Brandt, SD, Kavanagh, PV, Westphal, F, Stratford, A, Odland, AU, Klein, AK, Dowling, G, Dempster, NM, Wallach, J, Passie, T and Halberstadt, AL

Return of the lysergamides. Part VI: Analytical and behavioural characterization of 1-cyclopropanoyl-d-lysergic acid diethylamide (1CP-LSD)

Return of the lysergamides. Part VI: Analytical and behavioural characterization of 1-cyclopropanoyl-*d*-lysergic acid diethylamide (1CP-LSD)

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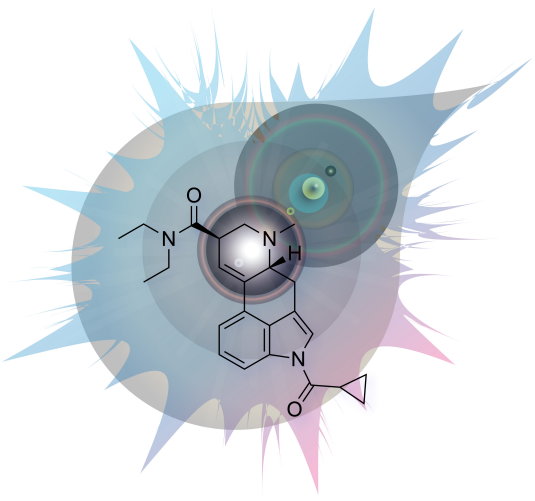
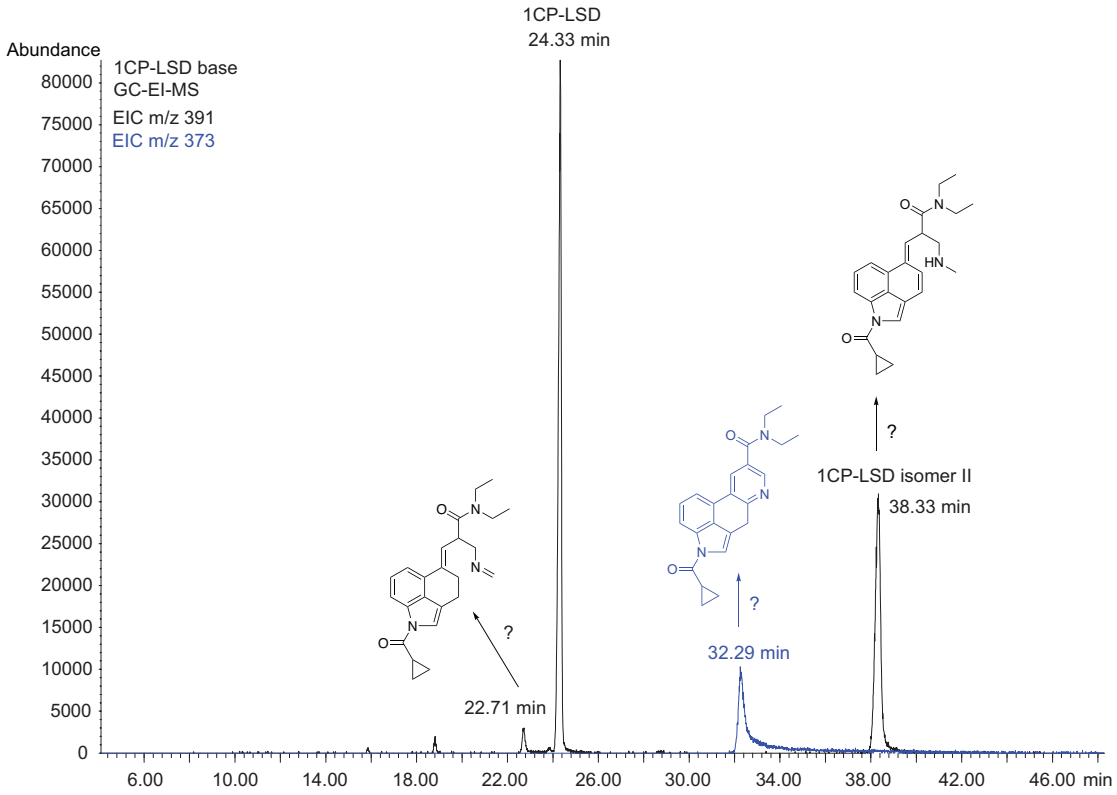
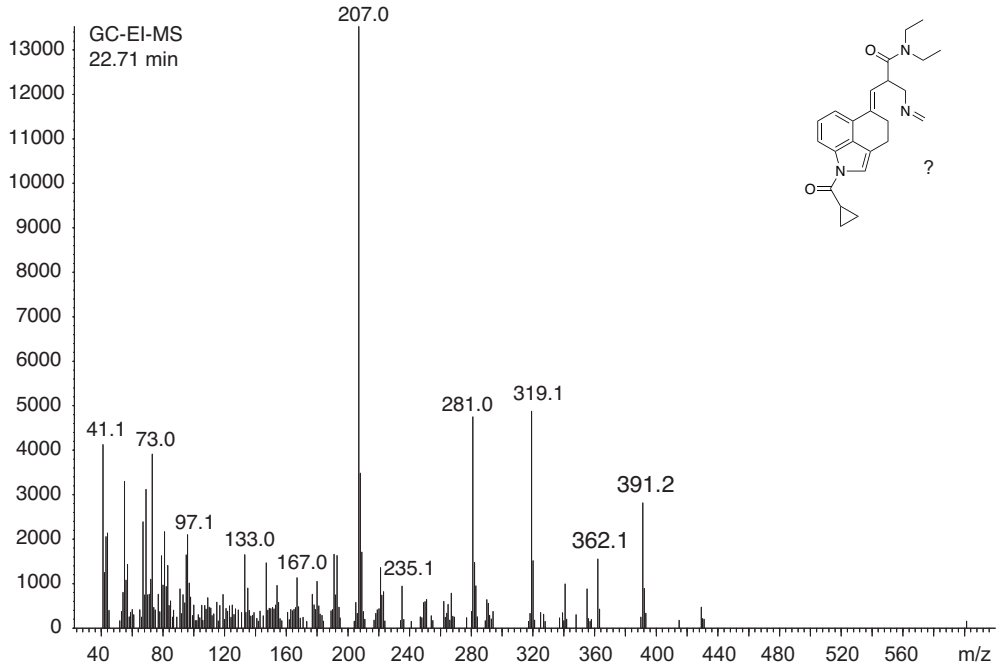
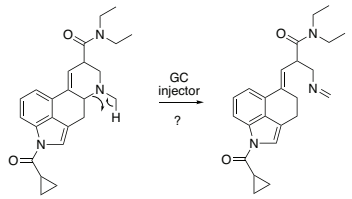
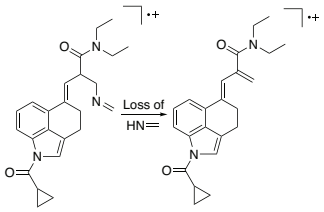


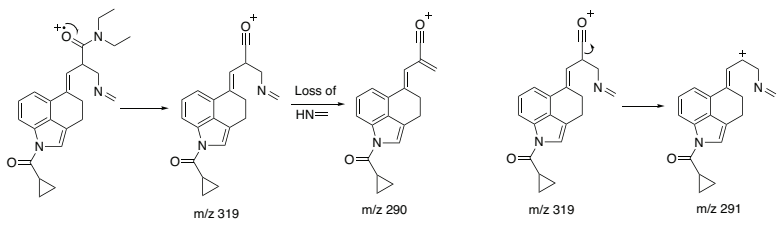


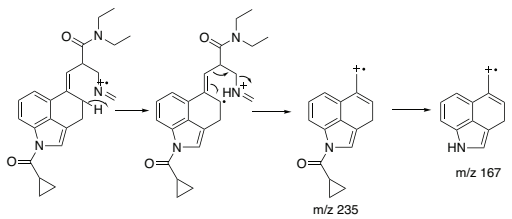
GC-induced formation of degradation products (GC-MS method 1; merged EIC traces)
(EI mass spectra next page; mass spectrum of 1CP-LSD in main text)

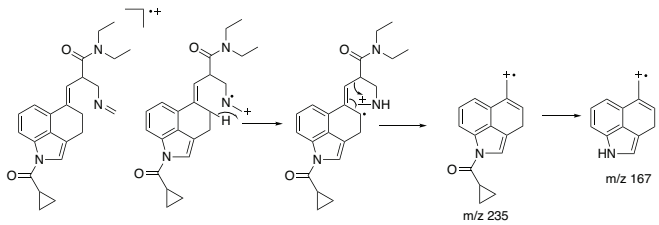

GC-EI-MS
22.71 min
207.0
281.0
319.1
391.2
362.1
41.1
73.0
97.1
133.0
167.0
235.1
m/z
?

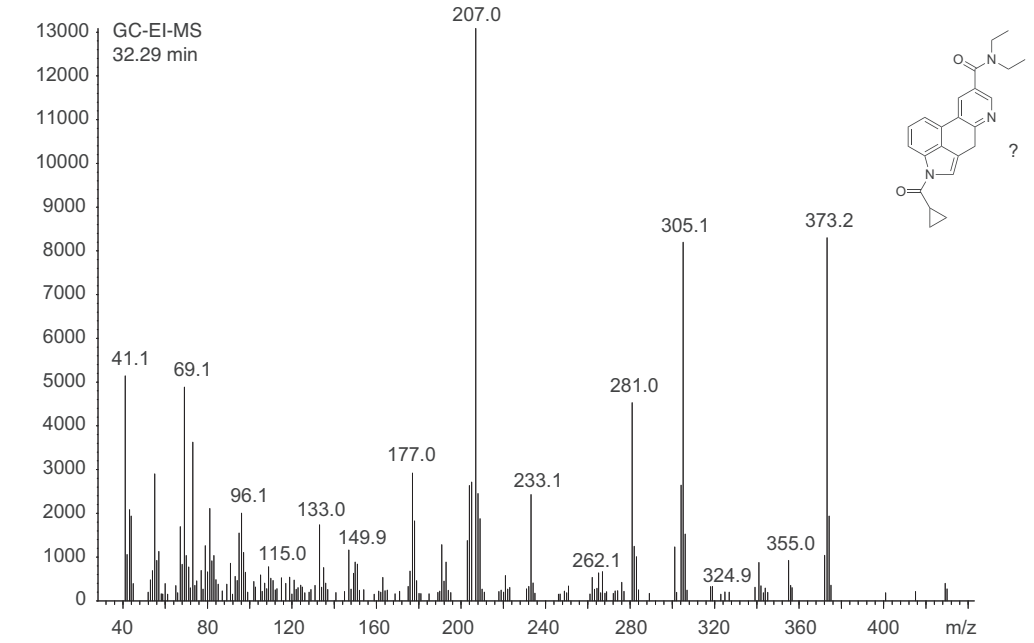

GC
injector
?

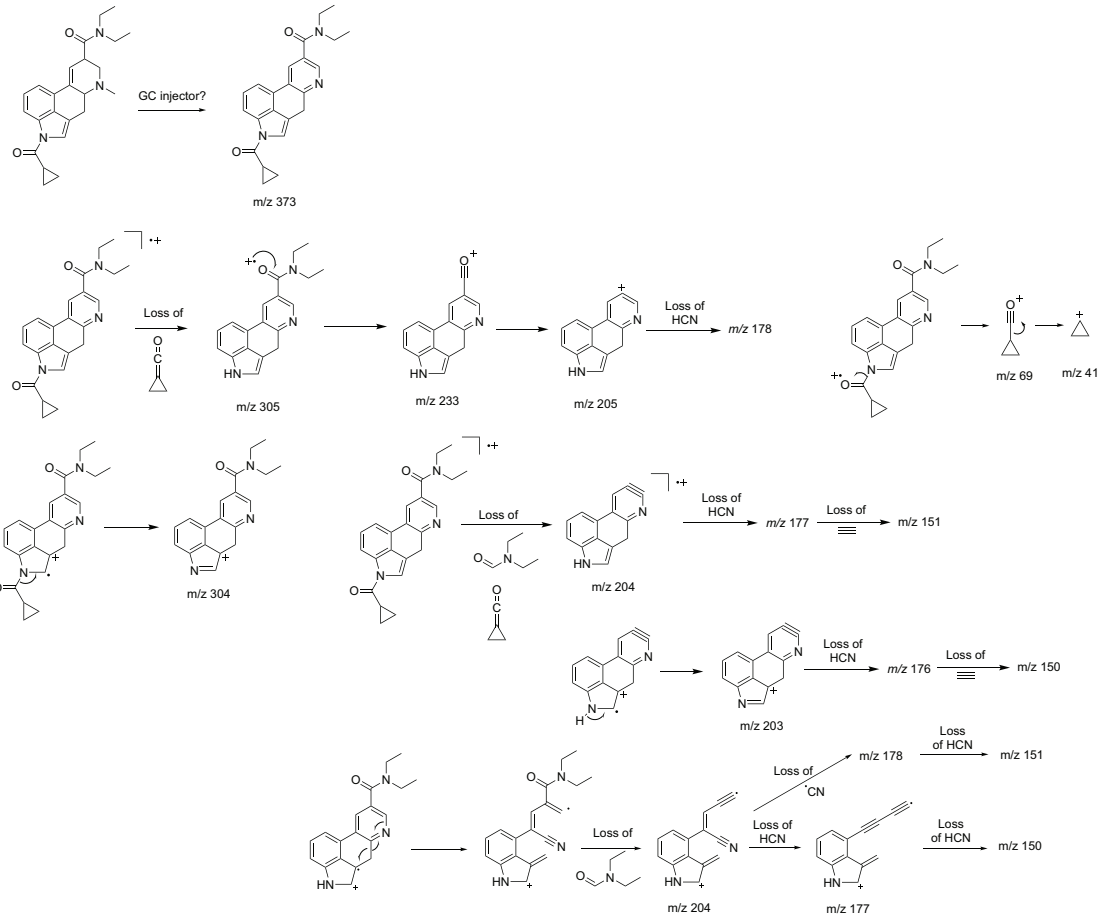

Loss of
HN=
m/z 362

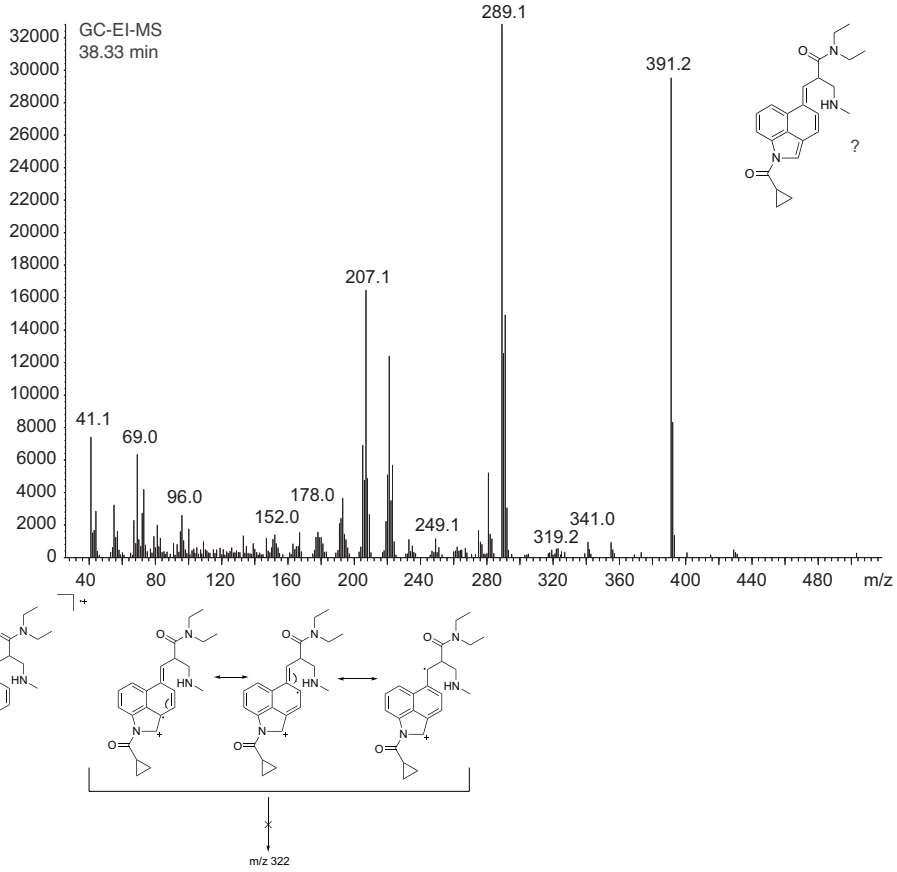

Loss of
HN=
m/z 319
m/z 290
m/z 319
m/z 291


m/z 235
m/z 167

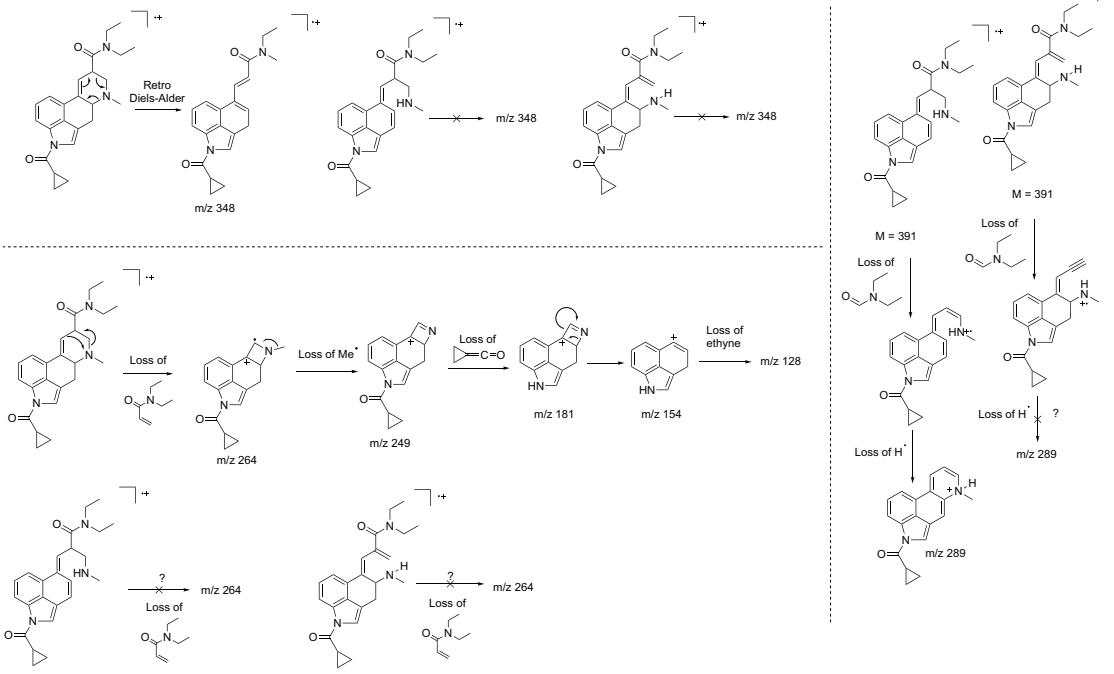

m/z 235
m/z 167

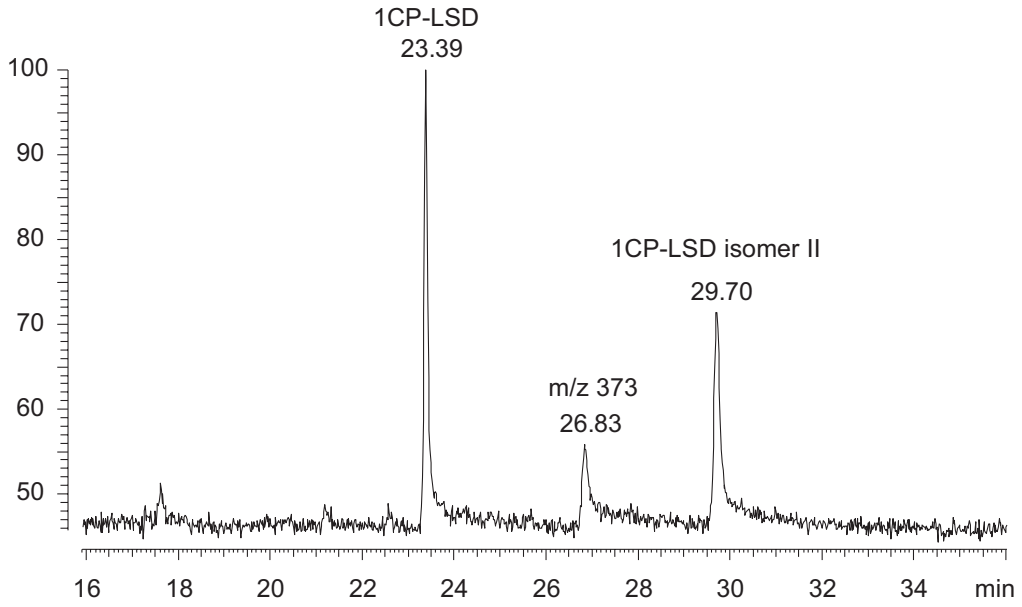

GC-EI-MS
32.29 min
13000
12000
11000
10000
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
40
80
120
160
200
240
280
320
360
400
m/z
207.0
305.1
373.2
41.1
69.1
281.0
177.0
233.1
96.1
133.0
149.9
115.0
262.1
324.9
355.0
?


GC injector?
m/z 373
Loss of
m/z 305
m/z 233
Loss of HCN
m/z 178
m/z 205
m/z 69
m/z 41
m/z 304
Loss of
Loss of HCN
m/z 177
Loss of
m/z 151
m/z 204
Loss of HCN
m/z 176
Loss of
m/z 150
m/z 203
Loss of HCN
m/z 178
Loss of HCN
m/z 151
Loss of CN
Loss of
Loss of HCN
Loss of HCN
m/z 150
m/z 204
m/z 177



Preferred radical radical cation delocalization to afford a thermodynamically stable naphthalene?

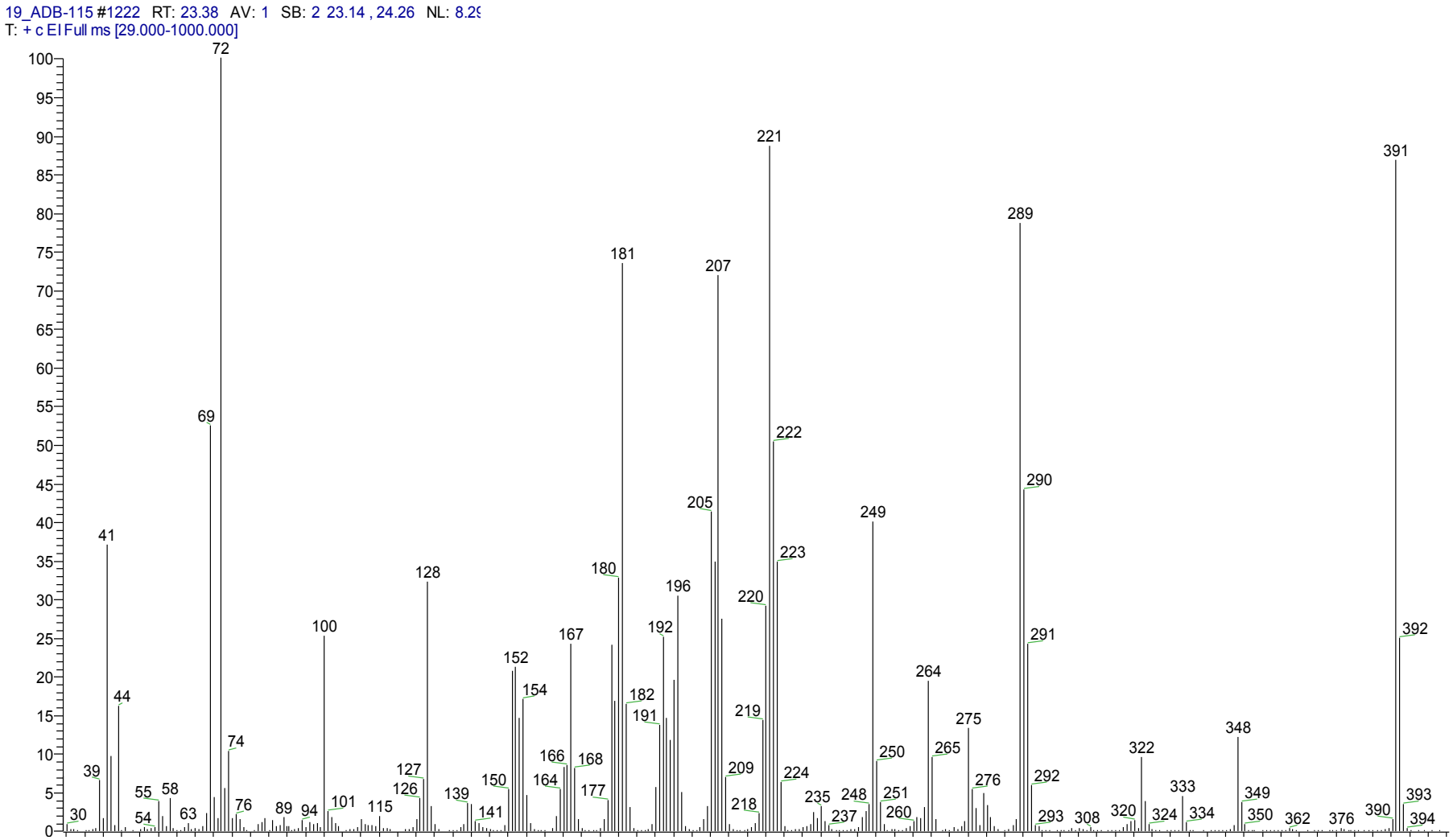


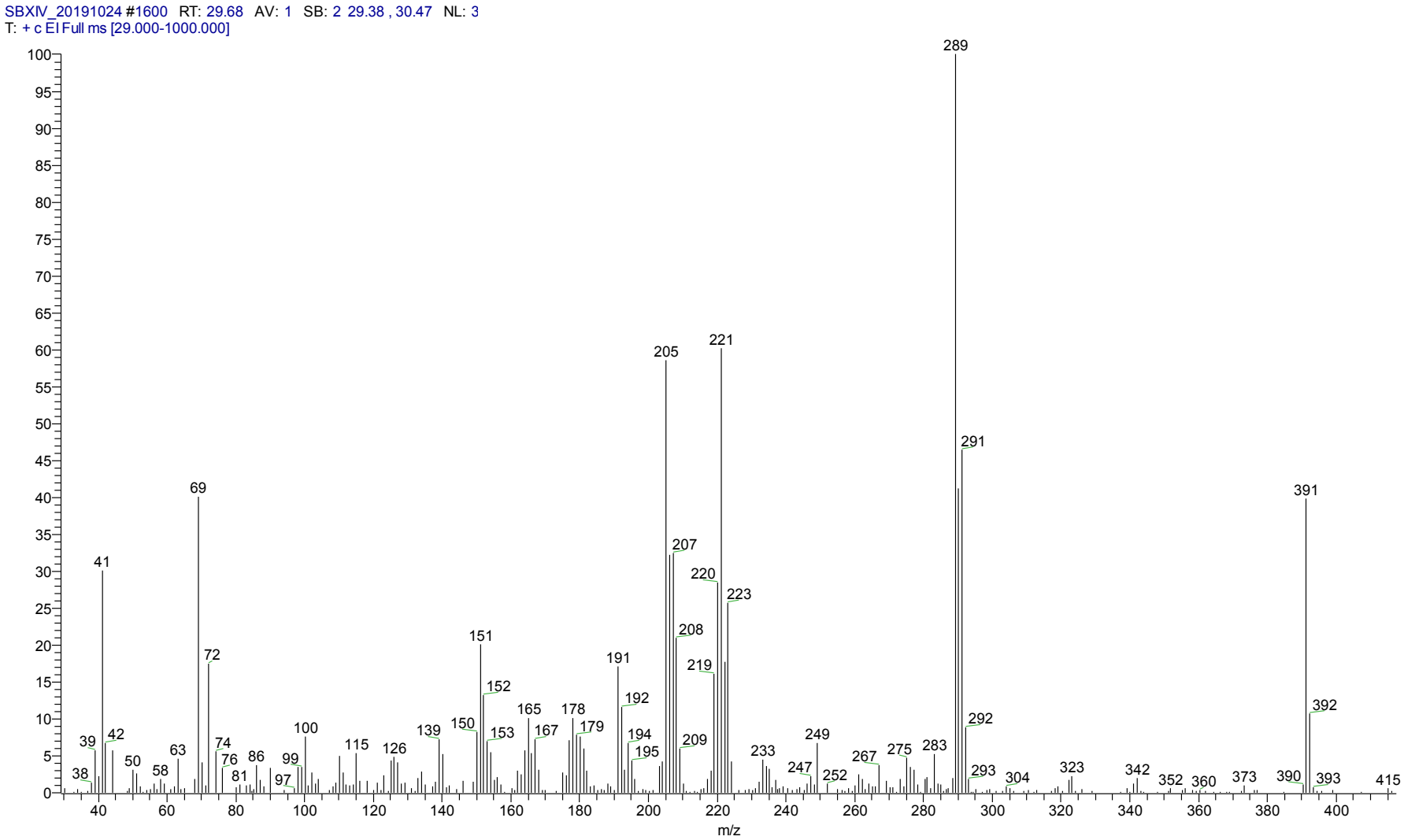


GC-induced formation of degradation products (GC-EI-MS method 2)

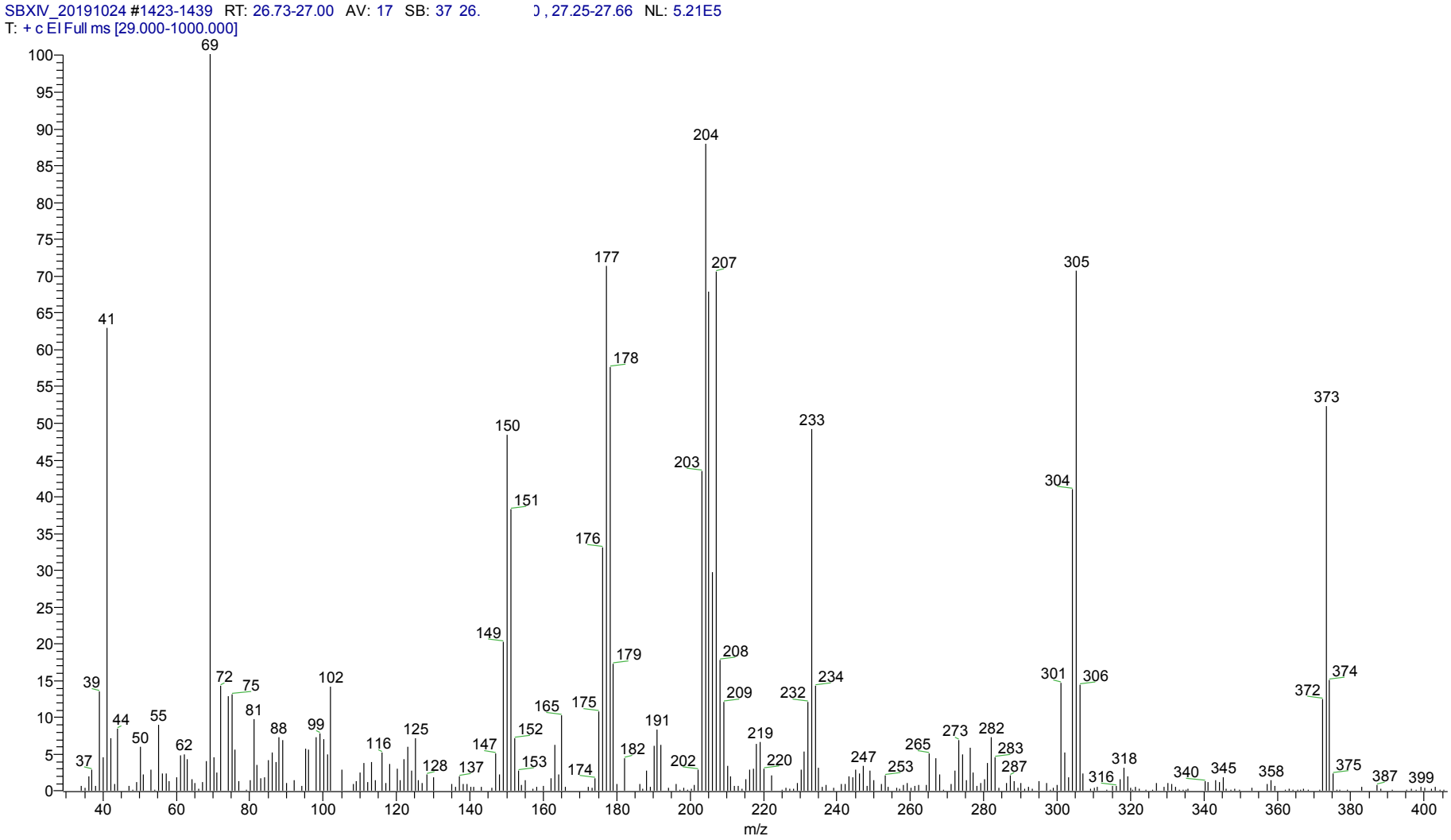
Electron ionization (EI) mass spectra (70 eV) were recorded using a Finnigan TSQ 8000 EVO triple stage quadrupole mass spectrometer coupled to a gas chromatograph (Trace 1310, Thermo Electron, Dreieich, Germany). Sample introduction was carried out using a Triplus RSH autosampler. The emission current was 200 µA and the scan time was 1 s spanning a scan range between m/z 29–600. The ion source temperature was maintained at 220°C. Samples were introduced via gas chromatography with splitless injection using a fused silica capillary DB-1 column (30 m × 0.25 mm, film thickness 0.25 µm). The temperature program consisted of an initial temperature of 80°C, held for 2 min, followed by a ramp to 310°C at 20°C/min. The final temperature was held for 23 min. The injector temperature and the transfer line temperature were 280°C and 300°C and the carrier gas was helium in constant flow mode at a flow rate of 1.2 mL/min. Approximately 2 mg were dissolved in 1.5 mL methanol. For analysis, 1 µL of sample solution was injected into the GC-MS system. Kovats retention indices (RI) were calculated from measurement of an *n*-alkane mixture analyzed with the above-mentioned temperature program.

