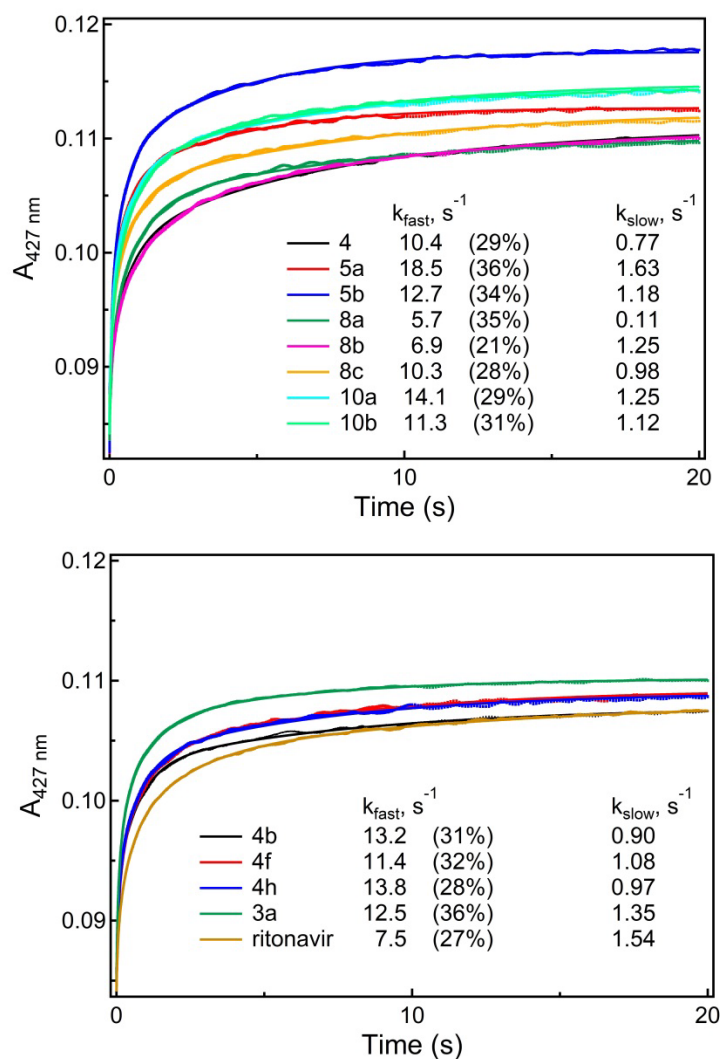


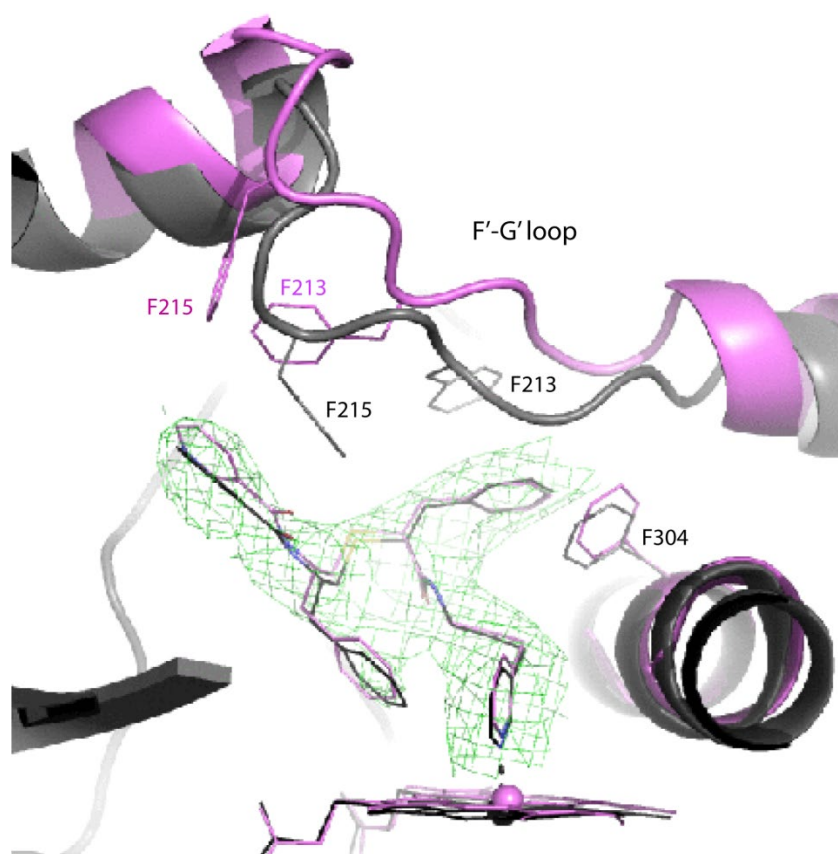
# Interaction of human drug-metabolizing CYP3A4 with rationally designed ritonavir analogues: Impact of steric constraints imposed on the heme-ligating group and the end-pyridine attachment

