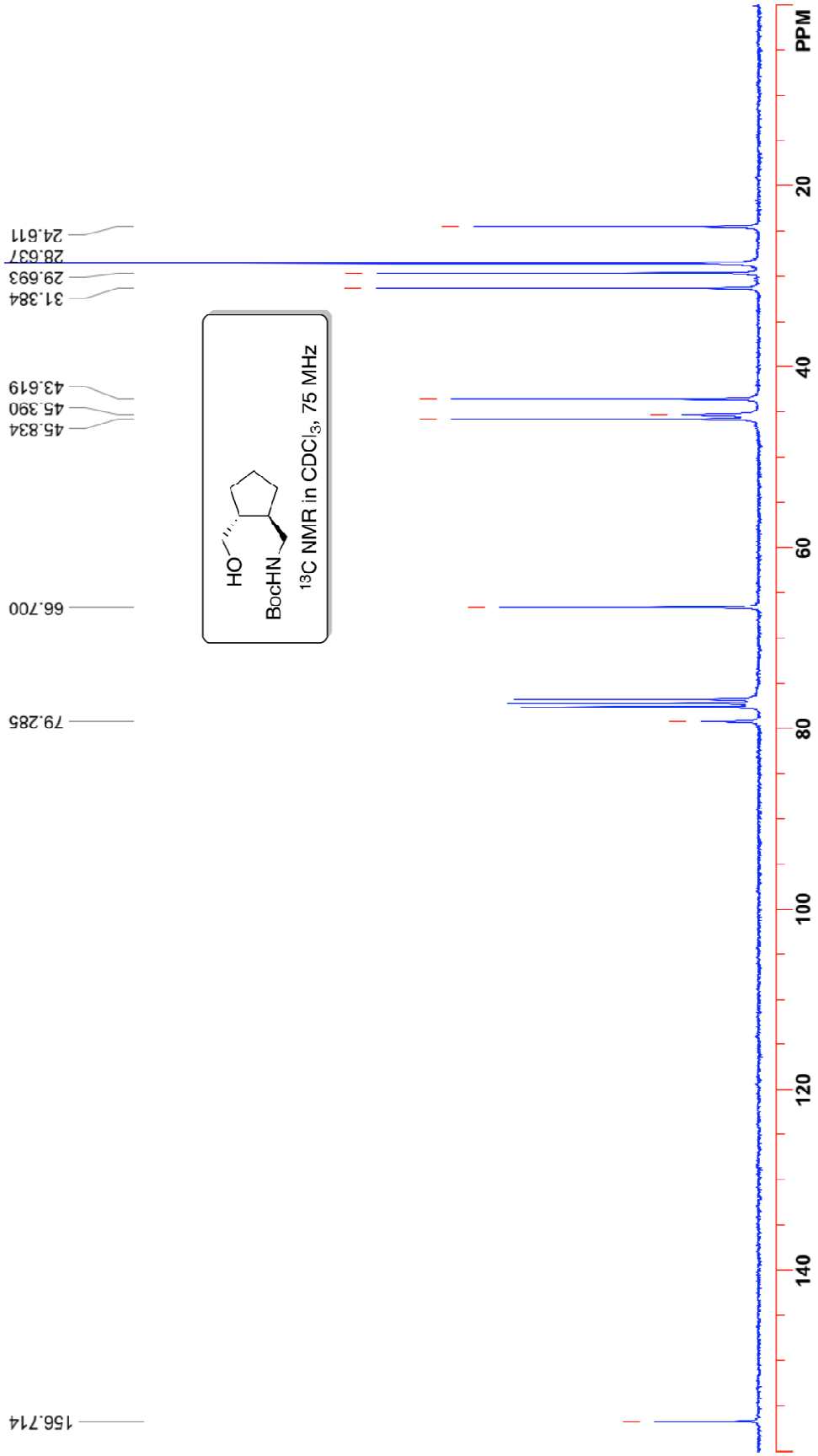


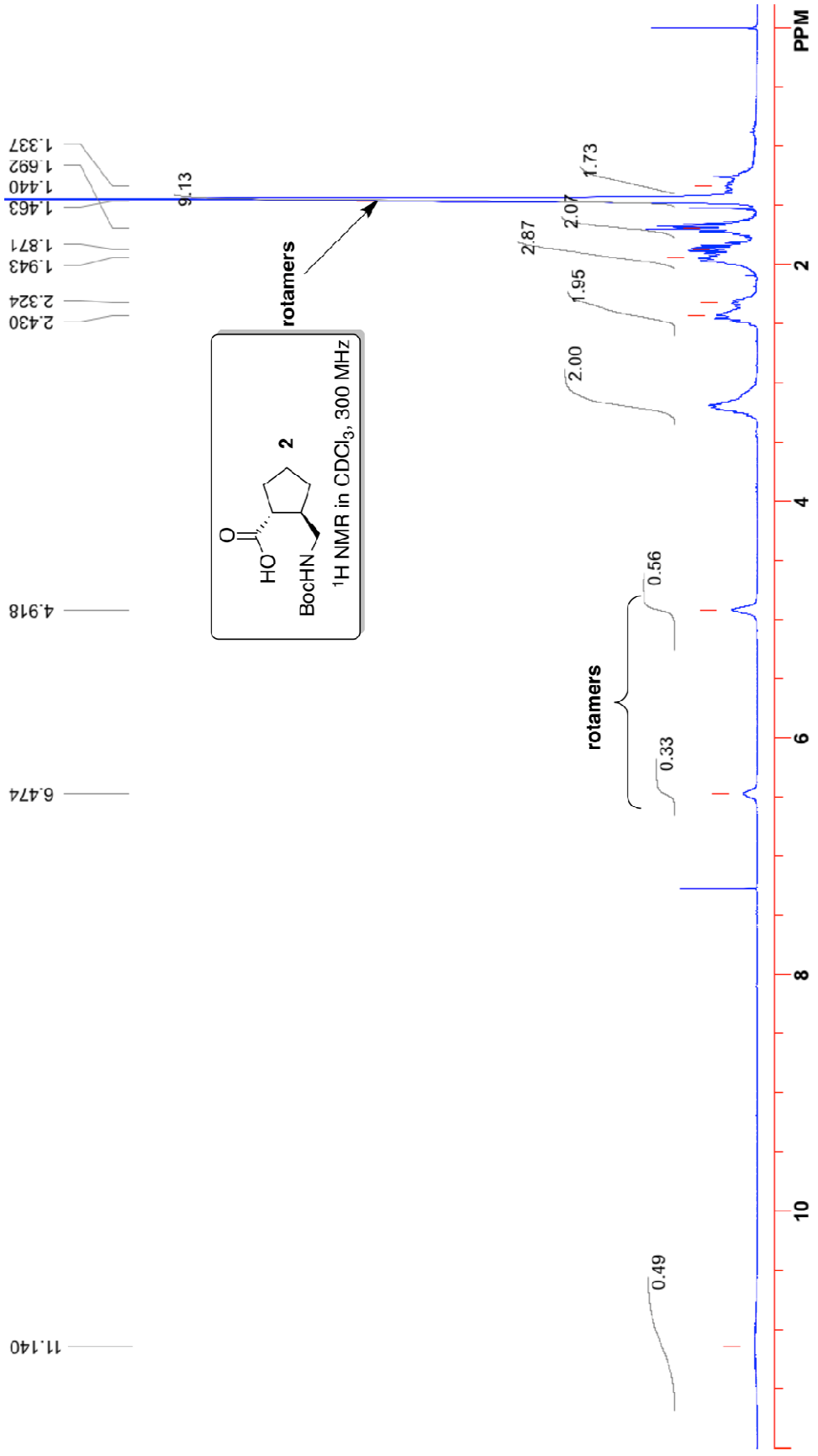
VII. 1D NMR Spectra for All New Compounds

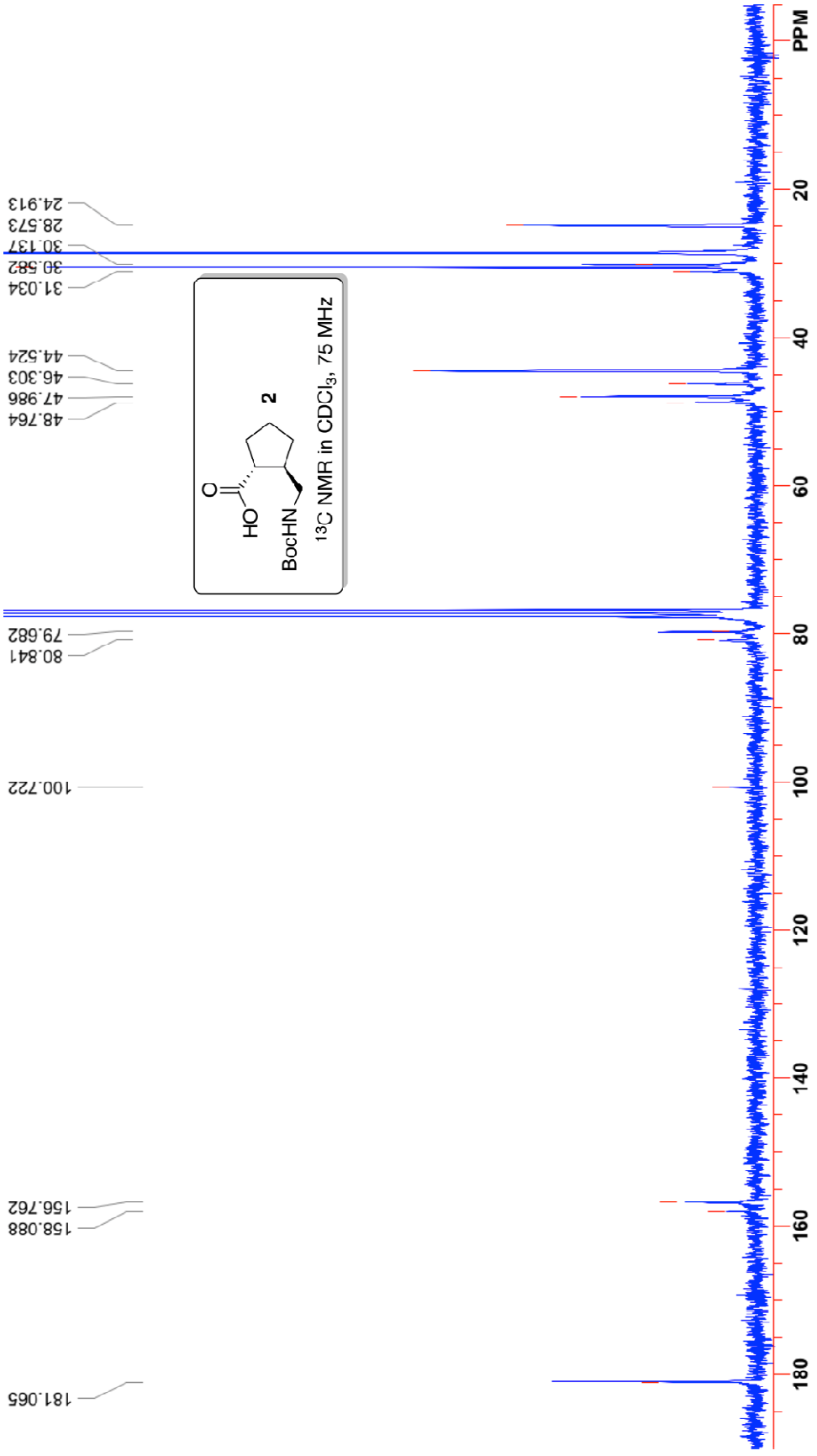

4.622
4.602
4.582
4.562
4.346
4.316
4.305
4.276
3.693
3.675
3.659
3.641
3.586
3.563
3.552
3.529
2.510
2.486
2.461
2.437
1.978
1.956
1.932
1.913
1.908
1.878
1.861
1.851
1.828
1.806
1.779
1.709
1.684
1.661
1.638
1.617
1.486
1.472
1.430
1.405
1.448
1.384
1.384
HO
O2N
1
1H NMR in CDCl3, 300 MHz
2.97
2.34
2.18
2.07
1.00
1.05
0.91
PPM

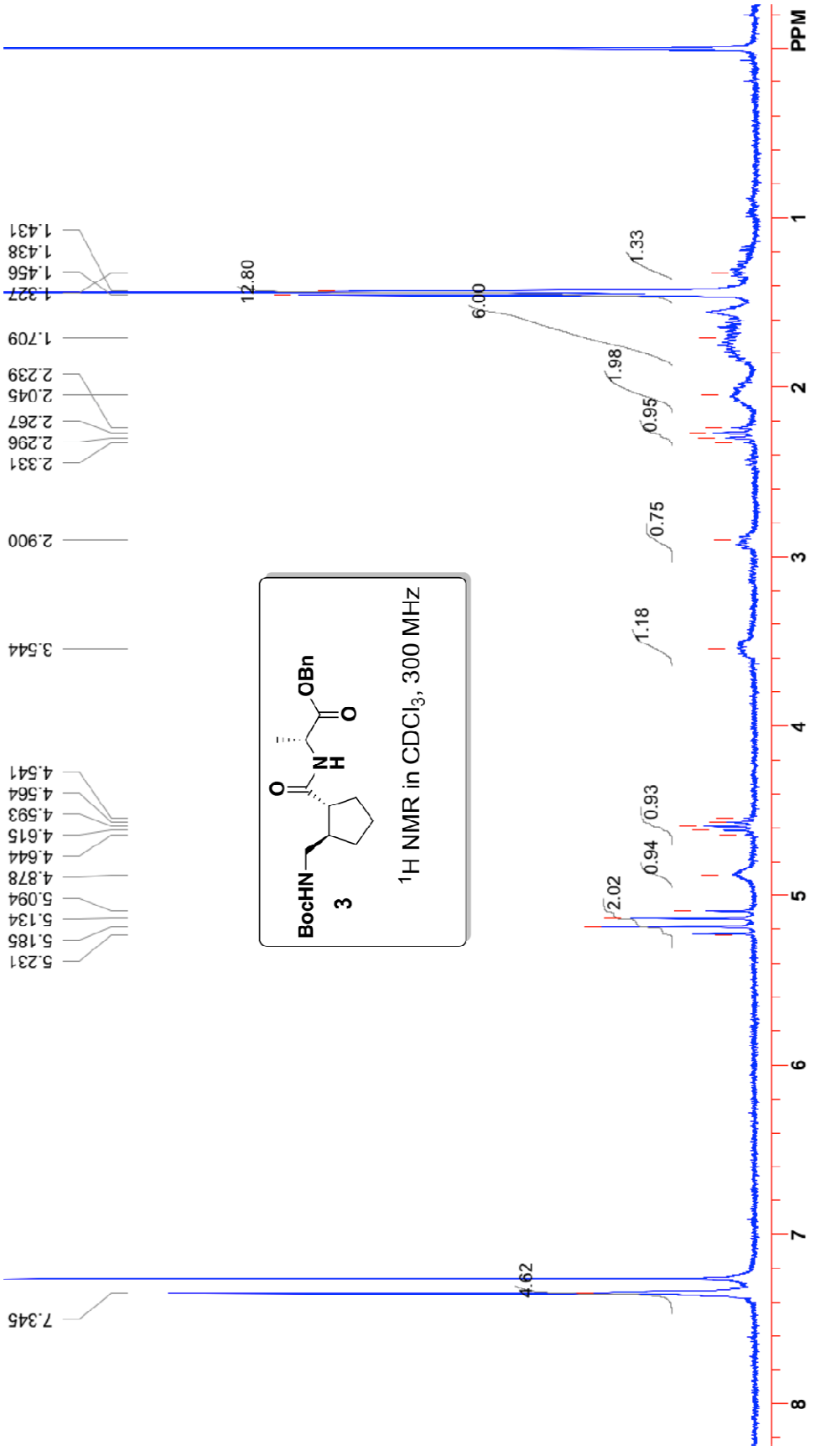

PPM
20
40
60
80
24.312
29.099
31.084
41.827
45.416
66.202
80.343
HO
O2N
1
13C NMR in CDCl3, 75 Hz