Samples were also analyzed using a GC-solid phase-IR-system (GC-sIR) that consisted of an Agilent GC 7890B (Waldbronn, Germany) with probe sampler Agilent G4567A and a DiscovIR-GC™ (Spectra Analysis, Marlborough, MA, USA). The column eluent was cryogenically accumulated on a spirally rotating ZnSe disk cooled by liquid nitrogen. IR spectra were recorded through the IR-transparent ZnSe disk using a nitrogen-cooled MCT detector. GC parameters: injection in splitless mode with the injection port temperature set at 240°C and a DB-1 fused silica capillary column (30 m × 0.32 mm i.d., 0.25 µm film thickness). The carrier gas was helium with a flow rate of 2.5 mL/min and the oven temperature program was as follows: 80°C for 2 min, ramped to 300°C at 20 °C/min, and held at for 22 min. The transfer line was heated at 280°C. Infrared conditions: oven temperature, restrictor temperature, disc temperature, and Dewar cap temperatures were 280°C, 280°C, -40°C, and 35°C, respectively. The vacuum was 0.2 mTorr, disc speed 3 mm/s, spiral separation was 1 mm, wavelength resolution 4 cm^{-1} and IR range 650–4000 cm^{-1}. Acquisition time was 0.6 s/file with 64 scans/spectrum. Data were processed using GRAMS/AI Ver. 9.1 (Grams Spectroscopy Software Suite, Thermo Fisher Scientific, Dreieich, Germany) followed by implementation of the OMNIC Software, Ver. 7.4.127 (Thermo Electron Corporation, Dreieich, Germany).

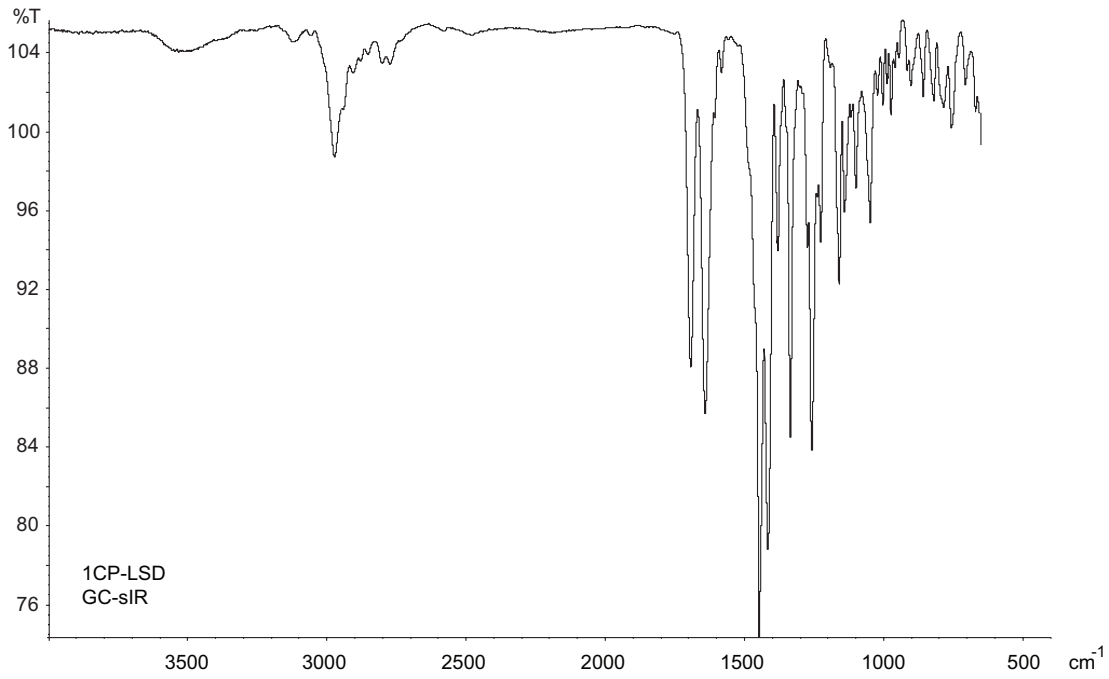

19_ADB-115 #1222 RT: 23.38 AV: 1 SB: 2 23.14 , 24.26 NL: 8.29
T: + c EI Full ms [29.000-1000.000]
1CP-LSD; RI: 3682 (DB-1,310)

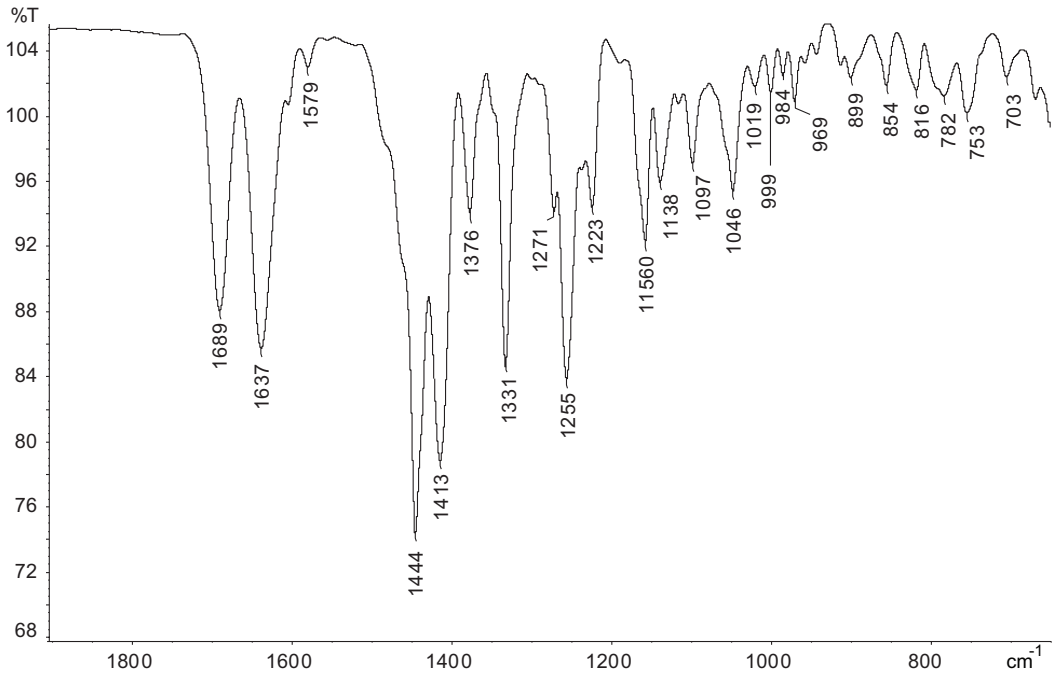


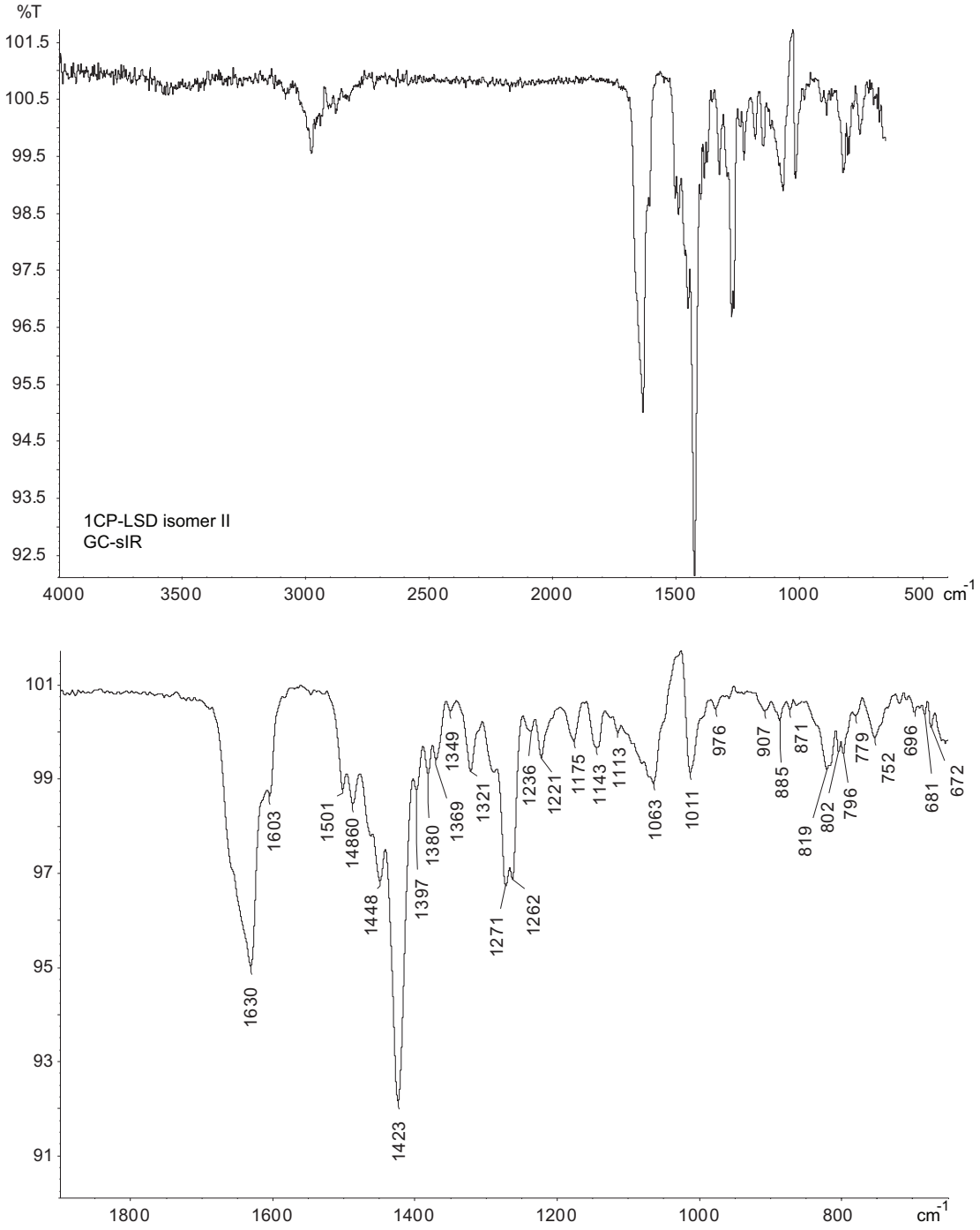
1CP-LSD Isomer II; RI: 3918 (DB-1,310)



Pyridine derivative degradation product (“m/z 373 species”)? RI: 3834 (DB-1,310)


%T
104
100
96
92
88
84
80
76
1CP-LSD
GC-sIR
3500
3000
2500
2000
1500
1000
500
cm-1


%T
104
100
96
92
88
84
80
76
72
68
1689
1637
1579
1444
1413
1376
1331
1271
1255
1223
1560
1138
1097
1046
999
1019
984
969
899
854
816
782
753
703
1800
1600
1400
1200
1000
800
cm-1


%T
101.5
100.5
99.5
98.5
97.5
96.5
95.5
94.5
93.5
92.5
1CP-LSD isomer II
GC-sIR
4000
3500
3000
2500
2000
1500
1000
500
cm-1
101
99
97
95
93
91
1630
1603
1501
1486
1448
1423
1397
1380
1369
1349
1321
1271
1262
1236
1221
1175
1143
1113
1063
1011
976
907
885
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819
802
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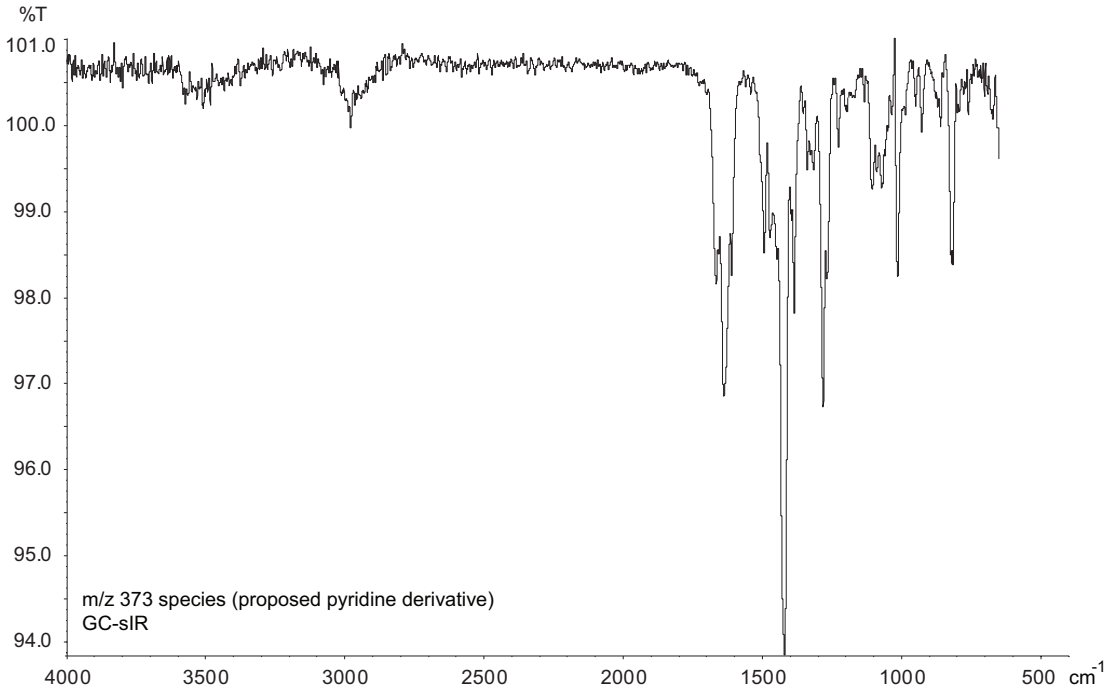
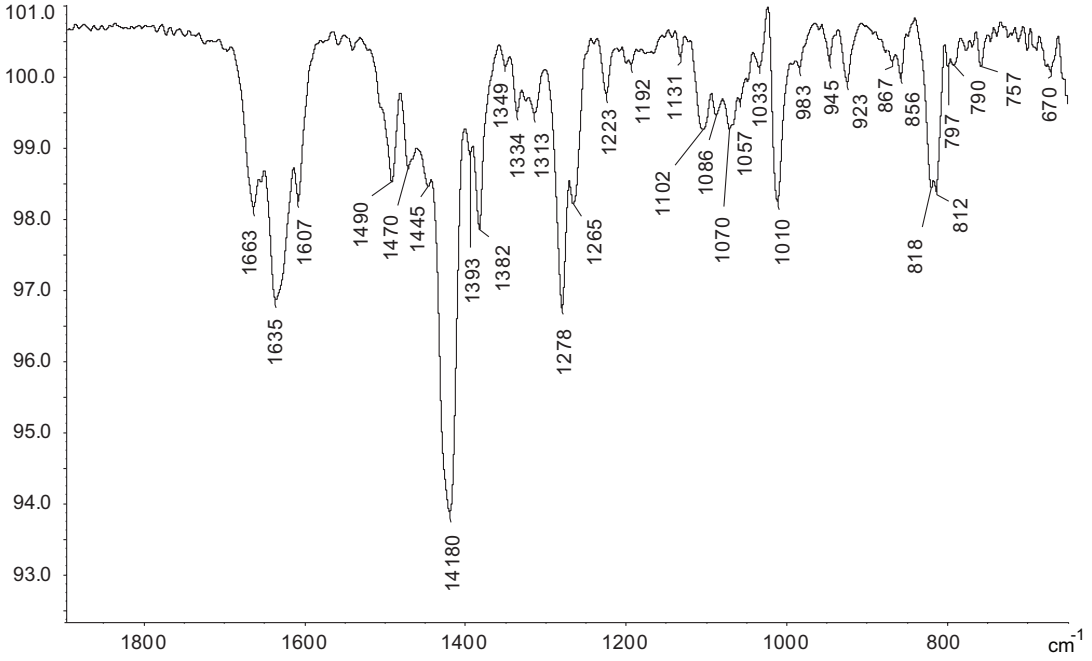
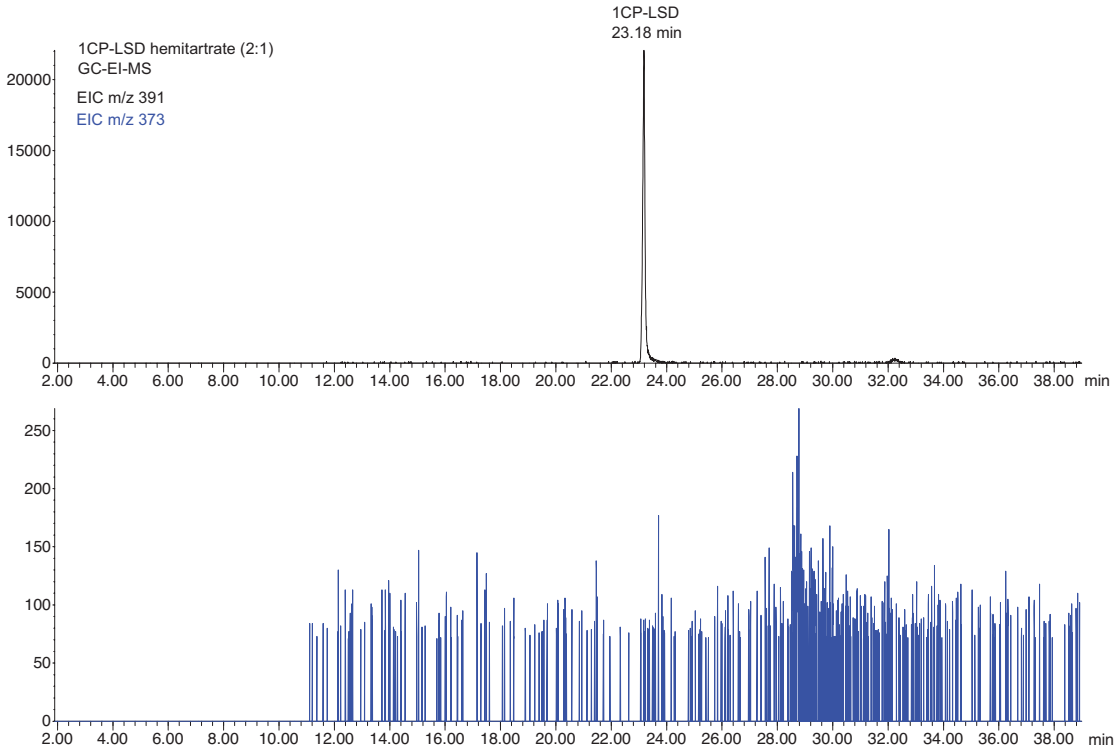
779
752
696
681
672
1800
1600
1400
1200
1000
800
cm-1


%T
101.0
100.0
99.0
98.0
97.0
96.0
95.0
94.0
m/z 373 species (proposed pyridine derivative)
GC-sIR
4000
3500
3000
2500
2000
1500
1000
500
cm-1

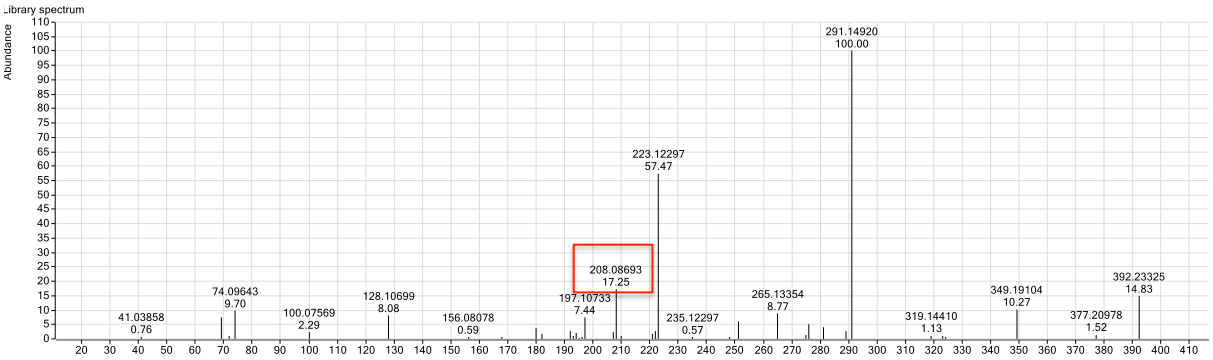

101.0
100.0
99.0
98.0
97.0
96.0
95.0
94.0
93.0
1663
1635
1607
1490
1470
1445
1418
0
1393
1382
1349
1334
1313
1278
1265
1223
1192
1131
1102
1086
1070
1057
1033
1010
983
945
923
867
856
818
812
797
790
757
670
1800
1600
1400
1200
1000
800
cm-1

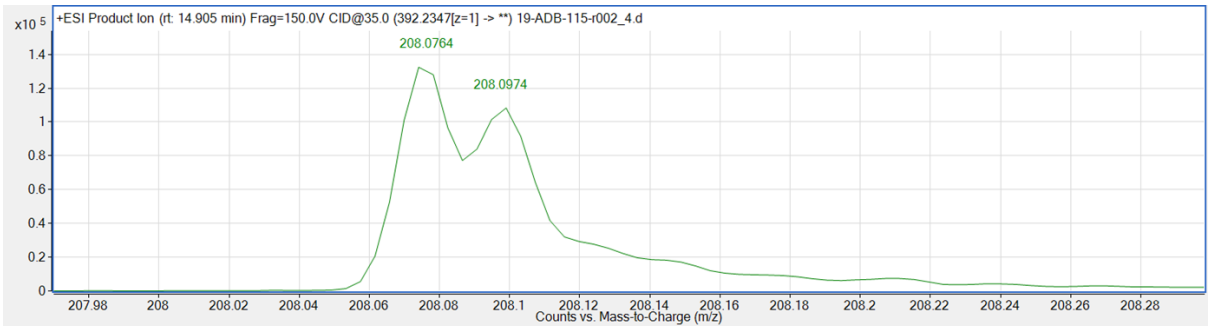
Samples were analyzed on an Agilent 7890A gas chromatograph coupled to a 5977A MSD. An AgilentHP-5MS UI column (30 m × 0.25 mm × 0.25 µm; Agilent Technologies, Stockport, UK) was used in split mode (1:50) with helium carrier gas at a constant flow of 1.0 mL/min. The injection port and transfer line temperatures were set at 275°C and 275°C, respectively. The initial oven temperature was 100°C, held for 1 min, ramped at 20 °C/min to 300°C and held at for 28 min (runtime 39 min). The ionization energy was set at 70 eV, the quadrupole at 150 °C, the ion source at 230°C and the mass range was set at m/z 29–500. The sample injection volume was 1 µL and a 1 mg/mL solution in methanol was analyzed.

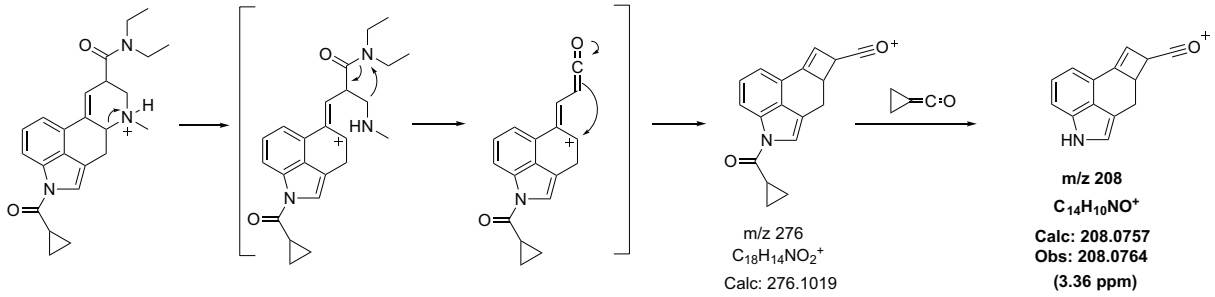


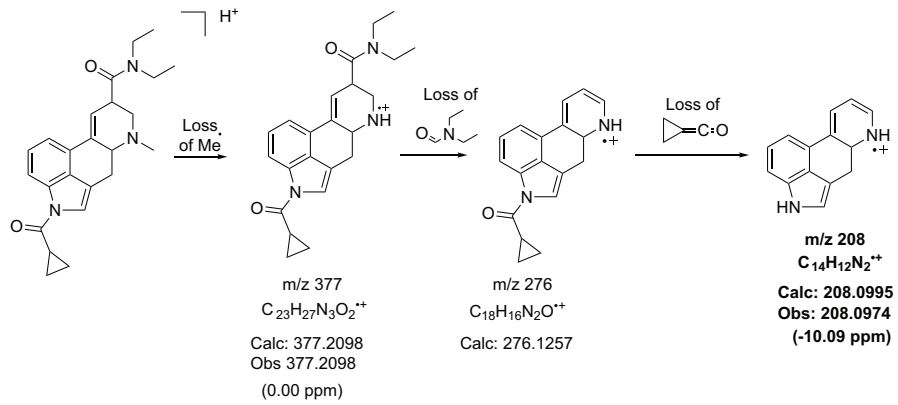
GC-EI-MS analysis (method 3; merged EIC traces)

Repeated mass measurements of the m/z 208.0869 species and detection of two distinct product ions (Agilent 6530 QTOF system) in profile mode.