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## SUPPLEMENTARY MATERIALS



**Figure S1.** Kinetics of ligand binding to CYP3A4. Kinetic traces were recorded by mixing 2  $\mu\text{M}$  CYP3A4 with 20  $\mu\text{M}$  solutions of series VI analogues (upper panel) or previously reported compounds and ritonavir (lower panel). Within the studied time interval, all reactions were biphasic. Fittings are shown as solid lines. The derived rate constants for the fast and slow phases and the percentage of the fast phase are indicated.



**Figure S2.** Superposition of **10a**-bound CYP3A4 crystallized in the I222 (magenta) and C2 space group (gray; molecule A). The ligand binding mode is only slightly affected by differences in crystal packing. Green mesh is polder omit electron density map contoured at 3  $\sigma$  level.

**Table S1.** Data collection and refinement statistics

Ligand	<b>5a</b>	<b>5b</b>	<b>8a</b>	<b>8b</b>
CYP3A4	WT	WT	WT	WT
PDB ID	7UF9	7UFA	7UFB	7UFC
<i>Data statistics</i>				
Space group	I222	I222	I222	I222
Unit cell	<i>a, b, c</i> = 77 x 101 x 128 Å; $\alpha, \beta, \gamma = 90^\circ$	<i>a, b, c</i> = 77 x 102 x 126 Å; $\alpha, \beta, \gamma = 90^\circ$	<i>a, b, c</i> = 77 x 102 x 128 Å; $\alpha, \beta, \gamma = 90^\circ$	<i>a, b, c</i> = 78 x 103 x 128 Å; $\alpha, \beta, \gamma = 90^\circ$
Resolution range (Å)	79.53-2.45 (2.58-2.45) <sup>a</sup>	50.86-2.50 (2.64-2.50)	79.62-2.25 (2.37-2.25)	80.35-2.35 (2.48-2.35)
Total reflections	82,809 (12,979)	124,746 (17,945)	186,616 (26,677)	82,093 (12,824)
Unique reflections	18,319 (2,694)	17,305 (2,503)	24,033 (3,473)	20,611 (3,070)
Redundancy	4.5 (4.6)	7.2 (7.2)	7.8 (7.7)	4.0 (4.2)
Completeness	98.1 (99.5)	99.8 (100.0)	99.5 (99.6)	95.3 (98.0)
Average <i>I</i> / $\sigma$	12.5 (1.1)	9.8 (1.0)	13.8 (1.3)	9.2 (1.1)
R <sub>merge</sub>	0.047 (1.630)	0.089 (2.524)	0.059 (1.604)	0.066 (2.695)
R <sub>pim</sub>	0.024 (0.842)	0.036 (1.006)	0.022 (0.610)	0.036 (1.362)
CC ½	0.999 (0.416)	0.998 (0.403)	0.999 (0.395)	0.994 (0.480)
<i>Refinement statistics</i>				
<i>R</i> / <i>R</i> <sub>free</sub> <sup>b</sup>	22.5/25.5	24.7/28.4	21.0/25.8	20.8/25.4
Number of atoms:				
Protein	3645	3735	3350	3727
Solvent	0	6	20	7
R.m.s. deviations				
Bond lengths, Å	0.004	0.003	0.003	0.003
Bond angles, °	0.634	0.558	0.517	0.535
Wilson B-factor, Å <sup>2</sup>	85	79	70	77
Average <i>B</i> -factor, Å <sup>2</sup> :				
Protein	119	119	101	107
Ligand	137	119	102	107
Ramachandran plot <sup>d</sup> (residues; %)				
Preferred	413 (94.3%)	421 (94.6%)	445 (96.7%)	434 (96.2%)
Allowed	23 (5.2%)	23 (5.2%)	15 (3.3%)	27 (3.8%)
Outliers	2 (0.5%)	1 (0.2%)	none	none