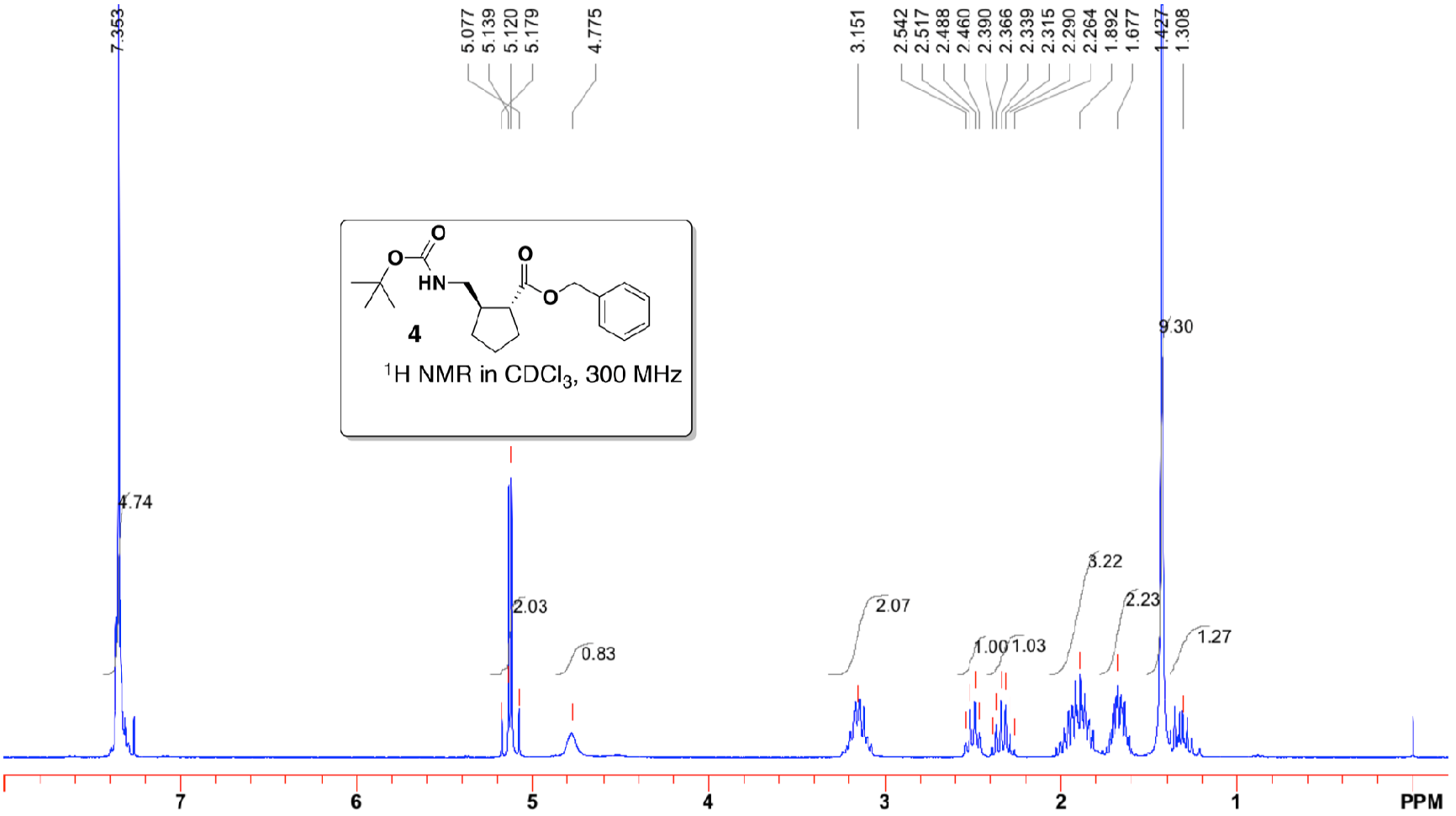

HO
BocHN
^{1}H NMR in $CDCl_3$, 300 MHz
PPM
1.299
1.439
1.592
1.802
2.402
3.113
3.446
3.470
3.480
3.502
3.567
3.623
3.638
3.657
3.674
5.166
3.98
2.27
1.95
0.72
1.92
2.00
0.95

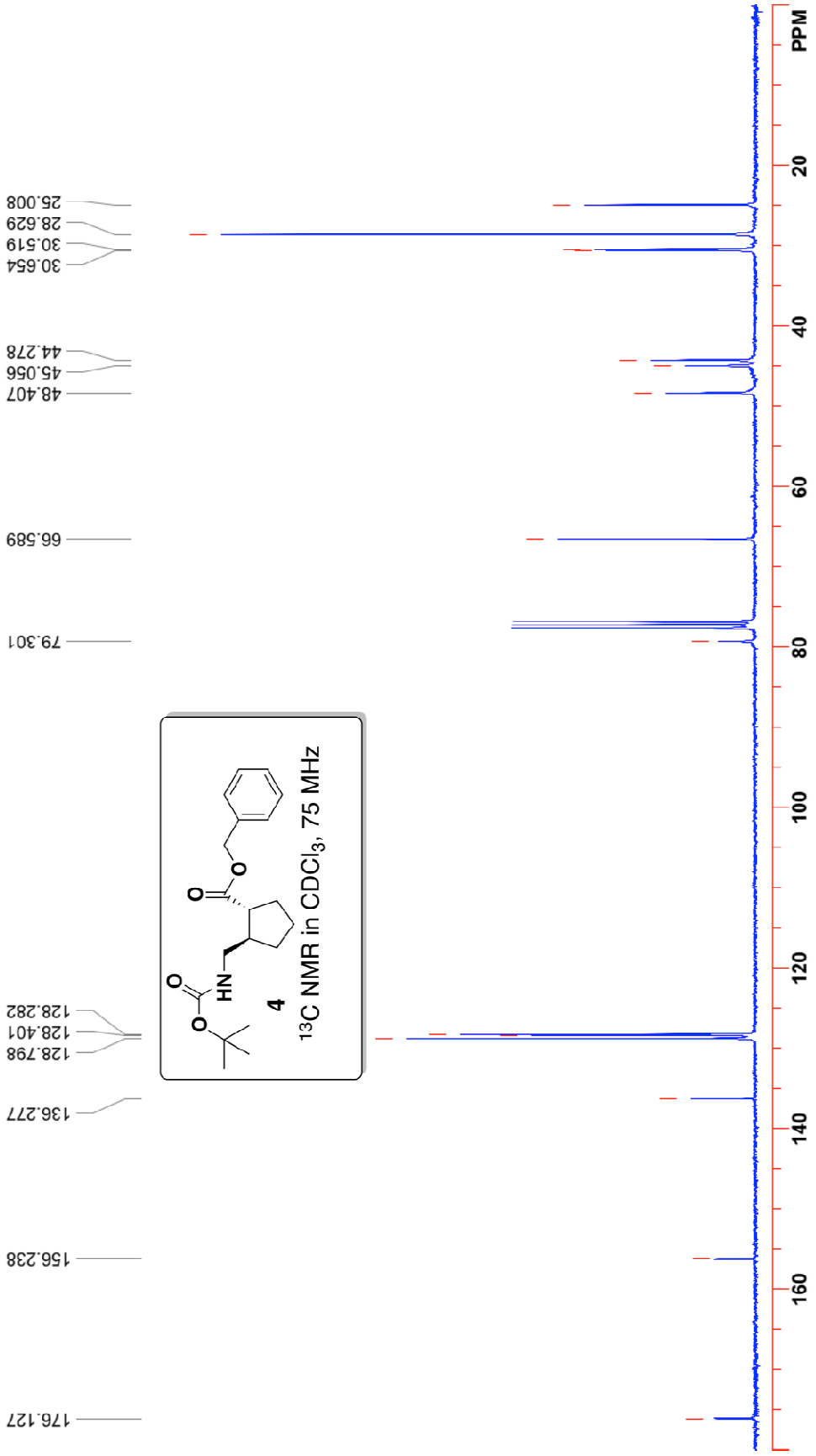

24.611
28.637
29.693
31.384
43.619
45.390
45.834
66.700
79.285
156.714
HO
BocHN
^{13}C NMR in $CDCl_3$, 75 MHz
PPM
20
40
60
80
100
120
140

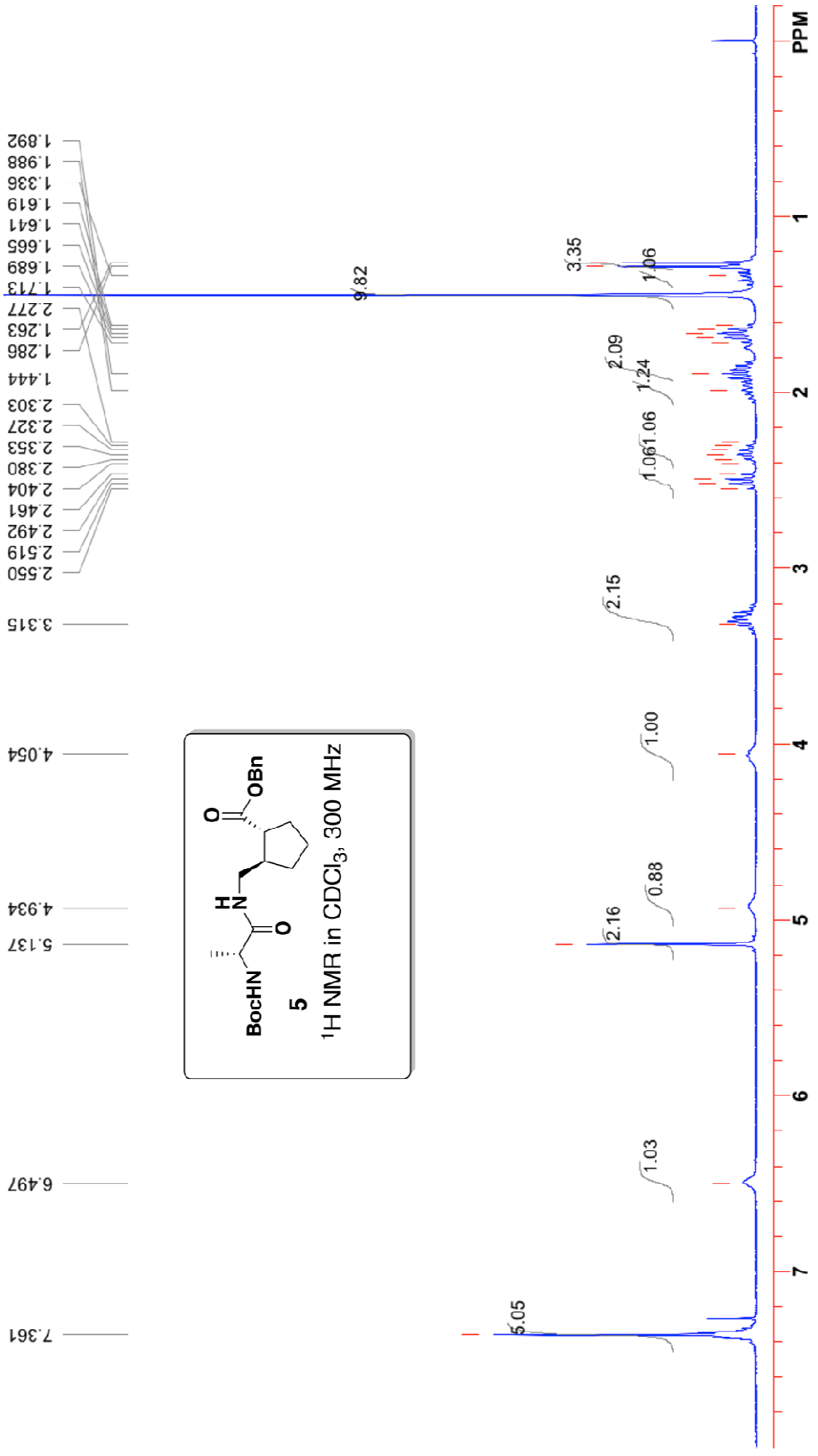

PPM
2
4
6
8
10
rotamers
rotamers
0.49
0.33
0.56
2.00
1.95
2.87
2.07
1.73
9.13
4.918
6.474
11.140
1.337
1.692
1.440
1.463
1.871
1.943
2.324
2.430
^{1}H NMR in CDCl$_3$, 300 MHz
BocHN
HO
O
2

