Supplementary Material

Efficient synthesis of 2-substituted 1-phenylchromen[3,4-*d*]imidazol-4(1*H*)-ones with possible anti-inflammatory activity

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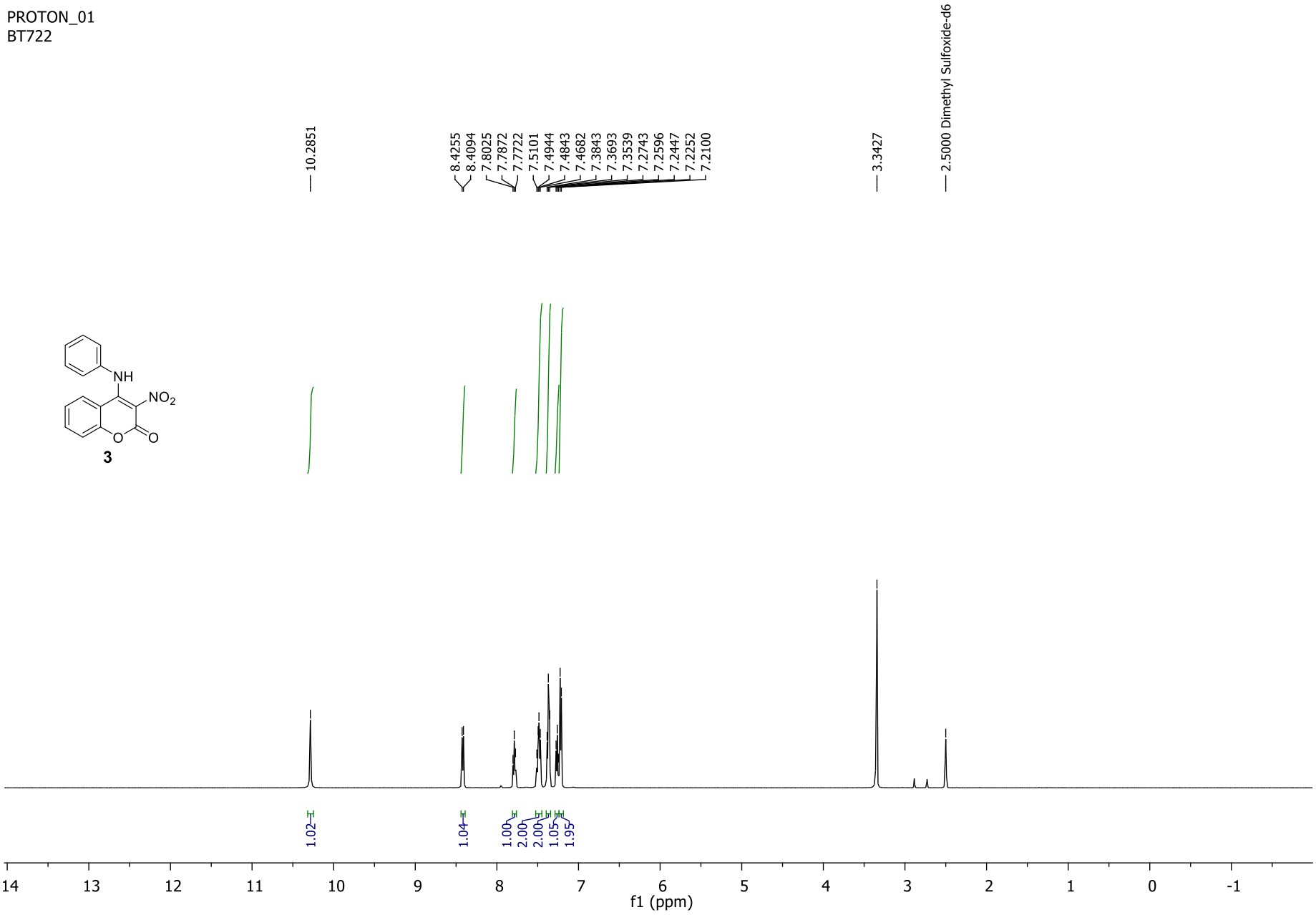
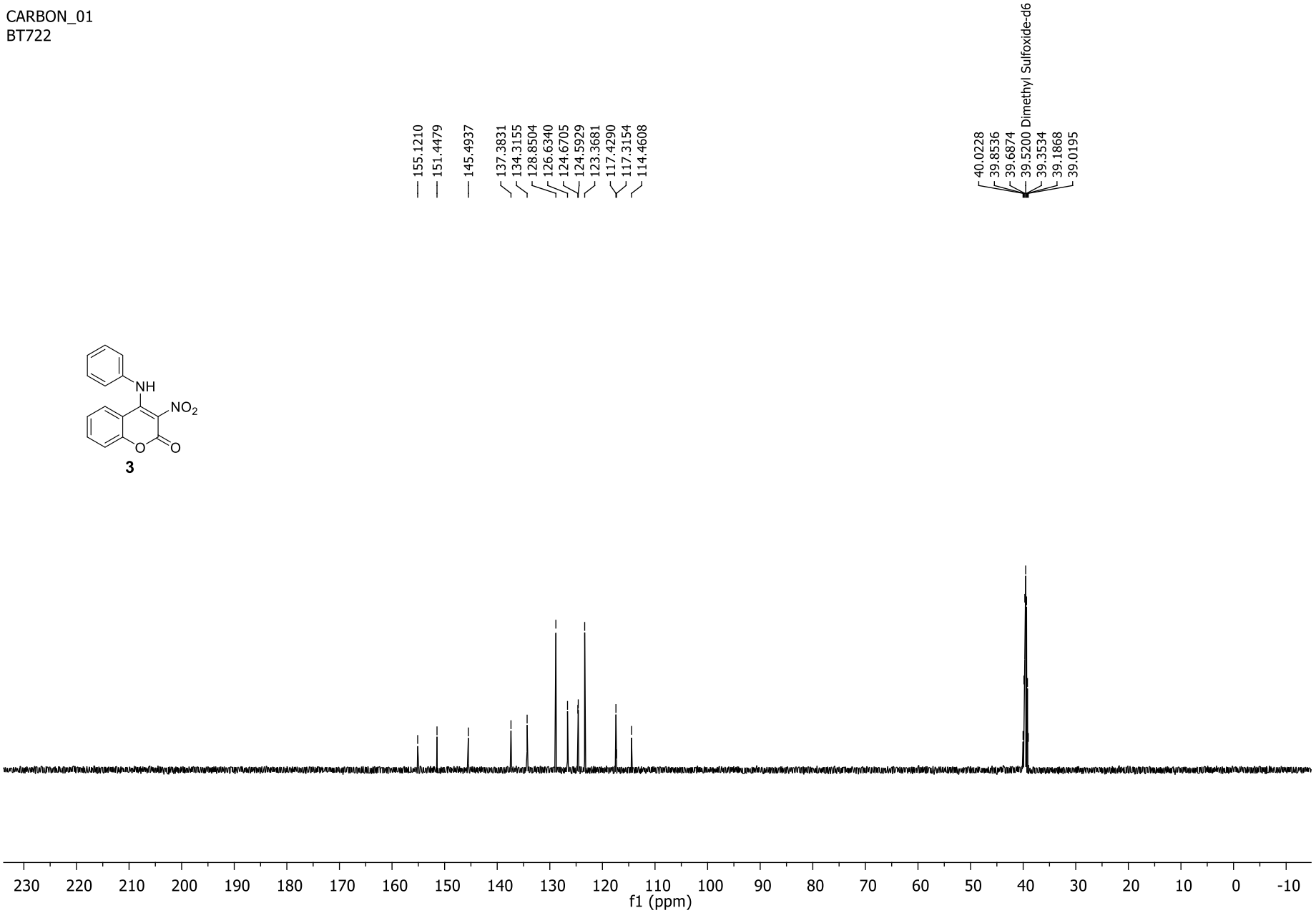
- **^{1}H-NMR and ^{13}C-NMR of compounds**

3-nitro-4-(phenylamino)-2*H*-chromen-2-one (3)

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145.4937
137.3831
134.3155
128.8504
126.6340
124.6705
124.5929
123.3681
117.4290
117.3154
114.4608
40.0228
39.8536
39.6874
39.5200 Dimethyl Sulfoxide-d6
39.3534
39.1868
39.0195
NH
NO2
O
O
3
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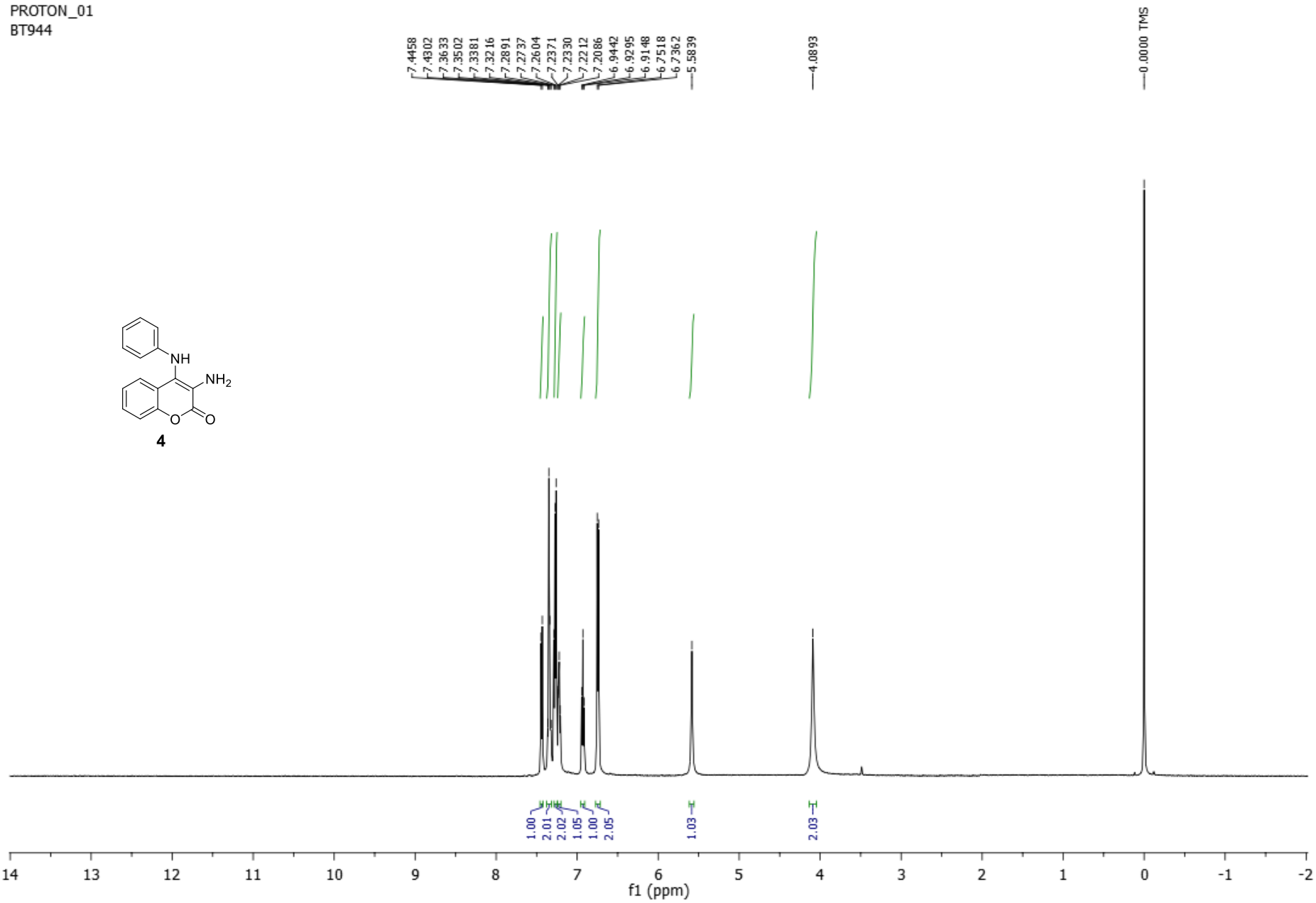
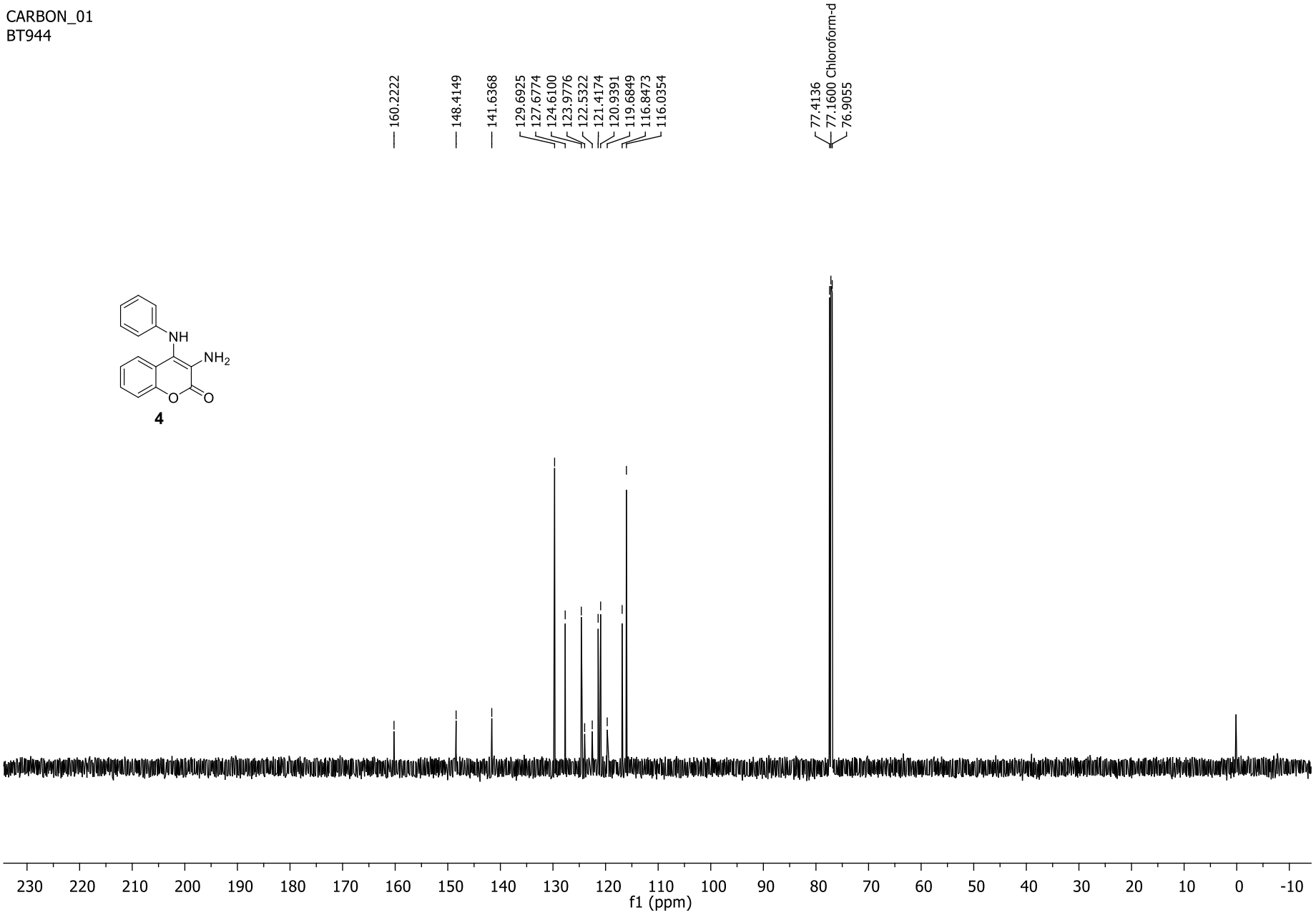
f1 (ppm)