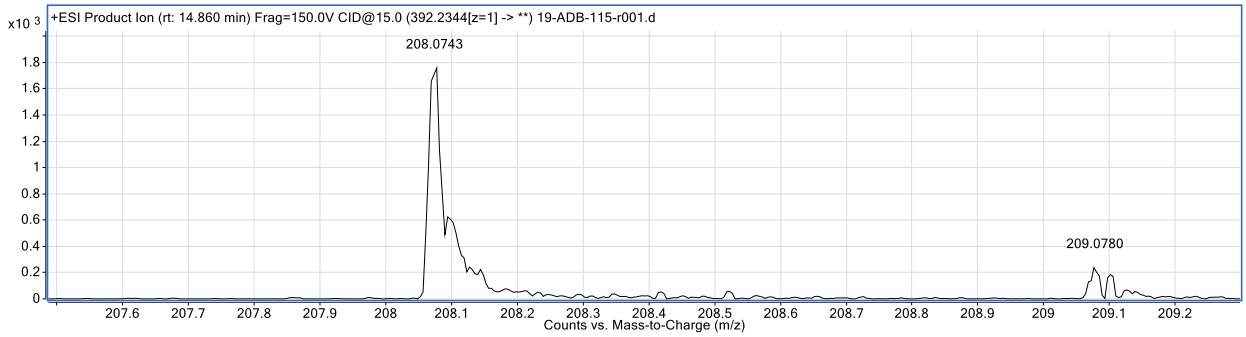




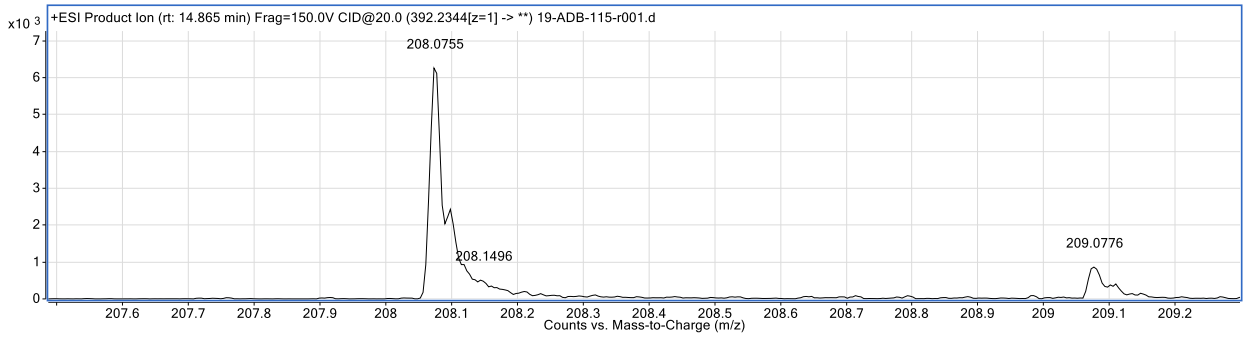
Dependence of both m/z 208 ions on collision energy

10V

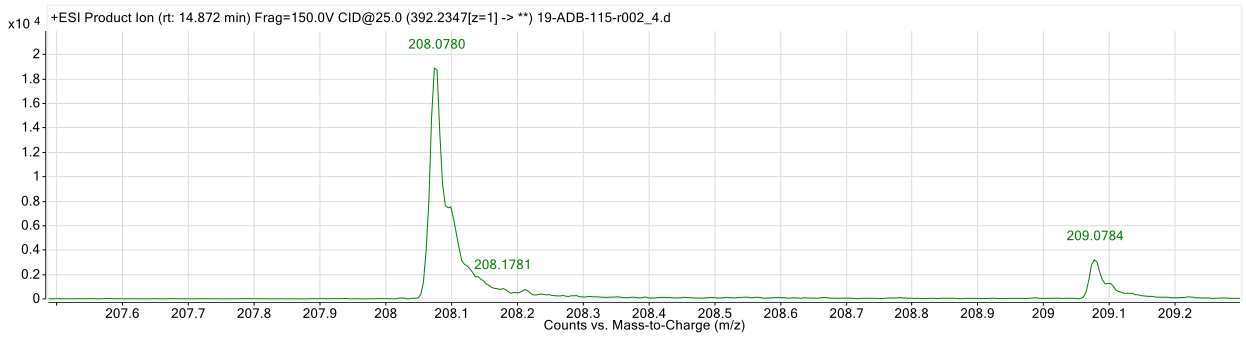
15V



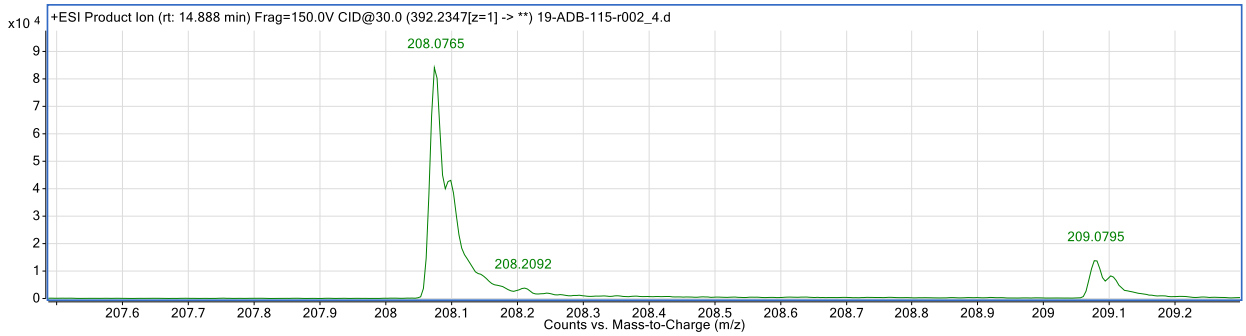
20V



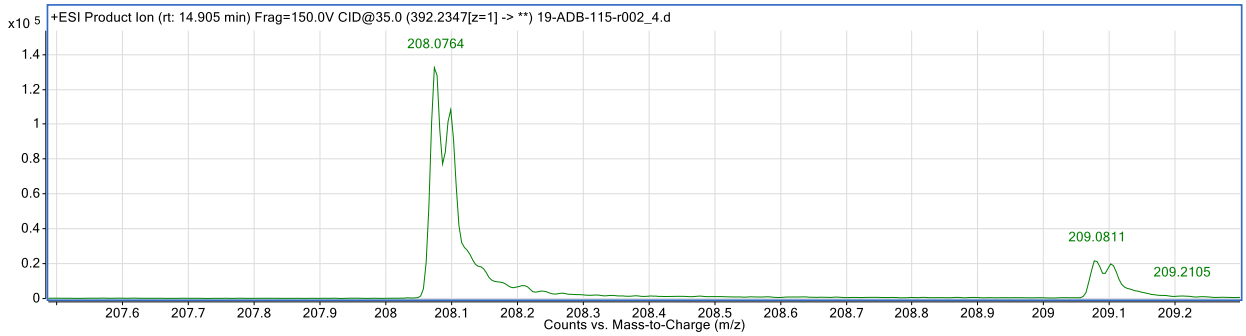
25V



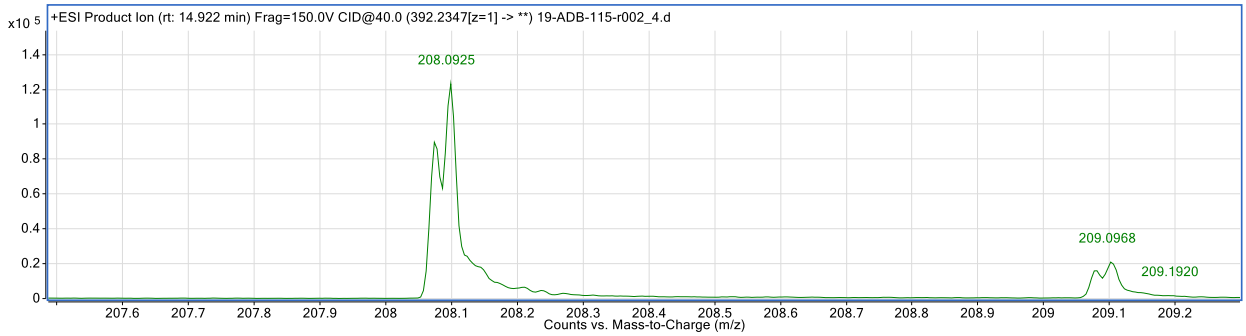
30V


+ESI Product Ion (rt: 14.888 min) Frag=150.0V CID@30.0 (392.2347[z=1] -> **) 19-ADB-115-r002_4.d
x10 4
208.0765
208.2092
209.0795
Counts vs. Mass-to-Charge (m/z)

35V


+ESI Product Ion (rt: 14.905 min) Frag=150.0V CID@35.0 (392.2347[z=1] -> **) 19-ADB-115-r002_4.d
x10 5
208.0764
209.0811
209.2105
Counts vs. Mass-to-Charge (m/z)

40V


+ESI Product Ion (rt: 14.922 min) Frag=150.0V CID@40.0 (392.2347[z=1] -> **) 19-ADB-115-r002_4.d
x10 5
208.0925
209.0968
209.1920
Counts vs. Mass-to-Charge (m/z)

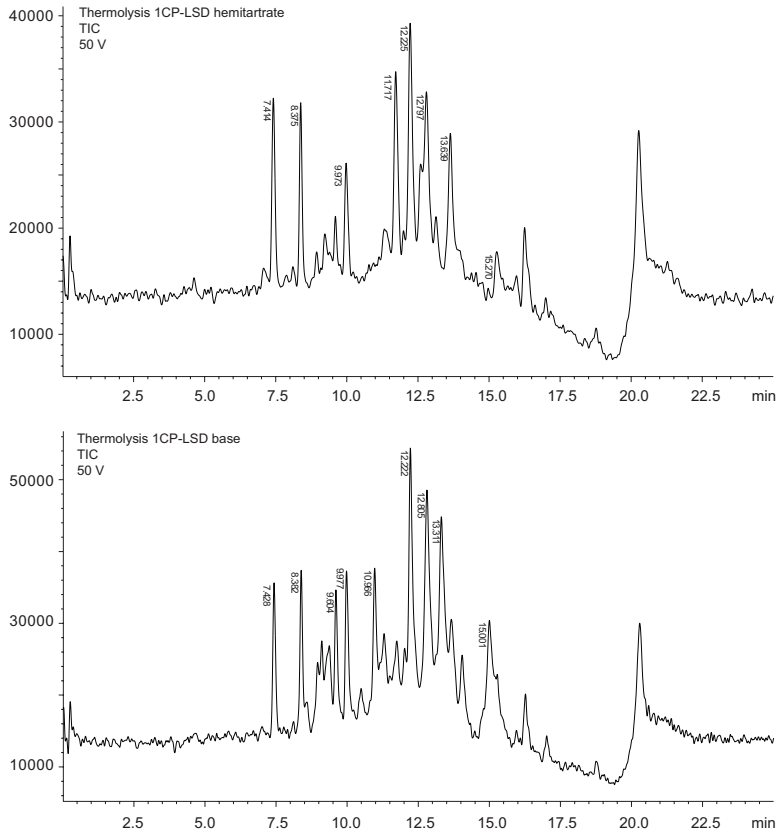
Thermolysis method

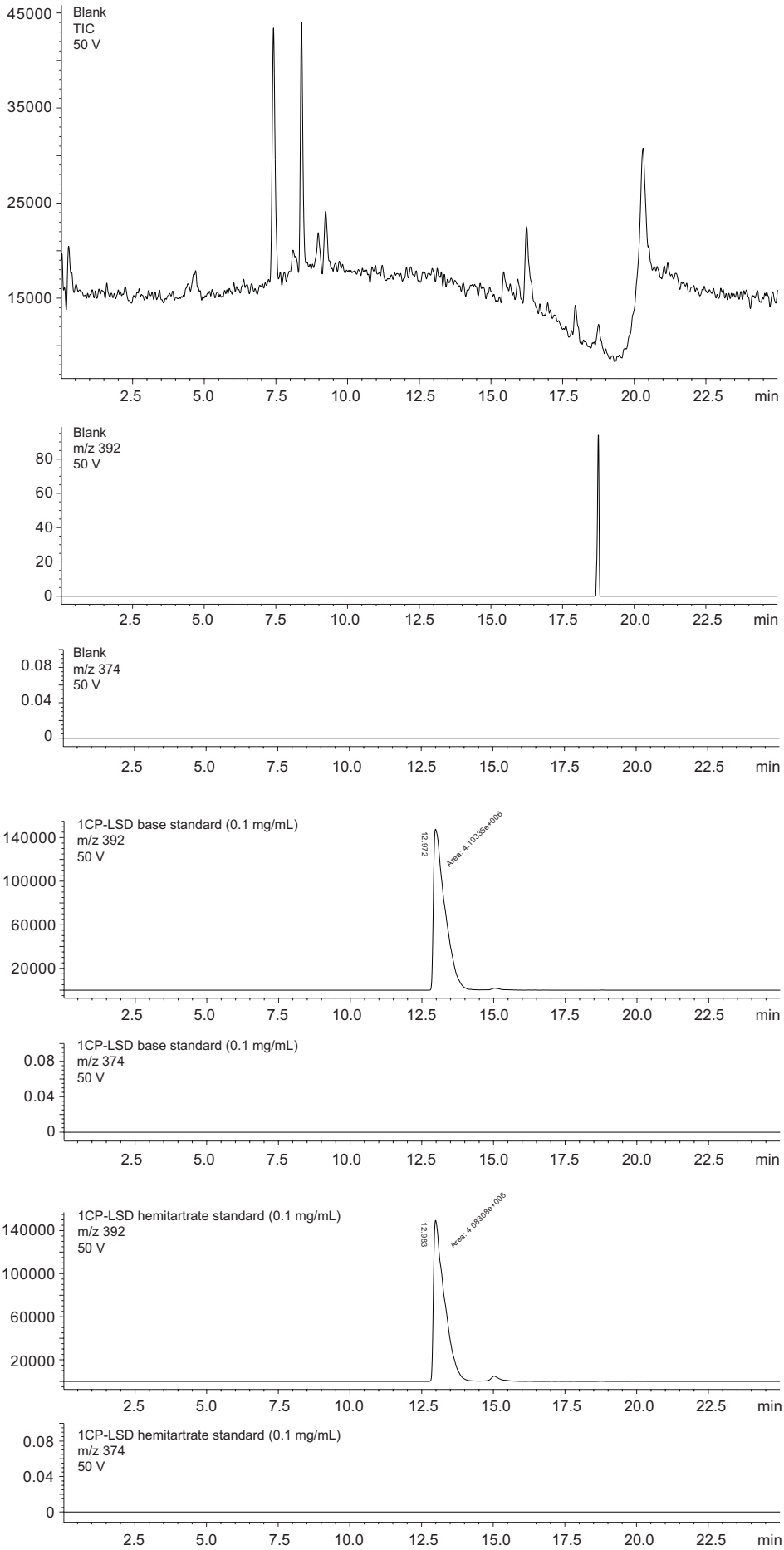
A sample (1 mg) in a glass vial (1.5 mL, purged with nitrogen and plugged with glass wool) was heated at 280°C for 3 min. This was allowed to cool to room temperature and the residue (dark brown for both the tartrate and freebase) was dissolved as much as possible (some insoluble material present) in methanol (500 µL). The mixture was centrifuged at 18,000 rpm (25,350 g) for 3 min and the supernatant was collected.

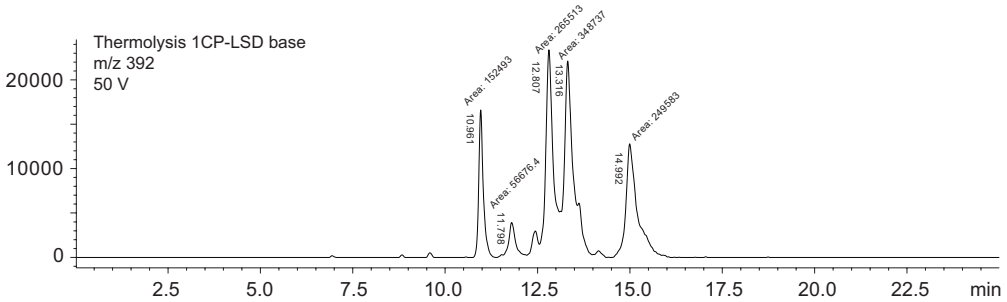
LC-ESI-MS
An aliquot (100 µL) was diluted with acetonitrile (150 µL, containing 0.1 % formic acid) and water (250 µL, containing 0.1 % formic acid). The mixture was passed through a spin filter (Costar Spin-X, nylon membrane, pore size 0.22 µm) and the filtrate was analyzed.

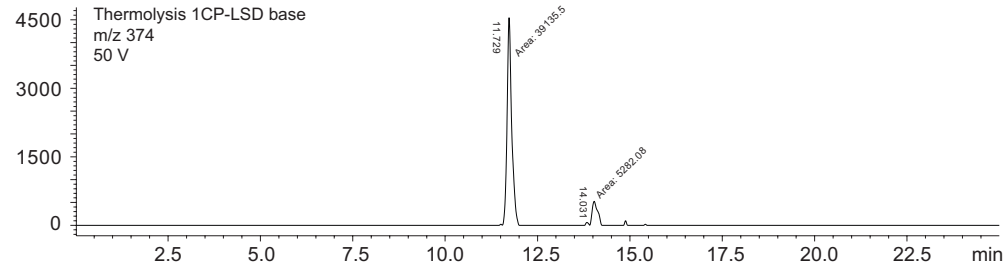
LC-MS was performed on Agilent 1100 LC system using an Allure® PFP Propyl (3 µm, pore size 60 Å; 50 mm x 2.1 mm) (Thames Restek, High Wycombe, UK). Mobile phase A: acetonitrile containing 0.1% formic acid' mobile phase B: water containing 0.1% formic acid). Elution profile: two % A (0–2 min), then linear gradient to 60 % A at 15 min; 60 % linear gradient to 80 % A at 18 min, and linear gradient down to 2 % A at 20 min and 2 % A for 5 min (run time 25 min); flow rate, 800 µL/min, 10 µL injected.

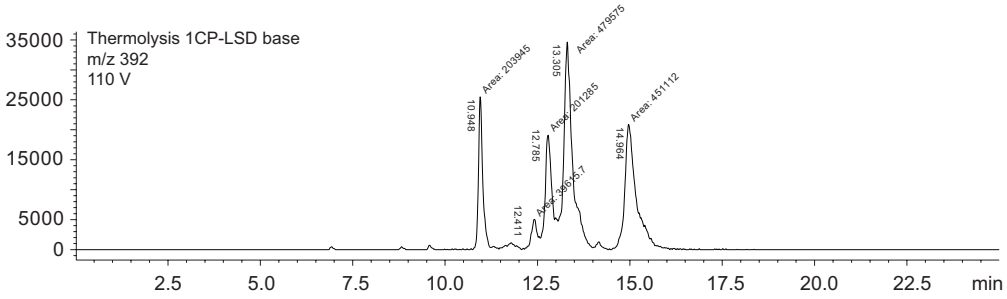
The LC system was coupled to a Hewlett Packard/Agilent 1100 MSD (Santa Clara, CA, USA) using the following conditions: positive ESI mode (full scan, m/z 70–500) with a fragmentor voltage as stated for in-source CID, capillary voltage 3500 V, drying gas (N_2) 12 L/min at 350 °C and nebulizer (N_2) pressure 50 psig. The mass spectrometer was tuned according to the manufacturer's instructions using ESI Tuning Mix G2421A (Agilent Technologies).

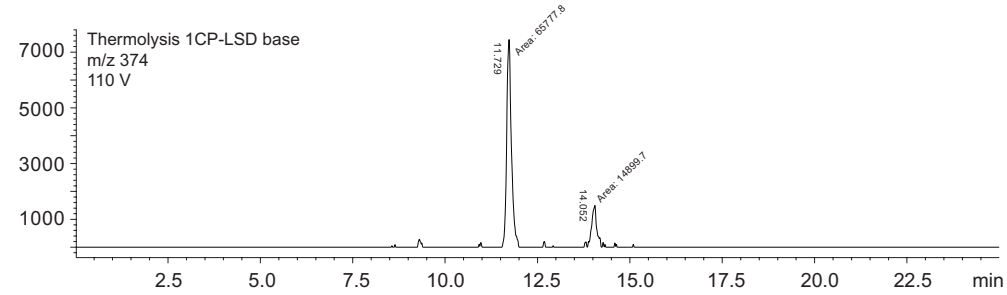


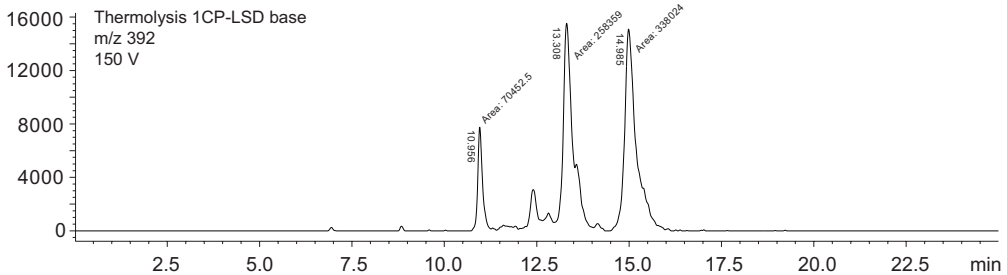

Blank
TIC
50 V
Blank
m/z 392
50 V
Blank
m/z 374
50 V
1CP-LSD base standard (0.1 mg/mL)
m/z 392
50 V
12.972
Area: 4.10358e+006
1CP-LSD base standard (0.1 mg/mL)
m/z 374
50 V
1CP-LSD hemitartrate standard (0.1 mg/mL)
m/z 392
50 V
12.983
Area: 4.08308e+006
1CP-LSD hemitartrate standard (0.1 mg/mL)
m/z 374
50 V
min

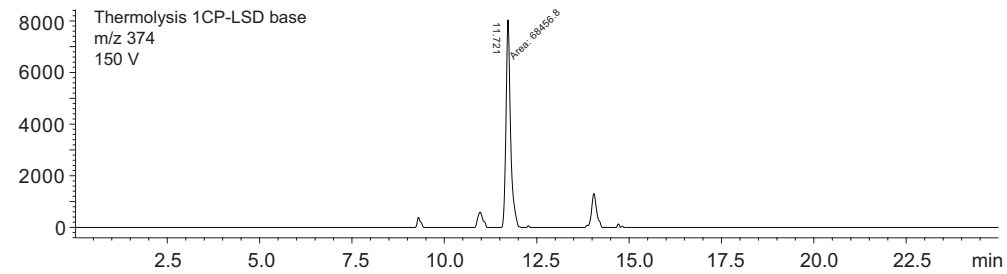

Thermolysis 1CP-LSD base
m/z 392
50 V
Area: 152493
10.961
Area: 56676.4
11.798
Area: 265513
12.807
Area: 348737
13.316
Area: 249583
14.992
20000
10000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

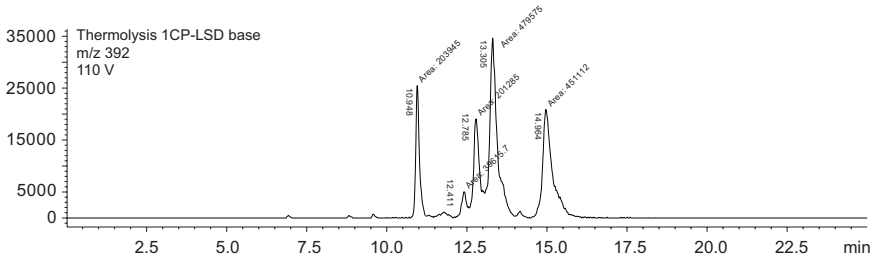

Thermolysis 1CP-LSD base
m/z 374
50 V
11.729
Area: 39135.5
14.031
Area: 5282.08
4500
3000
1500
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

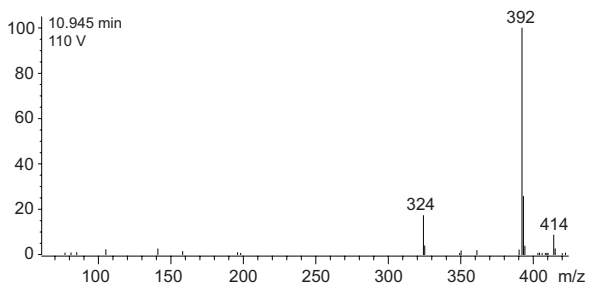

Thermolysis 1CP-LSD base
m/z 392
110 V
Area: 203945
10.948
12.411
Area: 38615.7
12.785
Area: 201285
13.305
Area: 475575
14.964
Area: 451112
35000
25000
15000
5000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

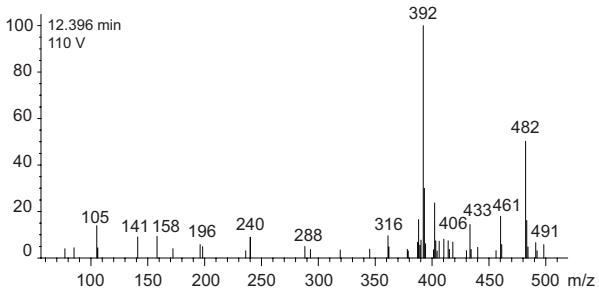

Thermolysis 1CP-LSD base
m/z 374
110 V
11.729
Area: 65777.8
14.052
Area: 14899.7
7000
5000
3000
1000
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

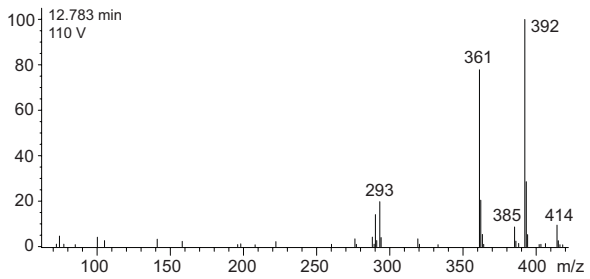

Thermolysis 1CP-LSD base
m/z 392
150 V
Area: 70452.5
10.956
13.308
Area: 258359
14.985
Area: 338024
16000
12000
8000
4000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

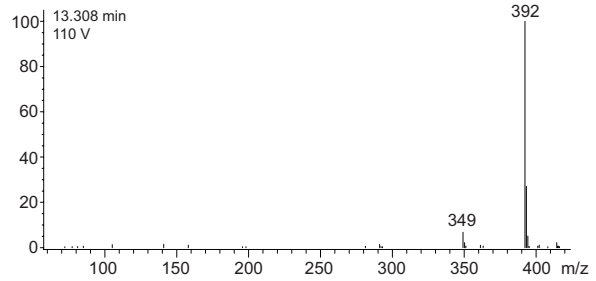

Thermolysis 1CP-LSD base
m/z 374
150 V
11.721
Area: 68466.8
8000
6000
4000
2000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min

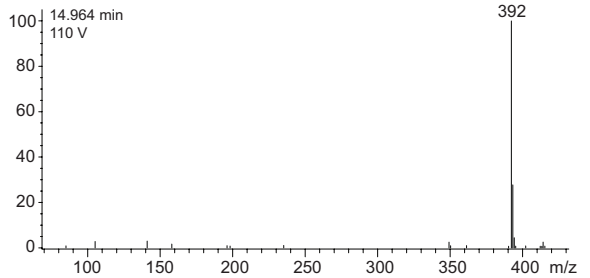

Thermolysis 1CP-LSD base
m/z 392
110 V
Area: 203945
Area: 479575
Area: 201285
Area: 451112
10.948
12.411
12.783
13.308
14.964
Thermolysis 1CP-LSD base
m/z 374
110 V
Area: 65777.8
Area: 14699.7
11.729
14.697
min

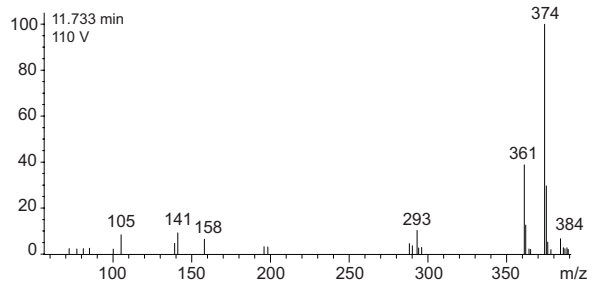

10.945 min
110 V
392
324
414
m/z

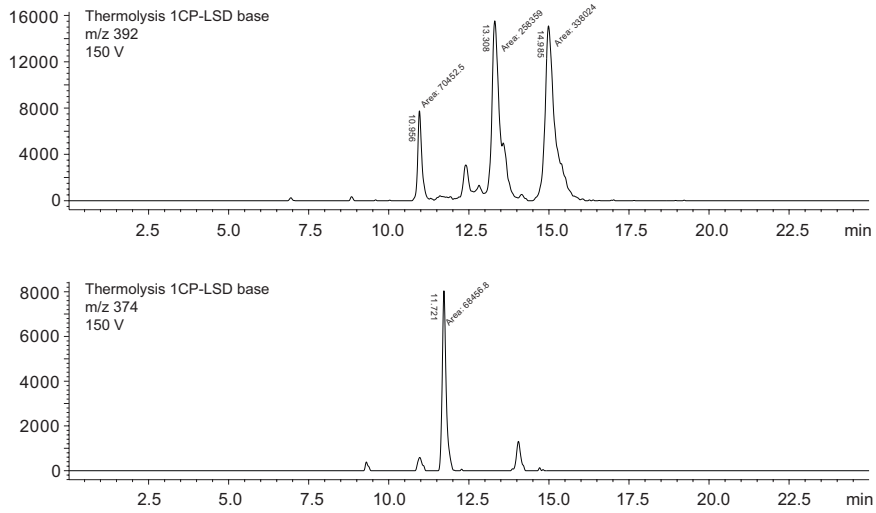

12.396 min
110 V
392
482
105
141
158
196
240
288
316
406
433
461
491
m/z

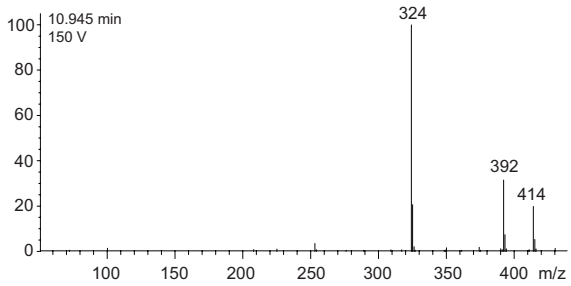

12.783 min
110 V
392
361
293
385
414
m/z

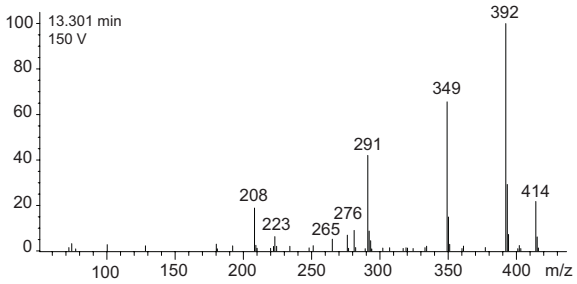

13.308 min
110 V
392
349
m/z

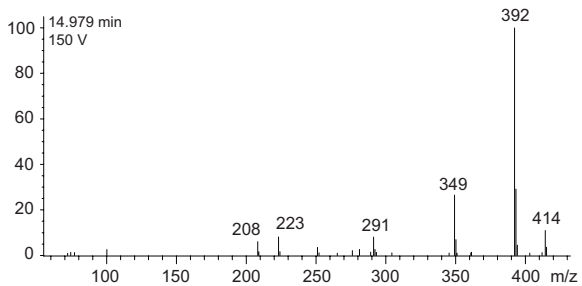

14.964 min
110 V
392
m/z

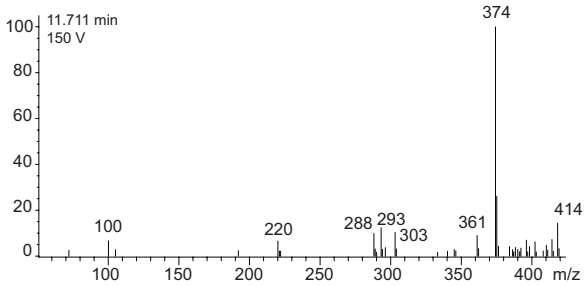

11.733 min
110 V
374
361
105
141
158
293
384
m/z

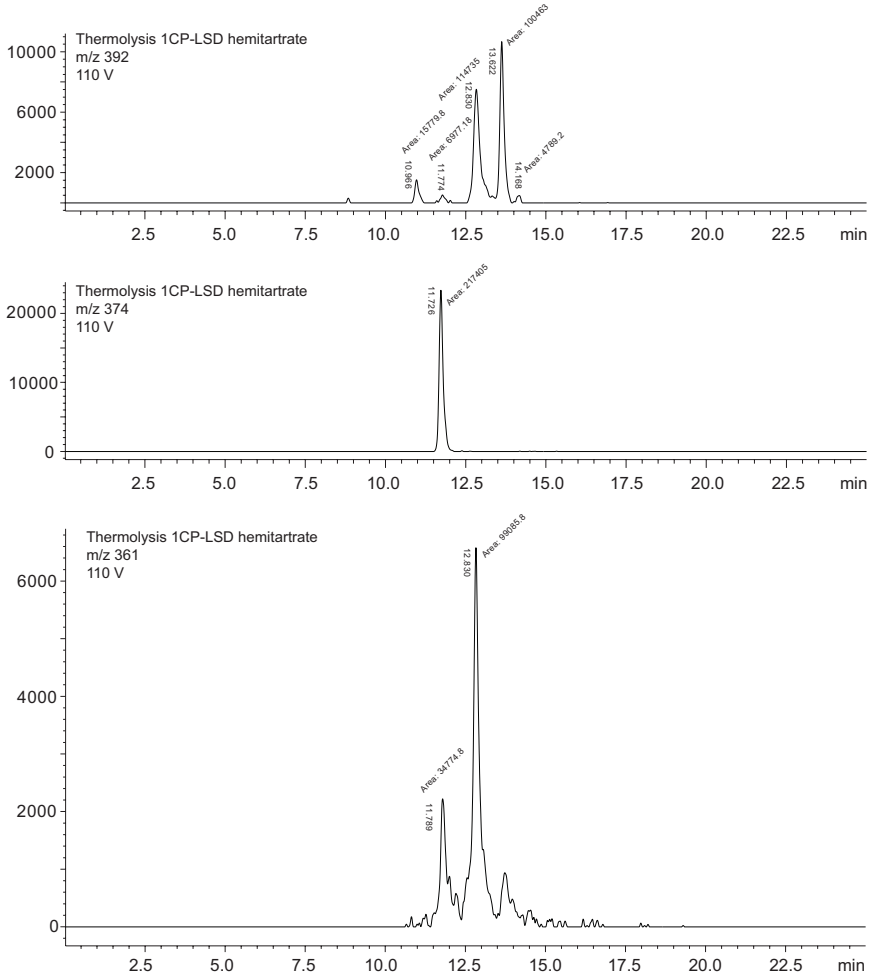

Thermolysis 1CP-LSD base
m/z 392
150 V
10.996
Area: 70452.5
13.308
Area: 258359
14.986
Area: 336024
Thermolysis 1CP-LSD base
m/z 374
150 V
11.721
Area: 68468.8
min