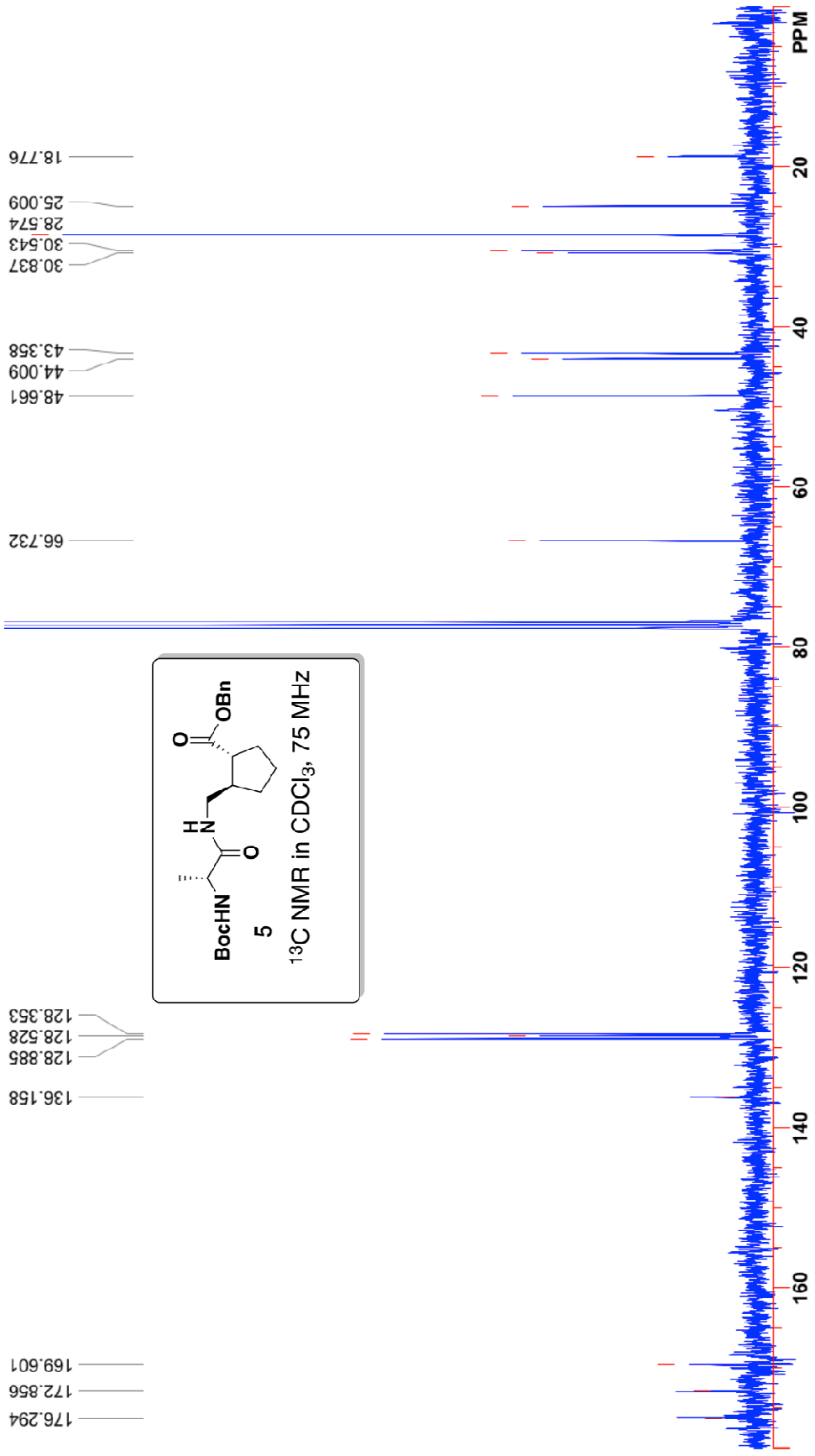

24.913
28.573
30.137
30.582
31.034
44.524
46.303
47.986
48.764
79.682
80.841
100.722
156.762
158.088
181.065
PPM
20
40
60
80
100
120
140
160
180
2
HO
O
BocHN
^{13}C NMR in $CDCl_3$, 75 MHz

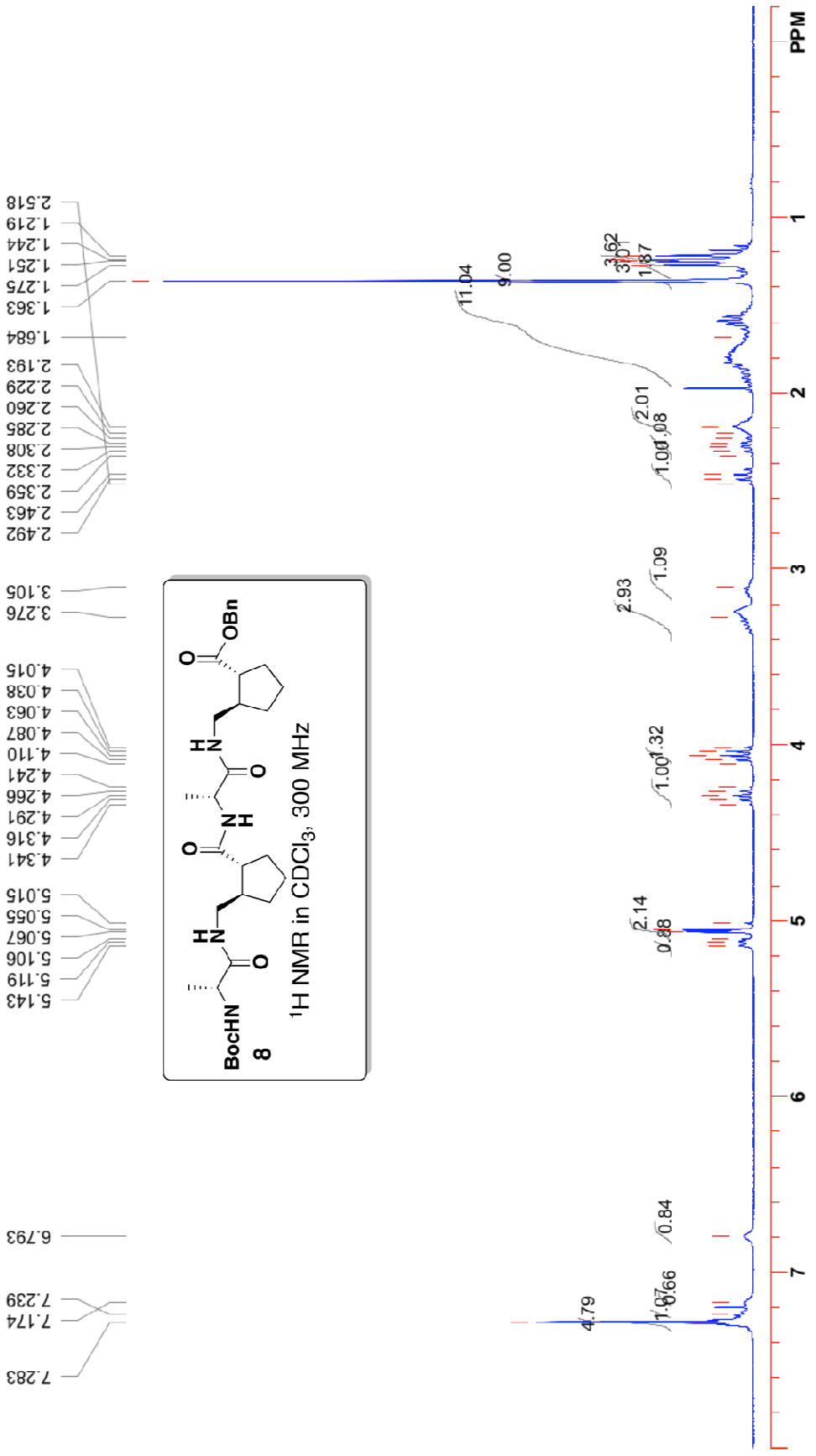

PPM
1
2
3
4
5
6
7
8
1.33
6.00
12.80
1.98
0.95
0.75
1.18
0.93
0.94
2.02
4.62
1.431
1.438
1.456
1.327
1.709
2.239
2.045
2.267
2.296
2.331
2.900
3.544
4.541
4.564
4.593
4.615
4.644
4.878
5.094
5.134
5.185
5.231
7.345
BocHN
O
N
H
OBn
O
3
^{1}H NMR in $CDCl_3$, 300 MHz

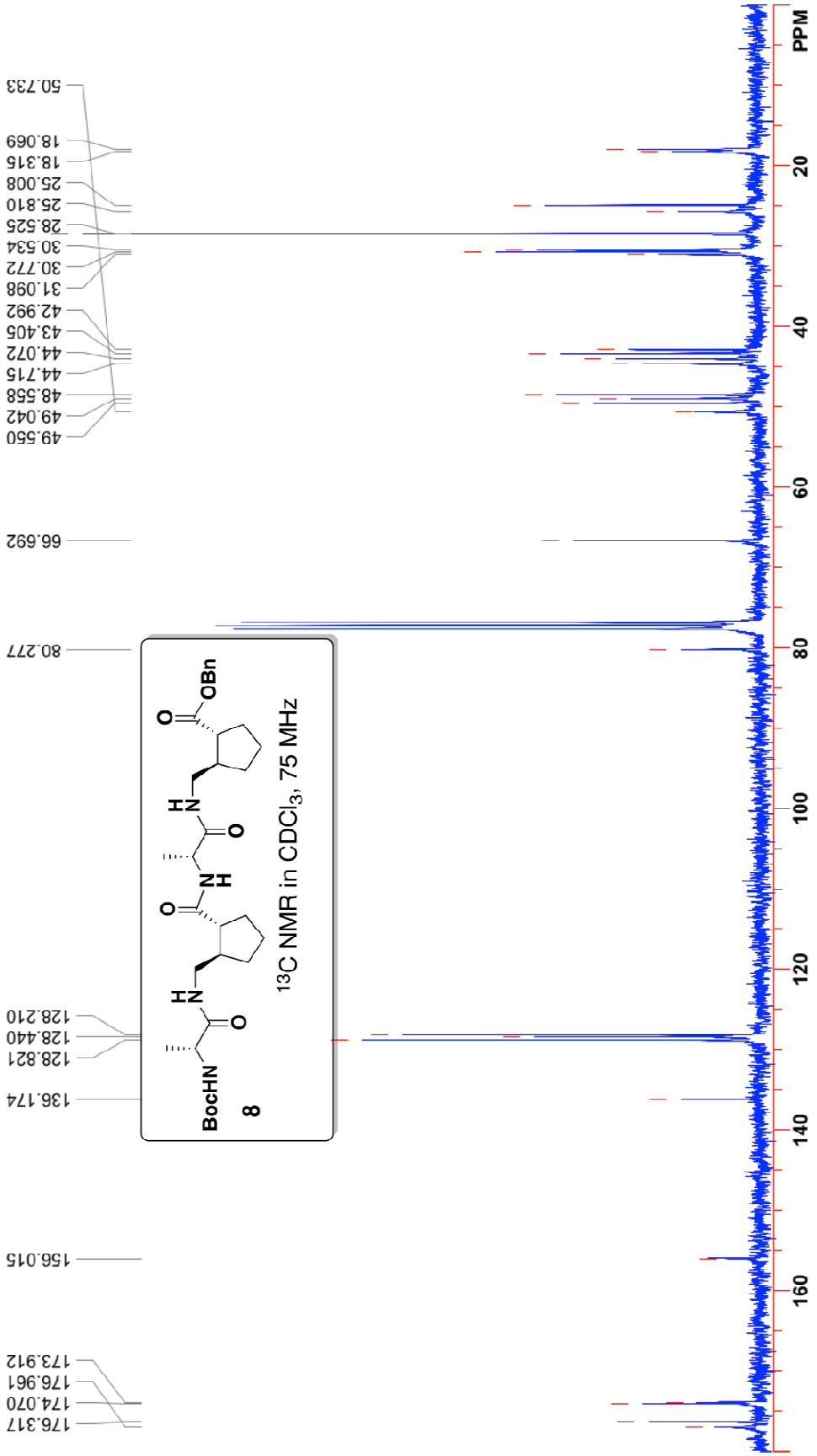

7.353
5.077
5.139
5.120
5.179
4.775
3.151
2.542
2.517
2.488
2.460
2.390
2.366
2.339
2.315
2.290
2.264
1.892
1.677
1.427
1.308
9.30
4.74
2.03
0.83
2.07
1.00
1.03
3.22
2.23
1.27
HN
4
^{1}H NMR in $CDCl_3$, 300 MHz
7
6
5
4
3
2
1
PPM