3-amino-4-(phenylamino)-2*H*-chromen-2-one (4)

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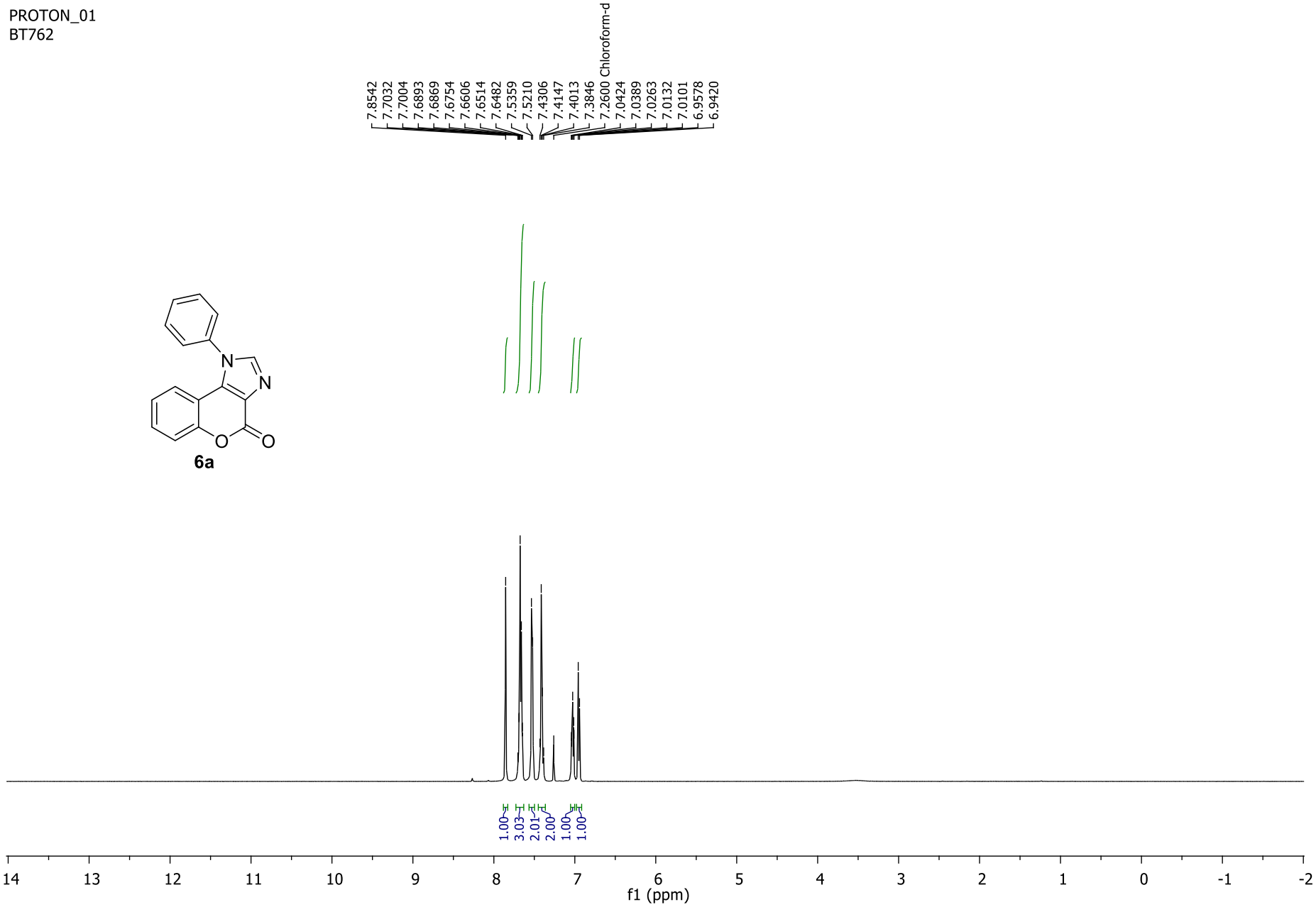
129.6925
127.6774
124.6100
123.9776
122.5322
121.4174
120.9391
119.6849
116.8473
116.0354
77.4136
77.1600 Chloroform-d
76.9055
NH
NH2
O
O
4
230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0 -10
f1 (ppm)

1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6a)



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BT762

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142.8893
135.9471
135.4430
130.8213
130.4772
130.0858
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77.4146
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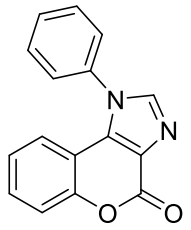
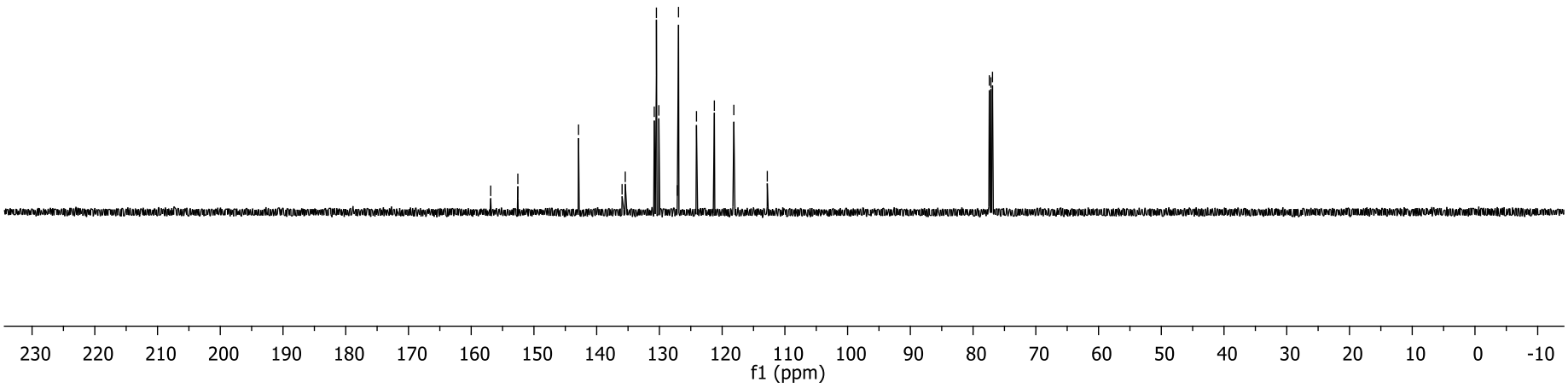


6a



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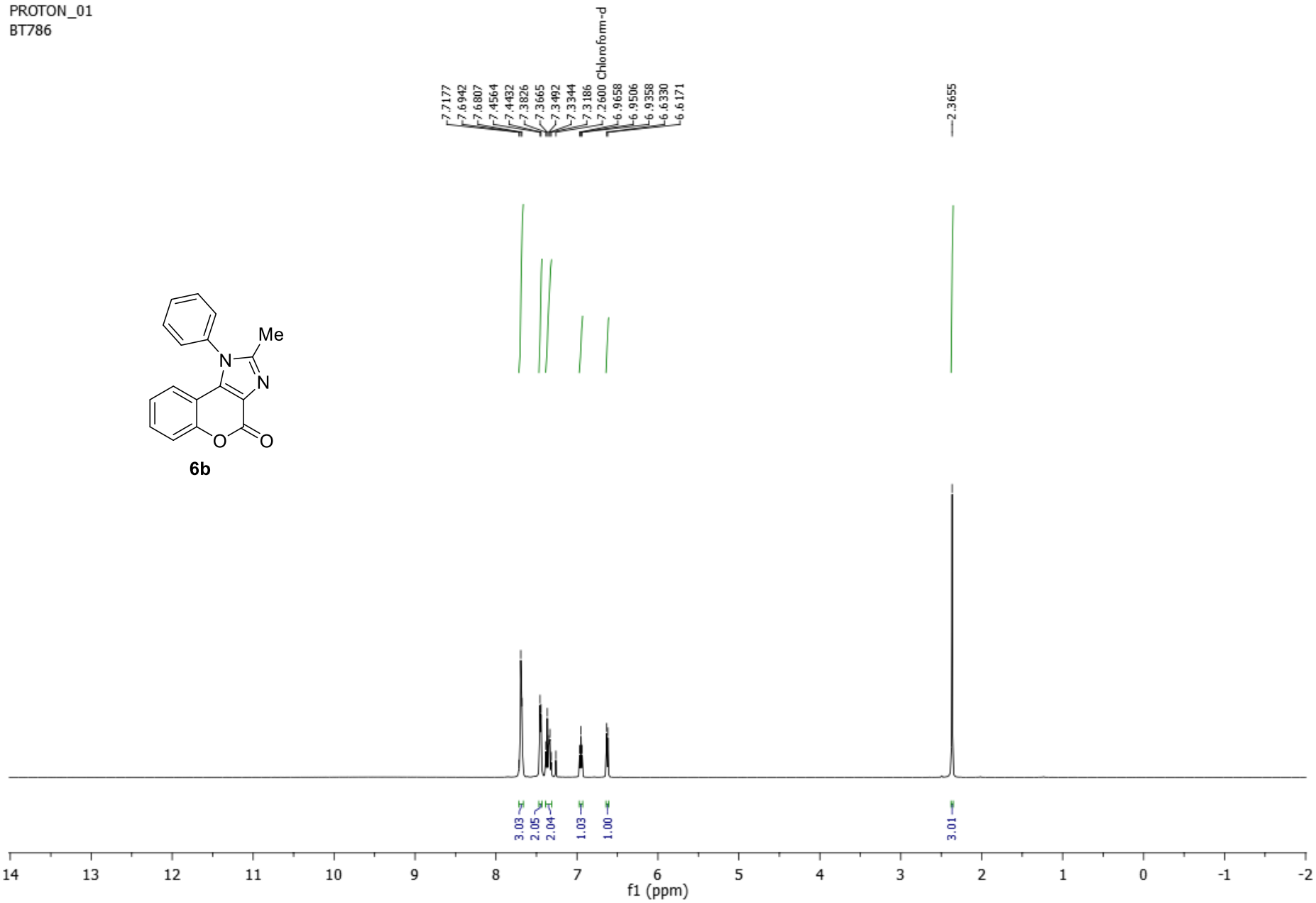