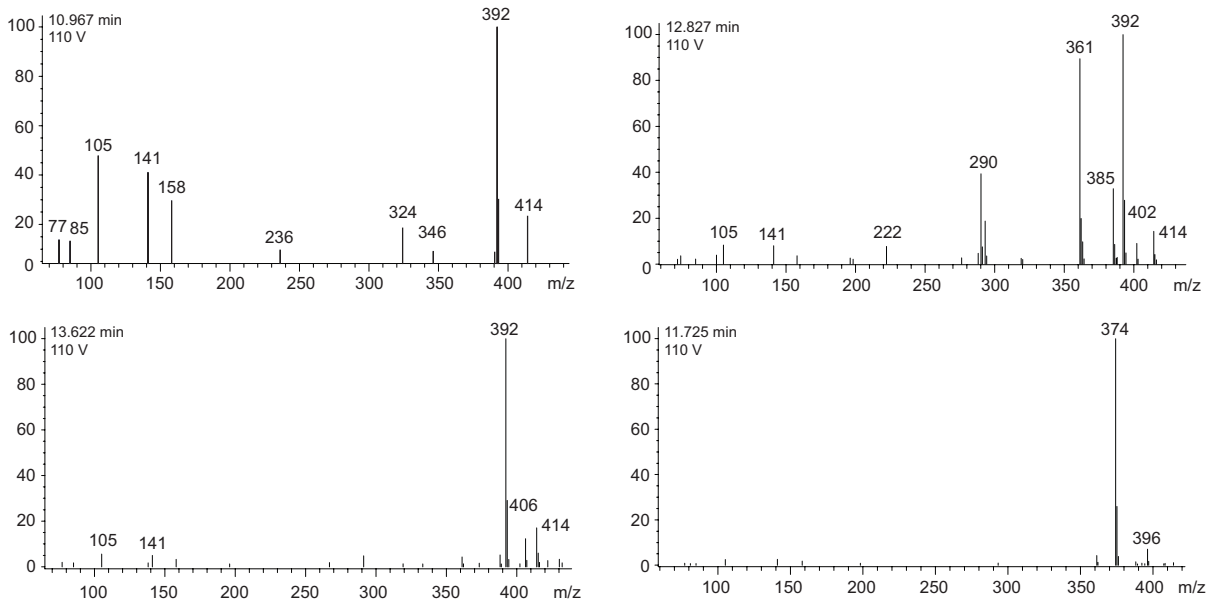

10.945 min
150 V
324
392
414
m/z

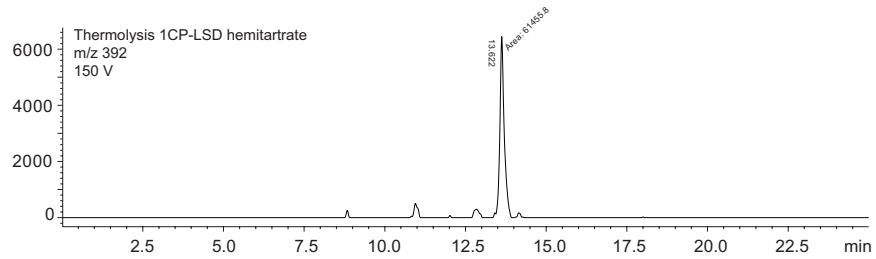

13.301 min
150 V
392
349
291
208
223
265
276
414
m/z

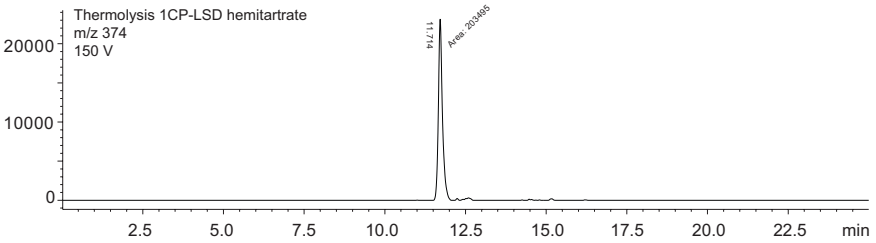

14.979 min
150 V
392
349
208
223
291
414
m/z

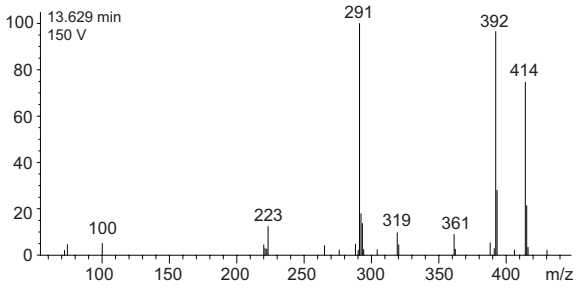

11.711 min
150 V
374
100
220
288
293
303
361
414
m/z

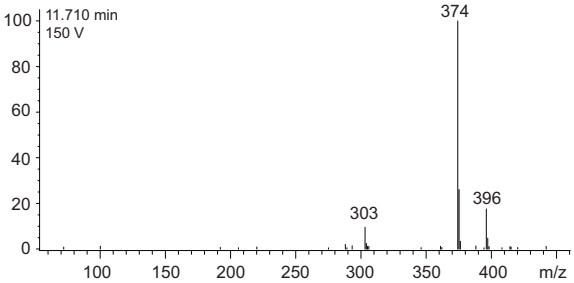

Thermolysis 1CP-LSD hemitartrate
m/z 392
110 V
Area: 15778.6
10.986
Area: 114735
12.830
Area: 6977.16
11.774
13.622
Area: 100463
Area: 4789.2
14.168
min
Thermolysis 1CP-LSD hemitartrate
m/z 374
110 V
11.726
Area: 217405
min
Thermolysis 1CP-LSD hemitartrate
m/z 361
110 V
12.830
Area: 99035.8
Area: 3474.8
11.789
min


10.967 min
110 V
392
105
141
158
77
85
236
324
346
414
m/z
12.827 min
110 V
392
361
290
385
402
105
141
222
414
m/z
13.622 min
110 V
392
406
414
105
141
m/z
11.725 min
110 V
374
396
m/z

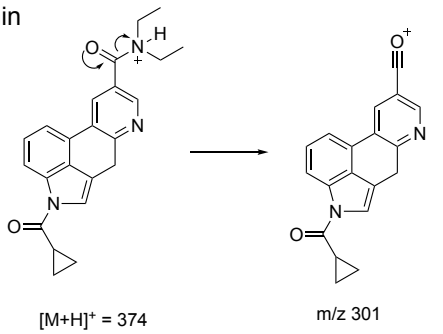

Thermolysis 1CP-LSD hemitartrate
m/z 392
150 V
13.622
Area: 61455.6
6000
4000
2000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min


Thermolysis 1CP-LSD hemitartrate
m/z 374
150 V
11.714
Area: 203485
20000
10000
0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
22.5
min


13.629 min
150 V
100
80
60
40
20
0
100
223
291
319
361
392
414
100
150
200
250
300
350
400
m/z

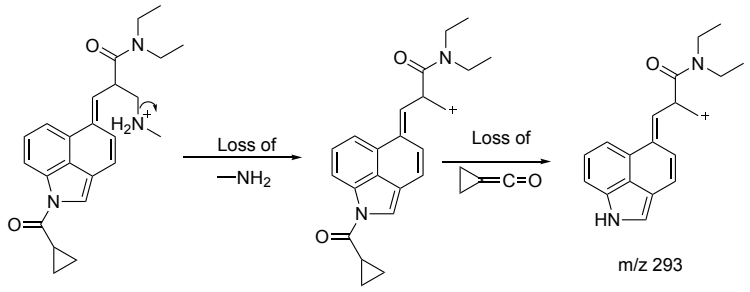

11.710 min
150 V
100
80
60
40
20
0
303
374
396
100
150
200
250
300
350
400
m/z

~11.7 min

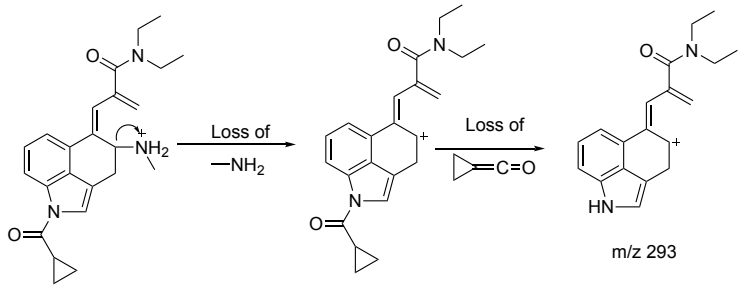


[M+H]+ = 374 m/z 301

~12.8 min - peak with m/z 361

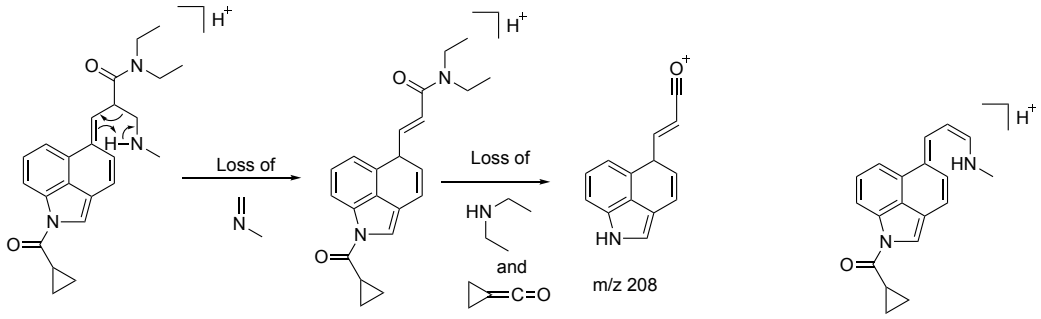


[M+H]+ = 392 m/z 361 m/z 293

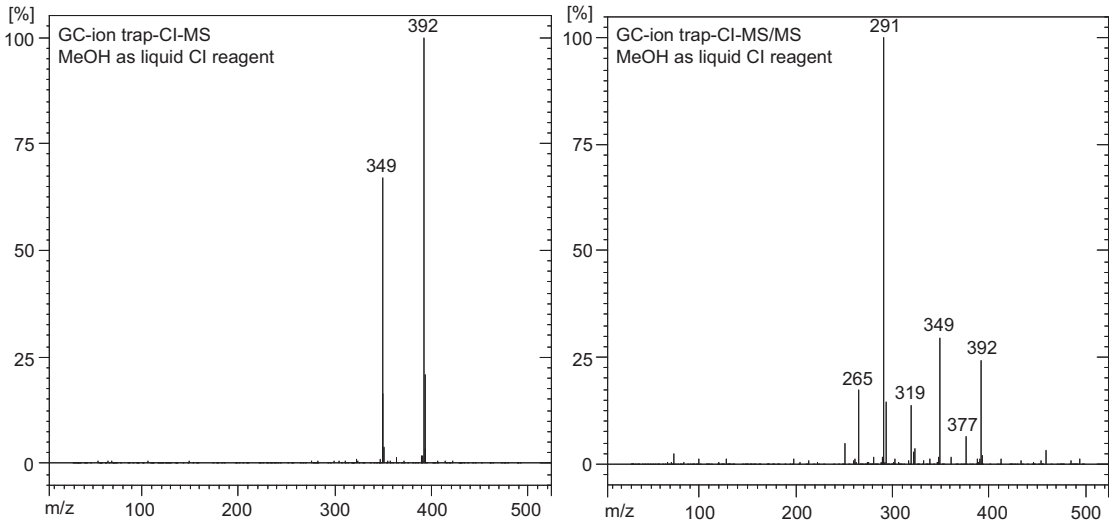


M+H = 392 m/z 361 m/z 293

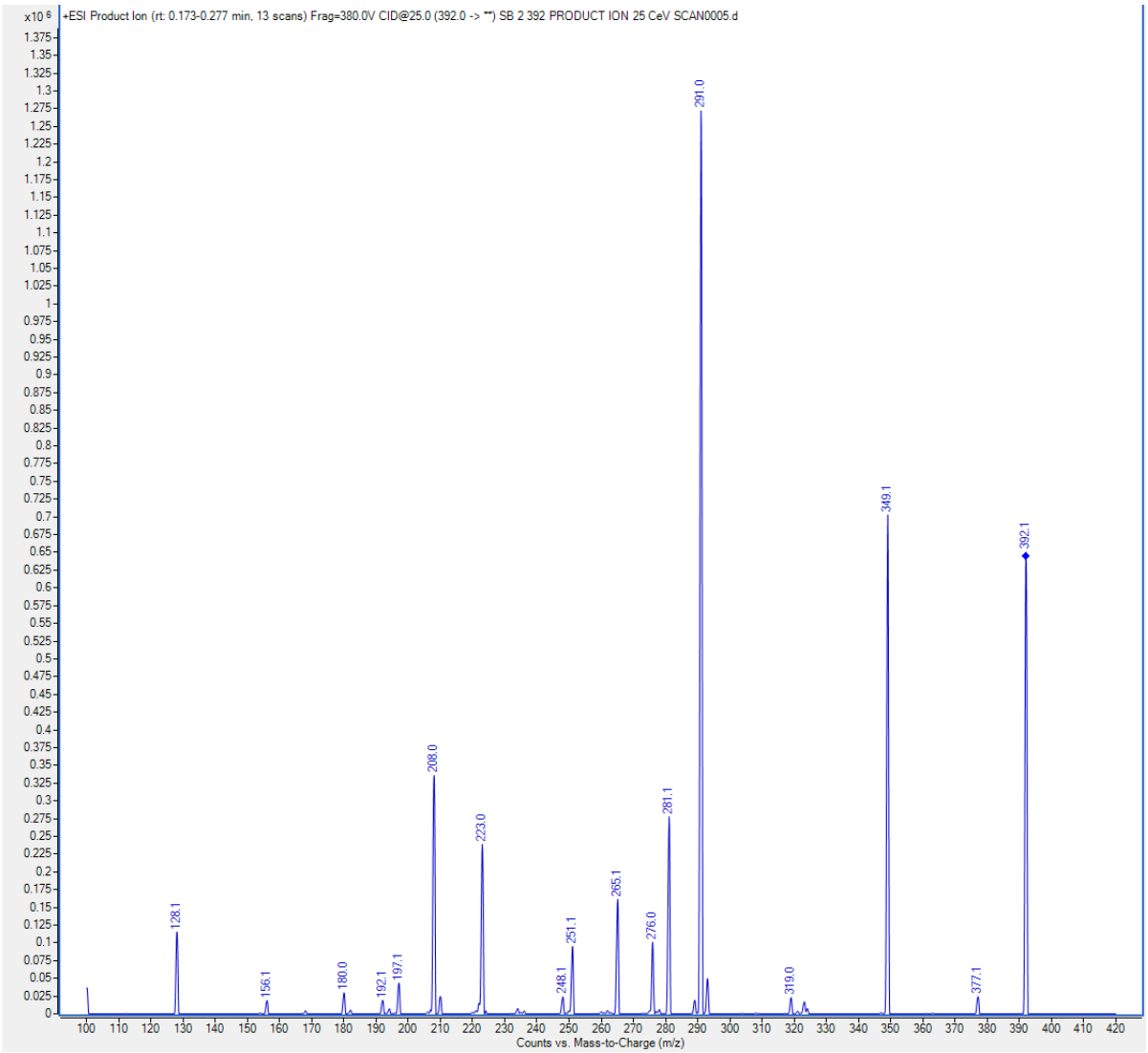
or ~13.3 min - peak with m/z 349



[M+H]+ = 392 m/z 349 m/z 208 m/z 291

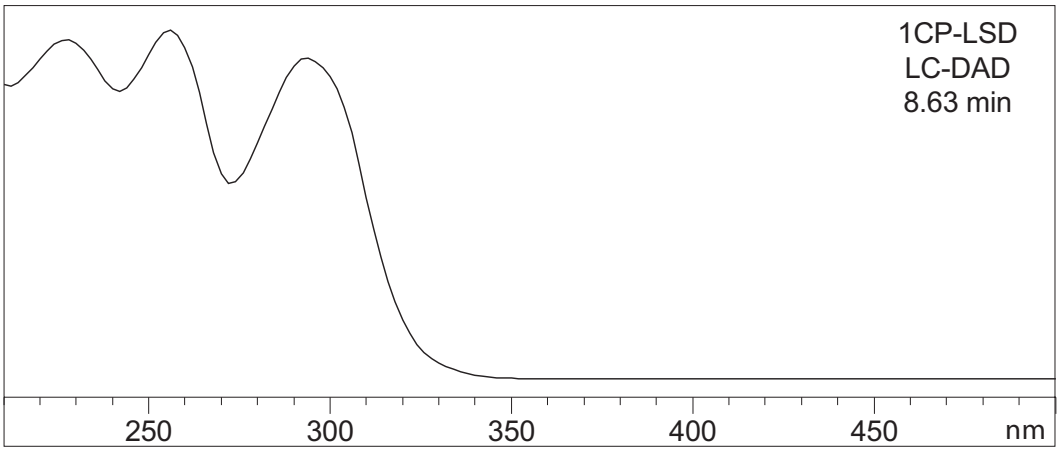


ESI-QqQ-MS/MS of 1CP-LSD



HPLC-DAD method

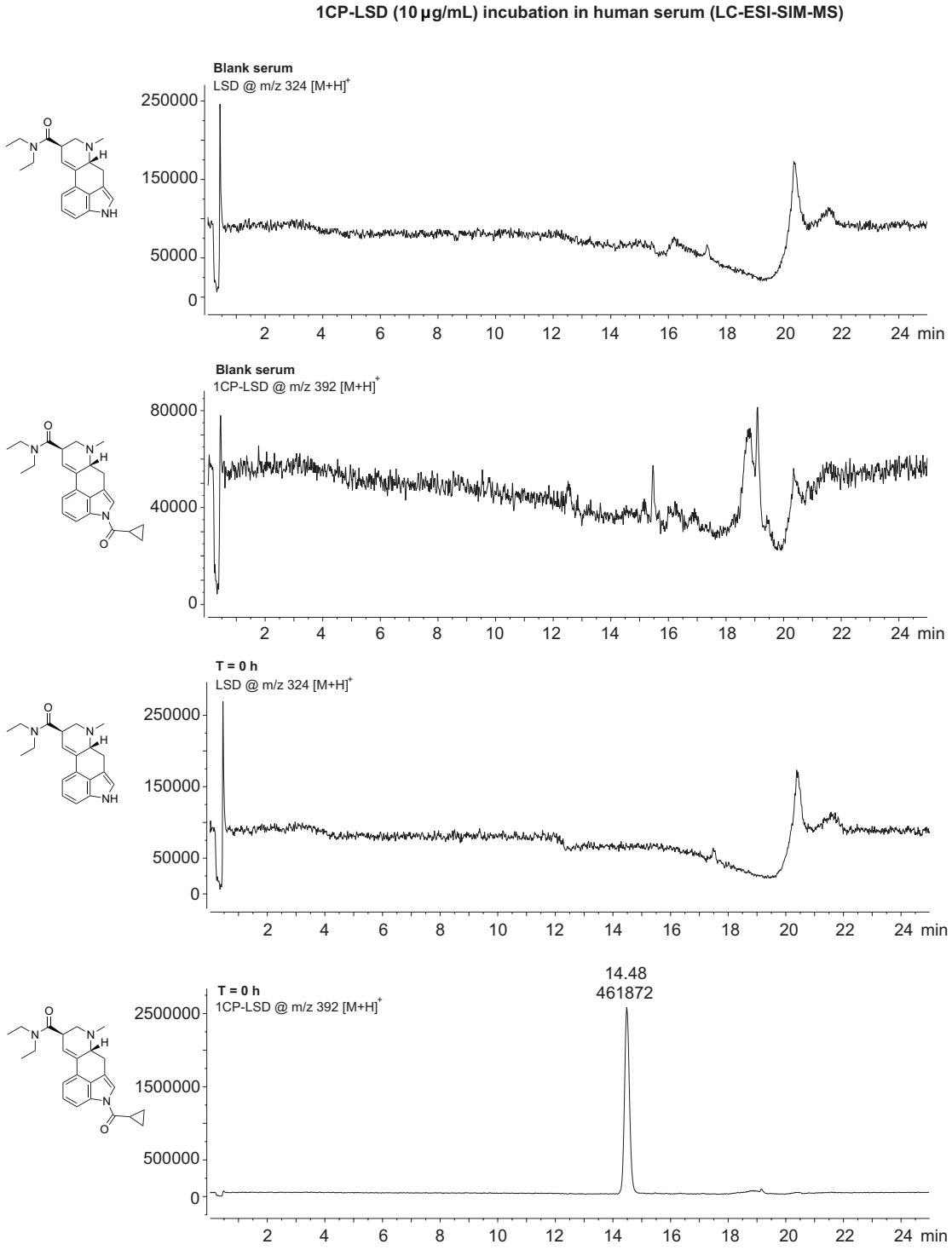
An Agilent 1100/1200 liquid chromatography system (quaternary pump G1311A, degasser G1322A, autosampler G1313A, column oven G1316A) coupled to a UV diode array detector (G1315D) was used using a Zorbax Eclipse XDB-C18 column (150 mm × 4.6 mm, 5 µm, Agilent). The column oven was set to 25°C. The mobile phases were 0.1% formic acid in water (A) and 0.1% formic acid in methanol (B). The gradient elution commenced with 100% A and ramped to 100% B in 10 min and held for 2 min, followed by a return to starting conditions at the 20 min time point. The flow rate was 1.0 mL/min. The injection volume was 10 µL. The diode array detection window was set at 195–500 nm (2 nm steps).



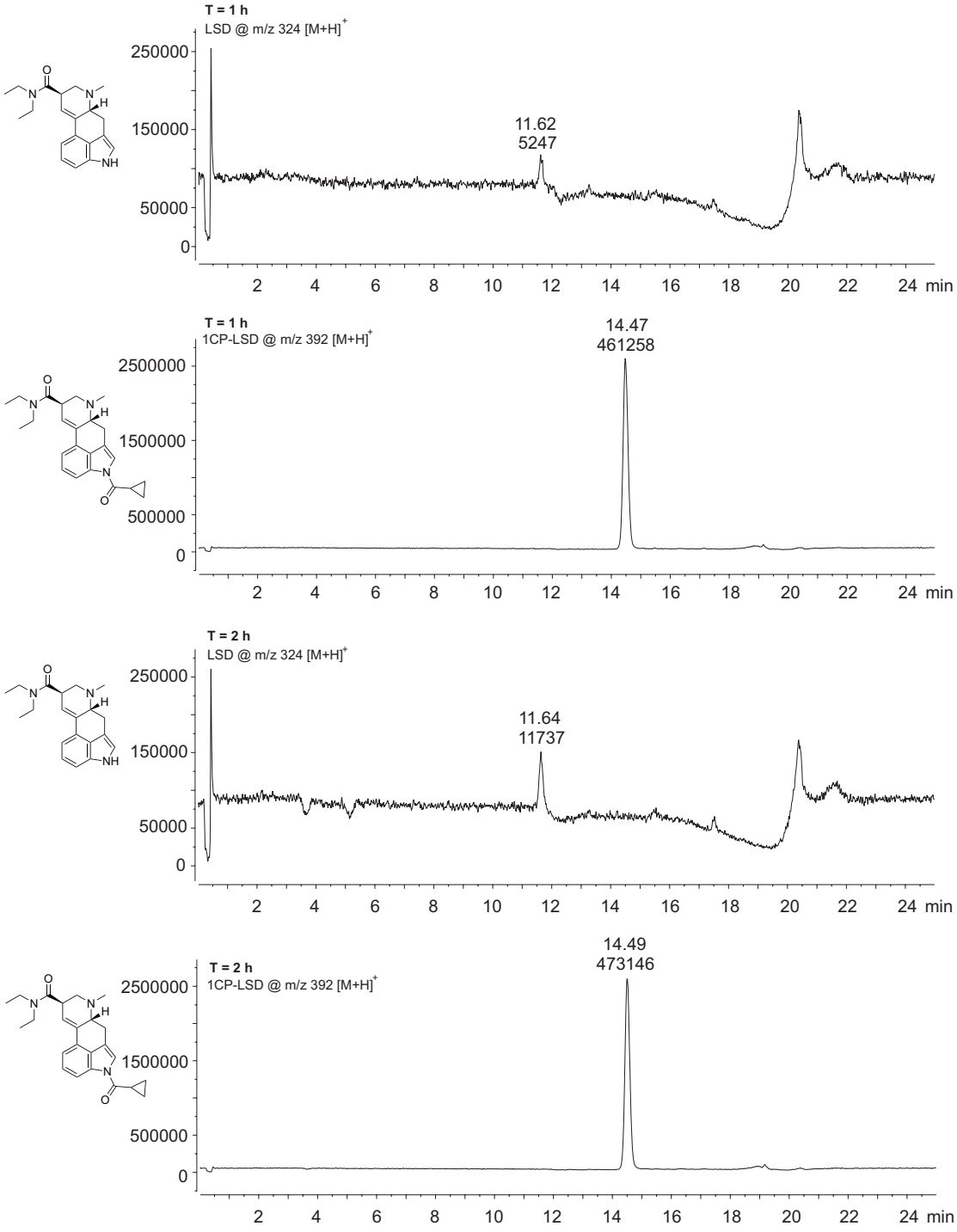
Serum containing 1CP-LSD or 1P-LSD (10 µg/mL, both as hemitartrates, 2:1) was incubated at 37°C and samples (10 µL) were removed at various times. These were diluted with acetonitrile/water (990 µL, 1:1, containing 0.1 % formic acid) and centrifuged at 18,000 rpm for 3 min. The supernatant was then passed through a Nylon filter (0.22 µm, Costar® Spin-X® centrifuge tube filter) and the filtrate was analysed by LC-ESI-MS.

LC-MS was performed on Agilent 1100 LC system using an Allure® PFP Propyl (3 µm, pore size 60 Å; 50 x 2.1 mm; part no. 9169552) (Thames Restek, High Wycombe HP14 4HW, UK): eluent A – acetonitrile containing 0.1% formic acid, eluent B – water containing 0.1% formic acid); 2 % A (0 - 2 min.) a linear gradient up to 60 % A at 15 min, 60 %, a linear gradient up to 80 % A at 18 min, a linear gradient down to 2 % A at 20 min and 2 % A for 5 min (run-time 25 min); flow rate, 800 µL/min, 10 µL injected.