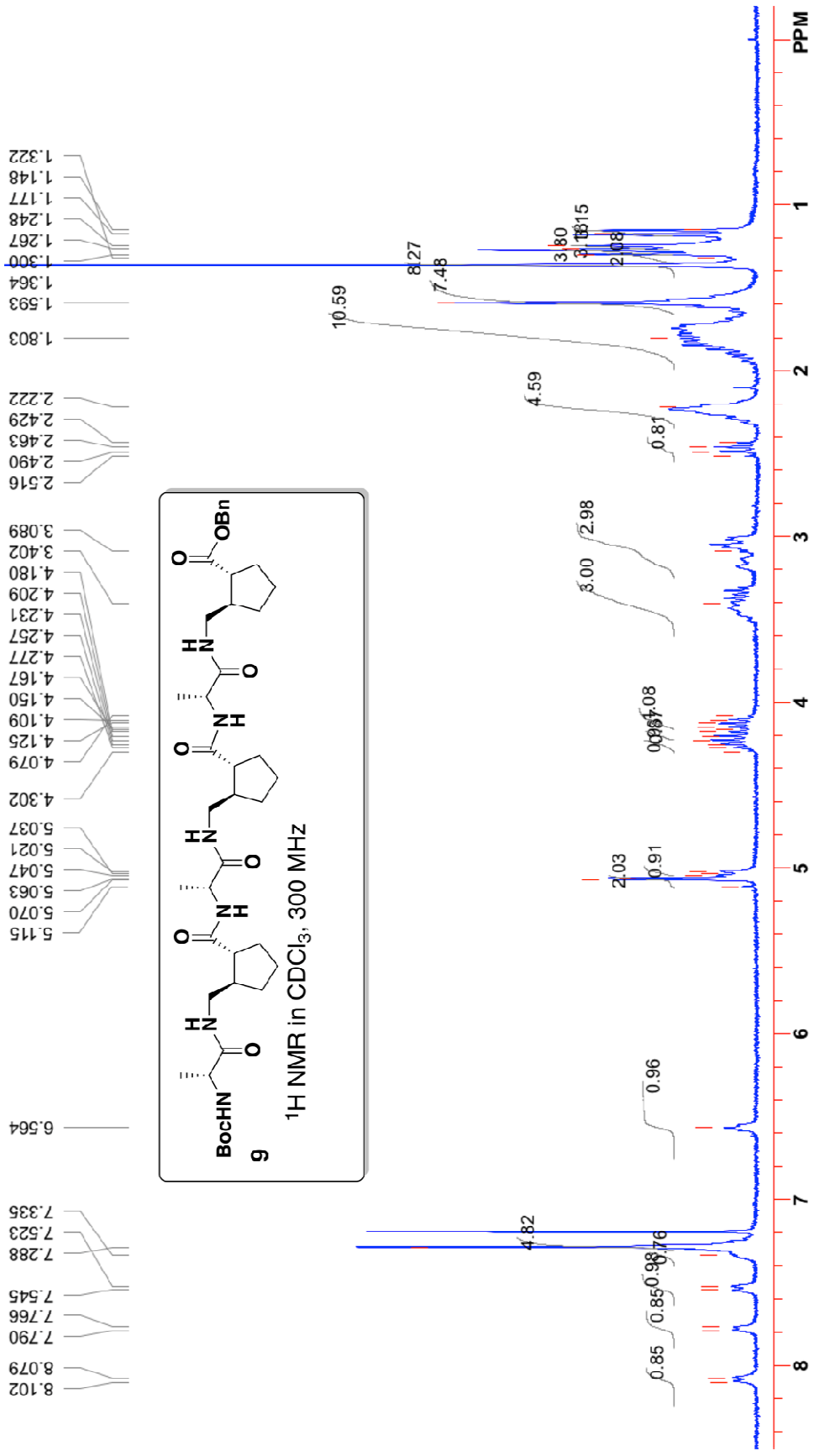

PPM
20
40
60
80
100
120
140
160
25.008
28.629
30.519
30.654
44.278
45.056
48.407
66.589
79.301
128.282
128.401
128.798
136.277
156.238
176.127
4
^{13}C NMR in $CDCl_3$, 75 MHz

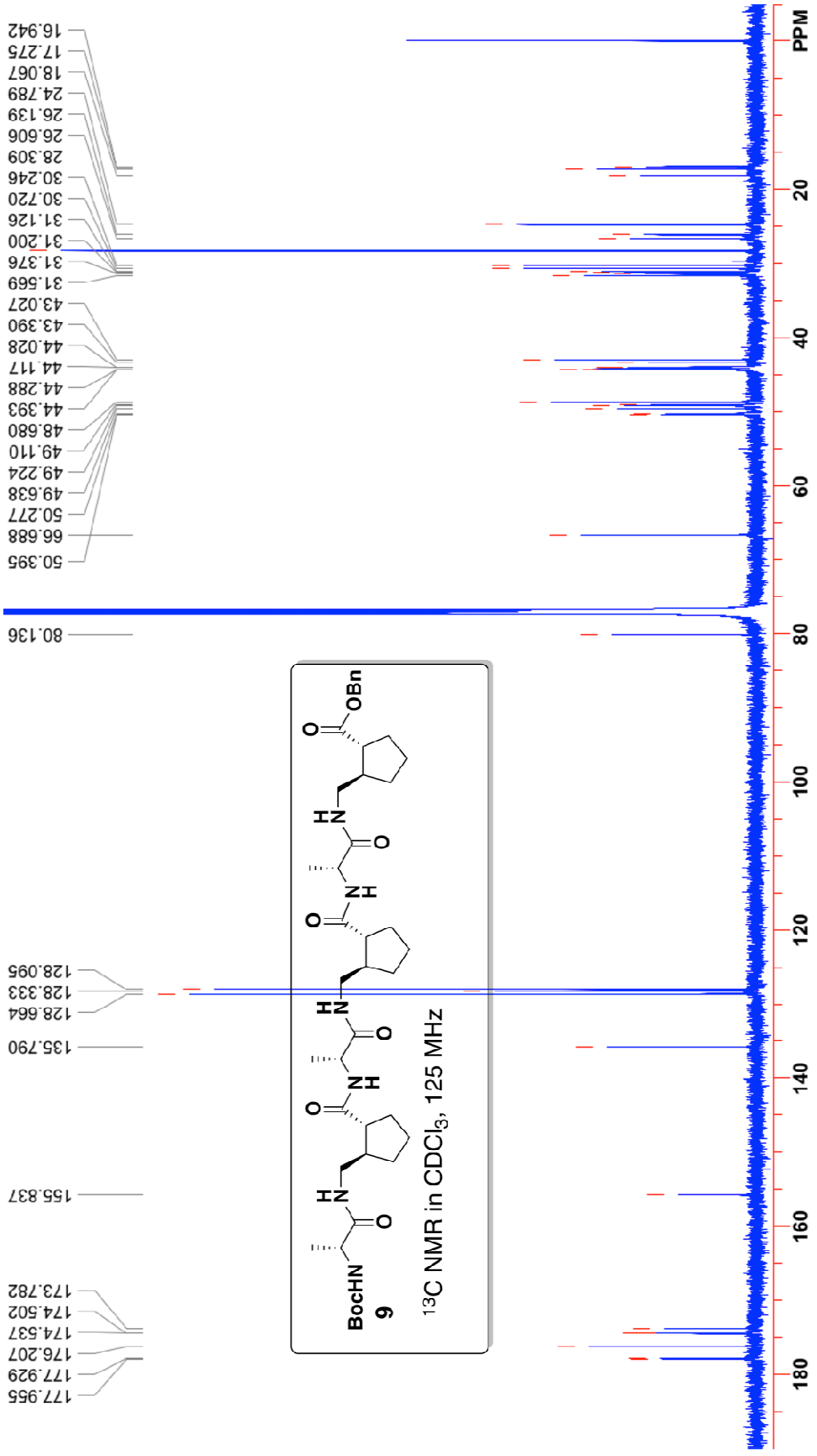

BocHN
O
H
N
O
OBn
5
^{1}H NMR in $CDCl_3$, 300 MHz
PPM
1
2
3
4
5
6
7
9.82
5.05
3.35
2.16
2.15
2.09
1.24
1.06
1.06
1.06
1.03
1.00
0.88
7.361
6.497
5.137
4.934
4.054
3.315
2.550
2.519
2.492
2.461
2.404
2.380
2.353
2.327
2.303
1.444
1.286
1.263
2.277
1.713
1.689
1.665
1.641
1.619
1.336
1.988
1.892

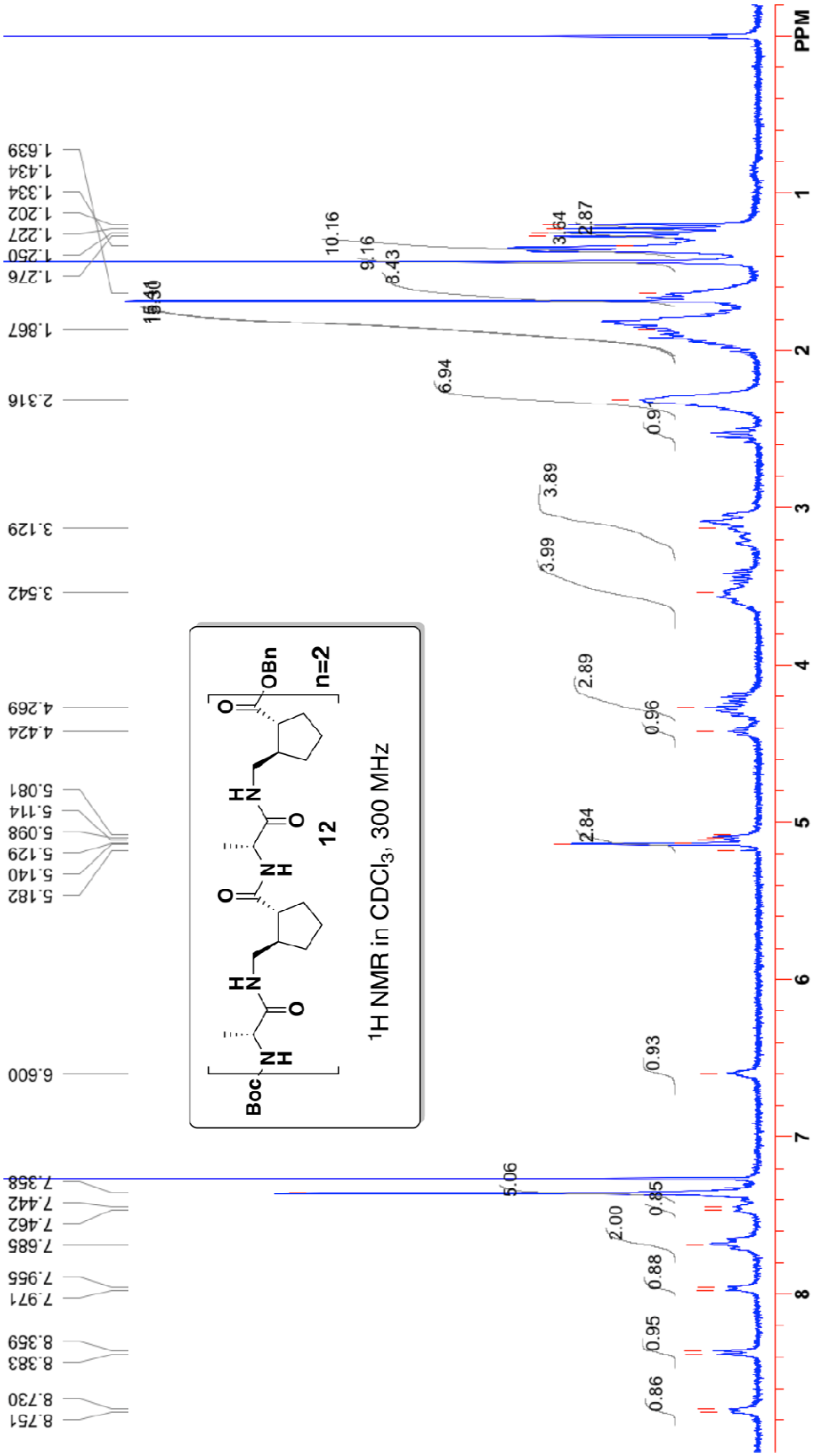

18.776
25.009
28.574
30.543
30.837
43.358
44.009
48.661
66.732
128.353
128.528
128.885
136.158
169.601
172.856
176.294
PPM
20
40
60
80
100
120
140
160
BocHN
O
H
N
O
OBn
5
^{13}C NMR in $CDCl_3$, 75 MHz

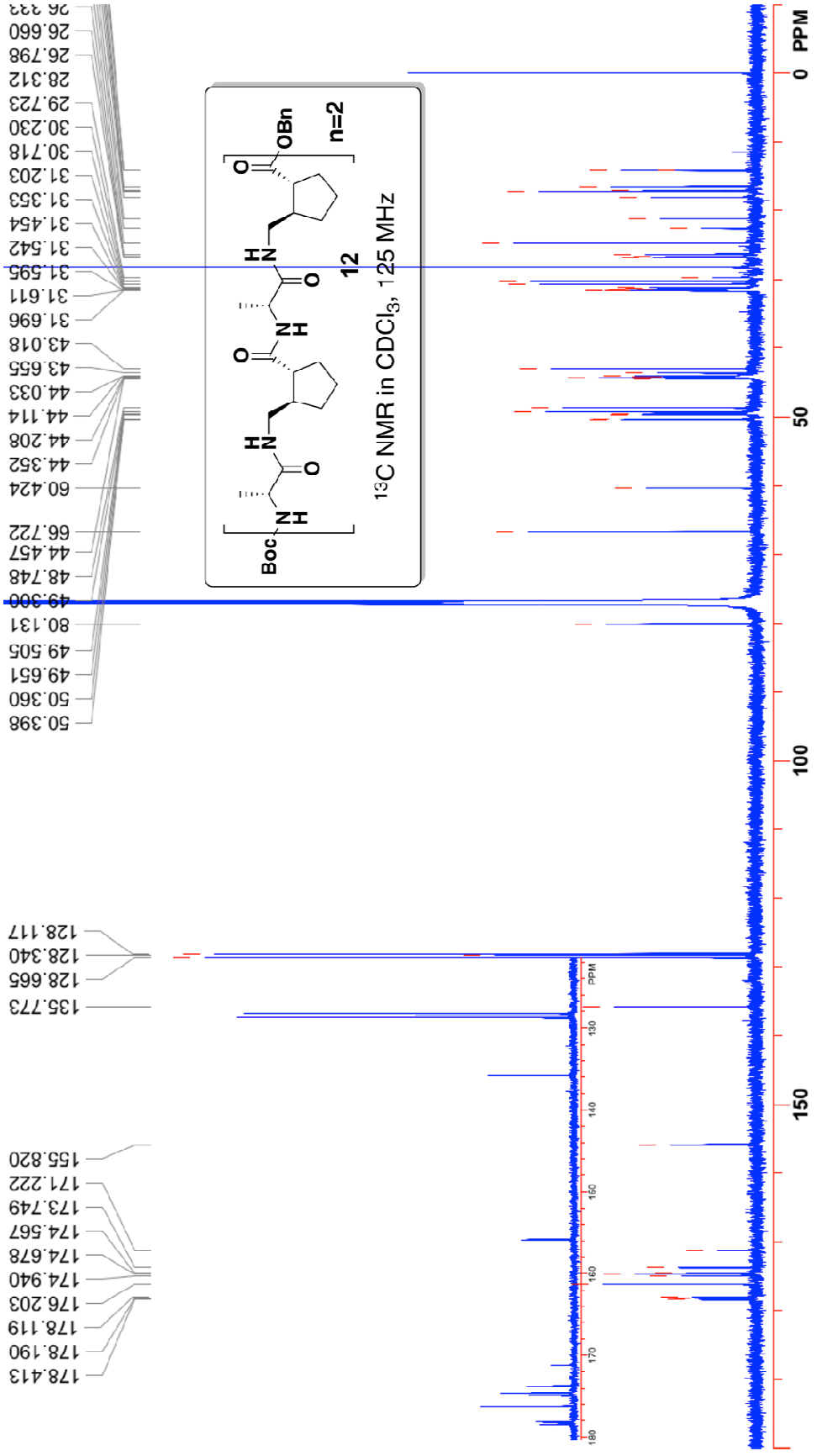

PPM
1
2
3
4
5
6
7
11.04
9.00
3.62
3.00
1.87
2.01
1.08
1.00
2.93
1.09
1.00
1.32
2.14
0.88
4.79
1.07
0.66
0.84
6.793
7.239
7.174
7.283
5.143
5.119
5.106
5.067
5.055
5.015
4.341
4.316
4.291
4.266
4.241
4.110
4.087
4.063
4.038
4.015
3.276
3.105
2.492
2.463
2.359
2.332
2.308
2.285
2.260
2.229
2.193
1.684
1.363
1.275
1.251
1.244
1.219
2.518
BocHN
8
OBn
^{1}H NMR in $CDCl_3$, 300 MHz