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127.6969
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77.4147
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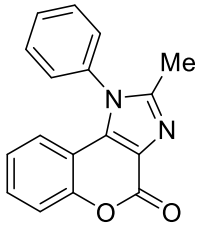
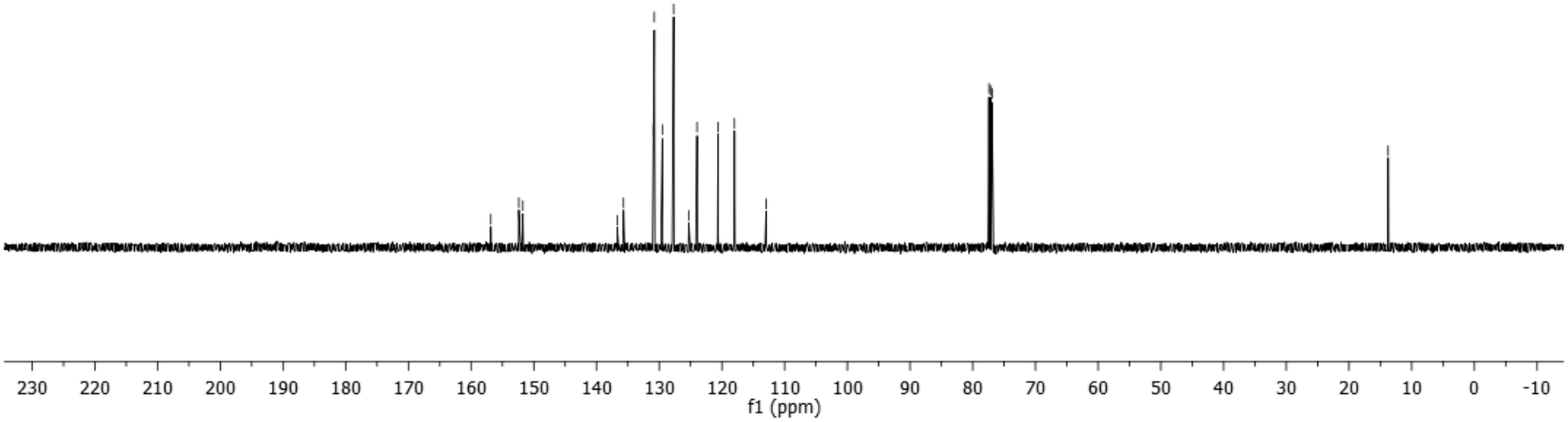
13.7499



6b



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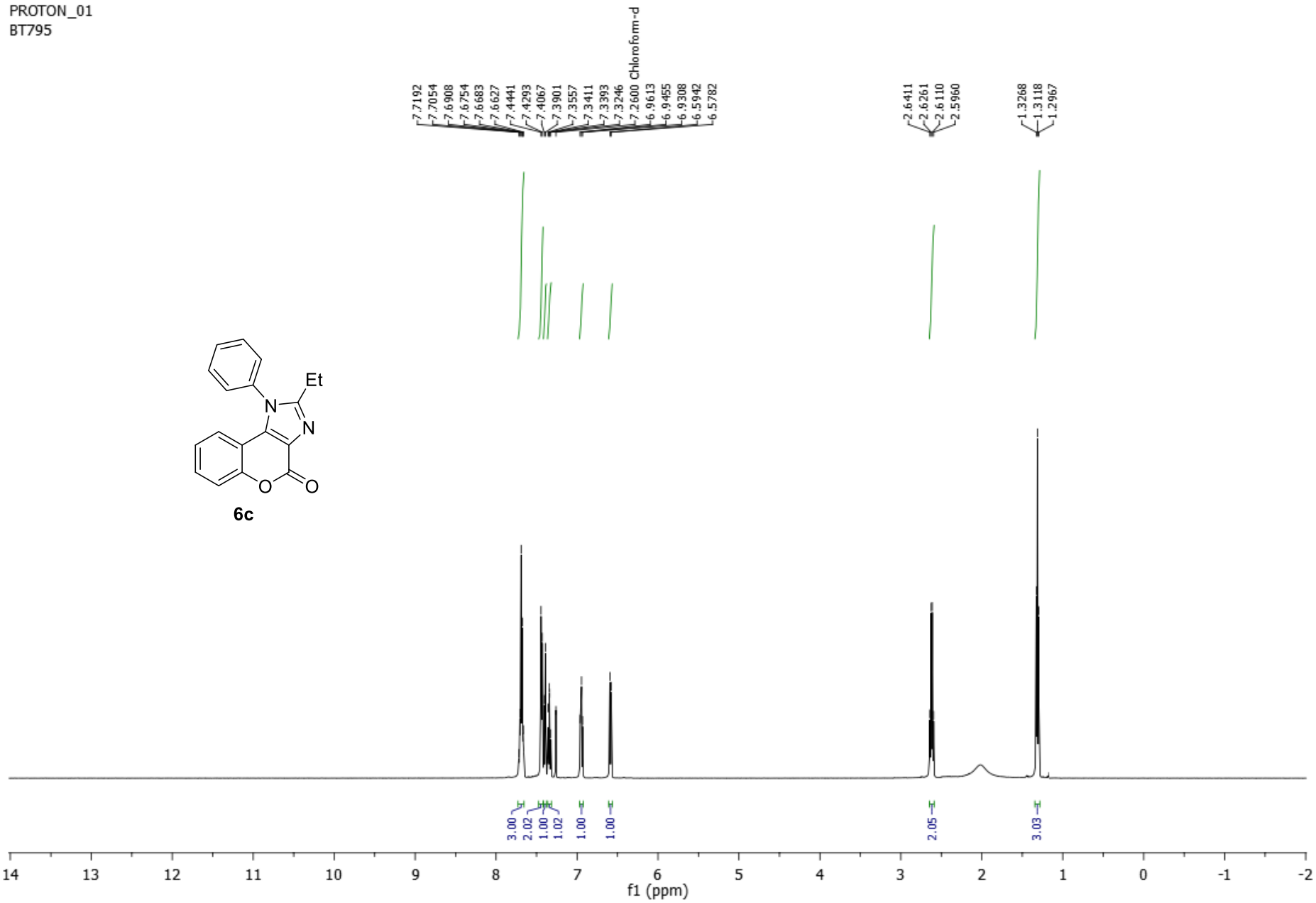

CARBON_01
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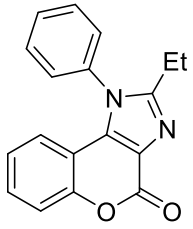
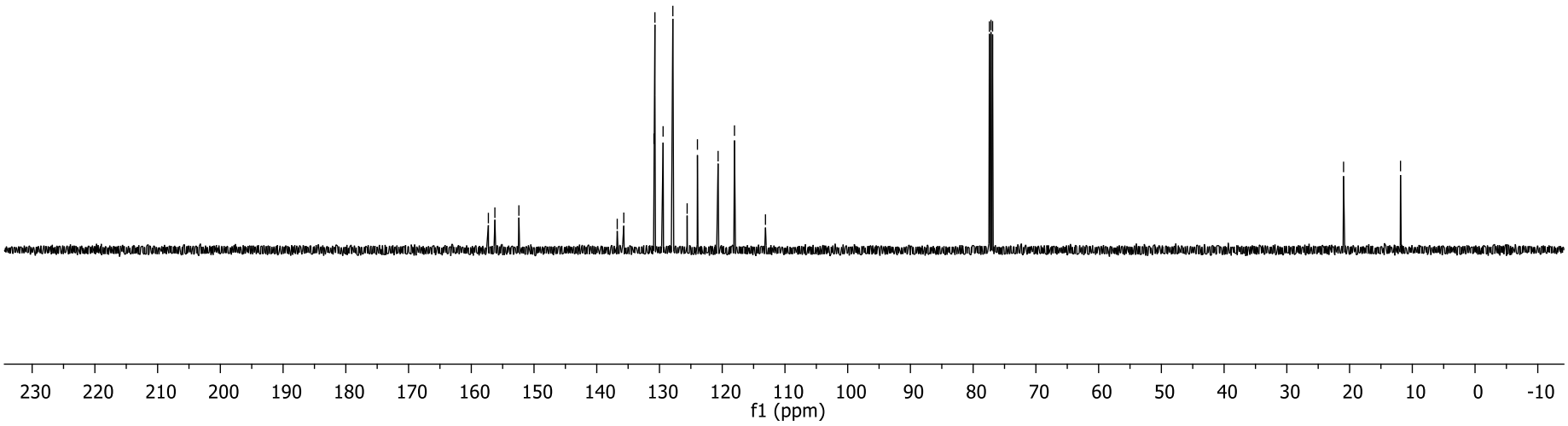


6c



1-phenyl-2-propylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6d)

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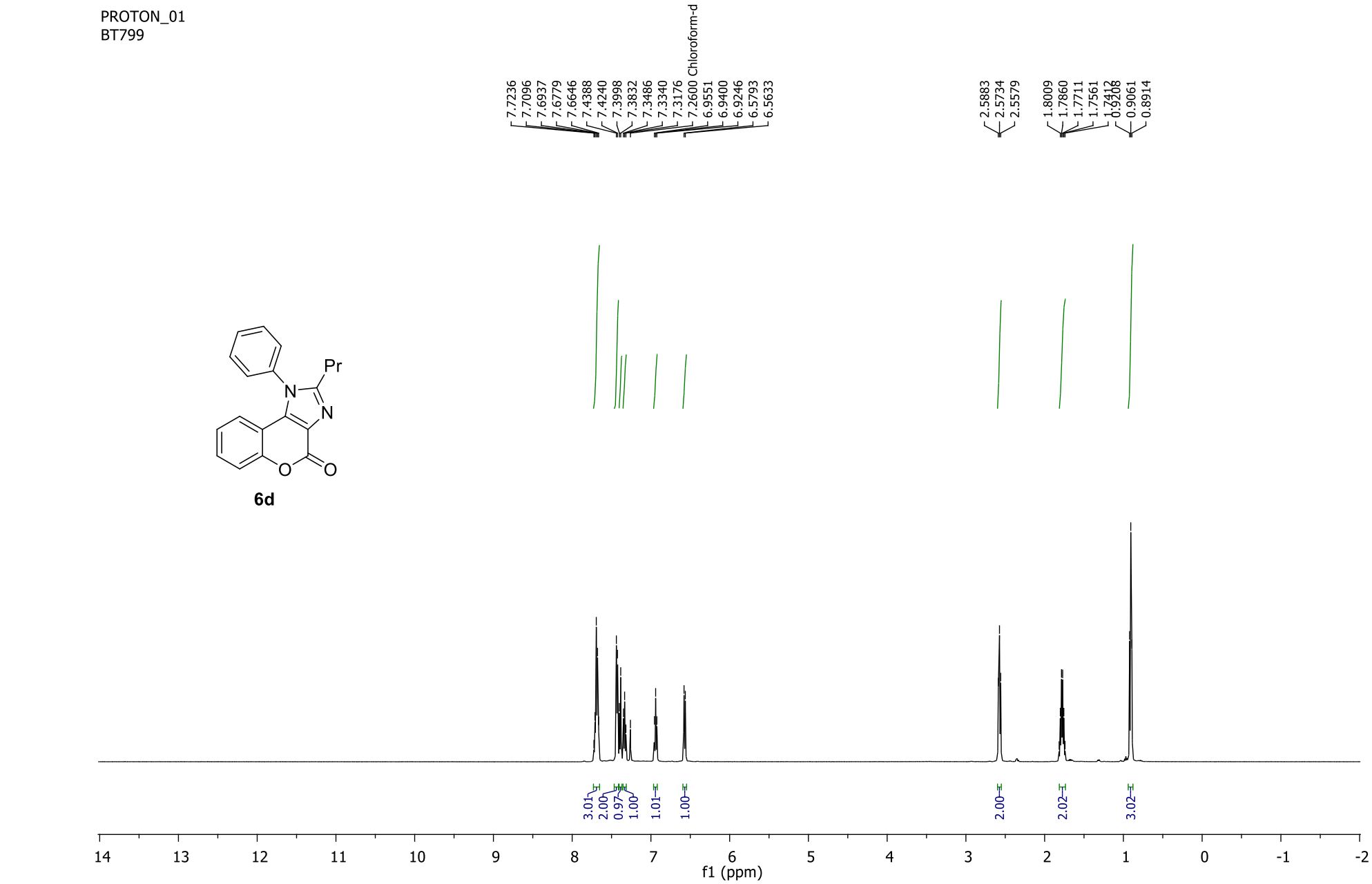
BT799