<sup>a</sup>Values in brackets are for the highest resolution shell.<sup>b</sup>*R*<sub>free</sub> was calculated from a subset of 5% of the data that were excluded during refinement.<sup>c</sup>Values for two molecules in the asymmetric unit.<sup>d</sup>Analyzed with PROCHECK.

**Table S2.** Data collection and refinement statistics

Ligand	<b>8c</b>	<b>10a</b>	<b>10b</b>
CYP3A4	WT	K421A/K424A	K421A/K424A
PDB ID	7UFD	7UFE	7UFF
<i>Data statistics</i>			
Space group	I222	C2	C2
Unit cell	<i>a, b, c</i> = 78 x103 x 130 Å; <i>α, β, γ</i> = 90	<i>a, b, c</i> = 154 x 97 x 94 Å; <i>α, β, γ</i> = 90 x 124 x 90°	<i>a, b, c</i> = 157 x 98 x 95 Å; <i>α, β, γ</i> = 90 x 125 x 90°
Resolution range (Å)	80.52-2.90 (3.06-2.90) <sup>a</sup>	77.63-2.40 (2.53-2.40)	77.75-2.70 (2.85-2.70)
Total reflections	57,848 (8,841)	148,105 (22,323)	183,071 (22,905)
Unique reflections	11,818 (1,714)	43,861 (6,382)	30,683 (4,113)
Redundancy	4.9 (5.2)	3.4 (3.5)	6.0 (5.5)
Completeness	99.8 (99.9)	98.7 (98.9)	95.1 (88.6)
Average <i>I</i> / <i>σ</i>	6.3 (2.5)	8.3 (1.1)	8.5 (1.0)
R <sub>merge</sub>	0.174 (1.203)	0.063 (1.257)	0.115 (1.774)
R <sub>pim</sub>	0.089 (0.570)	0.039 (0.777)	0.050 (0.818)
CC ½	0.972 (0.354)	0.998 (0.506)	0.997 (0.405)
<i>Refinement statistics</i>			
<i>R</i> / <i>R</i> <sub>free</sub> <sup>b</sup>	20.1/27.8	22.1/25.3	24.4/28.1
Number of atoms:			
Protein	3727	3706/3575 <sup>c</sup>	3685/3575 <sup>c</sup>
Solvent	0	53	13
R.m.s. deviations	0.002	0.002	0.002
Bond angles, °	0.476	0.503	0.511
Wilson B-factor, Å <sup>2</sup>	94	71	83
Average <i>B</i> -factor, Å <sup>2</sup> :			
Protein	107	90/111 <sup>c</sup>	92/123 <sup>c</sup>
Ligand	103	80/90 <sup>c</sup>	83/115 <sup>c</sup>
Ramachandran plot <sup>d</sup> (residues; %)			
Preferred	429 (95.1%)	820 (92.3%)	822 (93.3%)
Allowed	22 (4.9%)	67 (7.6%)	58 (6.6%)
Outliers	none	1 (0.1%)	1 (0.1%)

<sup>a</sup>Values in brackets are for the highest resolution shell.<sup>b</sup>*R*<sub>free</sub> was calculated from a subset of 5% of the data that were excluded during refinement.<sup>c</sup>Values for two molecules in the asymmetric unit.<sup>d</sup>Analyzed with PROCHECK.