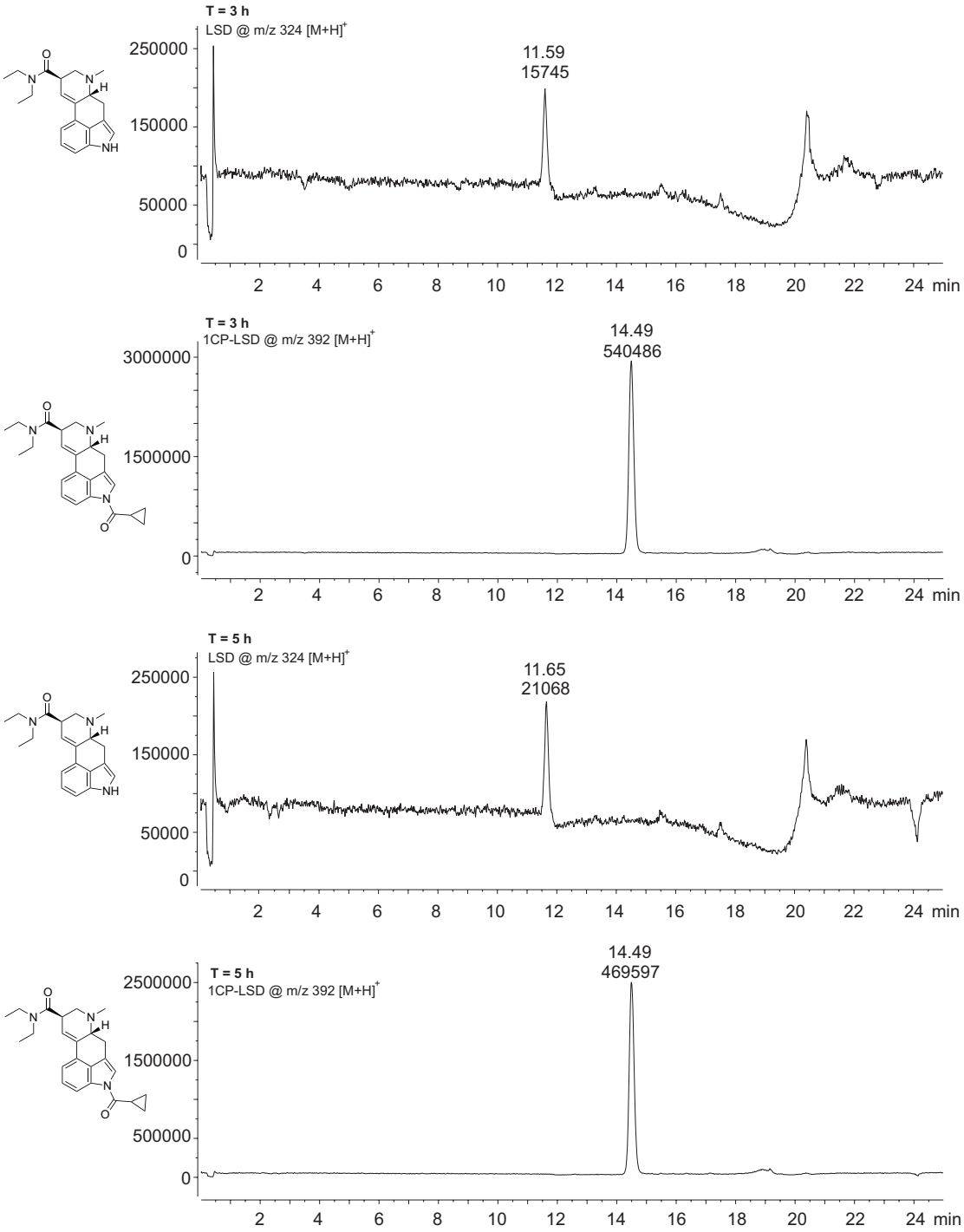
The LC system was coupled to a Hewlett Packard/Agilent 1100 MSD (Santa Clara, CA, USA) using the following conditions: positive ESI mode with a fragmentor voltage of 50 V for in-source CID), capillary voltage 3500 V, drying gas (N_2) 12 L/min at 350 °C and nebulizer (N_2) pressure 50 psig. The mass spectrometer was tuned according to the manufacturer's instructions using ESI Tuning Mix G2421A (Agilent Technologies). For SIM, m/z's 392, 380 and 324 were used for 1CP-LSD, 1P-LSD and LSD respectively. For full scan, a range of m/z 70-500 was used.

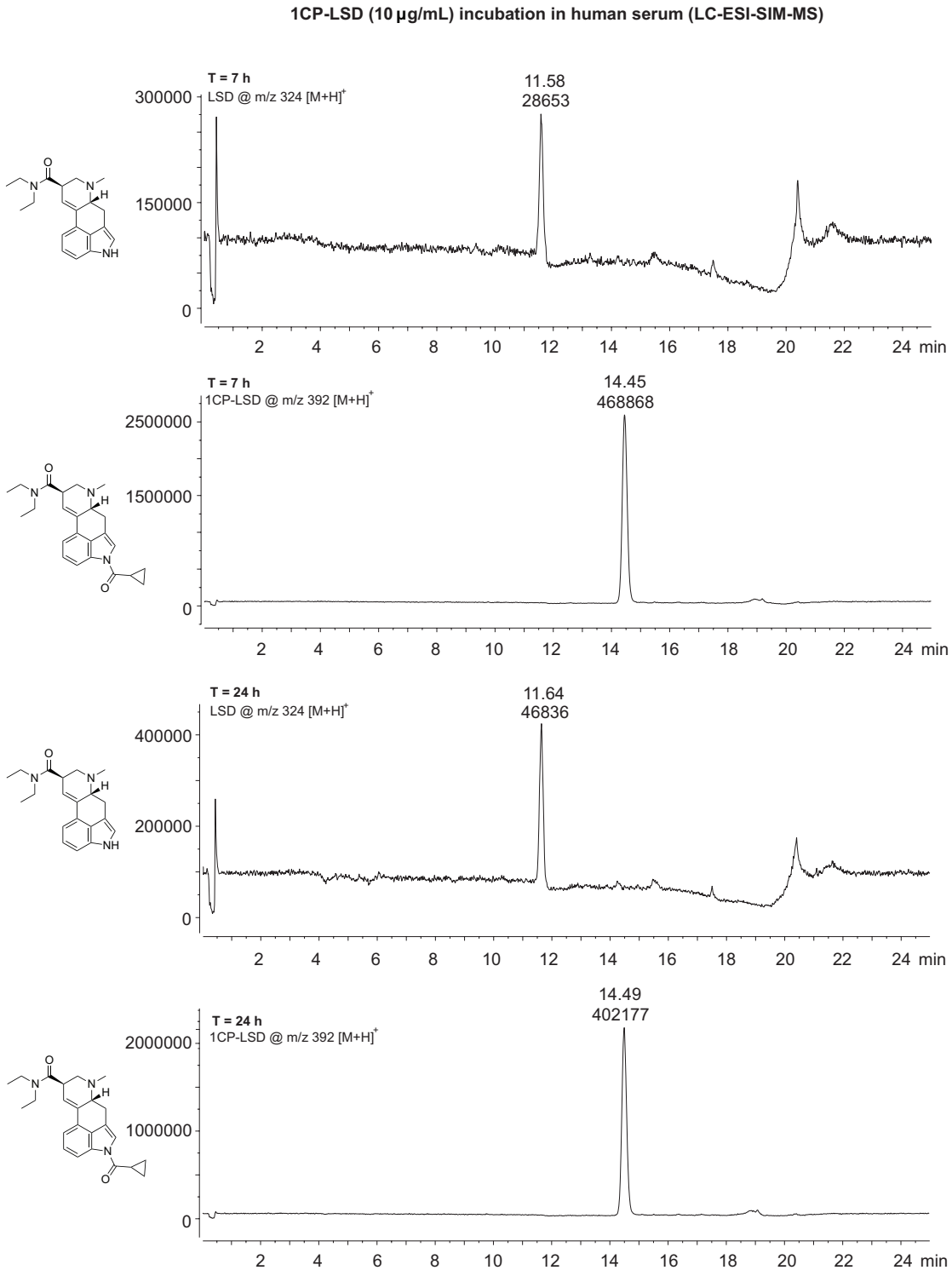

1CP-LSD (10 µg/mL) incubation in human serum (LC-ESI-SIM-MS)
Blank serum
LSD @ m/z 324 [M+H]+
250000
150000
50000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
Blank serum
1CP-LSD @ m/z 392 [M+H]+
80000
40000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
T = 0 h
LSD @ m/z 324 [M+H]+
250000
150000
50000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
T = 0 h
1CP-LSD @ m/z 392 [M+H]+
14.48
461872
2500000
1500000
500000
0
2 4 6 8 10 12 14 16 18 20 22 24 min

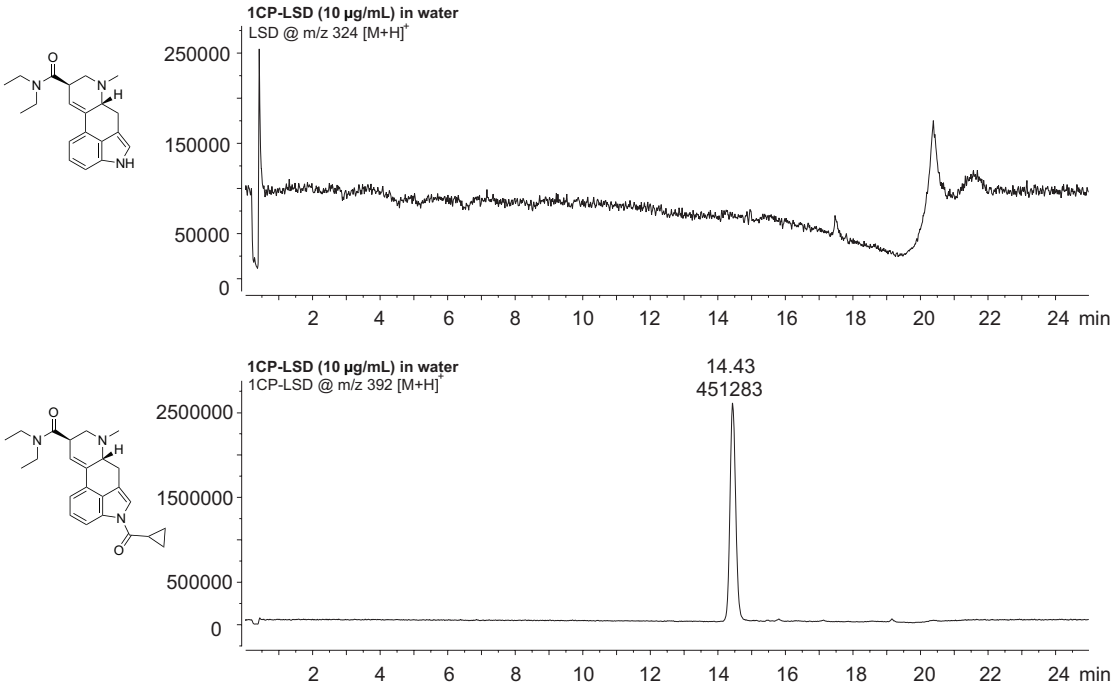
1CP-LSD (10 µg/mL) incubation in human serum (LC-ESI-SIM-MS)



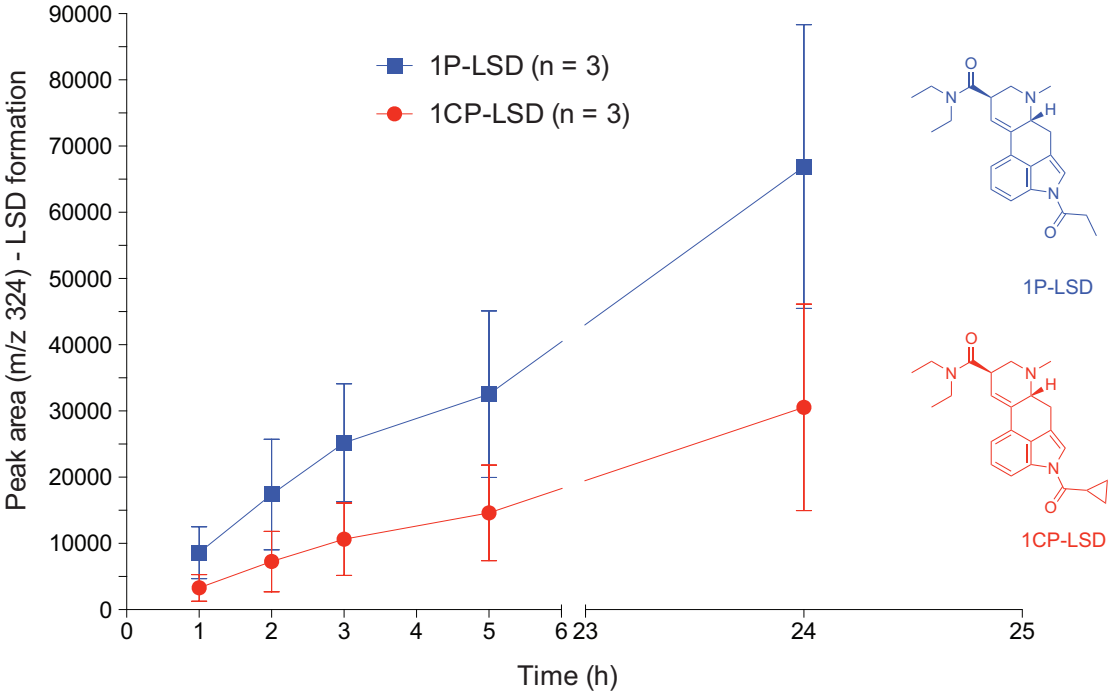
1CP-LSD (10 µg/mL) incubation in human serum (LC-ESI-SIM-MS)

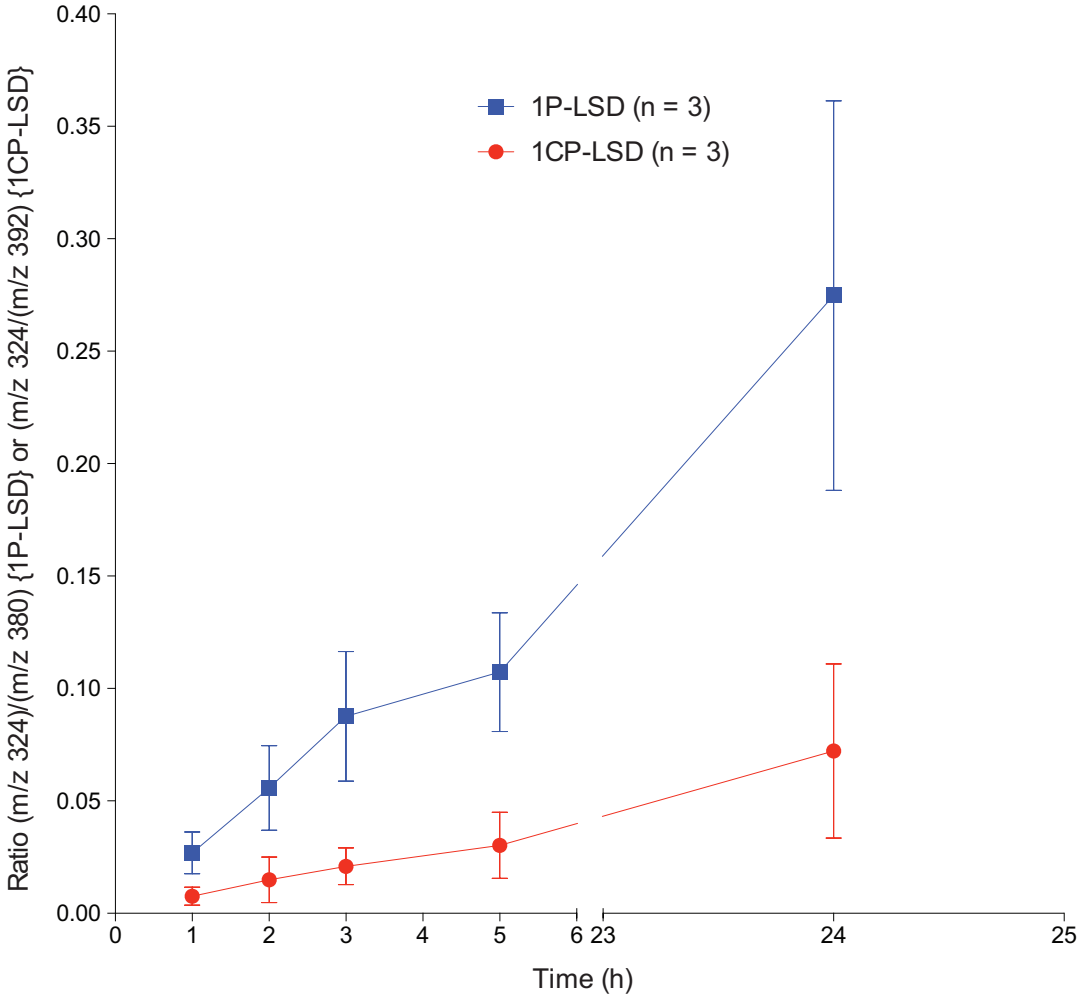



1CP-LSD (10 µg/mL) incubation in human serum (LC-ESI-SIM-MS)
T = 7 h
LSD @ m/z 324 [M+H]+
11.58
28653
300000
150000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
T = 7 h
1CP-LSD @ m/z 392 [M+H]+
14.45
468868
2500000
1500000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
T = 24 h
LSD @ m/z 324 [M+H]+
11.64
46836
400000
200000
0
2 4 6 8 10 12 14 16 18 20 22 24 min
T = 24 h
1CP-LSD @ m/z 392 [M+H]+
14.49
402177
2000000
1000000
0
2 4 6 8 10 12 14 16 18 20 22 24 min


1CP-LSD (10 µg/mL) in water
LSD @ m/z 324 [M+H]+
250000
150000
50000
0
2
4
6
8
10
12
14
16
18
20
22
24 min
1CP-LSD (10 µg/mL) in water
1CP-LSD @ m/z 392 [M+H]+
14.43
451283
2500000
1500000
500000
0
2
4
6
8
10
12
14
16
18
20
22
24 min

LSD formation after incubation of 1P-LSD and 1CP-LSD with human serum





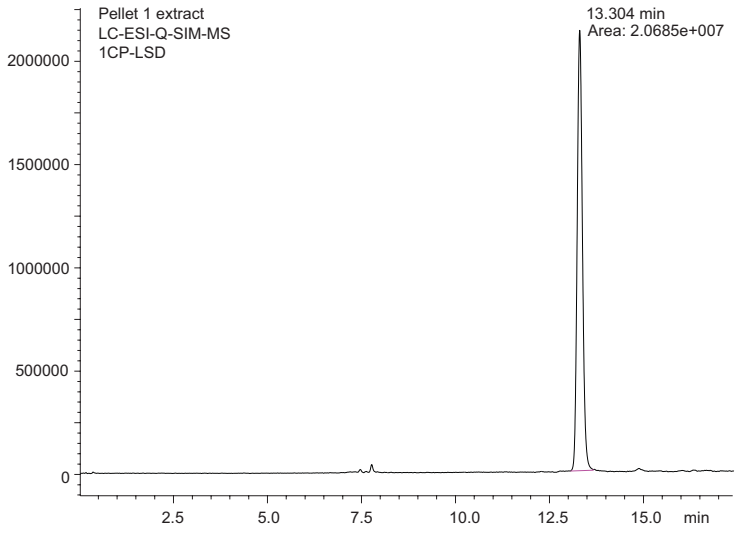
Pellet and blotter extraction

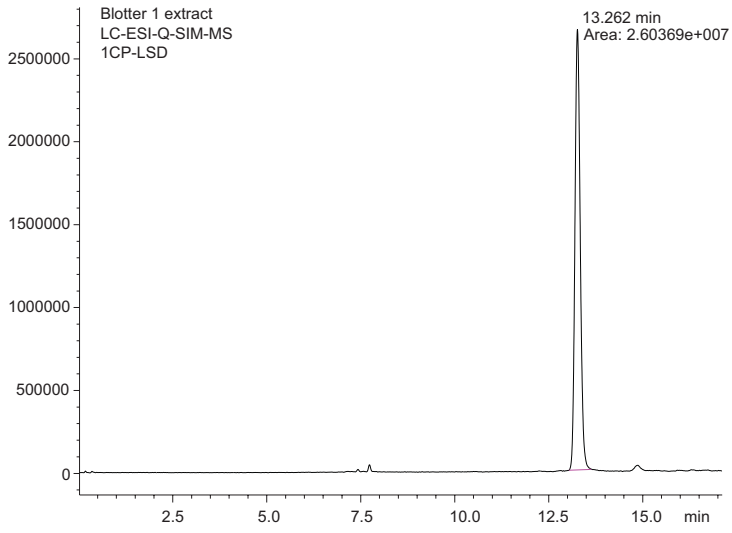
The sample (pellet - labeled to contain 150 µg 1CP-LSD hemitartrate or blotter – labeled to contain 100 µg 1CP-LSD freebase) was sonicated with acetonitrile/water (1:1, containing 0.1 % formic acid (AWFA); 4 x 2 mL for 5 min each time), centrifuged (5,000 rpm for 3 min.) and the supernatant was collected. The supernatants were combined and centrifuged (5,000 rpm for 5 min). The supernatant was collected and made up to 10 mL with AWFA. An aliquot (100 µL) was diluted to 10 mL with AWFA. A 1CP-LSD standard curve (0.3750, 0.1875, 0.0938, 0.0469, 0.0234 and 0.0117 µg/per mL) was prepared in AWFA.

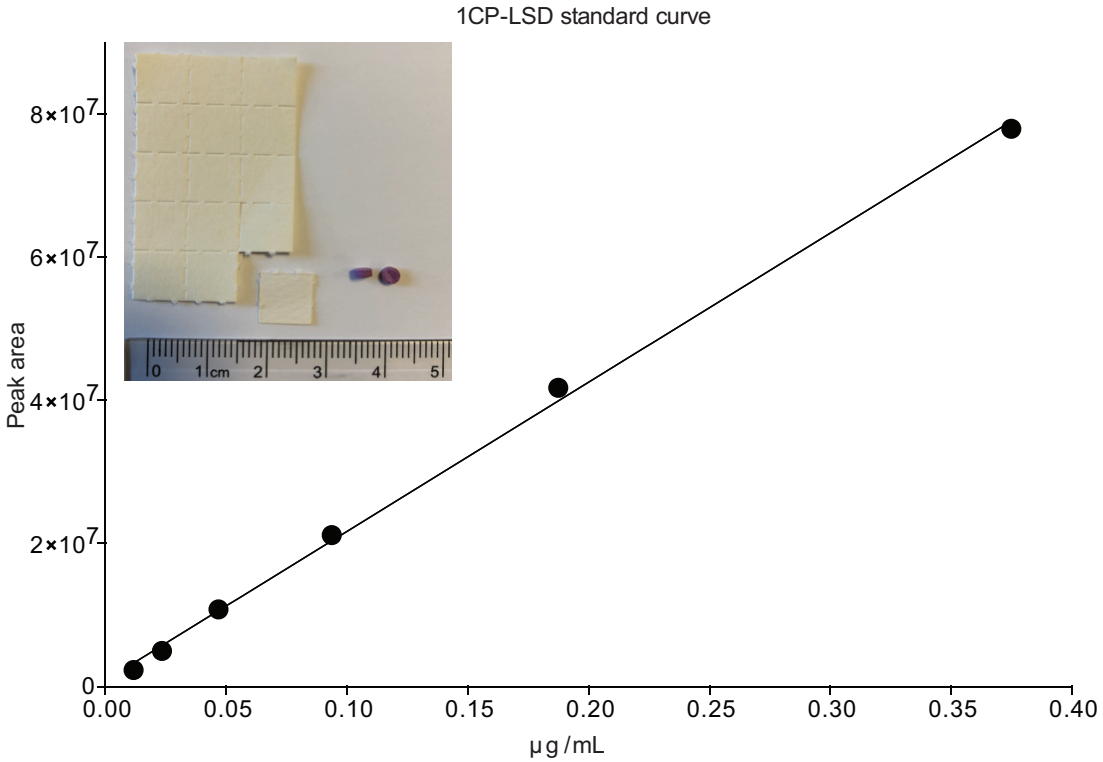
Results:

Pellet 1: 97 µg freebase (116 µg hemitartrate equivalent; pellet weight 14.9 mg)
Pellet 2: 105 µg freebase (125 µg hemitartrate equivalent; pellet weight 14.2 mg)

Blotter 1: 120 µg freebase (blotter weight 16.0 mg)
Blotter 2: 112 µg freebase (blotter weight 15.5 mg)





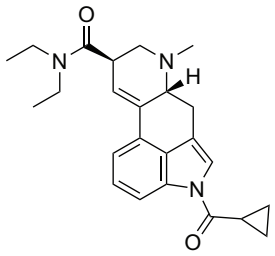


	µg/mL		Peak area		
	X	Err. Bar	Y1	Y2	Y3
	0.011719		2311890.00000	2343940.00000	2307770.00000
	0.023438		4941250.00000	5029580.00000	5006670.00000
	0.046875		1.05214e+007	1.14813e+007	1.04113e+007
	0.093750		2.10664e+007	2.12056e+007	2.12797e+007
	0.187500		4.17822e+007	4.19014e+007	4.15572e+007
	0.375000		7.87946e+007	7.75800e+007	7.74465e+007
Pellet 1			2.06850e+007	2.12446e+007	2.12866e+007
Pellet 2			2.25967e+007	2.27479e+007	2.31372e+007
Blotter 1			2.60369e+007	2.59435e+007	2.54800e+007
Blotter 2			2.41236e+007	2.41803e+007	2.41447e+007

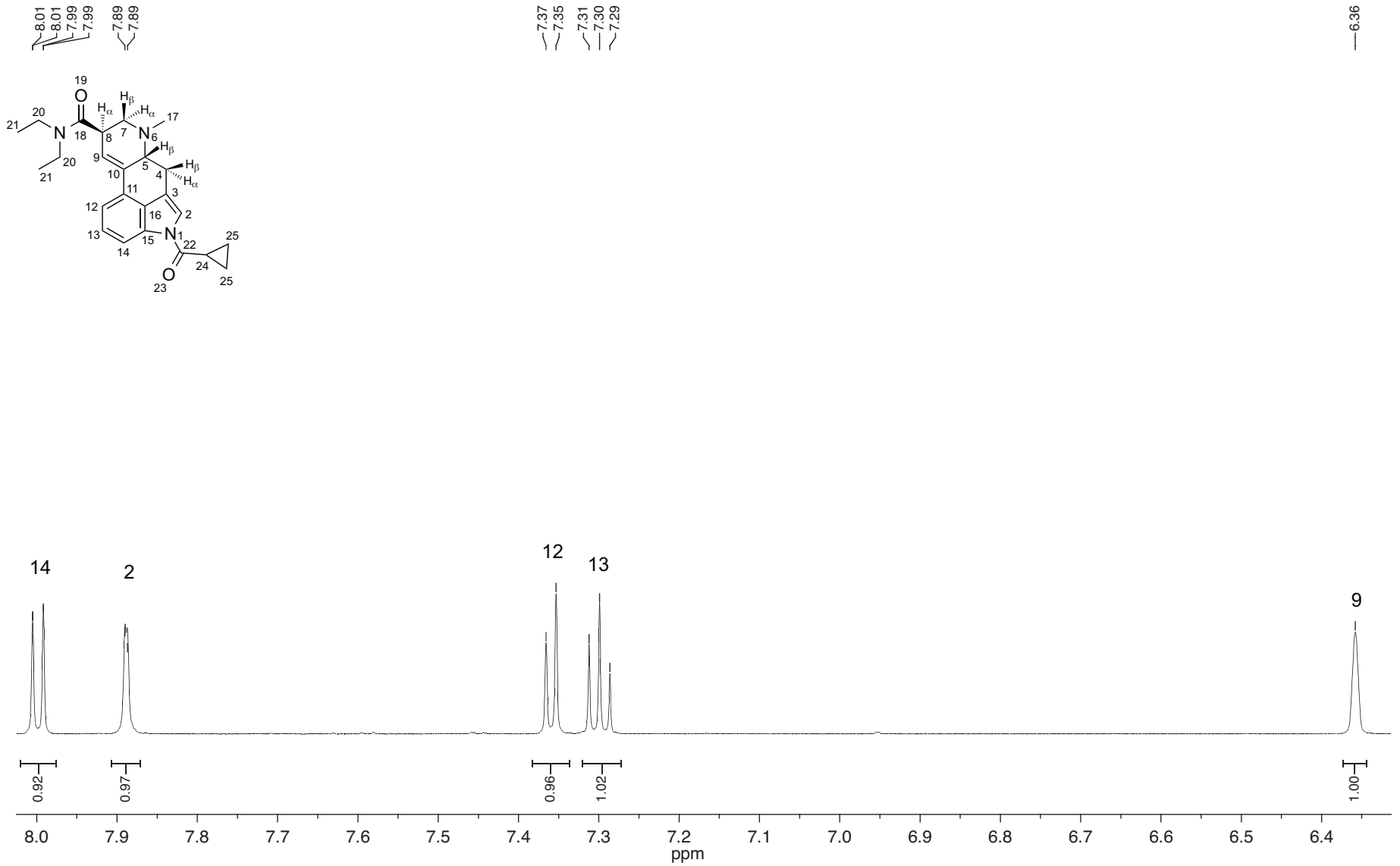
	Peak area
Slope	2.083e+008 ± 2.163e+006
Y-intercept when X=0.0	861720 ± 382333
X-intercept when Y=0.0	-0.004136
1/slope	4.800e-009
95% Confidence Intervals	
Slope	2.038e+008 to 2.129e+008
Y-intercept when X=0.0	51174 to 1.672e+006
X-intercept when Y=0.0	-0.008153 to -0.0002419
Goodness of Fit	
R square	0.9983

	µg/mL	Peak area
Pellet 1	0.097	2.107e+007
Pellet 2	0.105	2.283e+007
Blotter 1	0.120	2.582e+007
Blotter 2	0.112	2.415e+007

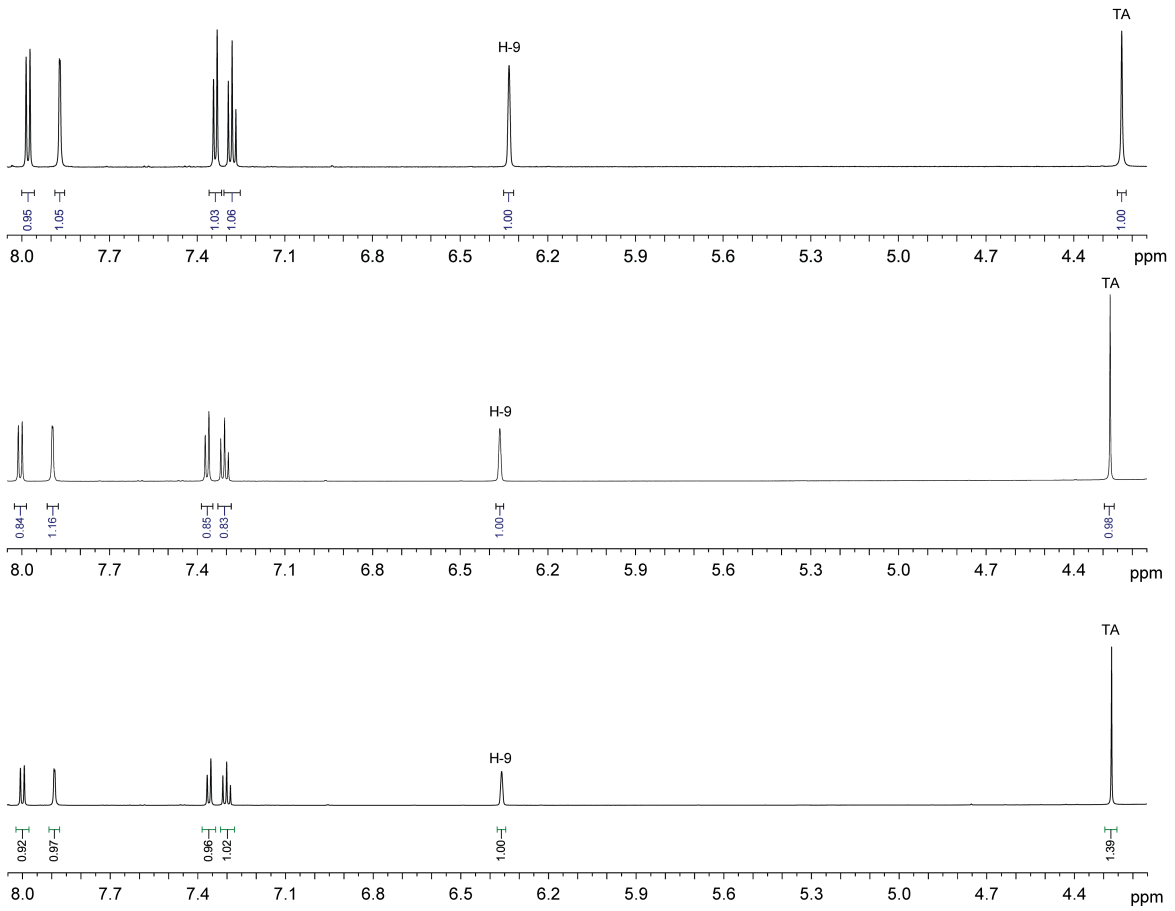
1CP-LSD hemitartrate (2:1)
^{1}H-NMR (600 MHz)
d_6-DMSO