6d

CARBON_01
BT799

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125.6498
123.9155
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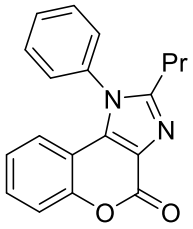
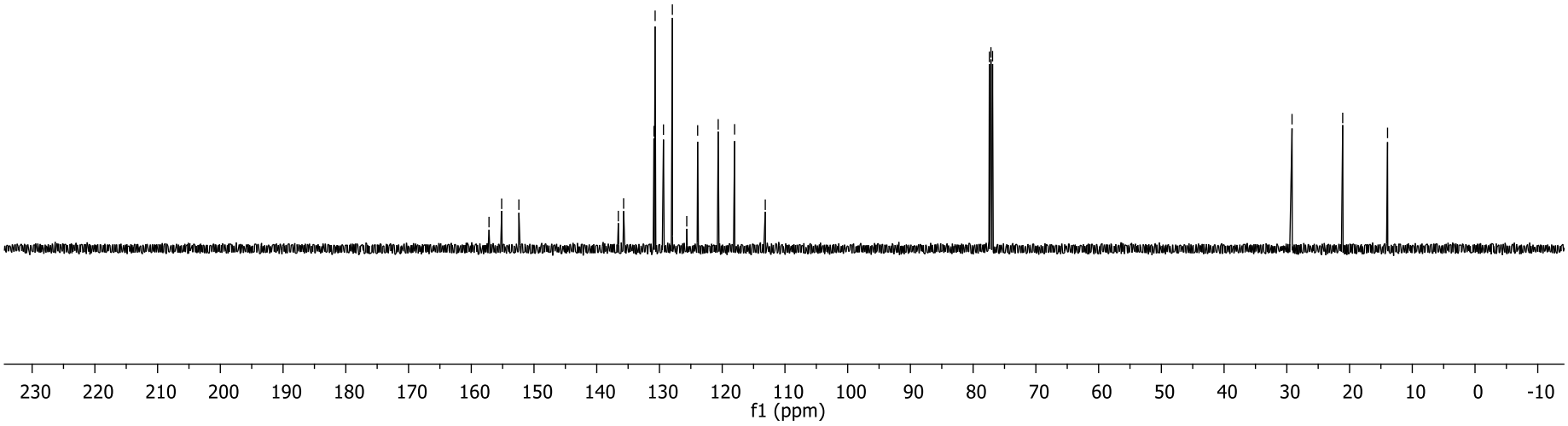
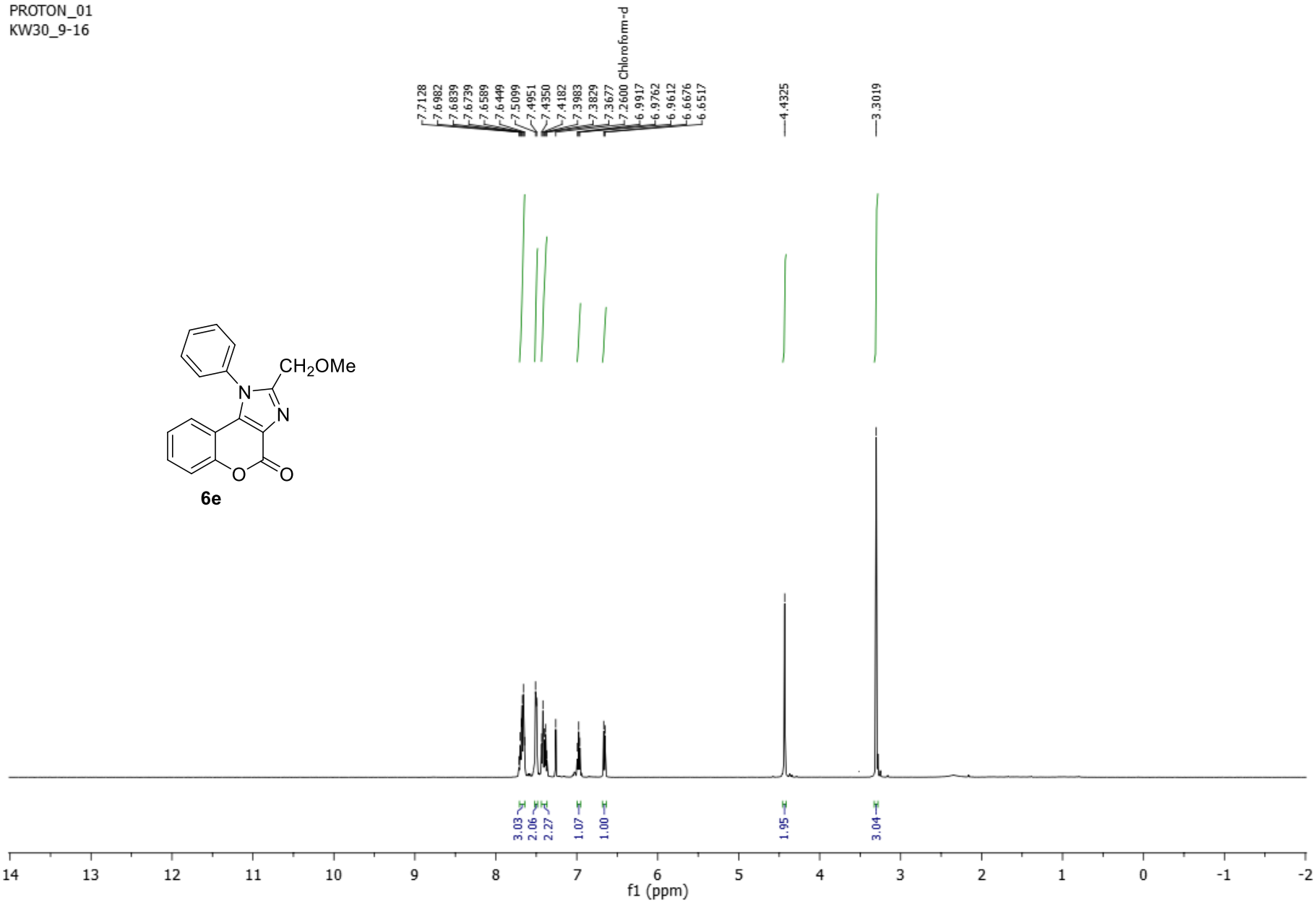


6d



2-(methoxymethyl)-1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6e)



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130.9285
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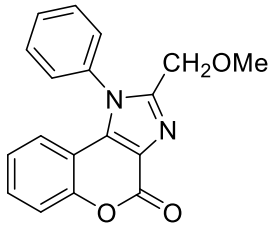
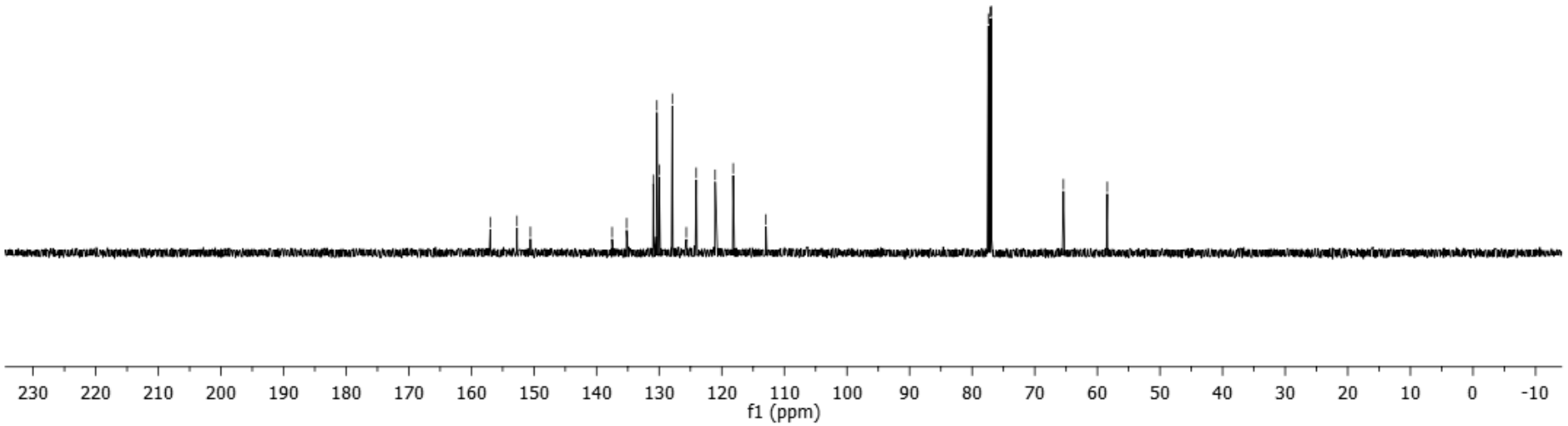
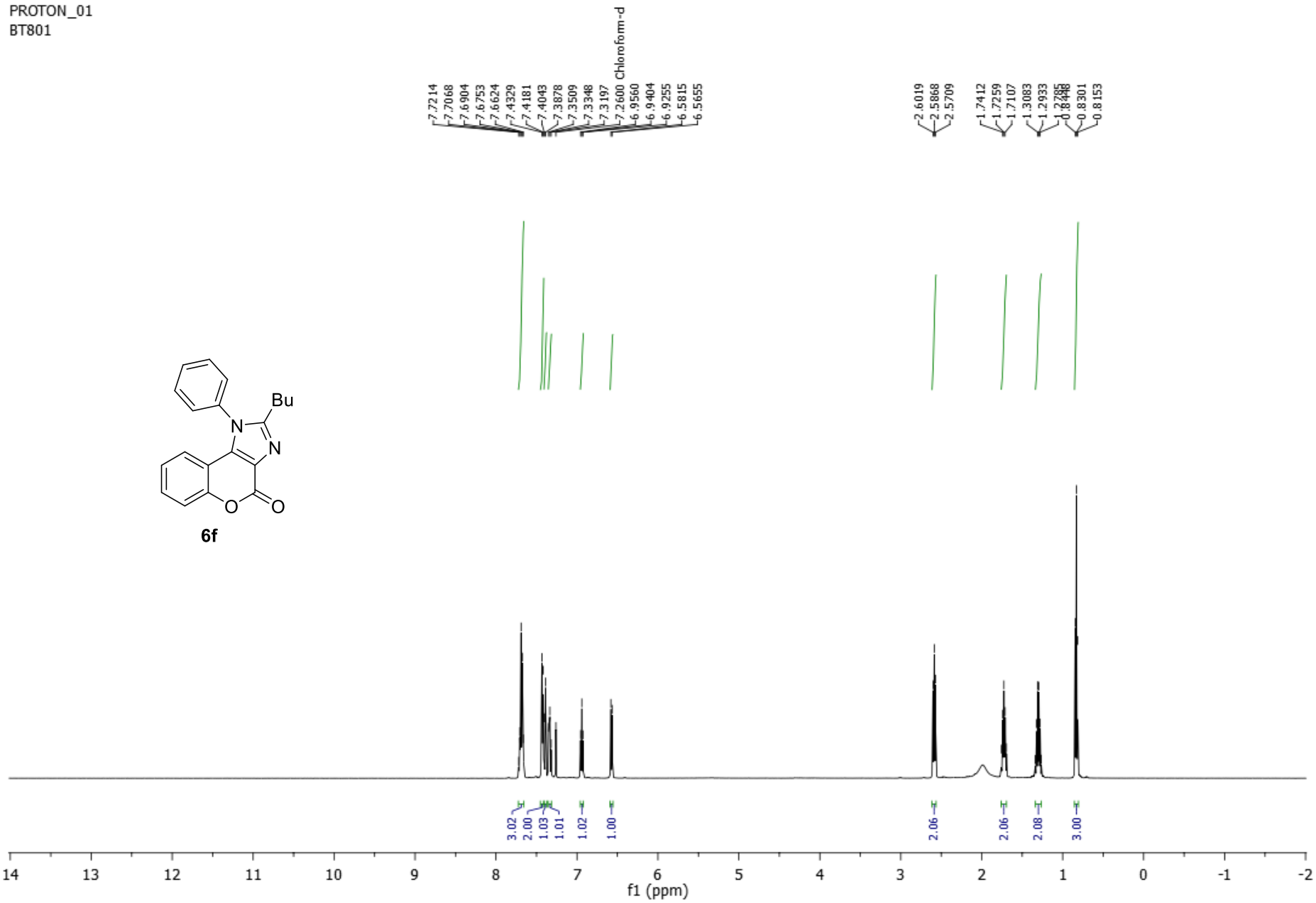
129.9857
127.9001
125.6547
124.0757
121.0488
118.1741
112.9319
77.4142
77.1600 Chloroform-d
76.9058
65.4215
58.4153