**Table S3.** Local correlation coefficients (CC) and  $CC_{\text{peak}}$  between three polder maps ( $F_{\text{obs}} = |F_{\text{model}}|$ )

Map 1 (m1), calculated  $F_{\text{obs}}$  assuming that the omitted ligand atoms are present. Map 2 (m2), calculated  $F_{\text{obs}}$  assuming that the omitted ligand atoms are not present. Map 3 (m3), polder map calculated using the experimental data.

		m1-m2		m1-m3		m2-m3	
Ligand/PDB ID		CC	$CC_{\text{peak}}$	CC	$CC_{\text{peak}}$	CC	$CC_{\text{peak}}$
<b>5a</b>	7UF9	0.6992	0.6672	0.9230	0.8715	0.6336	0.5914
<b>5b</b>	7UFA	0.4962	0.4570	0.8256	0.7698	0.4460	0.4101
<b>8a</b>	7UFB	0.7025	0.7522	0.9062	0.8803	0.7123	0.7491
<b>8b</b>	7UFC	0.5861	0.5493	0.8972	0.8544	0.5939	0.5425
<b>8c</b>	7UFD	0.6629	0.6702	0.9049	0.8783	0.5949	0.6046
<b>10a</b>	7UFE	0.5353	0.5100	0.9200	0.8496	0.5071	0.4826
<b>10b</b>	7UFF	0.5257	0.5584	0.8700	0.8496	0.4717	0.4749

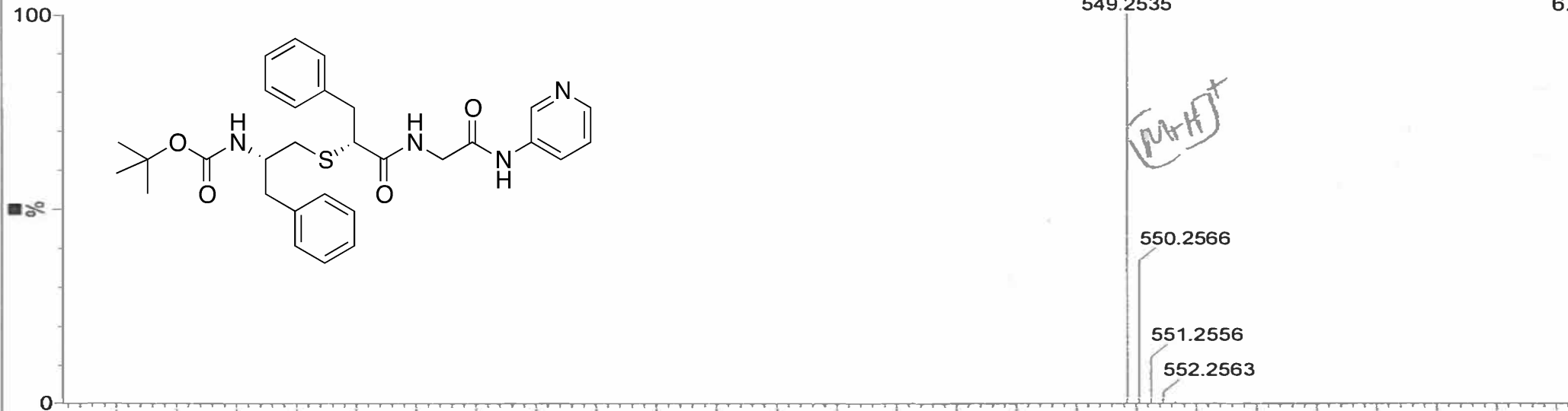
Correlation coefficients for polder maps were calculated with PHENIX.

For all ligands, pairwise comparisons of correlation coefficients indicate that m3 correlates best with m1. This means that the polder maps m3 (displayed in Figures 3, 5 and 7 of the main text) show the omitted ligand atoms.\*

\*Liebschner D., Afonine P.V.; Moriarty N.W.; Poon B.K.; Sobolev O.V.; Terwilliger T.C.; Adams P.D. Polder maps: improving OMIT maps by excluding bulk solvent. *Struct. Biol.* **2016**, D73, 148-157.