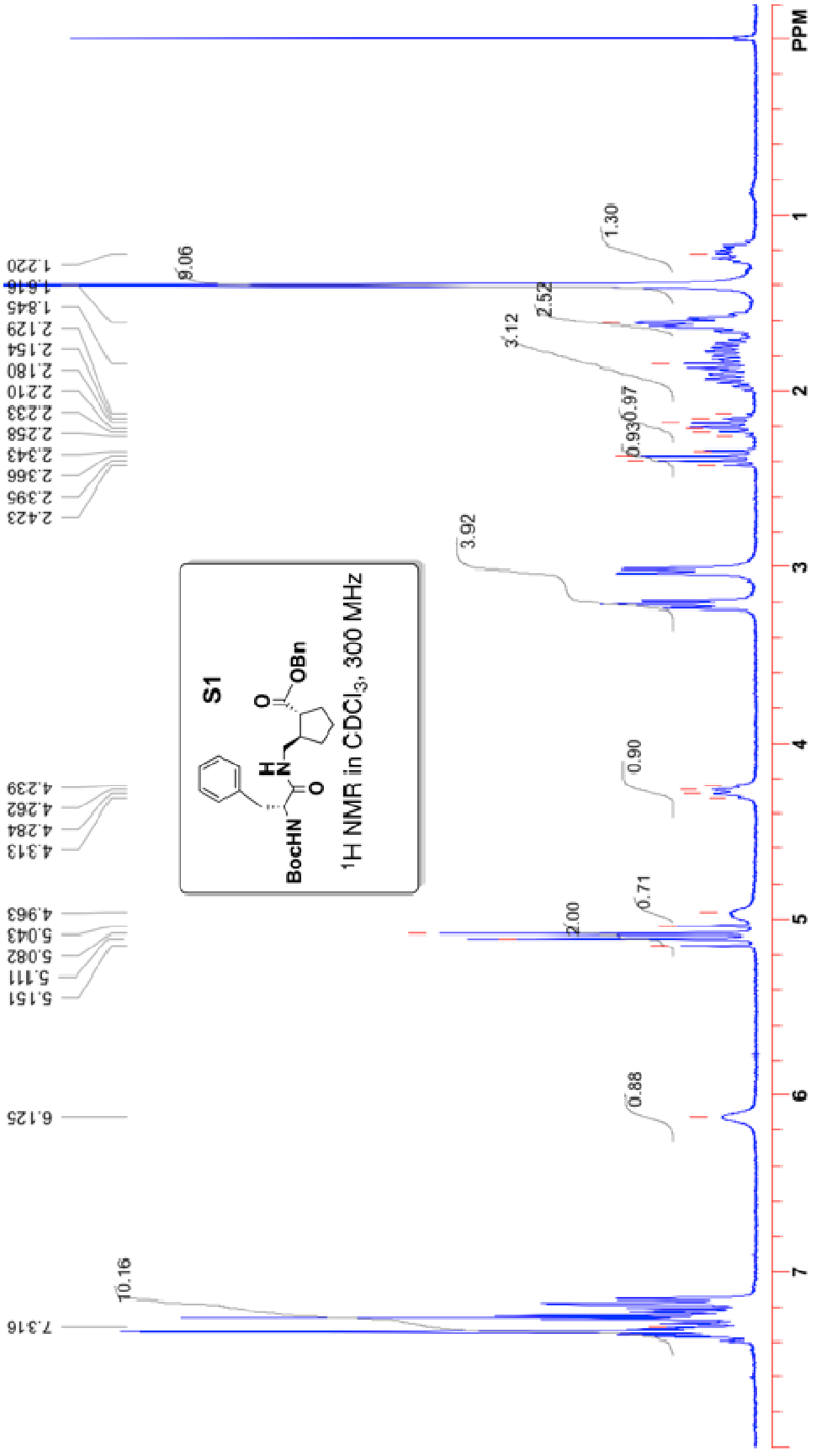

50.733
18.069
18.315
25.008
25.810
28.525
30.534
30.772
31.098
42.992
43.405
44.072
44.715
48.558
49.042
49.550
66.692
80.277
128.210
128.440
128.821
136.174
156.015
173.912
176.961
174.070
176.317
PPM
20
40
60
80
100
120
140
160
^{13}C NMR in $CDCl_3$, 75 MHz
BocHN
OBn
8

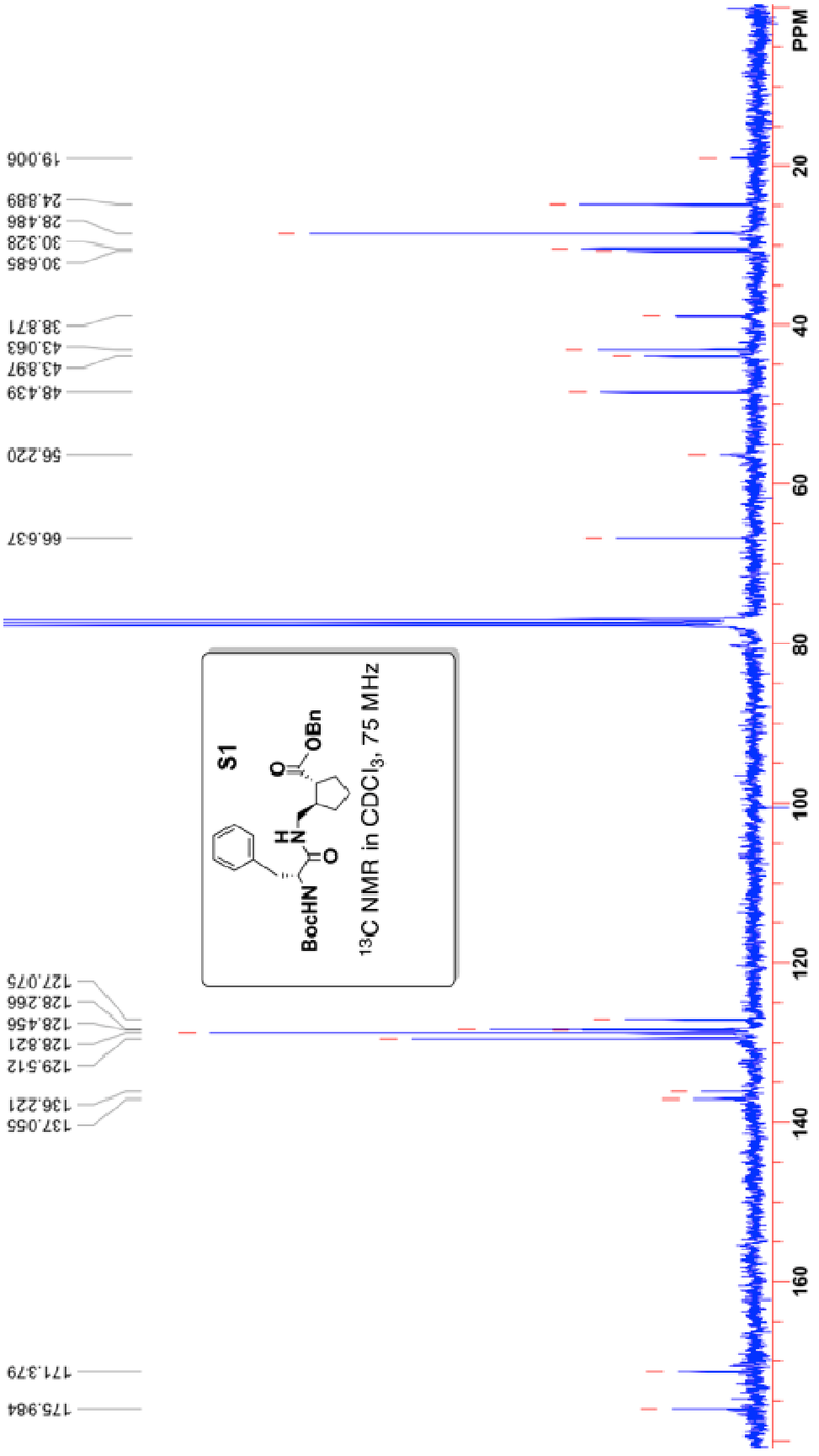

BocHN
OBn
6
g
^{1}H NMR in $CDCl_3$, 300 MHz
PPM

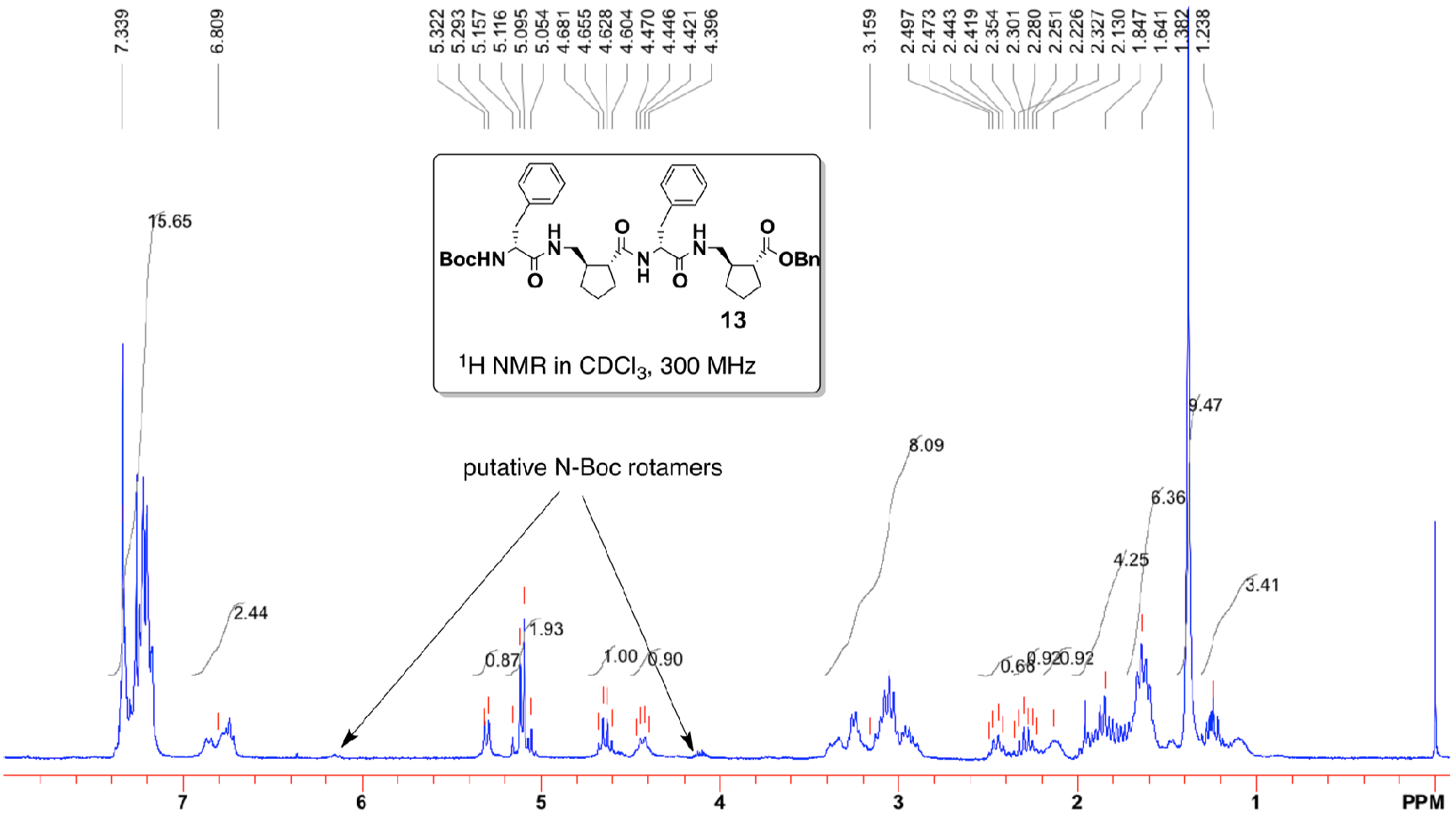

16.942
17.275
18.067
24.789
26.139
26.606
28.309
30.246
30.720
31.126
31.200
31.376
31.569
43.027
43.390
44.028
44.117
44.288
44.393
48.680
49.110
49.224
49.638
50.277
66.688
50.395
80.136
128.095
128.333
128.664
135.790
155.837
173.782
174.502
174.537
176.207
177.929
177.955
PPM
20
40
60
80
100
120
140
160
180
OBn
BocHN
9
^{13}C NMR in $CDCl_3$, 125 MHz