6e



2-butyl-1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6f)



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130.6858
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127.9310
125.6593
123.9335
120.6316
118.0312
113.1294
77.4139
77.1600 Chloroform-d
76.9053
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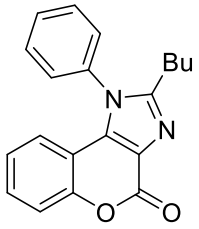
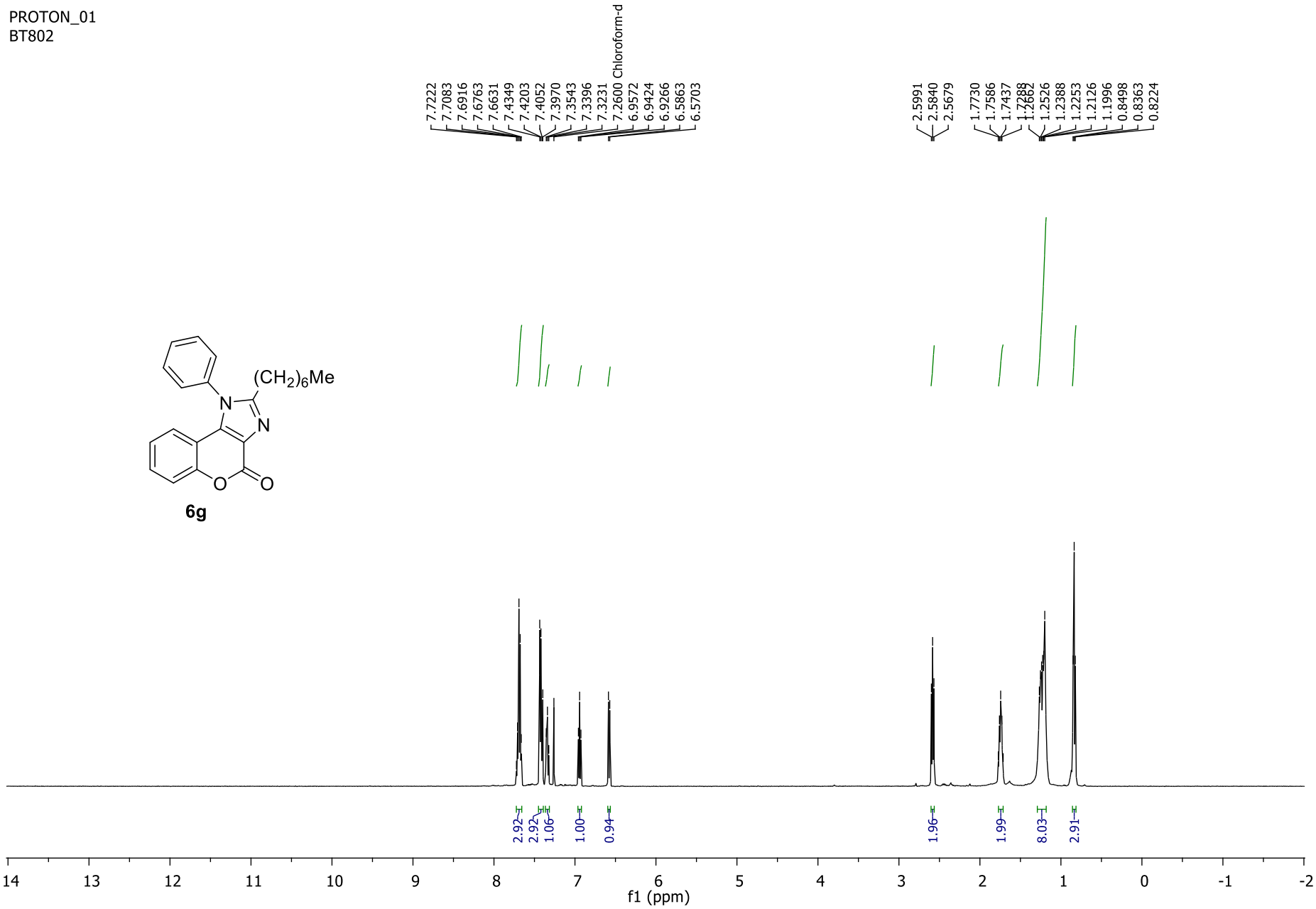
26.9506
22.3986
13.7340



6f

2-heptyl-1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6g)

PROTON_01
BT802



6g

CARBON_01
BT802

157.2587
155.3785
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136.5600
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130.8485
130.6750
129.3419
127.9693
125.7858
123.8978
120.6260
118.0656
113.1993
77.4137
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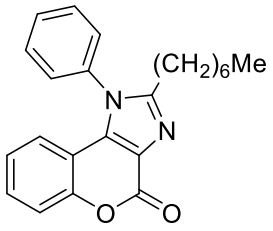
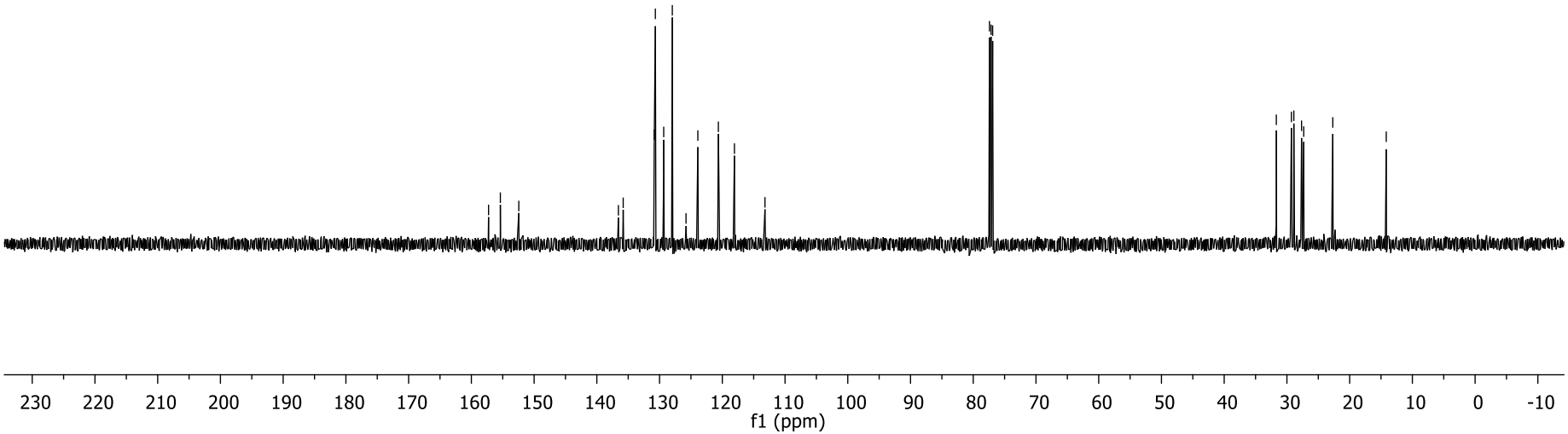
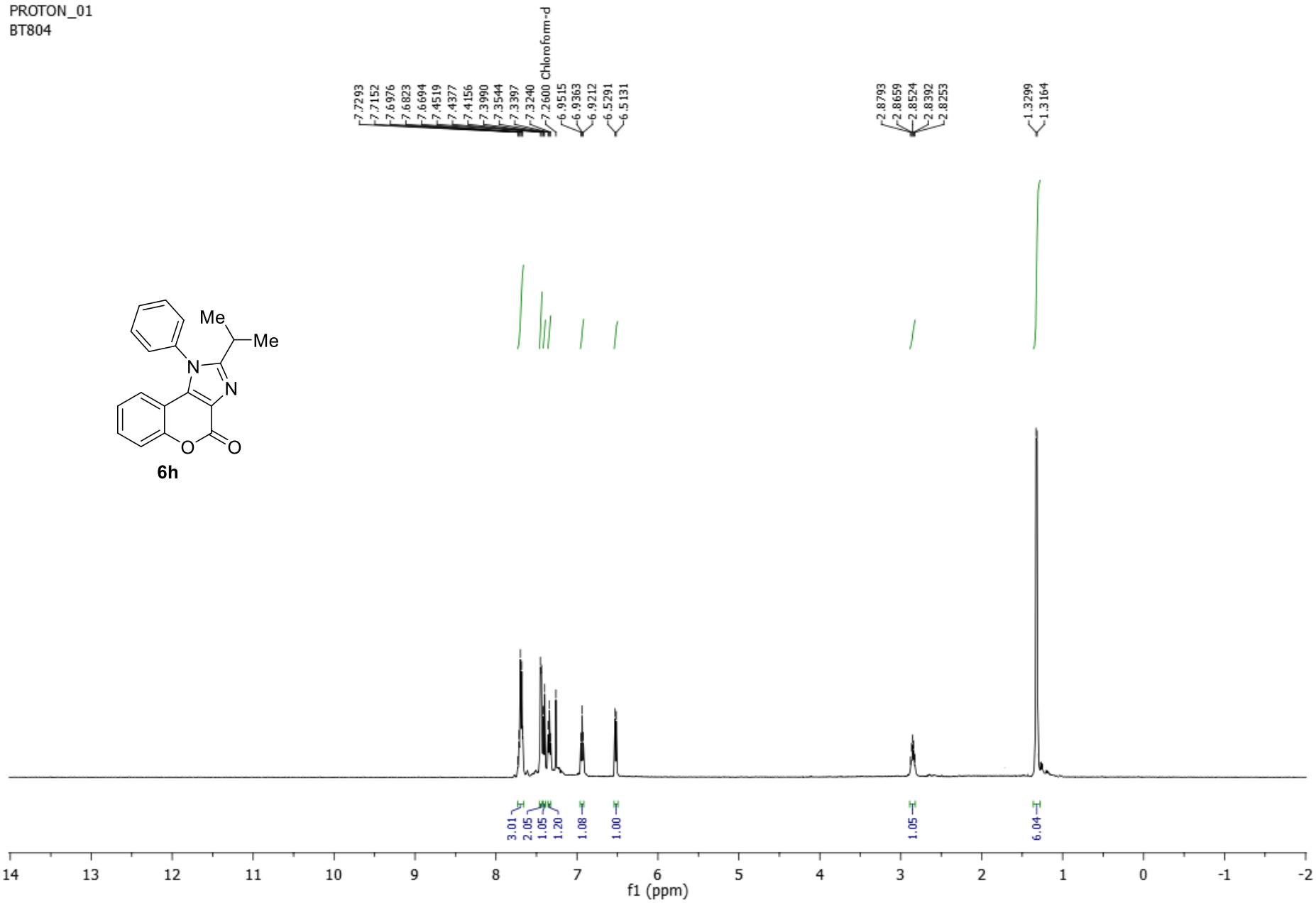
28.8957
27.6678
27.3195
22.6872
14.1650



6g



2-isopropyl-1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6h)