1CP-LSD hemitartrate (2:1)
^{1}H-NMR (600 MHz)
d_6-DMSO

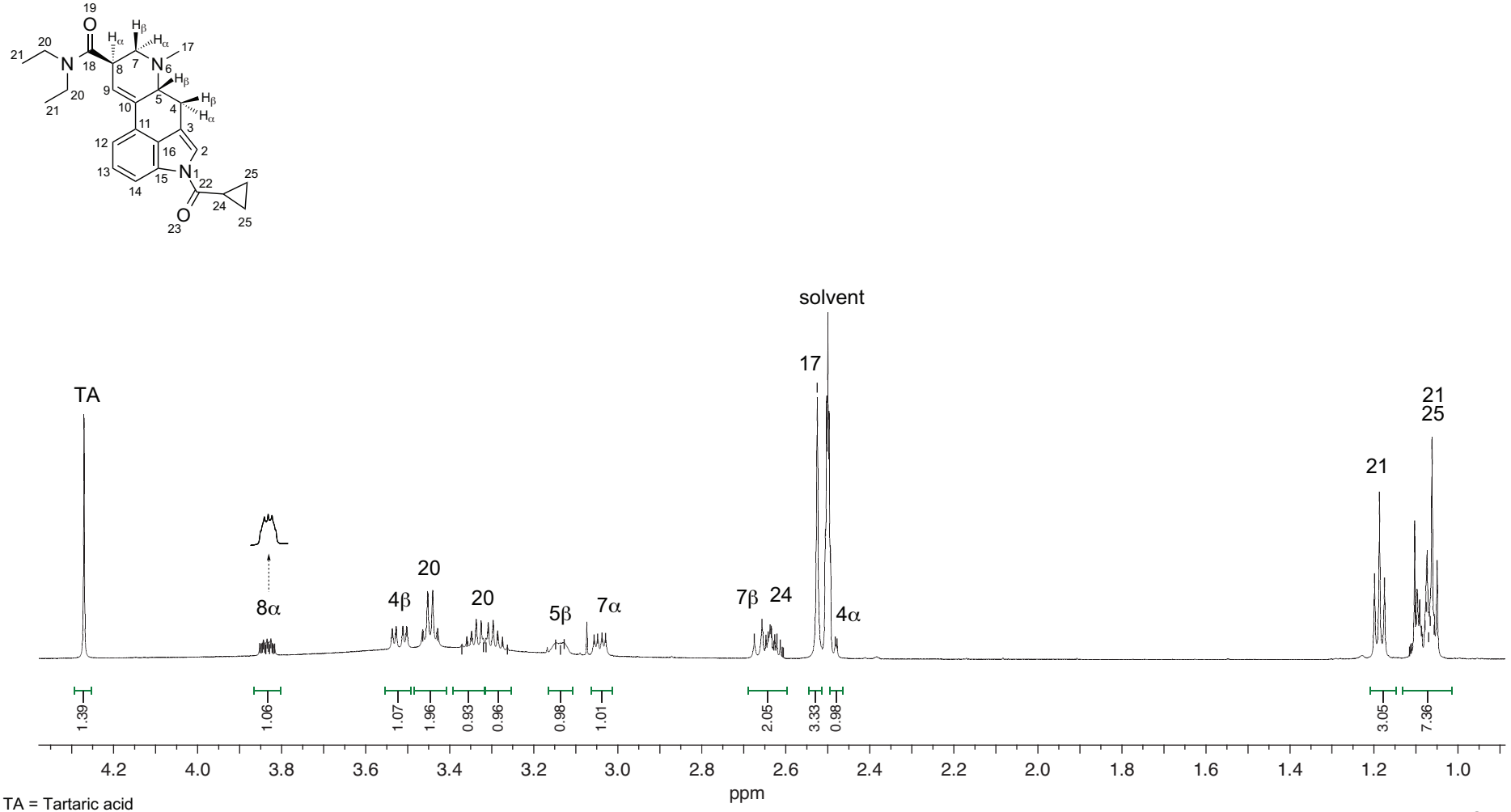


1CP-LSD:tartaric acid (TA) integration ratios



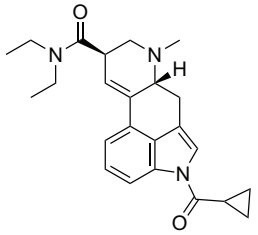
	1CPL:TA int. ratio	1CPL:TA mole ratio	MW	% 1CP-LSD
Analysis 1	1.00:1.00	1.00:0.50	466.57	83.92
Analysis 2	1.00:0.98	1.00:0.49	465.06	84.19
Analysis 3	1.00:1.39	1:0.69(5)	495.83	78.96
		Mean	**475.82**	**82.35**

1CP-LSD hemitartrate (2:1)
^{1}H-NMR (600 MHz)
d_6-DMSO

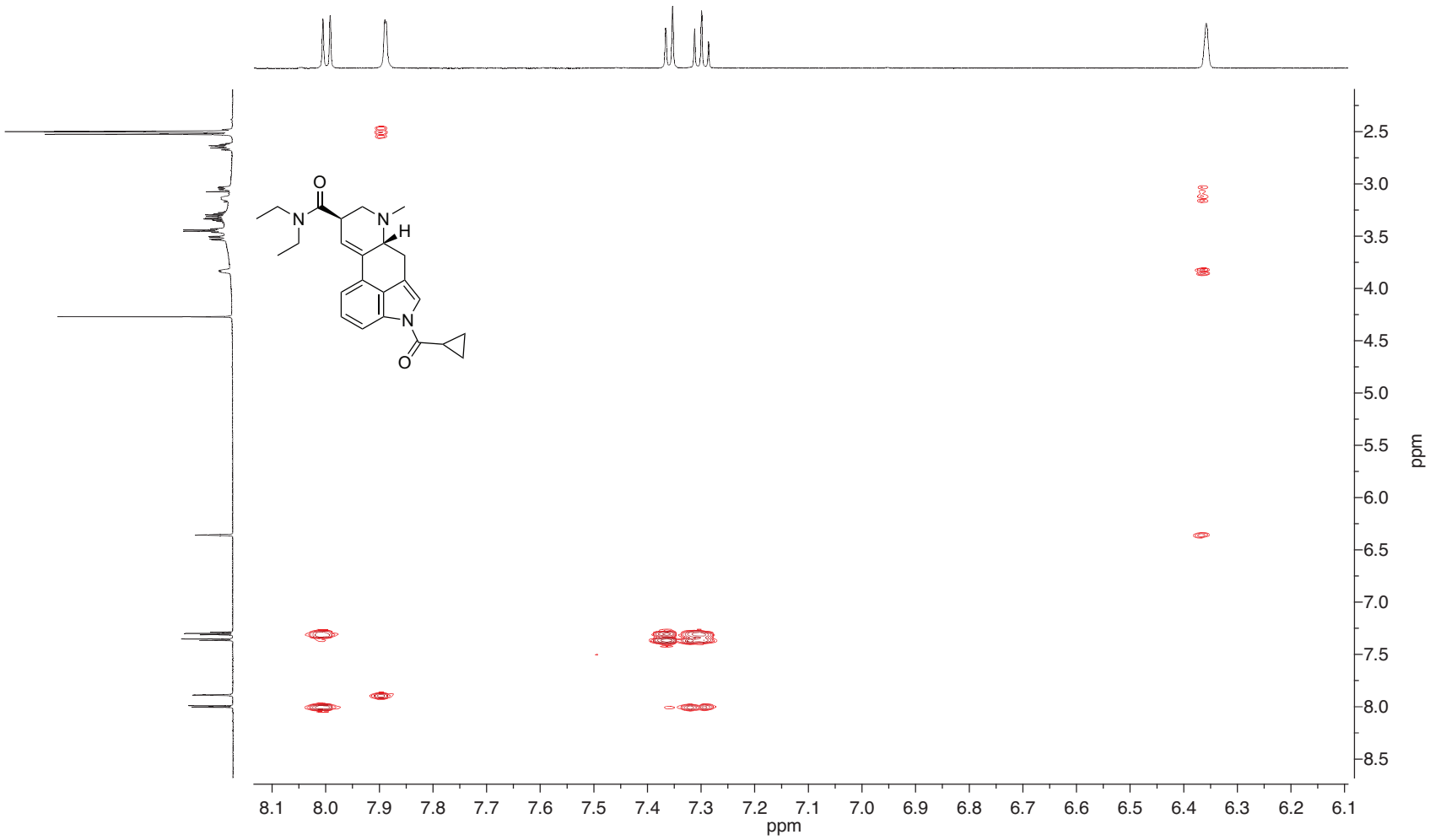


TA = Tartaric acid

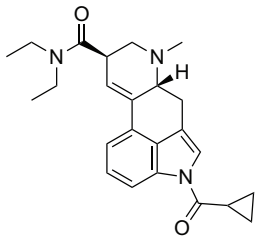
1CP-LSD hemitartrate (2:1)
COSY (600 MHz)
d_6-DMSO

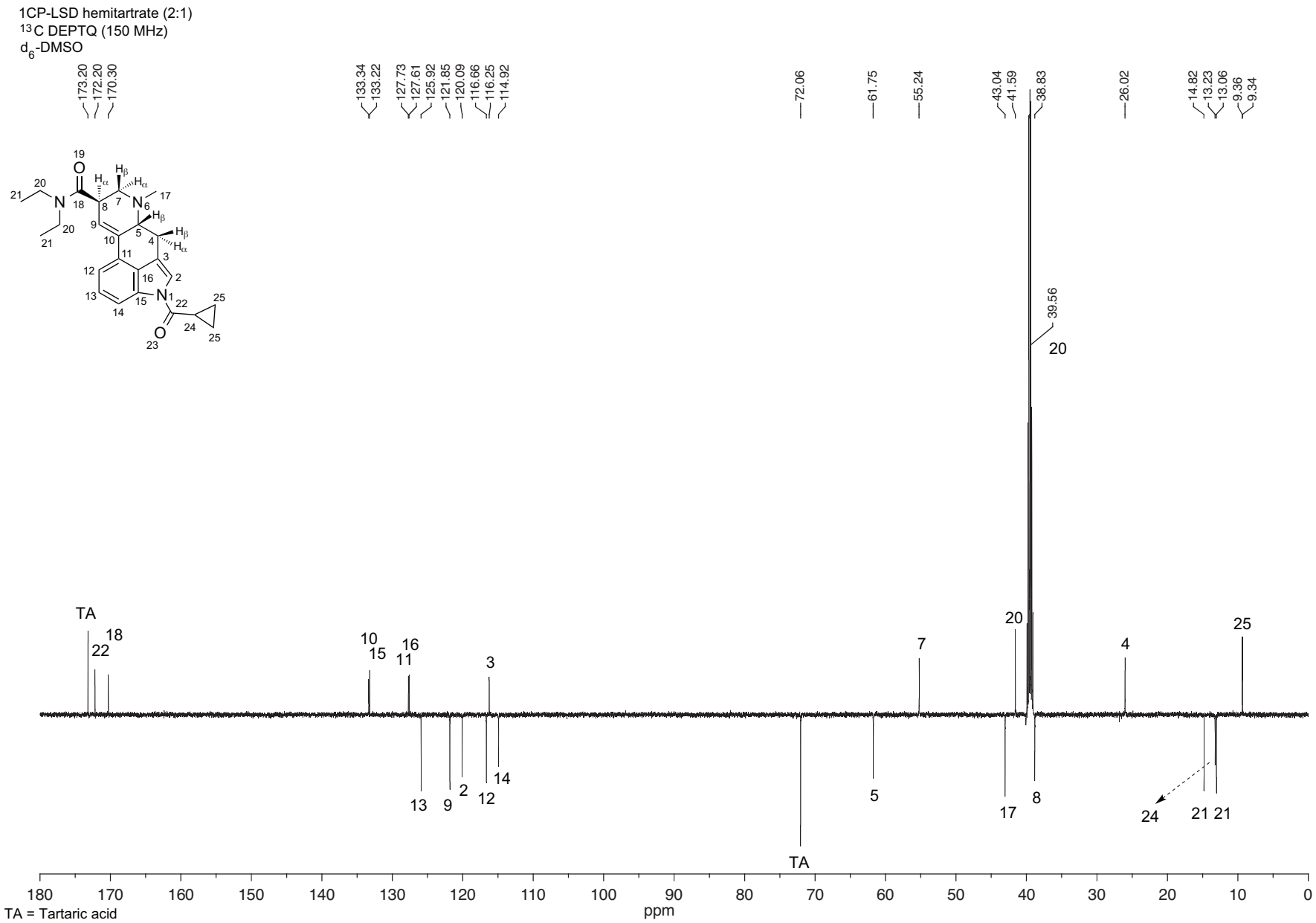


1CP-LSD hemitartrate (2:1)
COSY (600 MHz)
d_6-DMSO

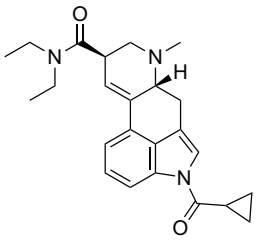


1CP-LSD hemitartrate (2:1)
COSY (600 MHz)
d_6-DMSO

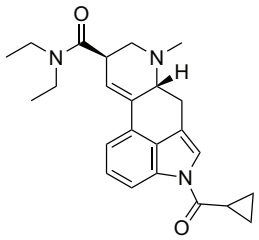


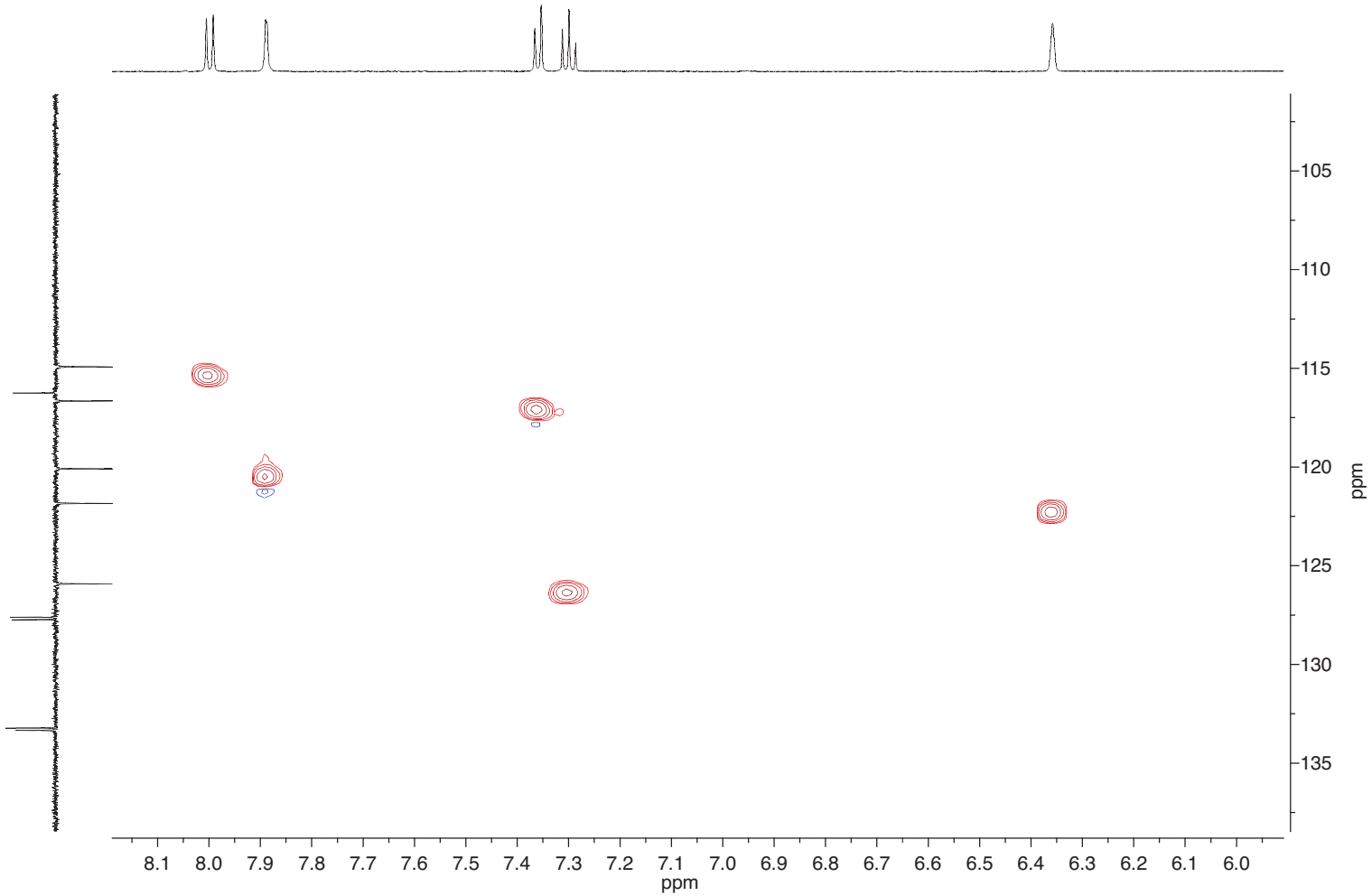

1CP-LSD hemitartrate (2:1)
13C DEPTQ (150 MHz)
d6-DMSO
173.20
172.20
170.30
133.34
133.22
127.73
127.61
125.92
121.85
120.09
116.66
116.25
114.92
72.06
61.75
55.24
43.04
41.59
38.83
26.02
14.82
13.23
13.06
9.36
9.34
39.56
20
TA
18
22
10
15
16
11
3
7
20
4
25
13
9
2
12
14
5
17
8
24
21
21
TA
180
170
160
150
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
ppm
TA = Tartaric acid

1CP-LSD hemitartrate (2:1)
HSQC
d_6-DMSO

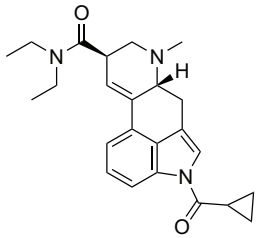


1CP-LSD hemitartrate (2:1)
HSQC
d_6-DMSO

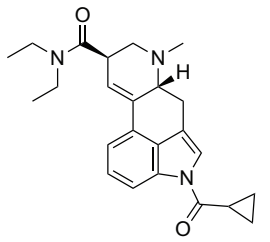




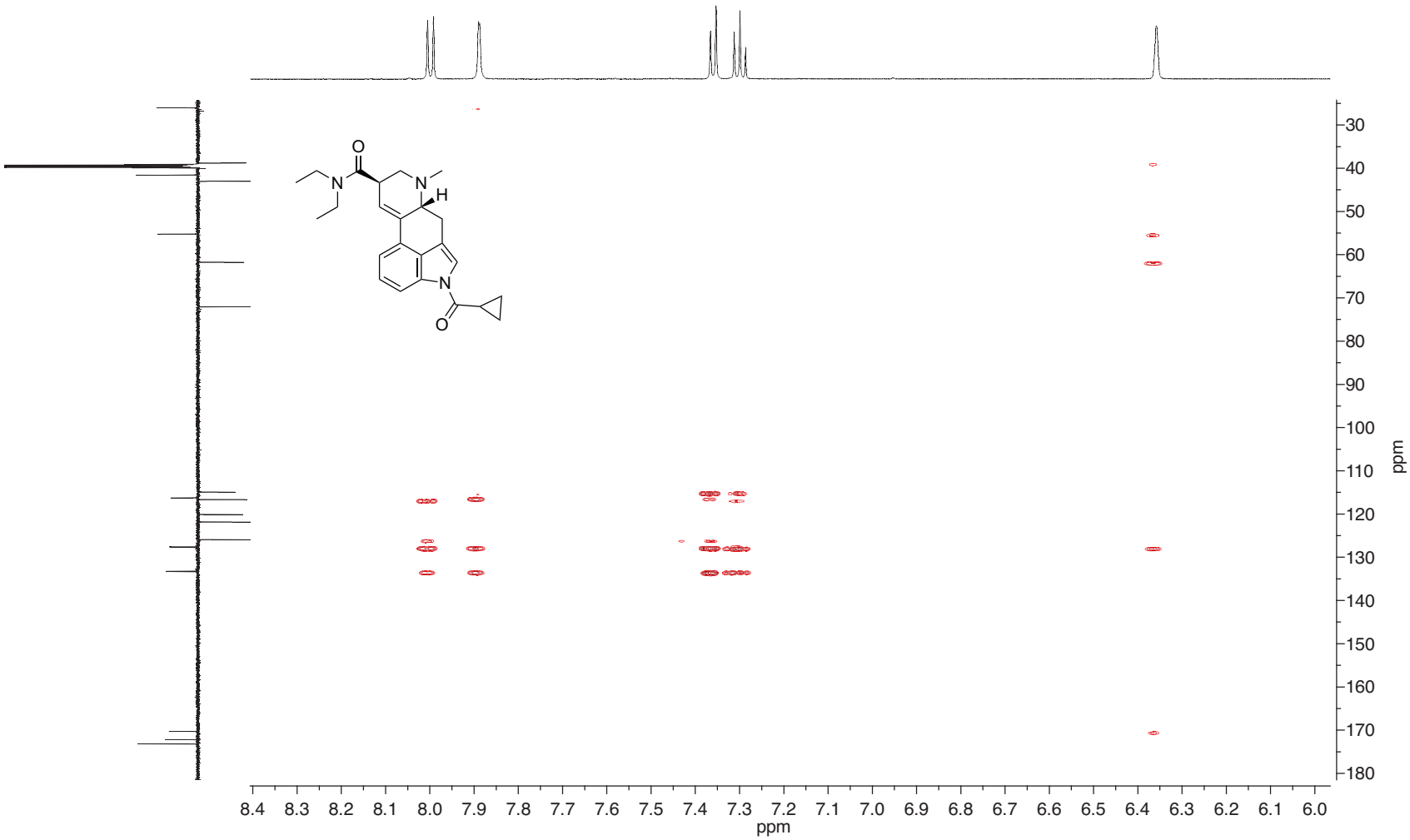
1CP-LSD hemitartrate (2:1)
HSQC
d_6-DMSO

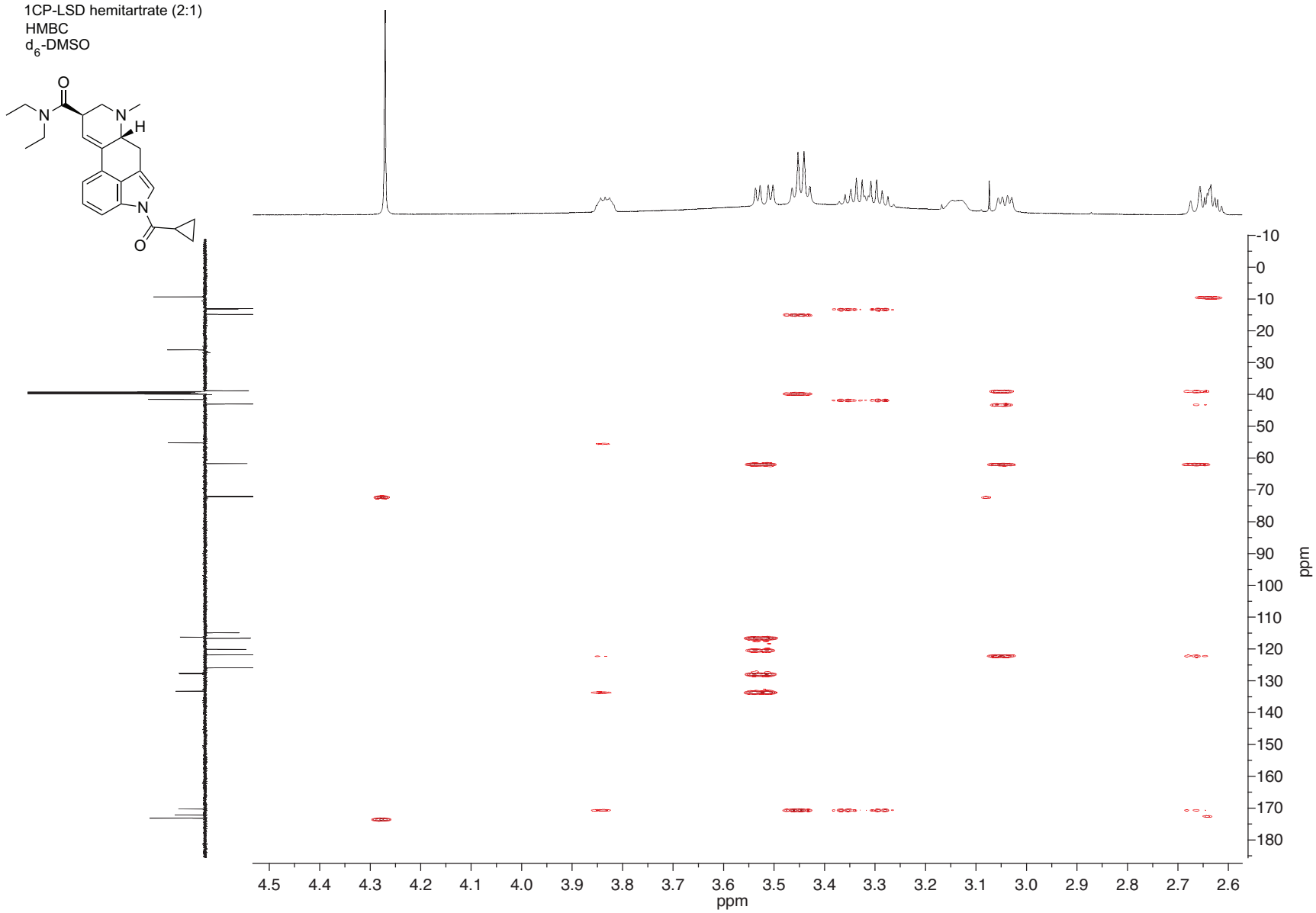


1CP-LSD hemitartrate (2:1)
HMBC
d_6-DMSO

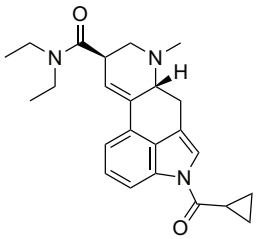


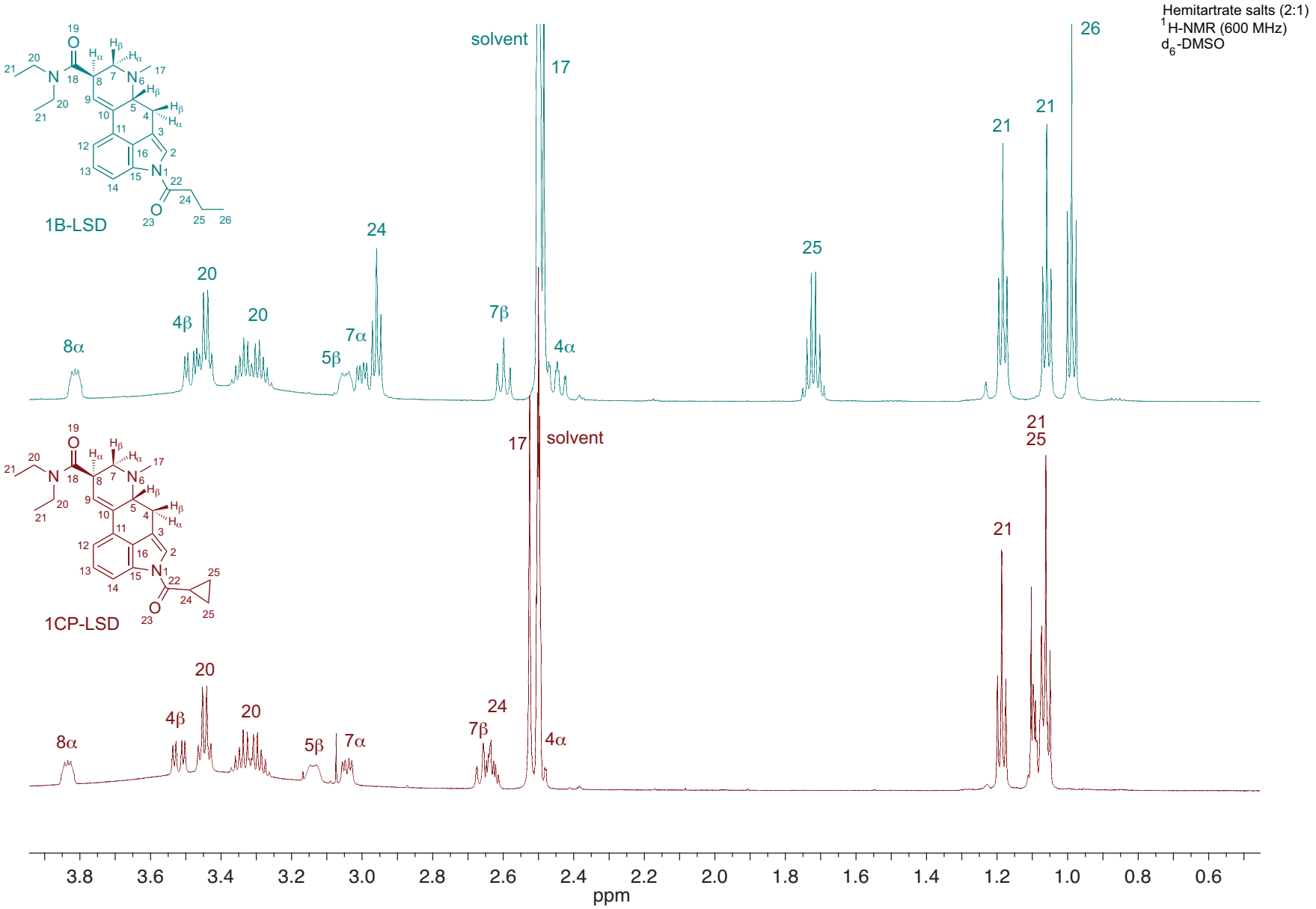
1CP-LSD hemitartrate (2:1)
HMBC
d_6-DMSO