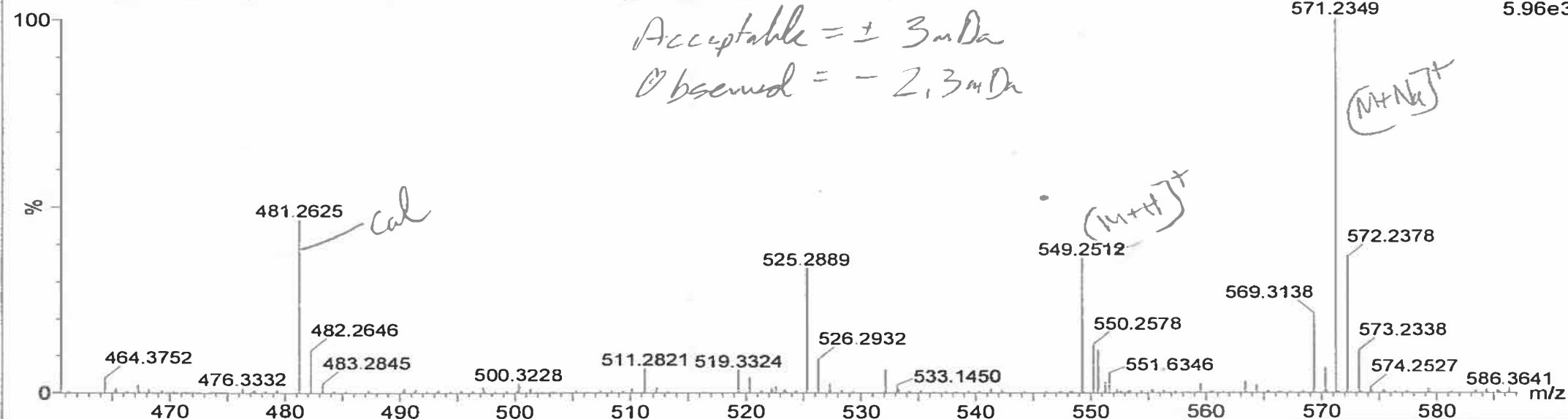
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TOF MS ES+  
6.62e12



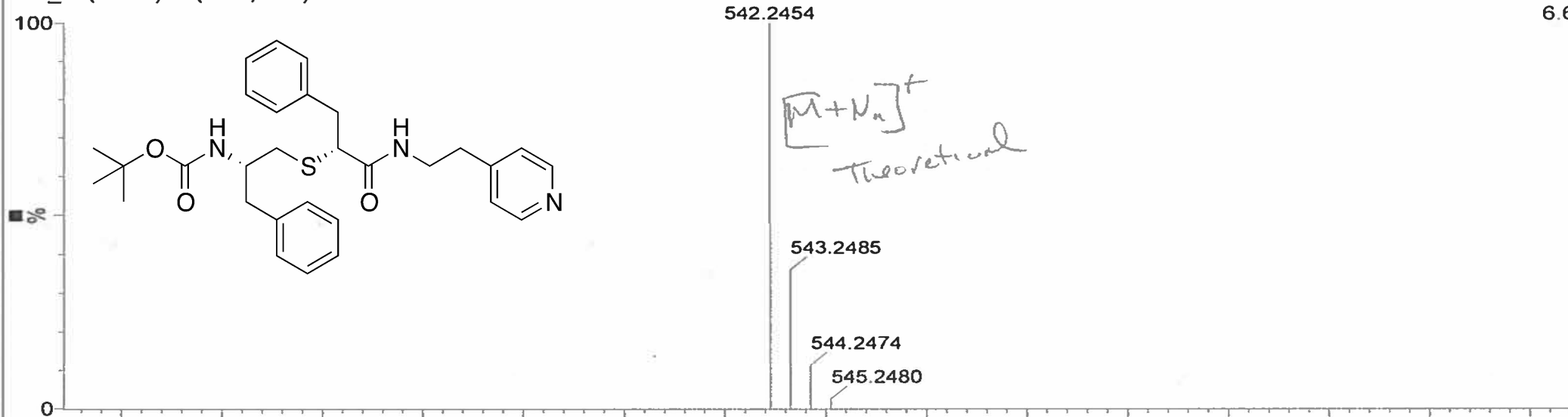
3124\_a 23 (0.422) AM (Cen,5, 80.00, Ar,8000.0,481.26,0.70); Sm (SG, 2x3.00); Sb (1,40.00 ); Cm (19:33)