CARBON_01
BT804

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135.7527
130.9011
130.6882
129.3489
128.1086
125.6721
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118.0780
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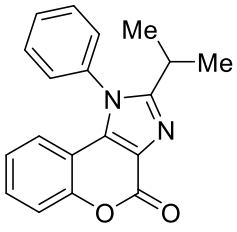
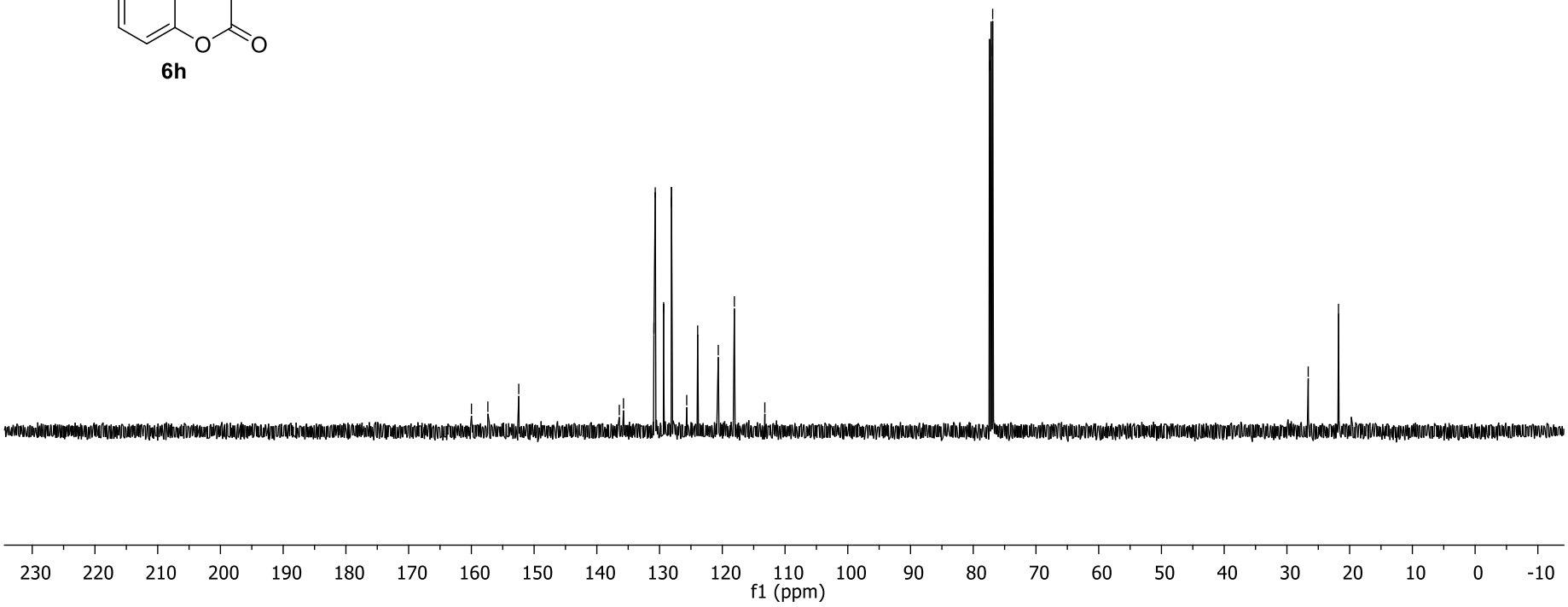
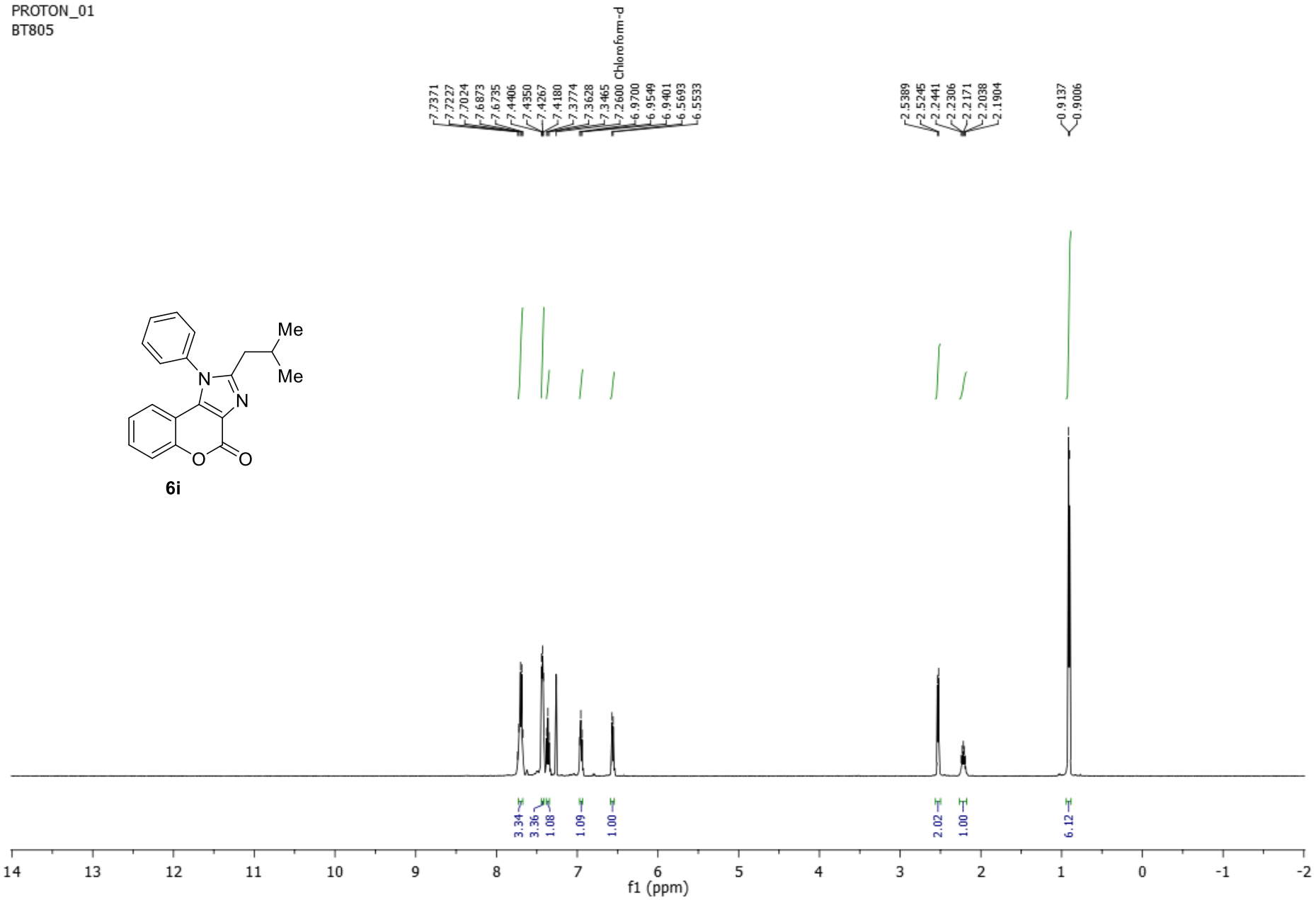
21.7791



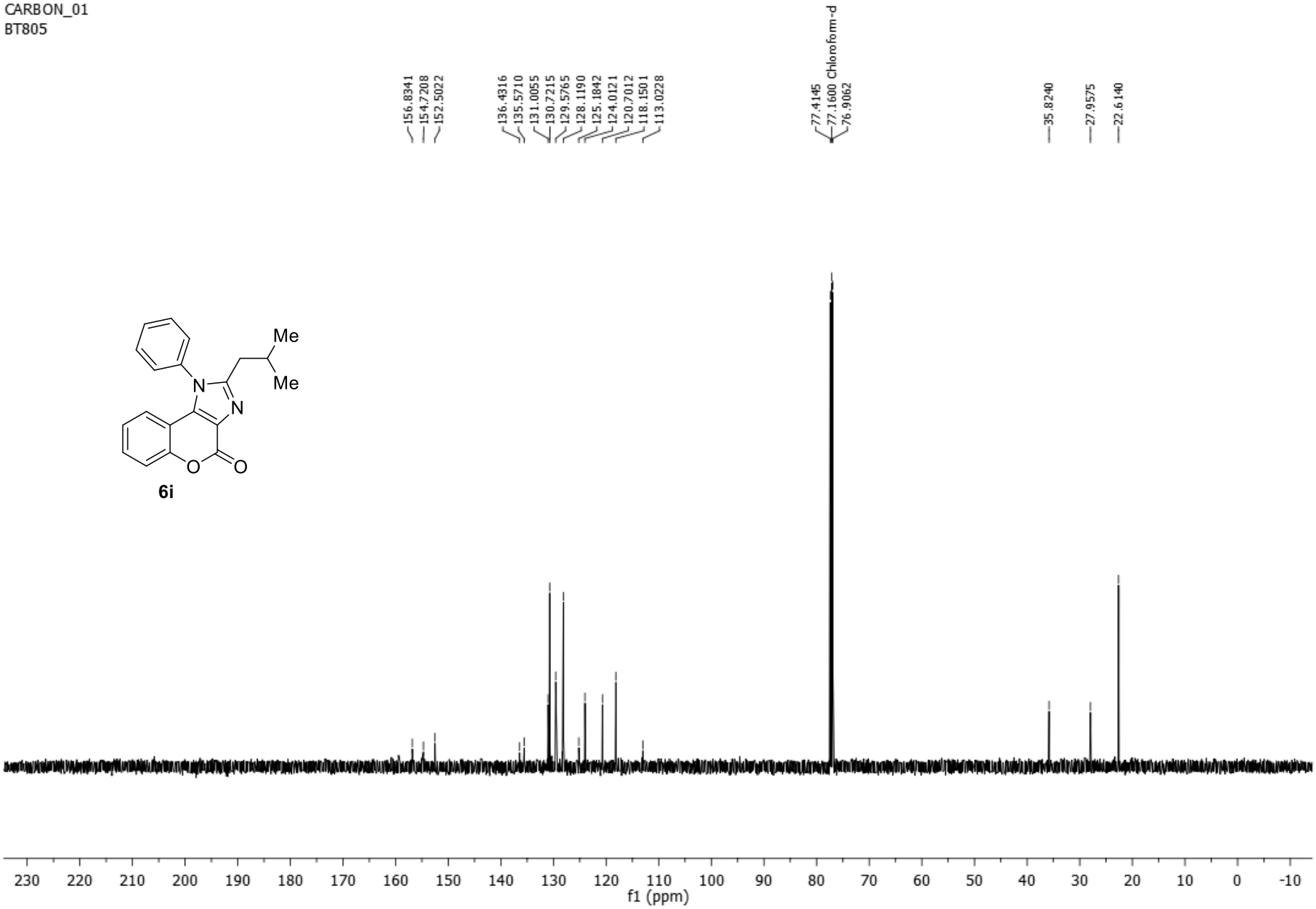
6h



2-isobutyl-1-phenylchromeno[3,4-*d*]imidazol-4(1*H*)-one (6i)