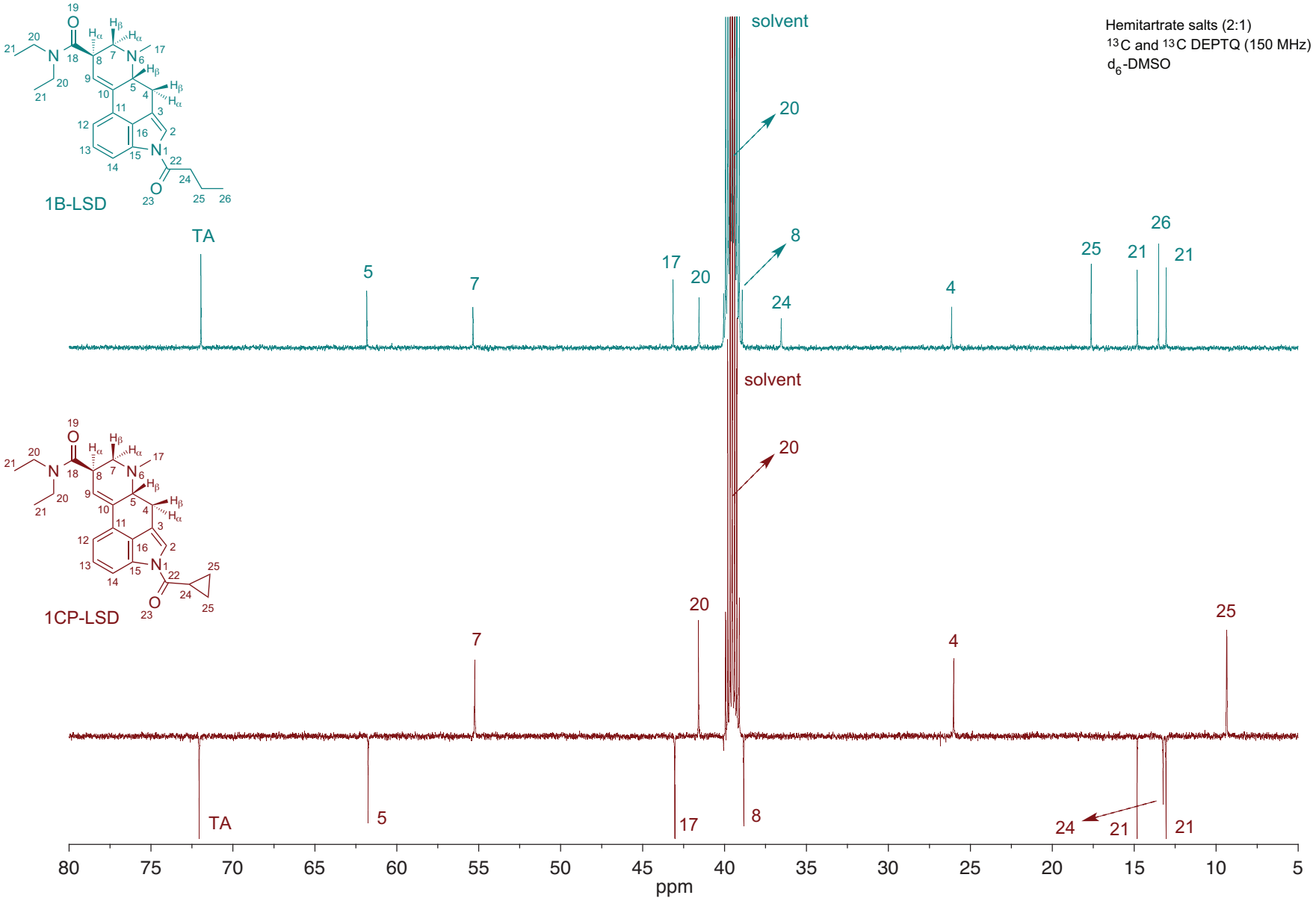



1CP-LSD hemitartrate (2:1)
HMBC
d6-DMSO
O
N
N
H
N
O
4.5 4.4 4.3 4.2 4.1 4.0 3.9 3.8 3.7 3.6 3.5 3.4 3.3 3.2 3.1 3.0 2.9 2.8 2.7 2.6
ppm
-10 0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180
ppm

1CP-LSD hemitartrate (2:1)
HMBC
d_6-DMSO

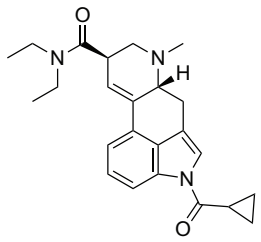


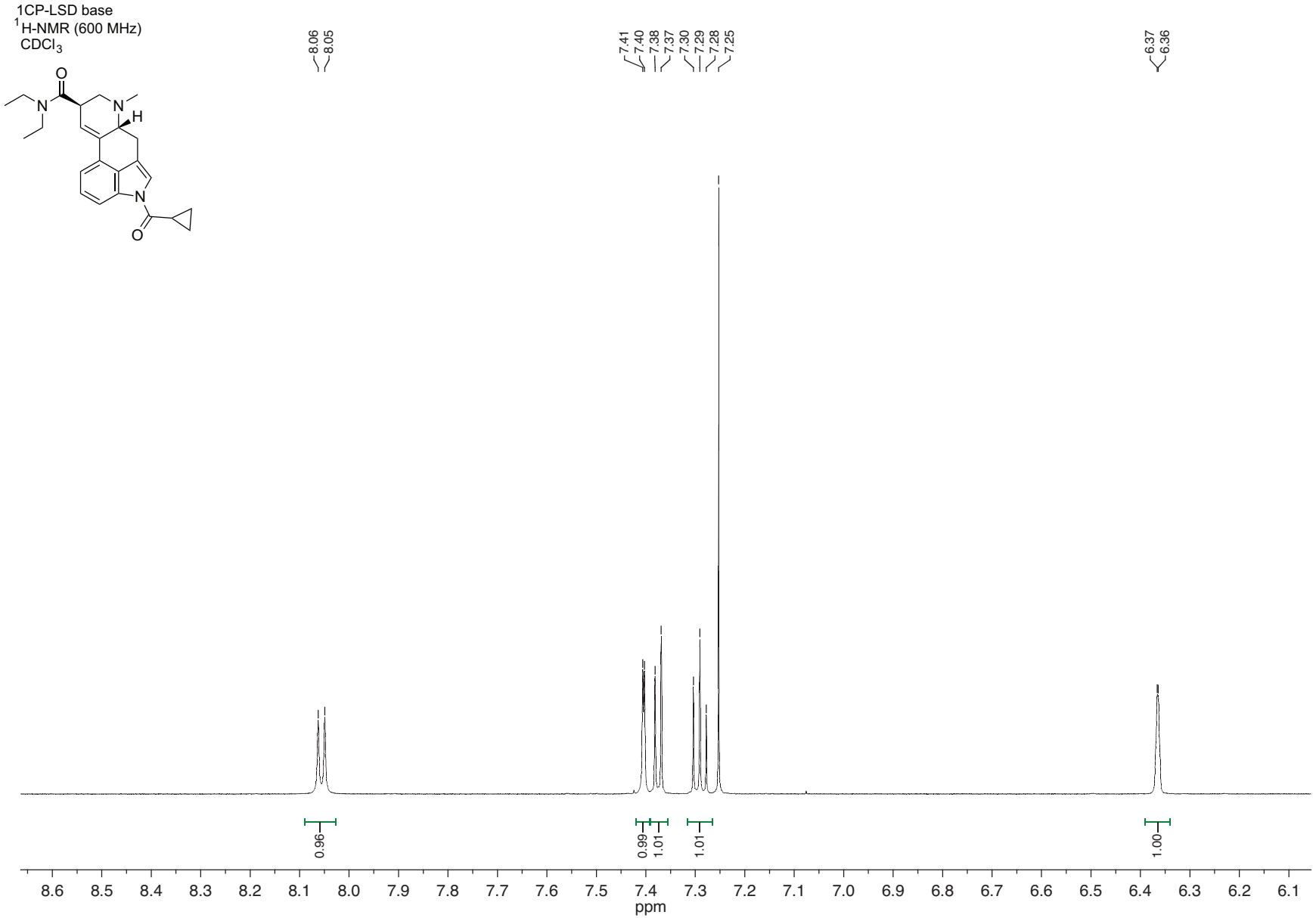

Hemitartrate salts (2:1)
1H-NMR (600 MHz)
d6-DMSO
1B-LSD
solvent
17
26
21
21
25
24
20
4β
20
8α
5β
7α
7β
4α
1CP-LSD
17
solvent
21
25
21
20
4β
20
8α
5β
7α
24
7β
4α
3.8
3.6
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
1.8
1.6
1.4
1.2
1.0
0.8
0.6
ppm

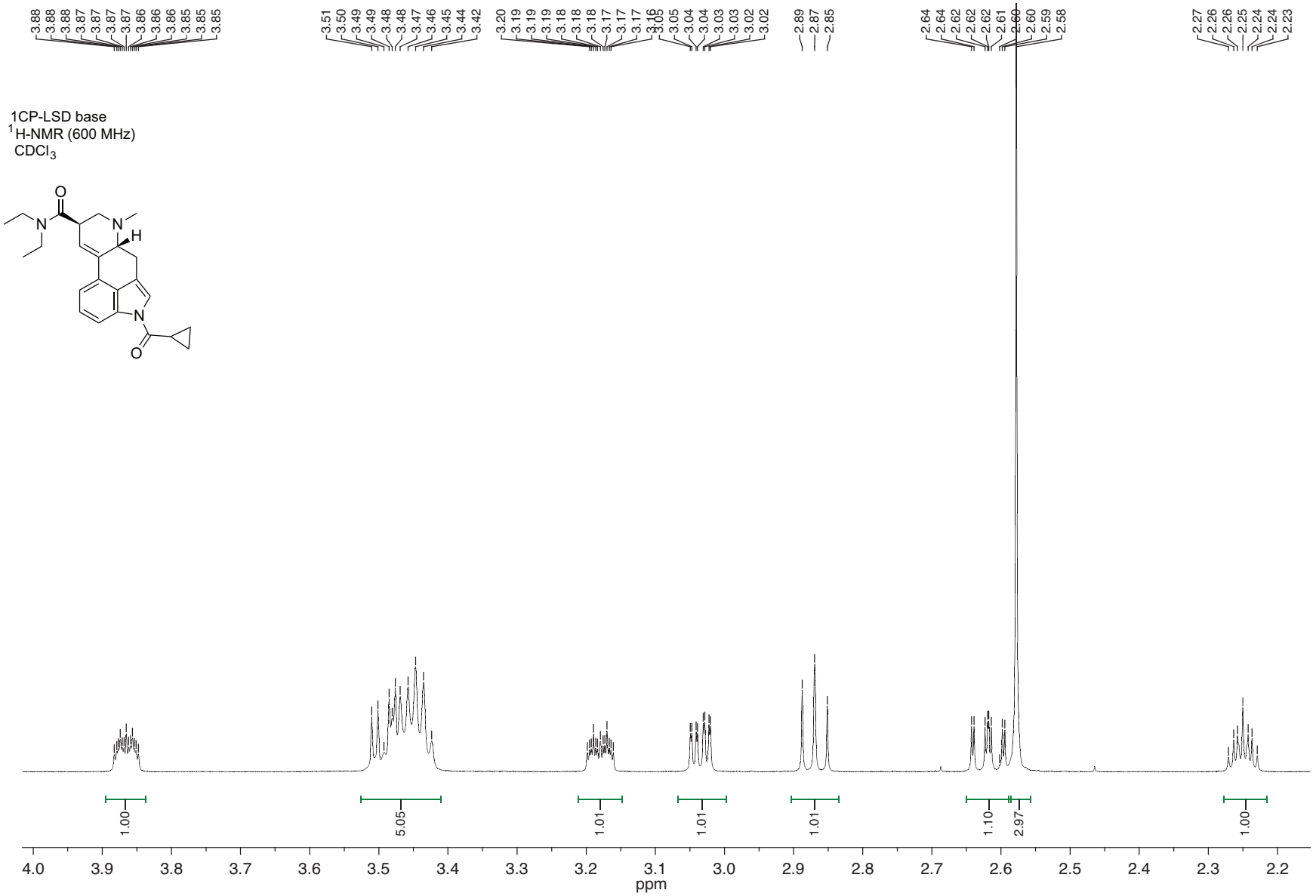


TA = Tartaric acid

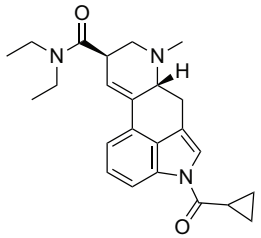
1CP-LSD base
^{1}H-NMR (600 MHz)
$CDCl_3$

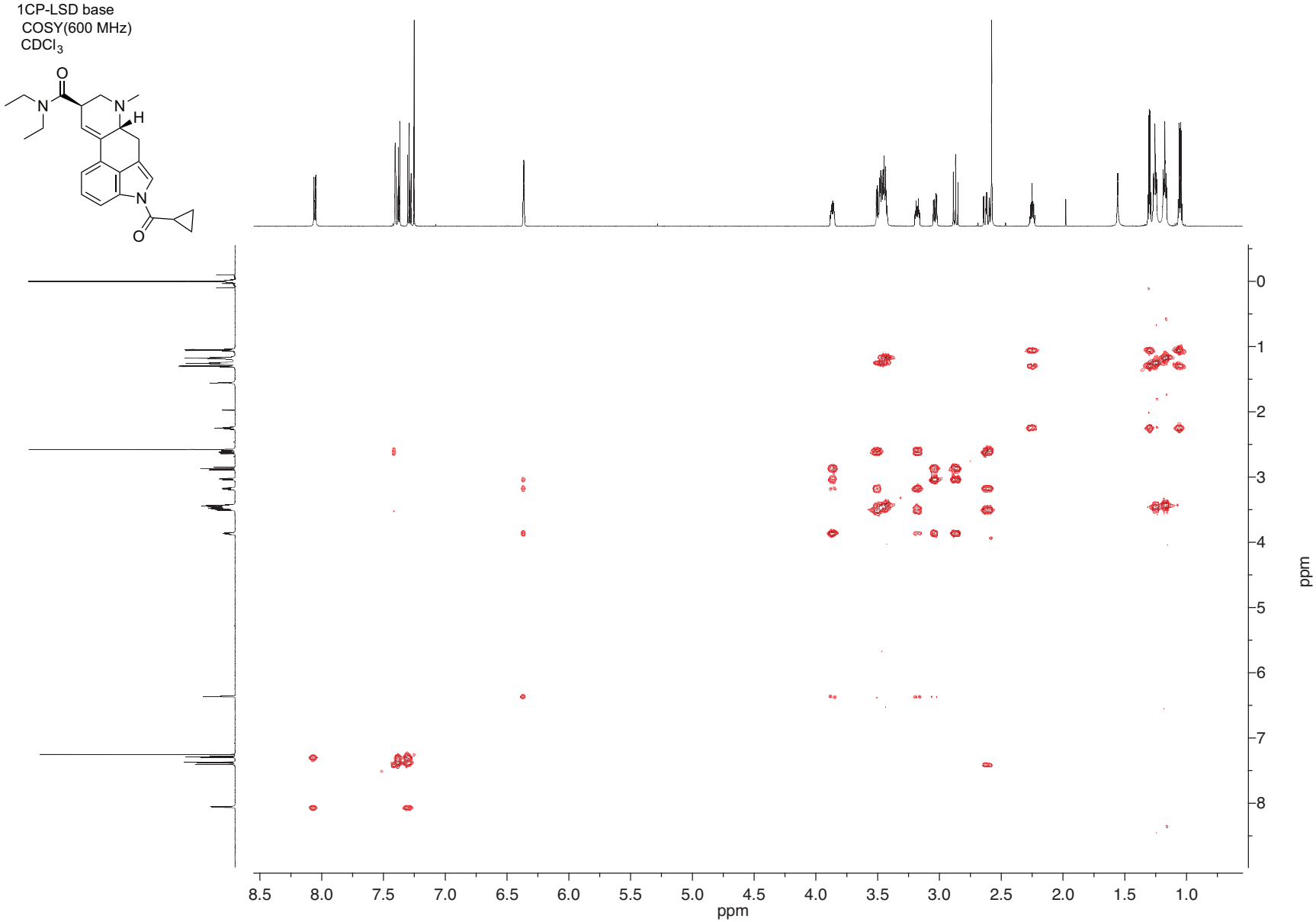


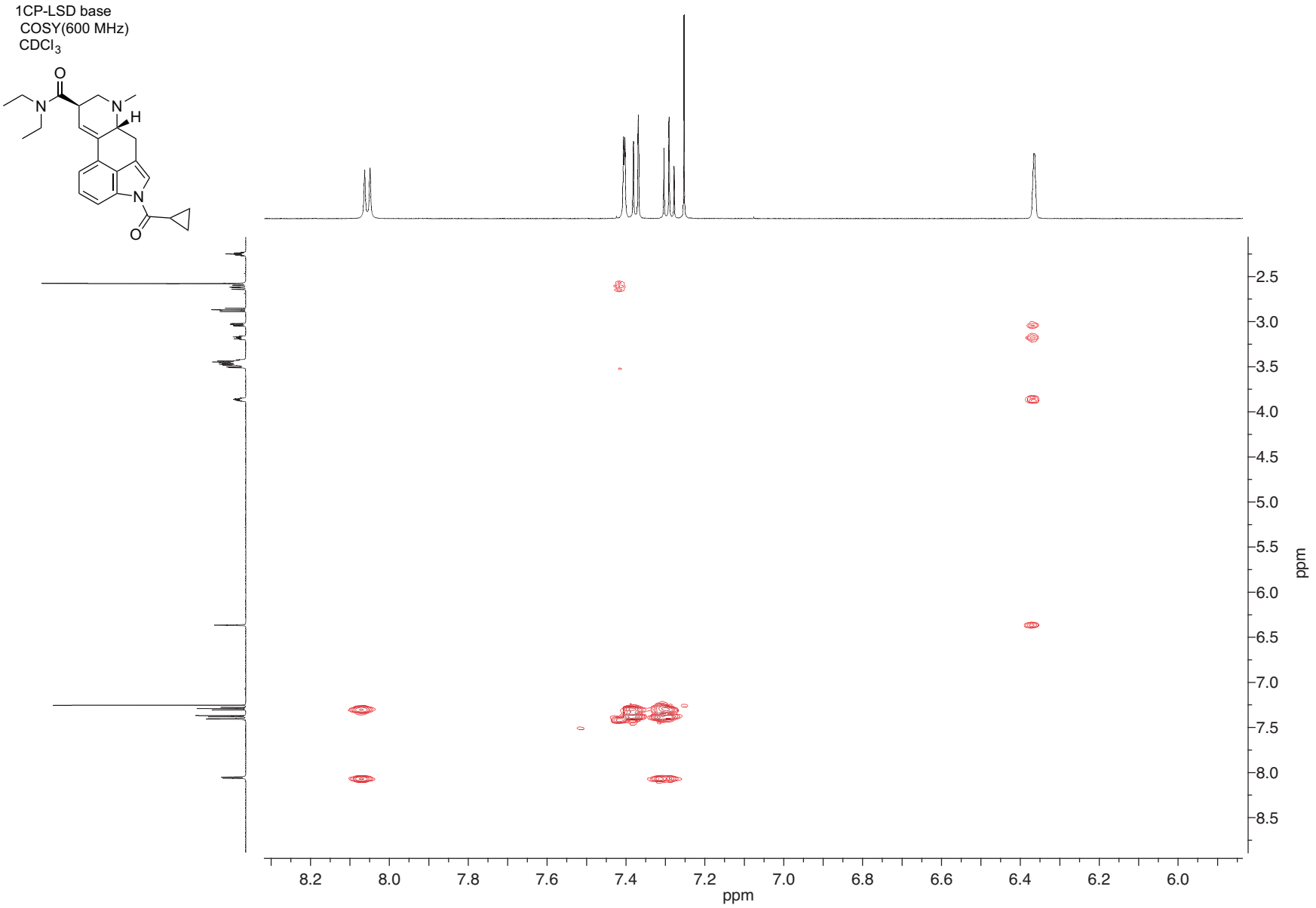

1CP-LSD base
1H-NMR (600 MHz)
CDCl3
8.06
8.05
7.41
7.40
7.38
7.37
7.30
7.29
7.28
7.25
6.37
6.36
0.96
0.99
1.01
1.01
1.00
8.6 8.5 8.4 8.3 8.2 8.1 8.0 7.9 7.8 7.7 7.6 7.5 7.4 7.3 7.2 7.1 7.0 6.9 6.8 6.7 6.6 6.5 6.4 6.3 6.2 6.1
ppm

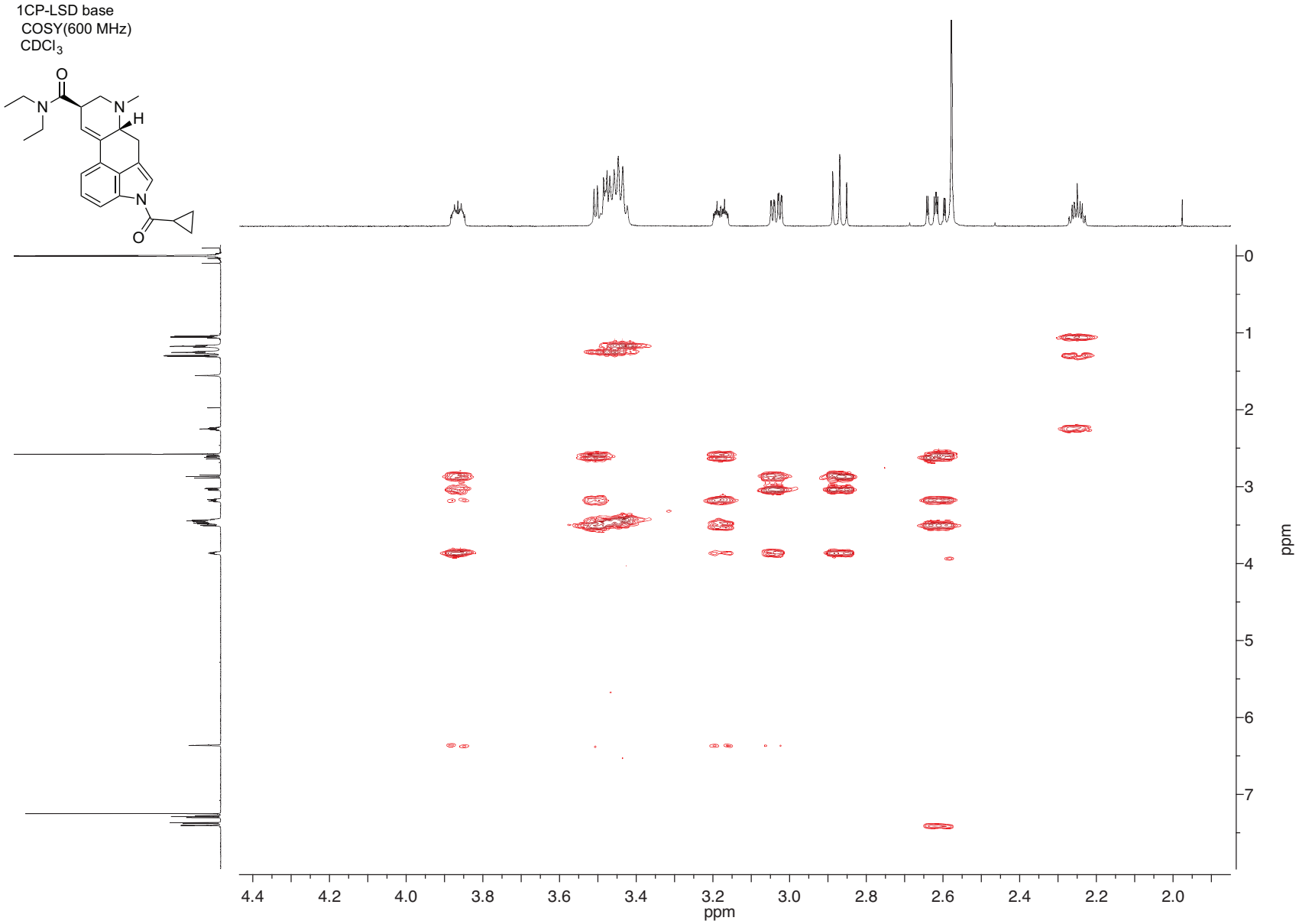

1CP-LSD base
1H-NMR (600 MHz)
CDCl3
3.88 3.88 3.88 3.87 3.87 3.87 3.87 3.86 3.86 3.86 3.85 3.85 3.85
3.51 3.50 3.49 3.49 3.48 3.48 3.47 3.46 3.45 3.44 3.42
3.20 3.19 3.19 3.18 3.18 3.17 3.17 3.16 3.05 3.05 3.04 3.04 3.03 3.03 3.02 3.02
2.89 2.87 2.85
2.64 2.64 2.62 2.62 2.62 2.61 2.60 2.60 2.59 2.58
2.27 2.26 2.26 2.25 2.24 2.24 2.23
1.00 5.05 1.01 1.01 1.01 1.10 2.97 1.00
4.0 3.9 3.8 3.7 3.6 3.5 3.4 3.3 3.2 3.1 3.0 2.9 2.8 2.7 2.6 2.5 2.4 2.3 2.2
ppm

1CP-LSD base
^{1}H-NMR (600 MHz)
$CDCl_3$

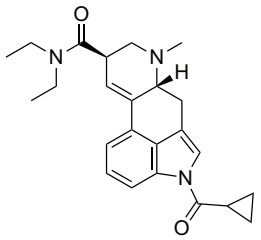



1CP-LSD base
COSY(600 MHz)
CDCl3
O
N
N
H
N
O
8.5
8.0
7.5
7.0
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
ppm
0
1
2
3
4
5
6
7
8
ppm

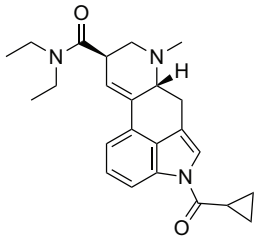

1CP-LSD base
COSY(600 MHz)
CDCl3
O
N
N
H
N
O
8.2
8.0
7.8
7.6
7.4
7.2
7.0
6.8
6.6
6.4
6.2
6.0
ppm
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
8.5
ppm


1CP-LSD base
COSY(600 MHz)
$CDCl_3$
O
N
N
H
N
O
4.4
4.2
4.0
3.8
3.6
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
ppm
0
1
2
3
4
5
6
7
ppm