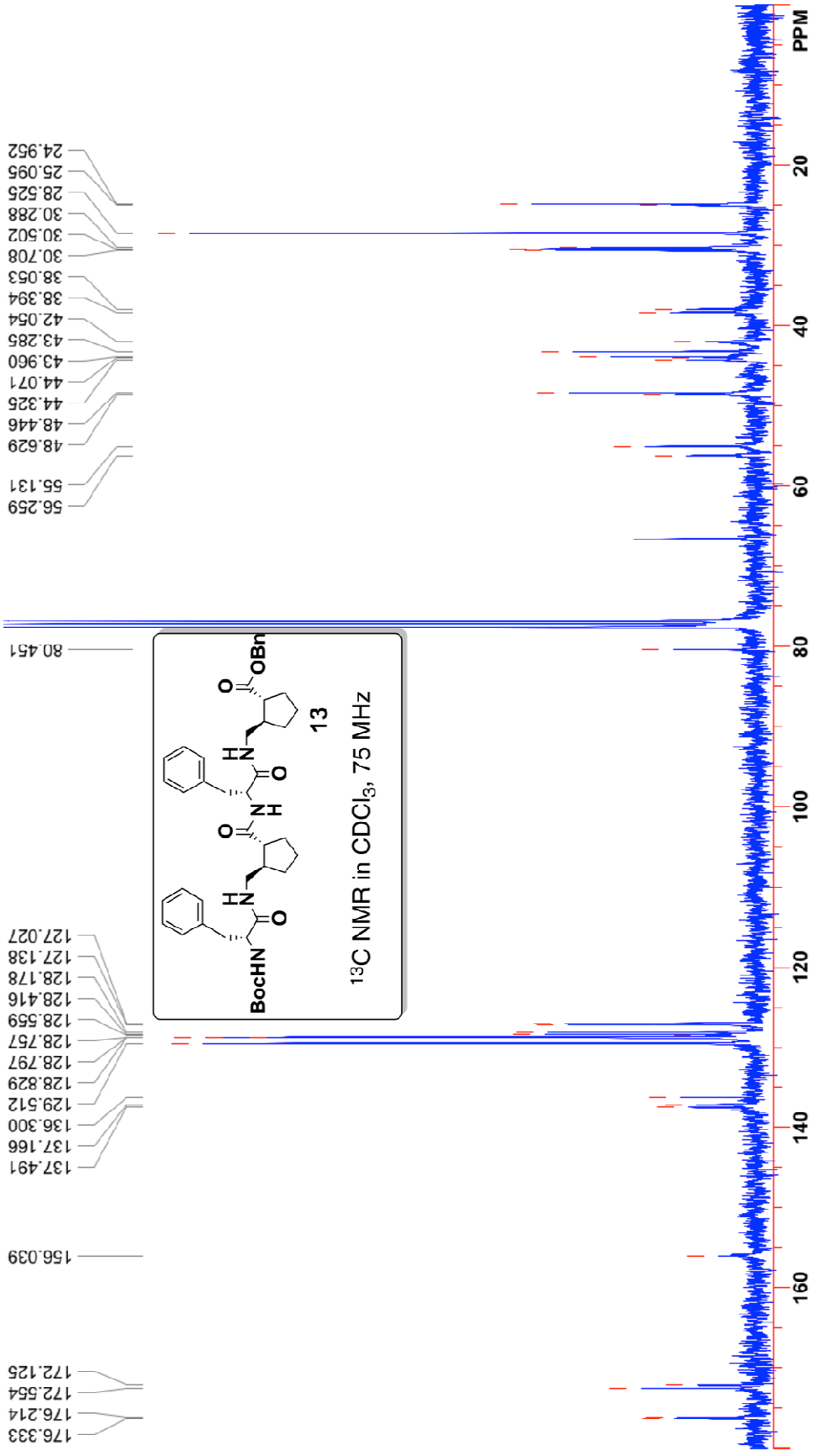

PPM
1 2 3 4 5 6 7 8
1.639
1.434
1.334
1.202
1.227
1.250
1.276
1.867
2.316
3.129
3.542
4.269
4.424
5.081
5.114
5.098
5.129
5.140
5.182
6.600
7.358
7.442
7.462
7.685
7.955
7.971
8.359
8.383
8.730
8.751
10.16
9.16
8.43
7.27
6.94
3.89
3.99
3.64
2.87
2.89
2.84
5.06
2.00
0.85
0.88
0.95
0.86
0.93
0.96
0.99
Boc
OBn
n=2
12
^{1}H NMR in $CDCl_3$, 300 MHz

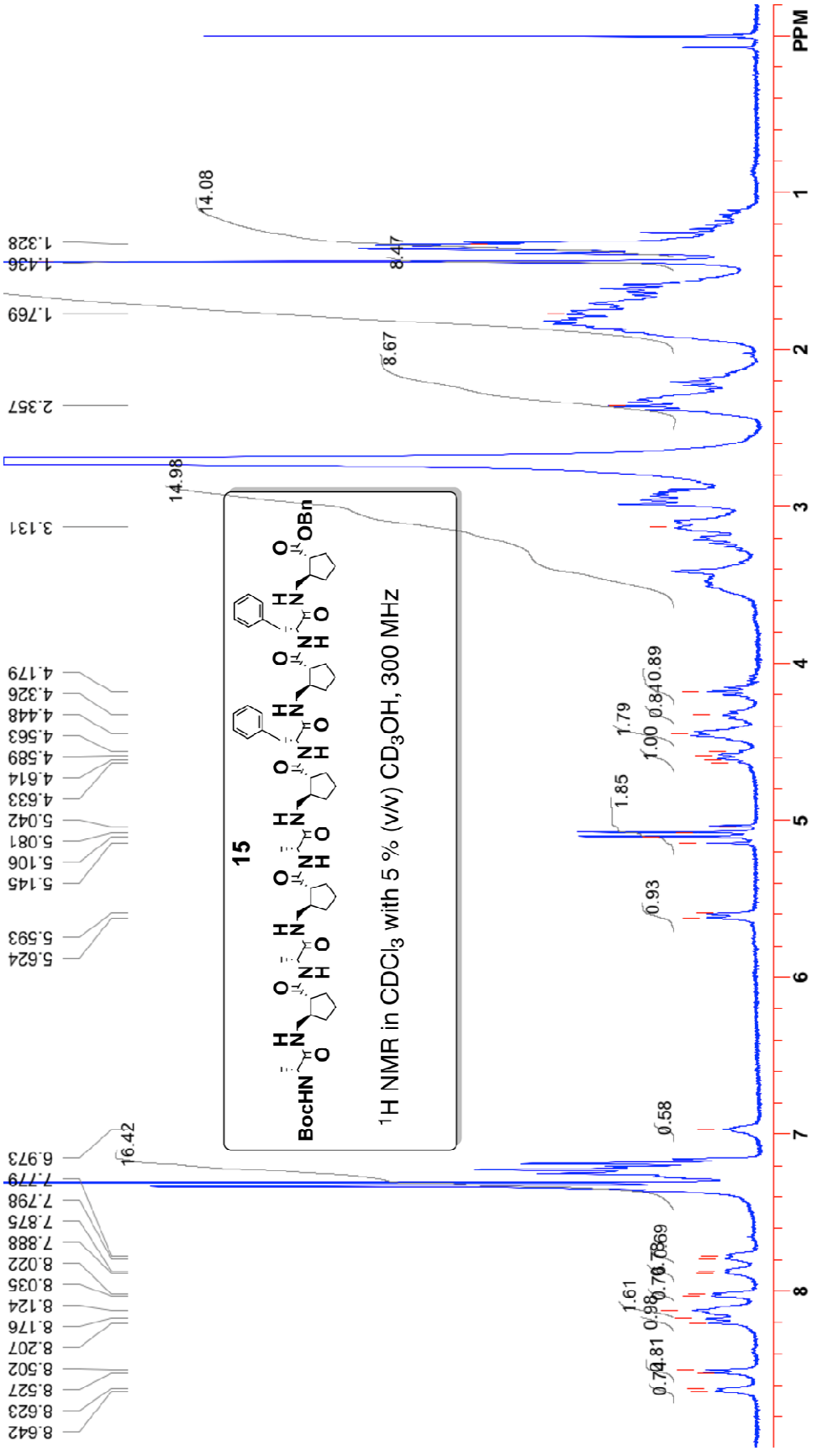

26.223
26.660
26.798
28.312
29.723
30.230
30.718
31.203
31.353
31.454
31.542
31.595
31.611
31.696
43.018
43.655
44.033
44.114
44.208
44.352
60.424
66.722
44.457
48.748
49.300
80.131
49.505
49.651
50.360
50.398
128.117
128.340
128.665
135.773
155.820
171.222
173.749
174.567
174.678
174.940
176.203
178.119
178.190
178.413
PPM
0
50
100
150
n=2
OBn
12
Boc
^{13}C NMR in $CDCl_3$, 125 MHz

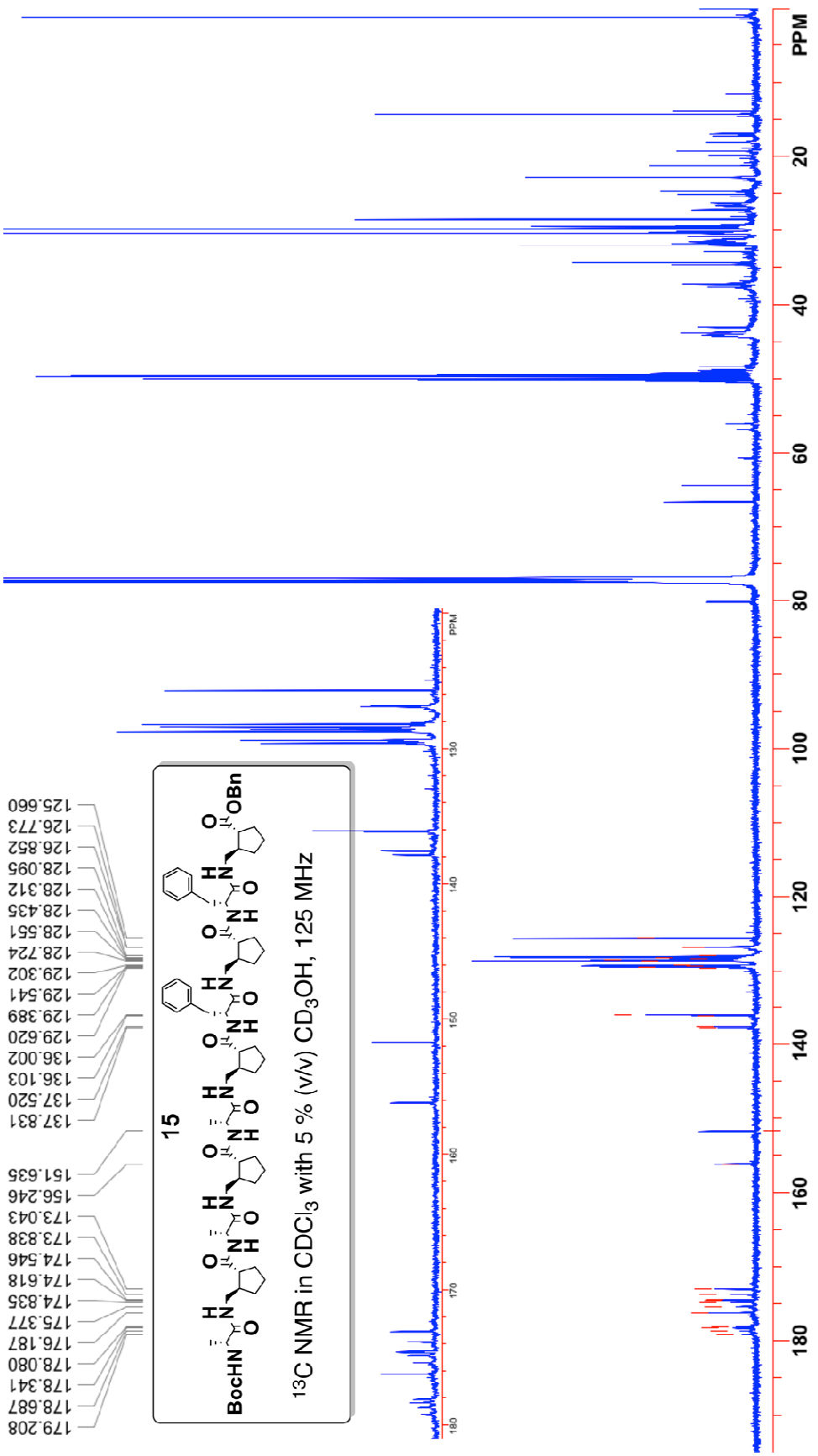

S1
OBn
O
H
N
O
BocHN
^{1}H NMR in $CDCl_3$, 300 MHz
PPM
1
2
3
4
5
6
7
1.220
1.616
1.845
2.129
2.154
2.180
2.210
2.233
2.258
2.343
2.366
2.395
2.423
4.239
4.262
4.284
4.313
4.963
5.043
5.082
5.111
5.151
6.125
7.316
10.16
9.06
1.30
2.52
3.12
0.97
0.93
3.92
0.90
0.71
2.00
0.88


S1
BocHN
OBn
^{13}C NMR in $CDCl_3$, 75 MHz
PPM
20
40
60
80
100
120
140
160
19.006
24.889
28.486
30.328
30.685
38.871
43.063
43.897
48.439
56.220
66.637
127.075
128.266
128.456
128.821
129.512
136.221
137.055
171.379
175.984


7.339
6.809
5.322
5.293
5.157
5.116
5.095
5.054
4.681
4.655
4.628
4.604
4.470
4.446
4.421
4.396
3.159
2.497
2.473
2.443
2.419
2.354
2.301
2.280
2.251
2.226
2.327
2.130
1.847
1.641
1.382
1.238
BocHN
OBn
13
1H NMR in CDCl3, 300 MHz
putative N-Boc rotamers
15.65
2.44
1.93
0.87
1.00
0.90
8.09
0.66
0.92
0.92
4.25
6.36
9.47
3.41
7
6
5
4
3
2
1
PPM


PPM
20
40
60
80
100
120
140
160
24.952
25.095
28.525
30.288
30.502
30.708
38.053
38.394
42.054
43.285
43.960
44.071
44.325
48.446
48.629
55.131
56.259
80.451
127.027
127.138
127.178
128.416
128.559
128.757
128.797
128.829
129.512
136.300
137.166
137.491
156.039
172.125
172.554
176.214
176.333
BocHN
OBn
13
^{13}C NMR in $CDCl_3$, 75 MHz


15
BocHN
OBn
^{1}H NMR in $CDCl_3$ with 5 % (v/v) CD_3OH, 300 MHz
PPM
1
2
3
4
5
6
7
8
14.08
8.47
8.67
14.98
16.42
1.328
1.436
1.769
2.357
3.131
4.179
4.326
4.448
4.563
4.589
4.614
4.633
5.042
5.081
5.106
5.145
5.593
5.624
6.973
7.779
7.798
7.875
7.888
8.022
8.035
8.124
8.176
8.207
8.502
8.527
8.623
8.642
0.58
0.93
1.85
1.79
1.00
0.84
0.89
1.61
0.98
0.81
0.76
0.78
0.69


15
BocHN
OBn
^{13}C NMR in $CDCl_3$ with 5 % (v/v) CD_3OH, 125 MHz
179.208
178.687
178.341
178.080
176.187
175.377
174.835
174.618
174.546
173.838
173.043
156.246
151.635
137.831
137.520
136.103
136.002
129.620
129.389
129.541
129.302
128.724
128.551
128.435
128.312
128.095
126.852
126.773
125.660
PPM

VIII. Crystallographic Report for Dipeptide 3

Crystallographic Experimental Section for Dipeptide **3** (gellman142)

Prepared by Ilia A. Guzei

Data Collection

A colorless crystal with dimensions 0.18 x 0.20 x 1.64 mm^3 was selected under oil under ambient conditions and attached to the tip of a MiTeGen MicroMount©. The crystal was mounted in a stream of cold nitrogen at 100(1) K and centered in the X-ray beam by using a video camera.