6i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BT805
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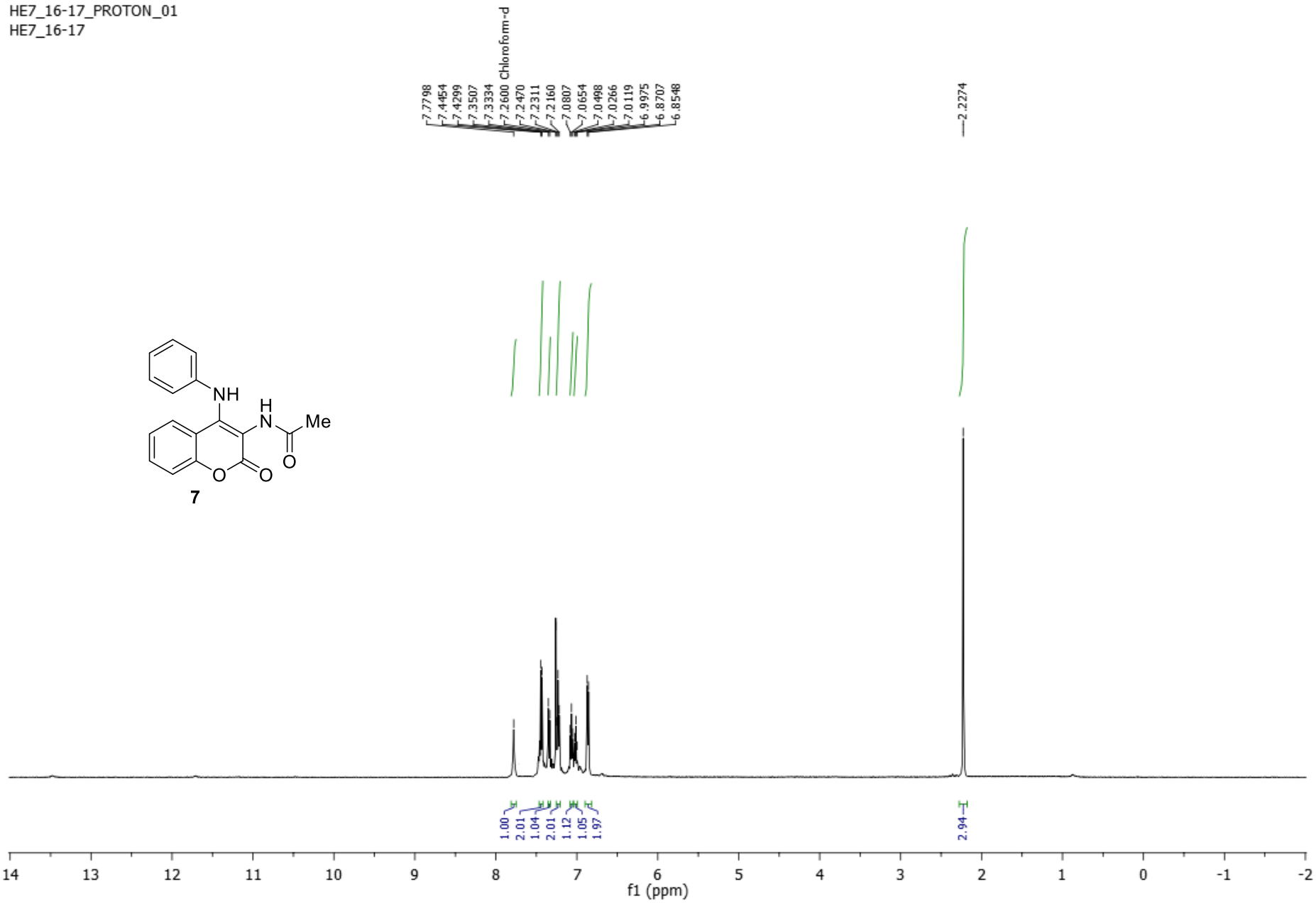
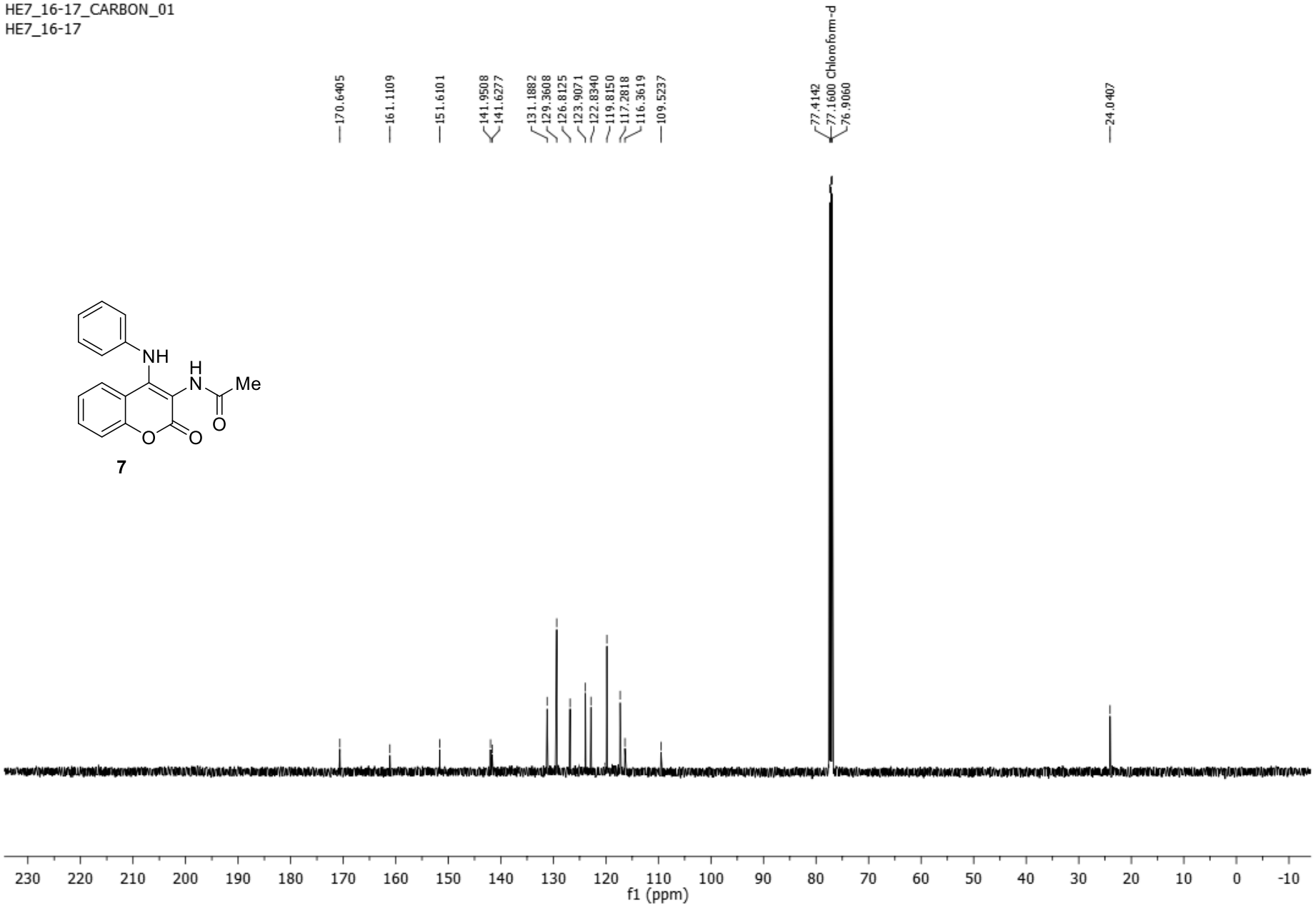
154.7208
152.5022
136.4316
135.5710
131.0055
130.7215
129.5765
128.1190
125.1842
124.0121
120.7012
118.1501
113.0228
77.4145
77.1600 Chloroform-d
76.9062
35.8240
27.9575
22.6140
Me
Me
N
N
O
O
6i
230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0 -10
f1 (ppm)

N-(2-oxo-4-(phenylamino)-2*H*-chromen-3-yl)acetamide (7)




HE7_16-17_CARBON_01
HE7_16-17
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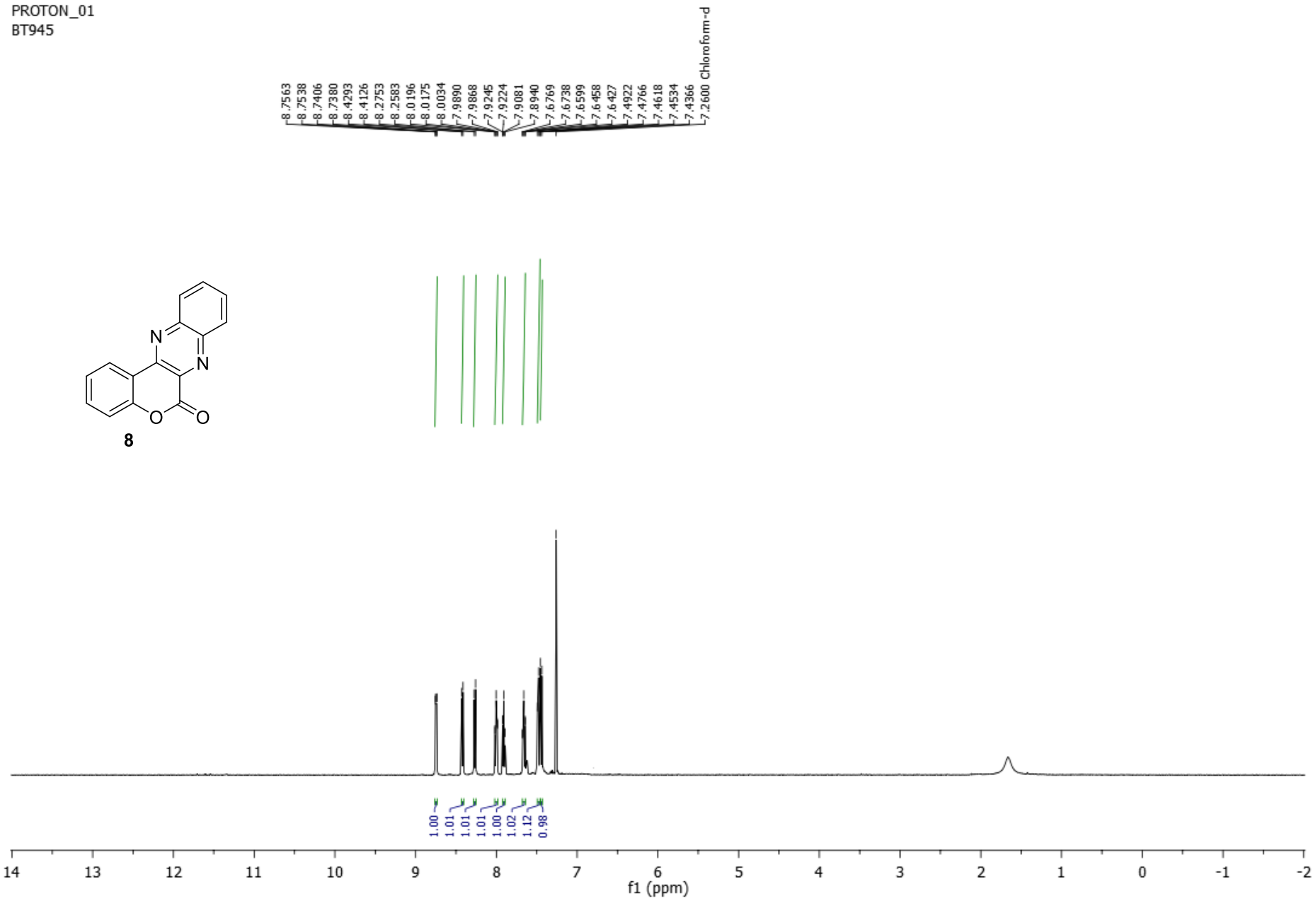
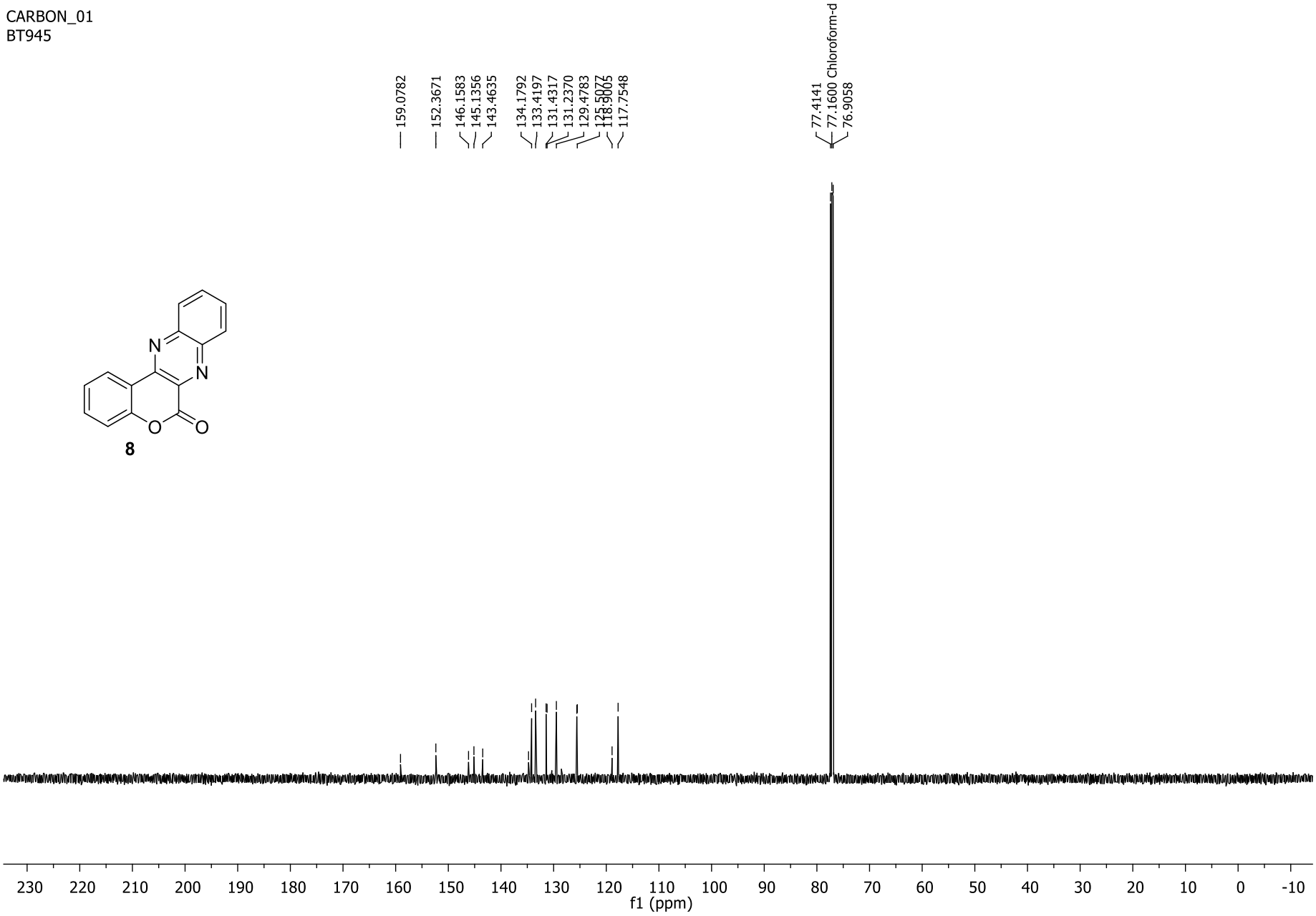
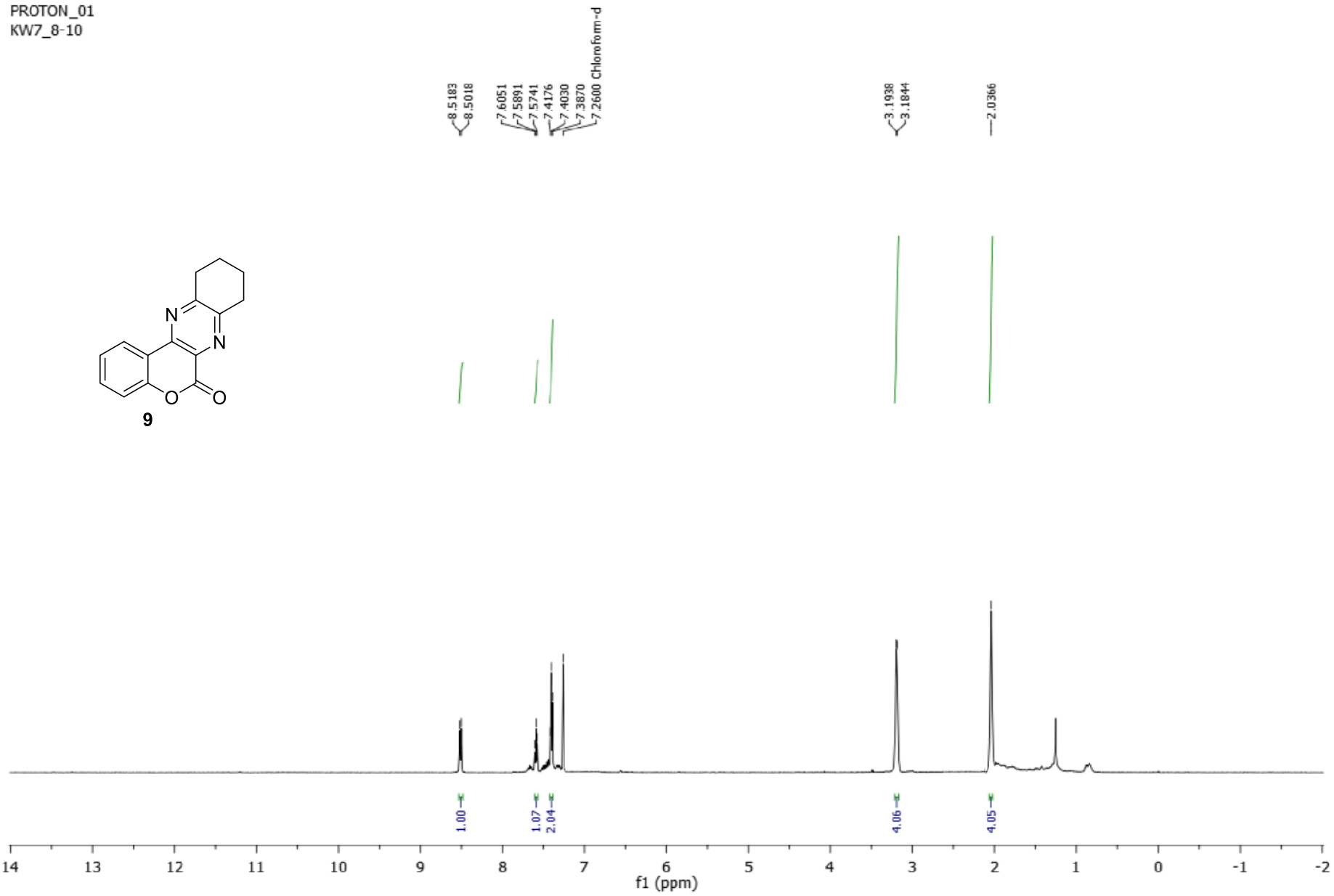
151.6101
141.9508
141.6277
131.1882
129.3608
126.8125
123.9071
122.8340
119.8150
117.2818
116.3619
109.5237
77.4142
77.1600 Chloroform-d
76.9060
24.0407
NH
H
N
Me
O
O
O
7
230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0 -10
f1 (ppm)