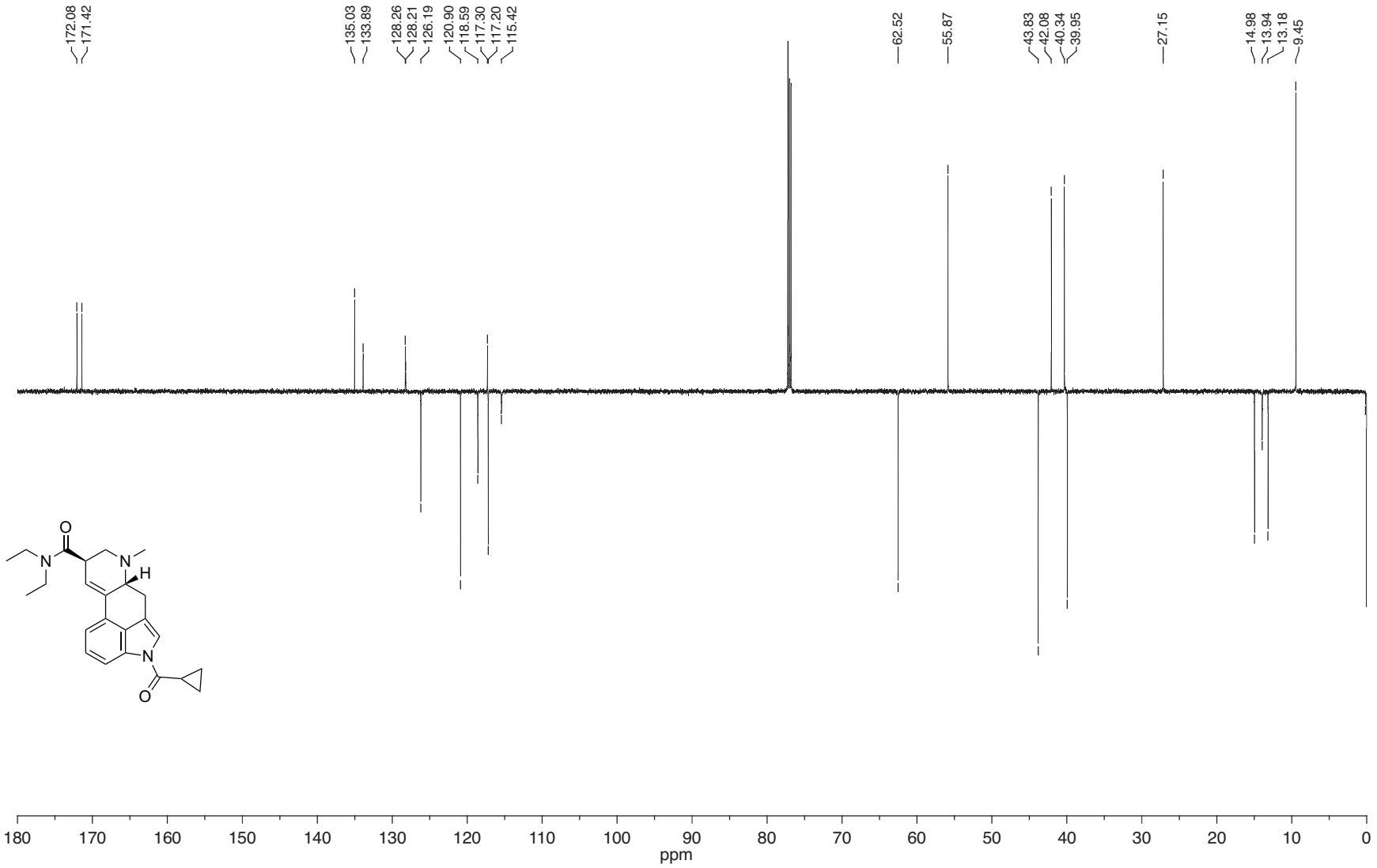
1CP-LSD base
COSY(600 MHz)
$CDCl_3$

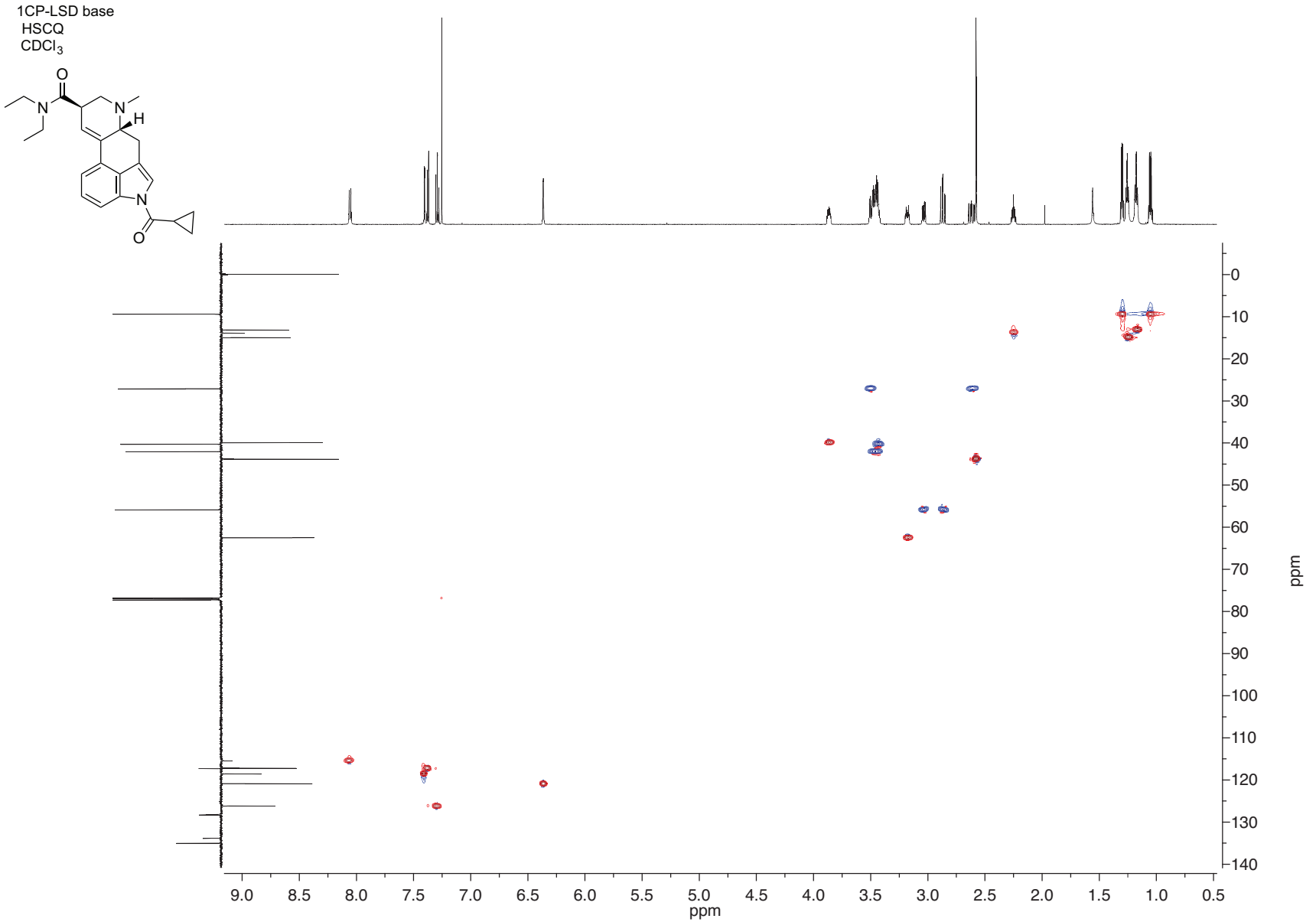


1CP-LSD base
^{13}C NMR (150 MHz)
$CDCl_3$

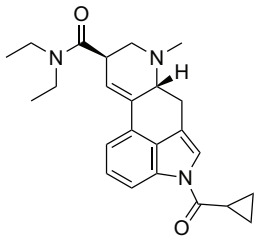


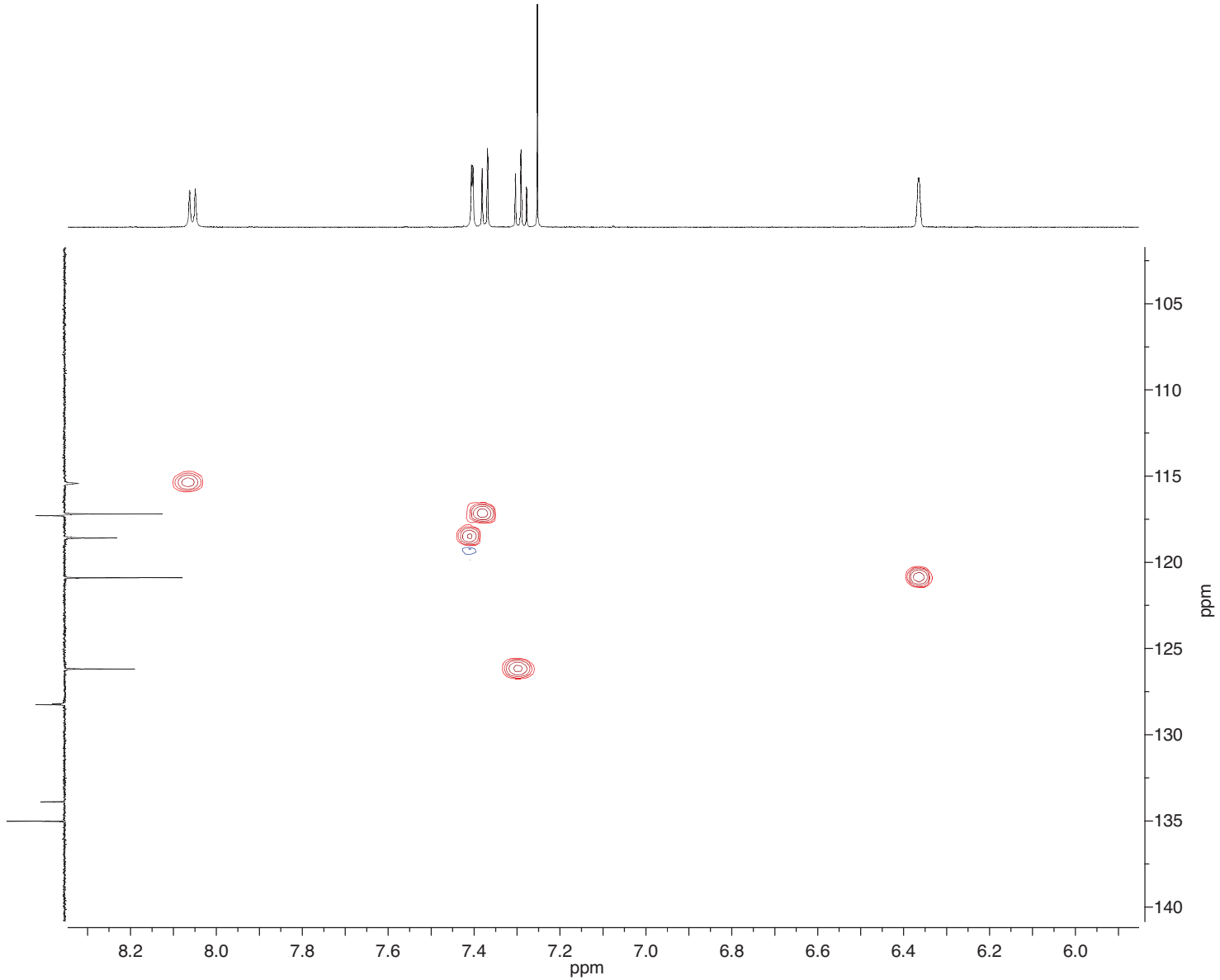
1CP-LSD base
^{13}C DEPTQ (150 MHz)
$CDCl_3$

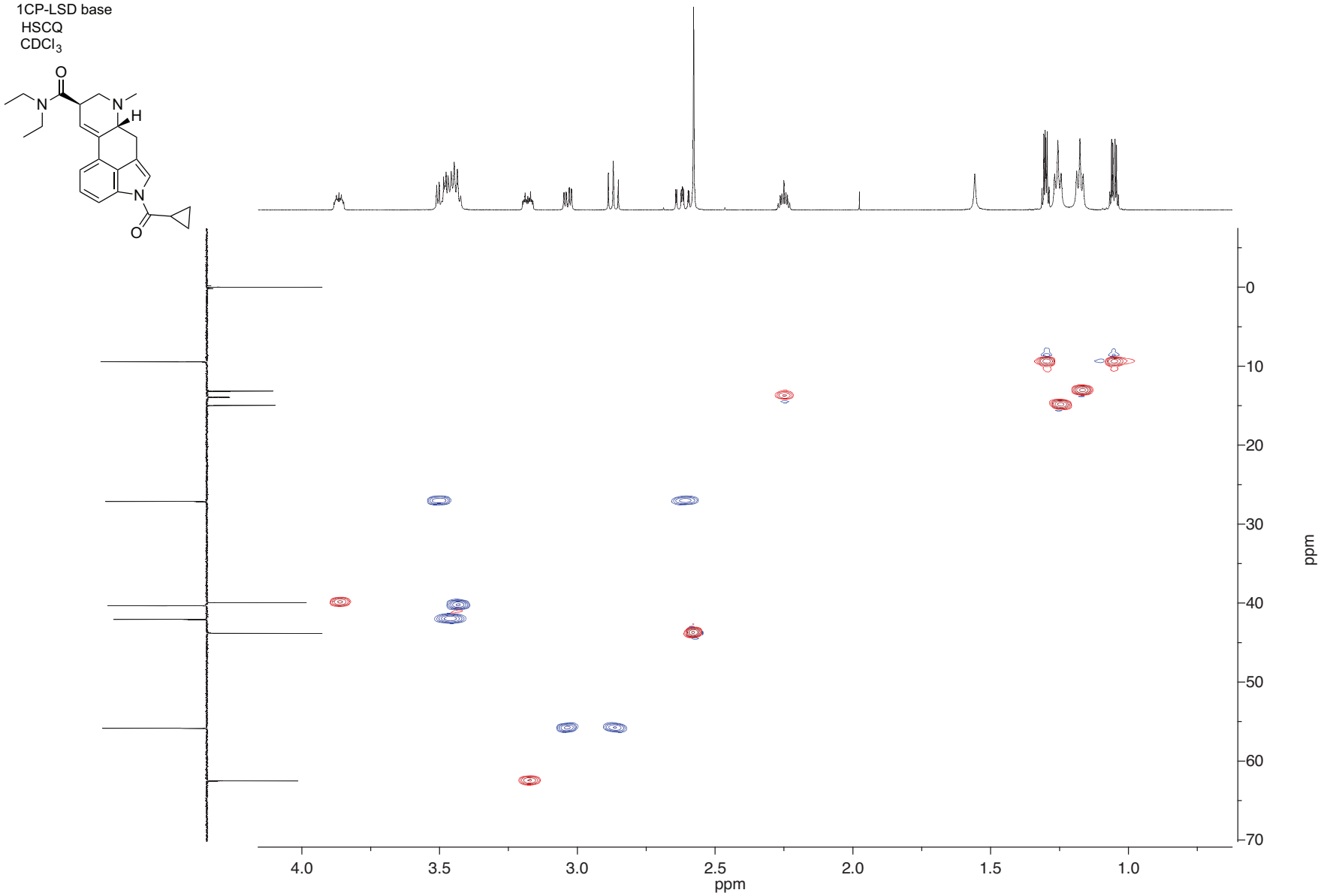


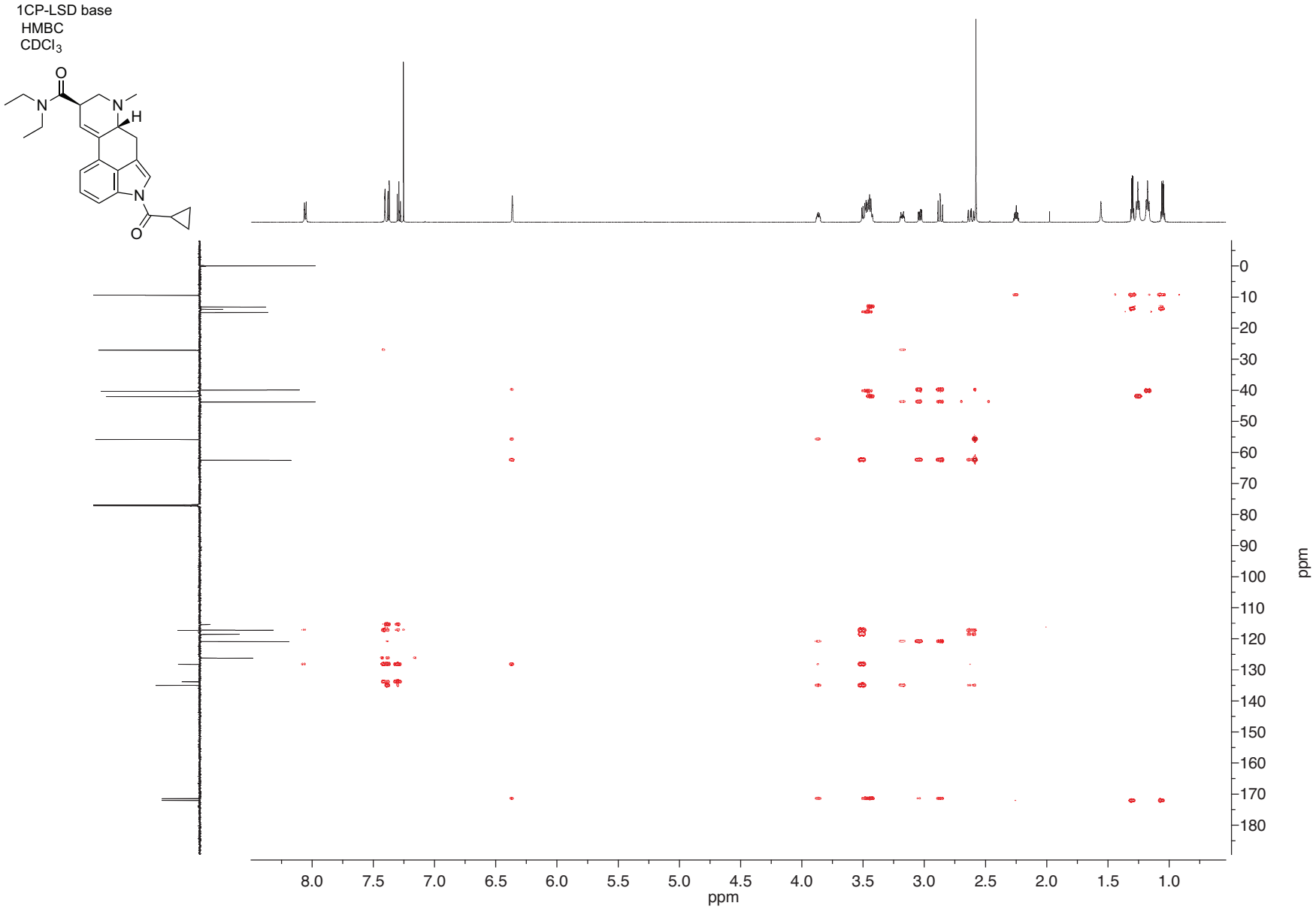

1CP-LSD base
HSCQ
CDCl3
O
N
N
H
N
O
9.0
8.5
8.0
7.5
7.0
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
ppm
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
ppm

1CP-LSD base
HSCQ
$CDCl_3$

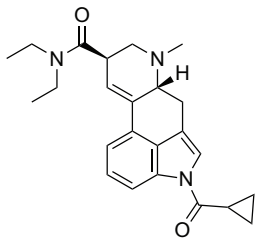


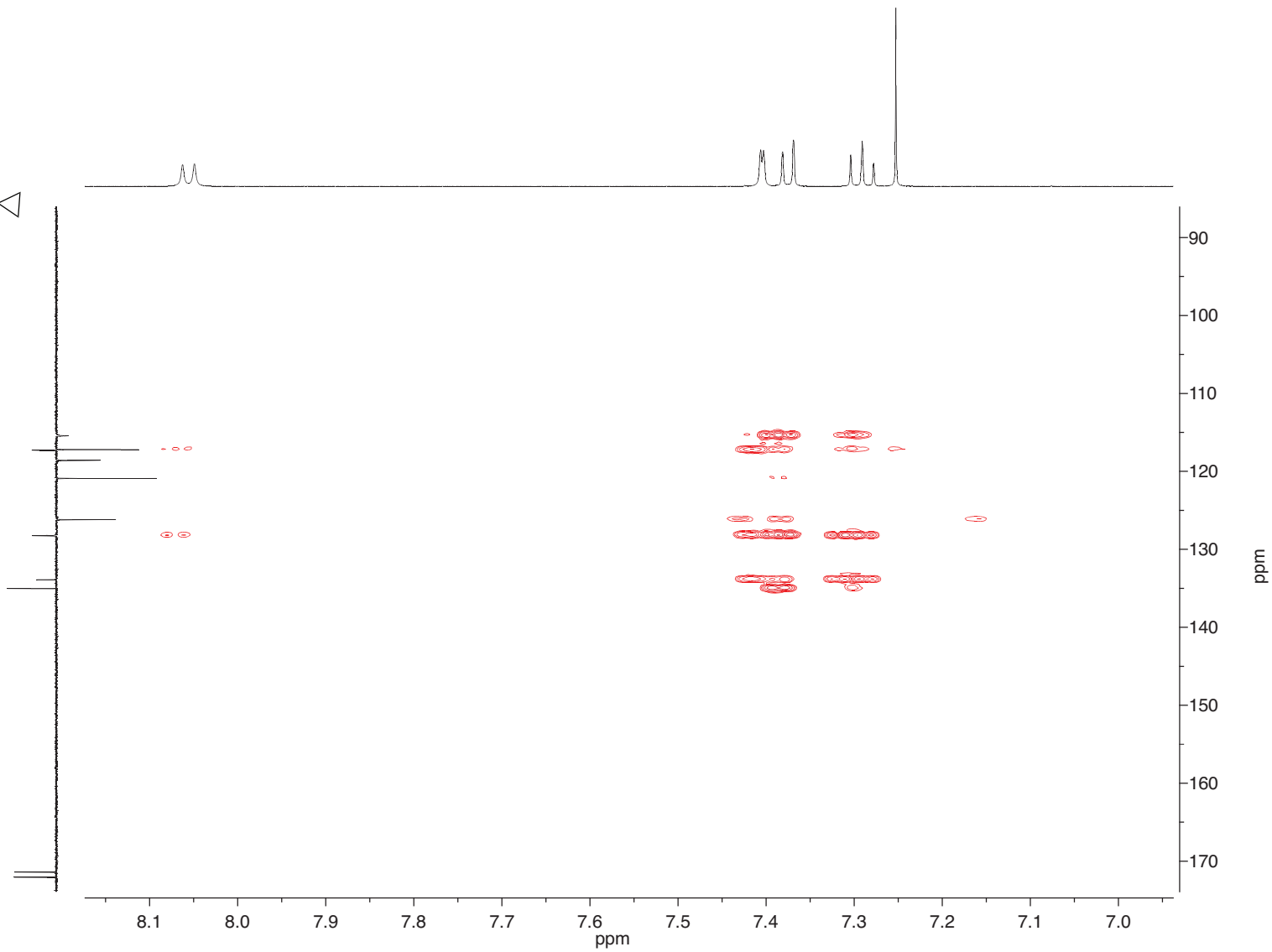


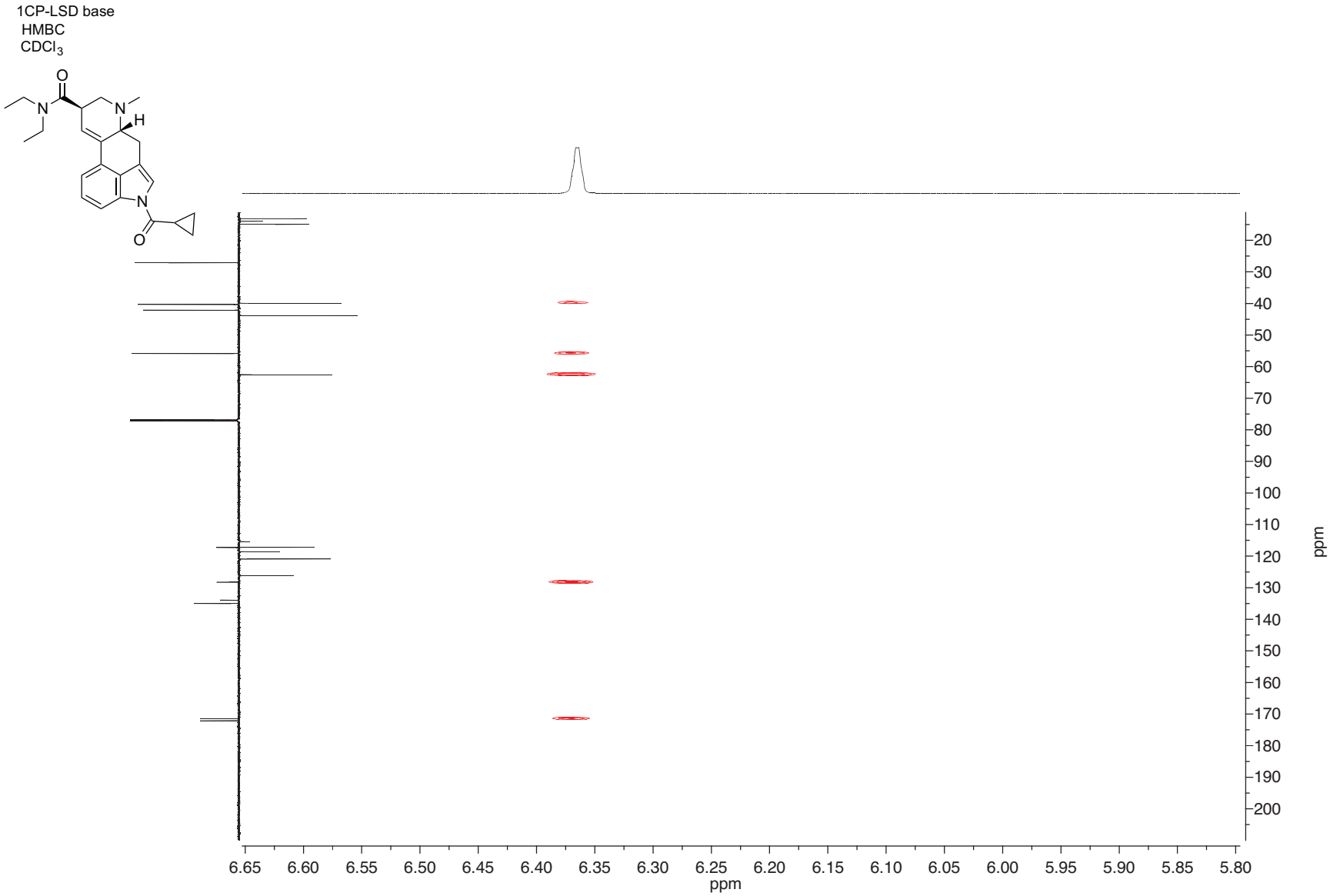

1CP-LSD base
HSCQ
CDCl3
O
N
N
H
N
O
0
10
20
30
40
50
60
70
ppm
4.0
3.5
3.0
2.5
2.0
1.5
1.0
ppm

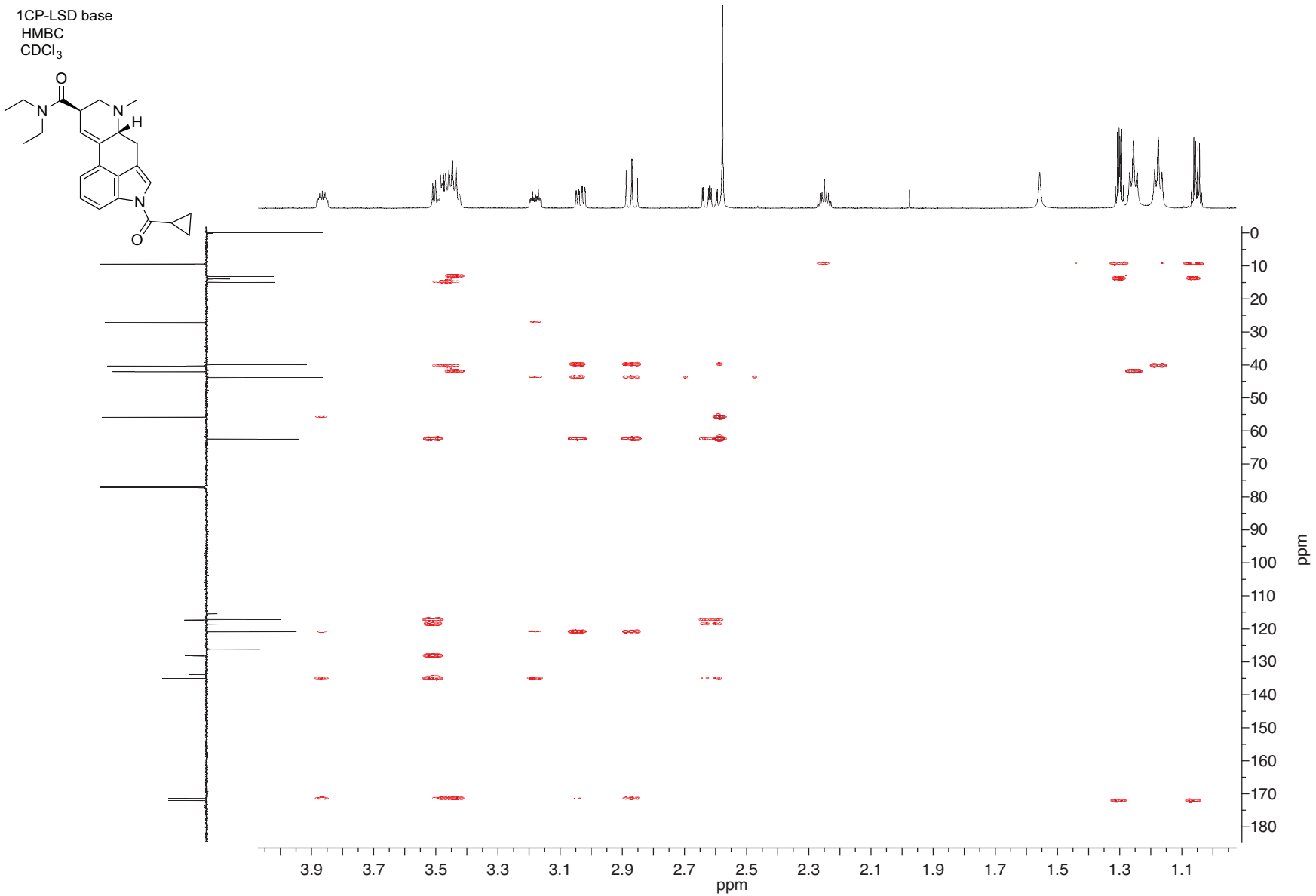

1CP-LSD base
HMBC
CDCl3
O
N
N
H
N
O
8.0
7.5
7.0
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
ppm
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
ppm

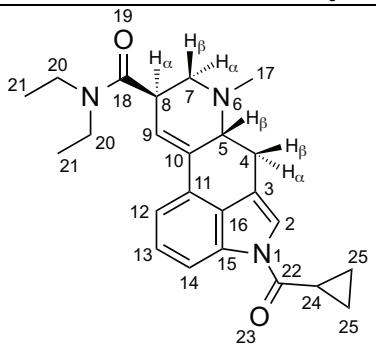
1CP-LSD base
HMBC
$CDCl_3$






1CP-LSD base
HMBC
CDCl3
O
N
N
H
N
O
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
ppm
6.65
6.60
6.55
6.50
6.45
6.40
6.35
6.30
6.25
6.20
6.15
6.10
6.05
6.00
5.95
5.90
5.85
5.80
ppm


1CP-LSD base
HMBC
CDCl3
O
N
N
H
N
O
3.9
3.7
3.5
3.3
3.1
2.9
2.7
2.5
2.3
2.1
1.9
1.7
1.5
1.3
1.1
ppm
0
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
ppm

^{1}H and ^{13}C DEPTQ NMR data for 1CP-LSD base in $CDCl_3$ at 600/150 MHz		
		
No.	^{13}C [δ / ppm]	^{1}H [δ / ppm]
1	–	–
2	118.57	7.41 (d, *J* = 2.0 Hz, 1H)
3	117.28	–
4	27.13	2.62 (ddd, *J* = 13.8, 11.8, 2.8 Hz, 4α-H, 1H) 3.50 (dd, *J* = 13.7, 5.4 Hz, 4β-H, 1 H) *overlap with H-20
5	62.50	3.19 (dddd, *J* = 11.2, 5.4, 3.5, 2.0 Hz, H-5β, 1H)
6	–	–
7	55.85	3.04 (ddd, *J* = 11.3, 5.0, 1.2 Hz, H-7α, 1H) 2.87 (t, *J* = 10.8 Hz, H-7β, 1H)
8	39.93	3.87 (dddd, *J* = 10.5, 4.9, 3.3, 2.1 Hz, H-8α, 1H)
9	120.88	6.38–6.35 (m, 1H)
10	135.01	–
11	128.24	–
12	117.18	7.38 (d, *J* = 7.4 Hz, 1H)
13	126.17	7.30 (t, *J* = 7.8 Hz, 1H)
14	115.40	8.06 (d, *J* = 8.1 Hz, 1H)
15	133.87	–
16	128.19	–
17	43.81	2.58 (s, 3H)
18	171.40	–
19	–	–
20	42.06	3.53-3.42 (m, 4H) *coalescing with 4β-H
20	40.31	
21	14.96	1.26 (t, *J* = 7.0 Hz, 3H)
21	13.16	1.18 (t, *J* = 7.0 Hz, 3H)
22	172.06	–
23	–	–
24	13.92	2.26 (tt, *J* = 8.0, 4.5 Hz, 1H)
25	9.42	1.32–1.29 (m, 2H) 1.08–1.04 (m, 2H)