The crystal evaluation and data collection were performed on a Bruker SMART APEXII diffractometer with Cu K_α (λ = 1.54178 Å) radiation and the diffractometer to crystal distance of 4.03 cm.

The initial cell constants were obtained from three series of ω scans at different starting angles. Each series consisted of 41 frames collected at intervals of 0.6º in a 25º range about ω with the exposure time of 10 seconds per frame. The reflections were successfully indexed by an automated indexing routine built in the APEXII program. The final cell constants were calculated from a set of 9966 strong reflections from the actual data collection.

The data were collected by using the full sphere data collection routine to survey the reciprocal space to the extent of a full sphere to a resolution of 0.82 Å. A total of 11924 data were harvested by collecting 31 sets of frames with 0.85º scans in ω with an exposure time 5-10 sec per frame. These highly redundant datasets were corrected for Lorentz and polarization effects. The absorption correction was based on fitting a function to the empirical transmission surface as sampled by multiple equivalent measurements. [1]

Structure Solution and Refinement

The systematic absences in the diffraction data were consistent for the space groups $P\bar{1}$ and $P1$. The *E*-statistics strongly suggested the non-centrosymmetric space group $P1$ that yielded chemically reasonable and computationally stable results of refinement [2-4].

A successful solution by the direct methods provided most non-hydrogen atoms from the *E*-map. The remaining non-hydrogen atoms were located in an alternating series of least-squares cycles and difference Fourier maps. All non-hydrogen atoms were refined with anisotropic displacement coefficients. All non-amido hydrogen atoms were included in the structure factor calculation at idealized positions and were allowed to ride on the neighboring atoms with relative isotropic displacement coefficients. The amido hydrogen atoms were located in the difference map and refined with restraints.

The three chiral centers in the molecule are in the R configuration.

The final least-squares refinement of 275 parameters against 3389 data resulted in residuals *R* (based on F^2 for $I \geq 2\sigma$) and *wR* (based on F^2 for all data) of 0.0307 and 0.0805, respectively. The final difference Fourier map was featureless.

The molecular diagram is drawn with 50% probability ellipsoids.

References

[1] Bruker-AXS. (2007) APEX2, SADABS, and SAINT Software Reference Manuals. Bruker-AXS, Madison, Wisconsin, USA.

[2] Sheldrick, G. M. (2008) SHELXL. *Acta Cryst.* **A64**, 112-122.

[3] Dolomanov, O.V.; Bourhis, L.J.; Gildea, R.J.; Howard, J.A.K.; Puschmann, H. "OLEX2: a complete structure solution, refinement and analysis program". *J. Appl. Cryst.* (2009) **42**, *339-341*.

[4] Guzei, I.A. (2006-2008). Internal laboratory computer programs "IG", "FCF_filter", "Modicifer".

Figure 1. A molecular drawing of Gellman142.

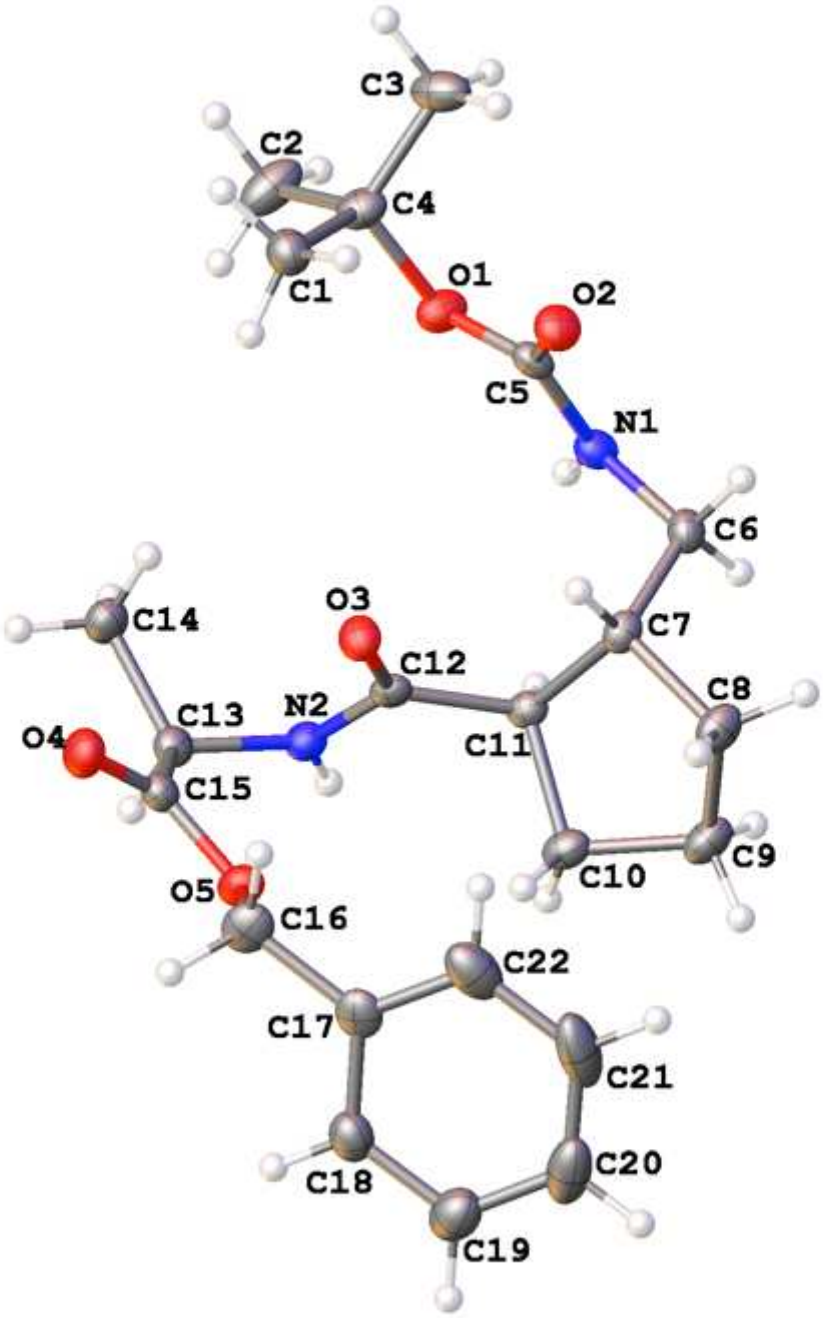


Table 1. Crystal data and structure refinement for gellman142.

Identification code	gellman142	
Empirical formula	$C_{22}\ H_{32}\ N_2\ O_5$	
Formula weight	404.50	
Temperature	100(1) K	
Wavelength	1.54178 Å	
Crystal system	Triclinic	
Space group	P1	
Unit cell dimensions	a = 5.041(3) Å	α= 92.56(3)°.
	b = 10.187(6) Å	β= 95.52(4)°.
	c = 10.943(7) Å	γ = 101.11(4)°.
Volume	547.7(5) $Å^3$	
Z	1	
Density (calculated)	1.226 Mg/m^3	
Absorption coefficient	0.706 mm^{-1}	
F(000)	218	
Crystal size	1.64 x 0.20 x 0.18 mm^3	
Theta range for data collection	4.07 to 69.46°.	
Index ranges	-6<=h<=5, -12<=k<=12, -13<=l<=13	
Reflections collected	11924	
Independent reflections	3389 [R(int) = 0.0187]	
Completeness to theta = 67.00°	97.5 %	
Absorption correction	Numerical with SADABS	
Max. and min. transmission	0.8835 and 0.3904	
Refinement method	Full-matrix least-squares on F^2	
Data / restraints / parameters	3389 / 5 / 275	
Goodness-of-fit on F^2	1.034	
Final R indices [I>2sigma(I)]	R1 = 0.0307, wR2 = 0.0803	
R indices (all data)	R1 = 0.0308, wR2 = 0.0805	
Absolute structure parameter Flack x	0.04(13)	
Absolute structure parameter Flack x	0.03(4)	
Largest diff. peak and hole	0.164 and -0.180 $e.Å^{-3}$	

Table 2. Atomic coordinates (x 10^4) and equivalent isotropic displacement parameters ($Å^2$x 10^3) for gellman142. U(eq) is defined as one third of the trace of the orthogonalized U^{ij} tensor.

	x	y	z	U(eq)
O(1)	2417(2)	-610(1)	4589(1)	24(1)
O(2)	6033(2)	1075(1)	4376(1)	24(1)
O(3)	2604(2)	693(1)	966(1)	22(1)
O(4)	1609(2)	-1153(1)	-1613(1)	27(1)
O(5)	-95(2)	729(1)	-1519(1)	23(1)
N(1)	1756(3)	1452(1)	4388(1)	19(1)
N(2)	-1956(3)	116(1)	639(1)	18(1)
C(1)	5458(4)	-1796(2)	3544(1)	27(1)
C(2)	1902(4)	-2911(2)	4800(2)	38(1)
C(3)	6004(4)	-1367(2)	5879(2)	33(1)
C(4)	4051(3)	-1658(2)	4703(1)	25(1)
C(5)	3612(3)	670(2)	4436(1)	19(1)
C(6)	2408(3)	2831(1)	4042(1)	21(1)
C(7)	2592(3)	2922(1)	2660(1)	19(1)
C(8)	2889(4)	4384(2)	2284(2)	26(1)
C(9)	27(4)	4505(2)	1776(2)	28(1)
C(10)	-1030(3)	3167(2)	1042(1)	24(1)
C(11)	-33(3)	2145(1)	1898(1)	18(1)
C(12)	360(3)	917(1)	1148(1)	18(1)
C(13)	-1856(3)	-980(2)	-253(1)	21(1)
C(14)	-1160(4)	-2205(2)	360(1)	26(1)
C(15)	129(3)	-497(1)	-1191(1)	21(1)
C(16)	1915(4)	1364(2)	-2298(2)	29(1)
C(17)	1583(3)	2793(2)	-2347(1)	26(1)
C(18)	-535(4)	3128(2)	-3096(1)	29(1)
C(19)	-921(4)	4435(2)	-3100(2)	37(1)
C(20)	809(5)	5429(2)	-2352(2)	42(1)
C(21)	2918(5)	5125(2)	-1611(2)	46(1)
C(22)	3327(4)	3804(2)	-1607(2)	38(1)

Table 3. Bond lengths [Å] and angles [°] for gellman142.

O(1)-C(5)	1.3519(19)	C(8)-H(8B)	0.9900
O(1)-C(4)	1.472(2)	C(8)-H(8A)	0.9900
O(2)-C(5)	1.220(2)	C(9)-C(10)	1.526(2)
O(3)-C(12)	1.229(2)	C(9)-H(9B)	0.9900
O(4)-C(15)	1.203(2)	C(9)-H(9A)	0.9900
O(5)-C(15)	1.3375(19)	C(10)-C(11)	1.554(2)
O(5)-C(16)	1.462(2)	C(10)-H(10A)	0.9900
N(1)-C(5)	1.339(2)	C(10)-H(10B)	0.9900
N(1)-C(6)	1.455(2)	C(11)-C(12)	1.520(2)
N(1)-H(1)	0.880(2)	C(11)-H(11)	1.0000
N(2)-C(12)	1.344(2)	C(13)-C(14)	1.526(2)
N(2)-C(13)	1.461(2)	C(13)-C(15)	1.533(2)
N(2)-H(2)	0.880(2)	C(13)-H(13)	1.0000
C(1)-C(4)	1.526(2)	C(14)-H(14C)	0.9800
C(1)-H(1B)	0.9800	C(14)-H(14A)	0.9800
C(1)-H(1A)	0.9800	C(14)-H(14B)	0.9800
C(1)-H(1C)	0.9800	C(16)-C(17)	1.499(2)
C(2)-C(4)	1.521(2)	C(16)-H(16B)	0.9900
C(2)-H(2A)	0.9800	C(16)-H(16A)	0.9900
C(2)-H(2B)	0.9800	C(17)-C(18)	1.387(3)
C(2)-H(2C)	0.9800	C(17)-C(22)	1.389(2)
C(3)-C(4)	1.524(2)	C(18)-C(19)	1.383(3)
C(3)-H(3B)	0.9800	C(18)-H(18)	0.9500
C(3)-H(3A)	0.9800	C(19)-C(20)	1.379(3)
C(3)-H(3C)	0.9800	C(19)-H(19)	0.9500
C(6)-C(7)	1.529(2)	C(20)-C(21)	1.367(3)
C(6)-H(6B)	0.9900	C(20)-H(20)	0.9500
C(6)-H(6A)	0.9900	C(21)-C(22)	1.400(3)
C(7)-C(8)	1.546(2)	C(21)-H(21)	0.9500
C(7)-C(11)	1.549(2)	C(22)-H(22)	0.9500
C(7)-H(7)	1.0000		
C(8)-C(9)	1.525(3)		
C(5)-O(1)-C(4)	120.52(13)		
C(15)-O(5)-C(16)	115.87(13)		
C(5)-N(1)-C(6)	121.51(13)		
C(5)-N(1)-H(1)	117.6(14)		
C(6)-N(1)-H(1)	118.6(14)		
C(12)-N(2)-C(13)	120.03(13)		
C(12)-N(2)-H(2)	121.7(12)		
C(13)-N(2)-H(2)	117.6(12)		
C(4)-C(1)-H(1B)	109.5		
C(4)-C(1)-H(1A)	109.5		
H(1B)-C(1)-H(1A)	109.5		
C(4)-C(1)-H(1C)	109.5		
H(1B)-C(1)-H(1C)	109.5		
H(1A)-C(1)-H(1C)	109.5		
C(4)-C(2)-H(2A)	109.5		
C(4)-C(2)-H(2B)	109.5		
H(2A)-C(2)-H(2B)	109.5		
C(4)-C(2)-H(2C)	109.5		
H(2A)-C(2)-H(2C)	109.5		
H(2B)-C(2)-H(2C)	109.5		
C(4)-C(3)-H(3B)	109.5		
C(4)-C(3)-H(3A)	109.5		