6*H*-chromeno[3,4-*b*]quinoxalin-6-one (8)



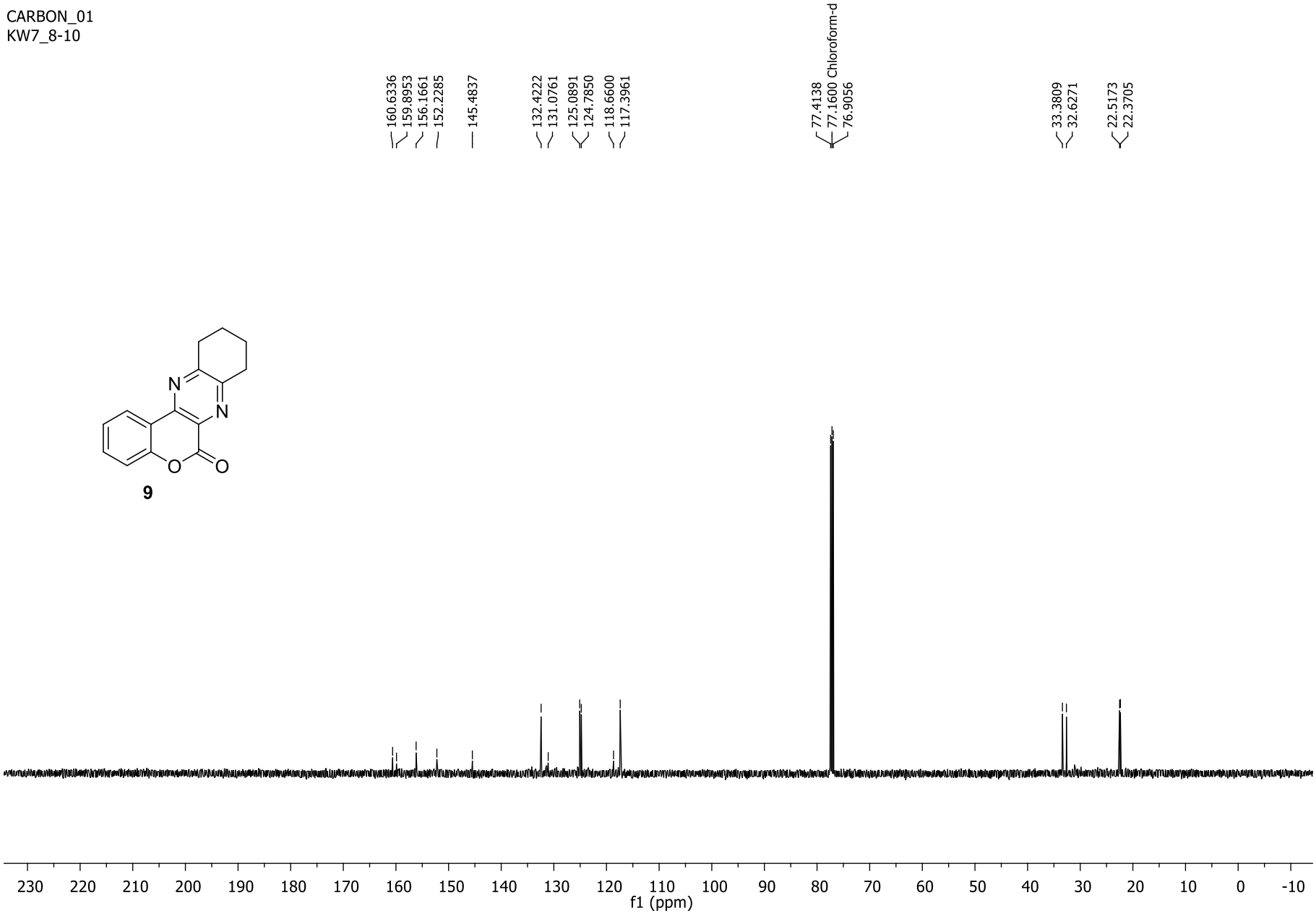

CARBON_01
BT945
159.0782
152.3671
146.1583
145.1356
143.4635
134.1792
133.4197
131.4317
131.2370
129.4783
125.5077
118.9005
117.7548
77.4141
77.1600 Chloroform-d
76.9058
N
N
O
O
8
230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0 -10
f1 (ppm)

8,9,10,11-tetrahydro-6*H*-chromeno[3,4-*b*]quinoxalin-6-one (9)



9

CARBON_01
KW7_8-10



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Visualization of the protein (PDB code: 3PZW) was performed using UCSF Chimera.[1] Water molecules were removed, missing residues were added with Modeller,[2] hydrogen atoms and AMBER99SB-ILDN charges were added and the charge on iron was set to +2.0, with no restraint applied to the iron atom and the ligands. Ligand 3D coordinates were generated and minimised with OpenBabel[3] using the MMFF94 force field.[4] ACPYPE (AnteChamber PYthon Parser interfacE)[5] was used to generate ligand topologies and parameters using Antechamber.[6] Energy minimizations were carried out using the AMBER99SB-ILDN force field[7] with GROMACS 4.6.5 as the molecular dynamics simulation toolkit.[8] Docking was performed with AutoDock Vina (1.1.2)[9] using a grid box of size 25 Å in X, Y, Z dimensions, centred on iron atom. UCSF-Chimera was used to generate docking input files and to analyze docking results. Docking was carried out with an exhaustiveness value of 10 and a maximum output of 20 docking modes.

1. Pettersen, E. F.; Goddard, T. D.; Huang, C. C.; Couch, G. S.; Greenblatt, D. M.; Meng, E. C.; Ferrin, T. E. *J. Comput. Chem.* **2004**, *25*, 1605.
2. Fiser, A.; Sali, A. *Meth. Enzymol.* **2003**, *374*, 461.
3. O'Boyle, N. M.; Banck, M.; James, C. A.; Morley, C.; Vandermeersch, T.; Hutchison, G. R. *J. Cheminform.* **2011**, *3*, 33.
4. Halgren, T. A. *J. Comput. Chem.* **1998**, *17*, 490.
5. Sousa de Silva, A. W.; Vranken, W. F. *BMC Research Notes* **2012**, *5*, 367.
6. Wang, J.; Wang, W.; Kollman, P. A.; Case, D. A. *J. Mol. Graph. Comput. Model.* **2006**, *25*, 247.
7. Lindorff-Larsen. K.; Piana, S.; Palmo, K. Maragakis, P.; Klepeis, J. L.; Dror, R. O.; Shaw, D. E. *Proteins* **2010**, 78, 1950.
8. Hess, B.; Kutzner, C.; van der Spoel, D.; Lindhal, E. *J. Chem. Theory Comput.* **2008**, *4*, 435.
9. Trott, O.; Olson, A. J. *J. Comput. Chem.* **2010**, 31, 455.