TOF MS ES+  
5.96e3



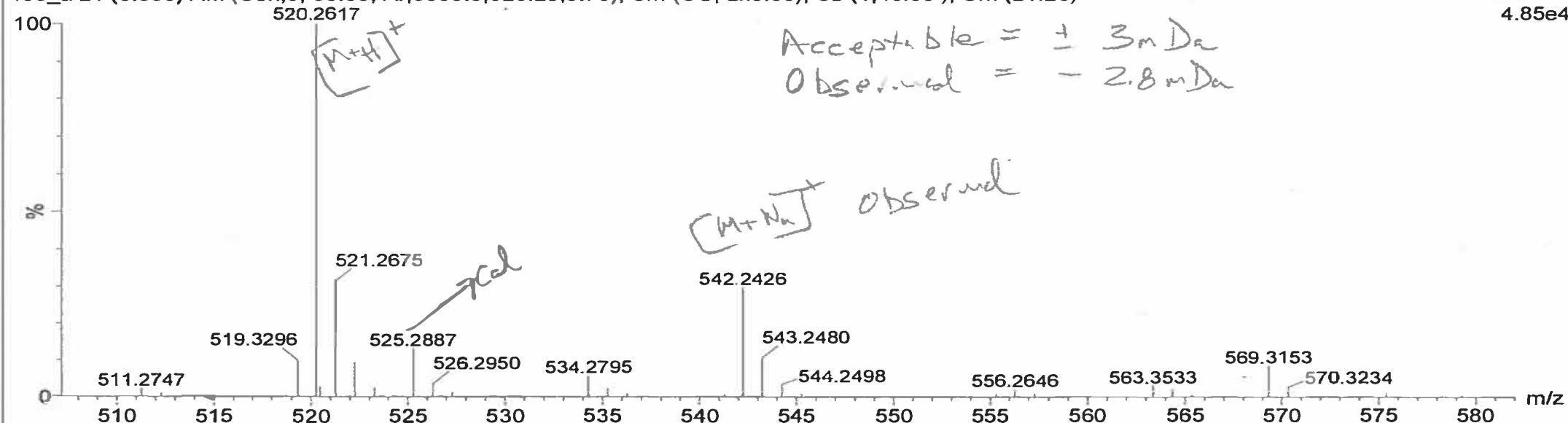
408\_a (0.019) Is (1.00,0.01) C<sub>30</sub>H<sub>37</sub>N<sub>3</sub>O<sub>3</sub>Na

TOF MS ES+  
6.66e12



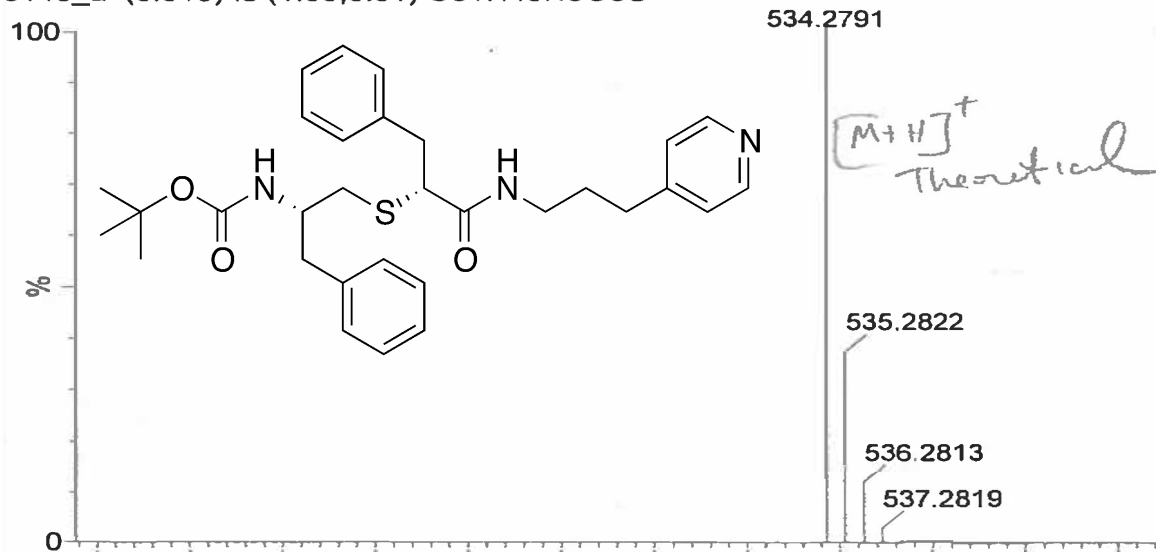
408\_a 21 (0.385) AM (Cen,5, 80.00, Ar,8000.0,525.29,0.70); Sm (SG, 2x3.00); Sb (1,40.00); Cm (21:26)