H(3B)-C(3)-H(3A)	109.5
C(4)-C(3)-H(3C)	109.5
H(3B)-C(3)-H(3C)	109.5
H(3A)-C(3)-H(3C)	109.5
O(1)-C(4)-C(2)	102.38(14)
O(1)-C(4)-C(3)	109.72(13)
C(2)-C(4)-C(3)	110.42(15)
O(1)-C(4)-C(1)	110.21(13)
C(2)-C(4)-C(1)	109.89(15)
C(3)-C(4)-C(1)	113.64(15)
O(2)-C(5)-N(1)	124.26(14)
O(2)-C(5)-O(1)	125.56(15)
N(1)-C(5)-O(1)	110.16(13)
N(1)-C(6)-C(7)	112.44(11)
N(1)-C(6)-H(6B)	109.1
C(7)-C(6)-H(6B)	109.1
N(1)-C(6)-H(6A)	109.1
C(7)-C(6)-H(6A)	109.1
H(6B)-C(6)-H(6A)	107.8
C(6)-C(7)-C(8)	111.68(12)
C(6)-C(7)-C(11)	111.48(12)
C(8)-C(7)-C(11)	105.28(13)
C(6)-C(7)-H(7)	109.4
C(8)-C(7)-H(7)	109.4
C(11)-C(7)-H(7)	109.4
C(9)-C(8)-C(7)	104.68(13)
C(9)-C(8)-H(8B)	110.8
C(7)-C(8)-H(8B)	110.8
C(9)-C(8)-H(8A)	110.8
C(7)-C(8)-H(8A)	110.8
H(8B)-C(8)-H(8A)	108.9
C(8)-C(9)-C(10)	102.70(14)
C(8)-C(9)-H(9B)	111.2
C(10)-C(9)-H(9B)	111.2
C(8)-C(9)-H(9A)	111.2
C(10)-C(9)-H(9A)	111.2
H(9B)-C(9)-H(9A)	109.1
C(9)-C(10)-C(11)	102.93(13)
C(9)-C(10)-H(10A)	111.2
C(11)-C(10)-H(10A)	111.2
C(9)-C(10)-H(10B)	111.2
C(11)-C(10)-H(10B)	111.2
H(10A)-C(10)-H(10B)	109.1
C(12)-C(11)-C(7)	114.05(13)
C(12)-C(11)-C(10)	110.54(12)
C(7)-C(11)-C(10)	105.85(12)
C(12)-C(11)-H(11)	108.8
C(7)-C(11)-H(11)	108.8
C(10)-C(11)-H(11)	108.8
O(3)-C(12)-N(2)	121.81(14)
O(3)-C(12)-C(11)	123.41(13)
N(2)-C(12)-C(11)	114.71(14)
N(2)-C(13)-C(14)	112.43(13)
N(2)-C(13)-C(15)	110.49(12)
C(14)-C(13)-C(15)	111.19(14)
N(2)-C(13)-H(13)	107.5
C(14)-C(13)-H(13)	107.5
C(15)-C(13)-H(13)	107.5
C(13)-C(14)-H(14C)	109.5
C(13)-C(14)-H(14A)	109.5
H(14C)-C(14)-H(14A)	109.5
C(13)-C(14)-H(14B)	109.5
H(14C)-C(14)-H(14B)	109.5
H(14A)-C(14)-H(14B)	109.5
O(4)-C(15)-O(5)	124.55(14)
O(4)-C(15)-C(13)	124.62(14)
O(5)-C(15)-C(13)	110.76(13)
O(5)-C(16)-C(17)	105.96(14)
O(5)-C(16)-H(16B)	110.5
C(17)-C(16)-H(16B)	110.5
O(5)-C(16)-H(16A)	110.5
C(17)-C(16)-H(16A)	110.5
H(16B)-C(16)-H(16A)	108.7
C(18)-C(17)-C(22)	118.49(16)
C(18)-C(17)-C(16)	120.77(15)
C(22)-C(17)-C(16)	120.70(17)
C(19)-C(18)-C(17)	120.91(16)
C(19)-C(18)-H(18)	119.5
C(17)-C(18)-H(18)	119.5
C(20)-C(19)-C(18)	120.07(19)
C(20)-C(19)-H(19)	120.0
C(18)-C(19)-H(19)	120.0
C(21)-C(20)-C(19)	120.10(18)
C(21)-C(20)-H(20)	120.0
C(19)-C(20)-H(20)	120.0
C(20)-C(21)-C(22)	120.08(17)
C(20)-C(21)-H(21)	120.0
C(22)-C(21)-H(21)	120.0
C(17)-C(22)-C(21)	120.35(19)
C(17)-C(22)-H(22)	119.8
C(21)-C(22)-H(22)	119.8

Table 4. Anisotropic displacement parameters ($Å^2 x\ 10^3$) for gellman142. The anisotropic displacement factor exponent takes the form: $-2\pi^2[\ h^2\ a^{*2}U^{11} + ...\ + 2\ h\ k\ a^*\ b^*\ U^{12}\ ]$

	U^{11}	U^{22}	U^{33}	U^{23}	U^{13}	U^{12}
O(1)	17(1)	25(1)	31(1)	8(1)	5(1)	4(1)
O(2)	16(1)	27(1)	28(1)	0(1)	2(1)	3(1)
O(3)	16(1)	25(1)	25(1)	-2(1)	4(1)	7(1)
O(4)	31(1)	26(1)	26(1)	-2(1)	7(1)	9(1)
O(5)	27(1)	25(1)	21(1)	6(1)	7(1)	8(1)
N(1)	14(1)	24(1)	19(1)	2(1)	3(1)	3(1)
N(2)	15(1)	21(1)	21(1)	3(1)	4(1)	5(1)
C(1)	27(1)	27(1)	26(1)	-1(1)	2(1)	6(1)
C(2)	30(1)	28(1)	61(1)	16(1)	16(1)	11(1)
C(3)	34(1)	47(1)	24(1)	8(1)	6(1)	21(1)
C(4)	21(1)	28(1)	29(1)	7(1)	6(1)	10(1)
C(5)	17(1)	25(1)	14(1)	1(1)	0(1)	2(1)
C(6)	20(1)	20(1)	23(1)	-3(1)	2(1)	4(1)
C(7)	16(1)	17(1)	25(1)	2(1)	6(1)	3(1)
C(8)	23(1)	19(1)	37(1)	5(1)	8(1)	3(1)
C(9)	29(1)	21(1)	36(1)	7(1)	8(1)	9(1)
C(10)	25(1)	25(1)	24(1)	7(1)	6(1)	10(1)
C(11)	17(1)	20(1)	18(1)	3(1)	5(1)	6(1)
C(12)	20(1)	20(1)	16(1)	6(1)	3(1)	6(1)
C(13)	20(1)	20(1)	22(1)	0(1)	0(1)	2(1)
C(14)	32(1)	21(1)	26(1)	3(1)	3(1)	5(1)
C(15)	23(1)	21(1)	18(1)	-1(1)	-1(1)	4(1)
C(16)	35(1)	32(1)	24(1)	8(1)	15(1)	8(1)
C(17)	31(1)	29(1)	18(1)	4(1)	11(1)	3(1)
C(18)	35(1)	28(1)	24(1)	0(1)	4(1)	3(1)
C(19)	48(1)	33(1)	32(1)	5(1)	10(1)	14(1)
C(20)	69(2)	24(1)	33(1)	2(1)	23(1)	5(1)
C(21)	61(1)	35(1)	31(1)	-7(1)	12(1)	-18(1)
C(22)	38(1)	44(1)	26(1)	3(1)	3(1)	-6(1)

Table 5. Hydrogen coordinates (x 10^4) and isotropic displacement parameters ($Å^2$x 10^3) for gellman142.

	x	y	z	U(eq)
H(1)	36(13)	1057(19)	4357(19)	28(5)
H(2)	-3559(17)	301(18)	737(17)	24(5)
H(1B)	6934	-1018	3520	40
H(1A)	4139	-1842	2817	40
H(1C)	6205	-2616	3550	40
H(2A)	684	-3094	4032	57
H(2B)	850	-2771	5485	57
H(2C)	2788	-3674	4945	57
H(3B)	4993	-1218	6577	49
H(3A)	7386	-564	5800	49
H(3C)	6890	-2132	6016	49
H(6B)	4166	3281	4495	26
H(6A)	994	3312	4287	26
H(7)	4184	2550	2429	23
H(8B)	3565	5025	3004	31
H(8A)	4162	4559	1649	31
H(9B)	71	5265	1239	33
H(9A)	-1104	4625	2447	33
H(10A)	-252	3151	246	28
H(10B)	-3039	2980	886	28
H(11)	-1436	1856	2470	21
H(13)	-3708	-1258	-713	25
H(14C)	-2545	-2537	902	40
H(14A)	622	-1955	844	40
H(14B)	-1110	-2909	-273	40
H(16B)	1585	911	-3134	35
H(16A)	3776	1321	-1943	35
H(18)	-1736	2449	-3613	35
H(19)	-2380	4649	-3618	44
H(20)	533	6325	-2352	50
H(21)	4108	5811	-1097	55
H(22)	4805	3598	-1096	46

Table 6. Torsion angles [°] for gellman142.

C(5)-O(1)-C(4)-C(2)	-177.67(13)
C(5)-O(1)-C(4)-C(3)	65.06(17)
C(5)-O(1)-C(4)-C(1)	-60.80(17)
C(6)-N(1)-C(5)-O(2)	10.9(2)
C(6)-N(1)-C(5)-O(1)	-170.49(11)
C(4)-O(1)-C(5)-O(2)	0.2(2)
C(4)-O(1)-C(5)-N(1)	-178.36(11)
C(5)-N(1)-C(6)-C(7)	74.93(17)
N(1)-C(6)-C(7)-C(8)	172.11(13)
N(1)-C(6)-C(7)-C(11)	54.65(17)
C(6)-C(7)-C(8)-C(9)	-99.05(15)
C(11)-C(7)-C(8)-C(9)	22.08(16)
C(7)-C(8)-C(9)-C(10)	-40.22(16)
C(8)-C(9)-C(10)-C(11)	42.26(15)
C(6)-C(7)-C(11)-C(12)	-112.94(14)
C(8)-C(7)-C(11)-C(12)	125.79(13)
C(6)-C(7)-C(11)-C(10)	125.32(13)
C(8)-C(7)-C(11)-C(10)	4.05(15)
C(9)-C(10)-C(11)-C(12)	-152.51(13)
C(9)-C(10)-C(11)-C(7)	-28.54(16)
C(13)-N(2)-C(12)-O(3)	-6.25(19)
C(13)-N(2)-C(12)-C(11)	170.63(12)
C(7)-C(11)-C(12)-O(3)	-13.25(19)
C(10)-C(11)-C(12)-O(3)	105.87(16)
C(7)-C(11)-C(12)-N(2)	169.92(11)
C(10)-C(11)-C(12)-N(2)	-70.96(16)
C(12)-N(2)-C(13)-C(14)	79.69(16)
C(12)-N(2)-C(13)-C(15)	-45.19(17)
C(16)-O(5)-C(15)-O(4)	-9.8(2)
C(16)-O(5)-C(15)-C(13)	173.03(12)
N(2)-C(13)-C(15)-O(4)	142.28(15)
C(14)-C(13)-C(15)-O(4)	16.7(2)
N(2)-C(13)-C(15)-O(5)	-40.53(16)
C(14)-C(13)-C(15)-O(5)	-166.11(12)
C(15)-O(5)-C(16)-C(17)	-169.85(12)
O(5)-C(16)-C(17)-C(18)	-77.86(18)
O(5)-C(16)-C(17)-C(22)	99.59(18)
C(22)-C(17)-C(18)-C(19)	-0.5(2)
C(16)-C(17)-C(18)-C(19)	176.97(16)
C(17)-C(18)-C(19)-C(20)	-0.1(3)
C(18)-C(19)-C(20)-C(21)	0.4(3)
C(19)-C(20)-C(21)-C(22)	-0.1(3)
C(18)-C(17)-C(22)-C(21)	0.8(2)
C(16)-C(17)-C(22)-C(21)	-176.67(16)
C(20)-C(21)-C(22)-C(17)	-0.5(3)

Symmetry transformations used to generate equivalent atoms:

Table 7. Hydrogen bonds for gellman142 [Å and °].

D-H...A	d(D-H)	d(H...A)	d(D...A)	<(DHA)
N(1)-H(1)...O(2)#1	0.880(2)	2.024(10)	2.835(2)	152.8(19)
N(2)-H(2)...O(3)#1	0.880(2)	2.084(3)	2.964(2)	178.7(18)

Symmetry transformations used to generate equivalent atoms:
#1 x-1,y,z