TOF MS ES+  
4.85e4



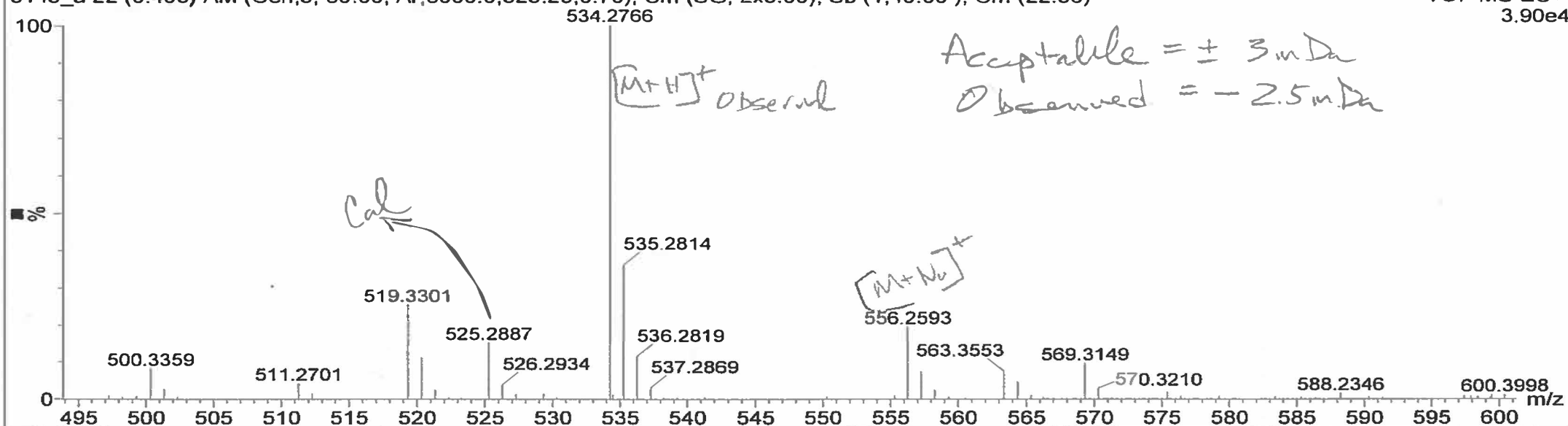
3145\_a (0.019) Is (1.00,0.01) C<sub>31</sub>H<sub>40</sub>N<sub>3</sub>O<sub>3</sub>S

TOF MS ES+  
6.58e12



3145\_a 22 (0.403) AM (Cen,5, 80.00, Ar,8000.0,525.29,0.70); Sm (SG, 2x3.00); Sb (1,40.00 ); Cm (22:36)

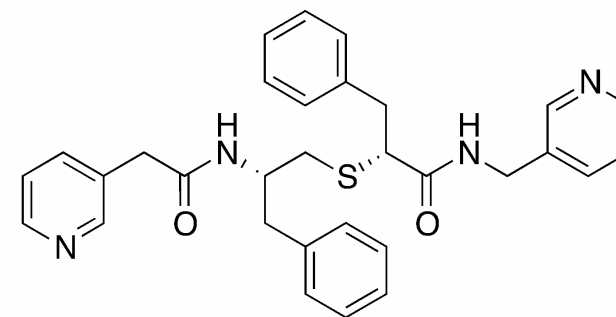
TOF MS ES+  
3.90e4





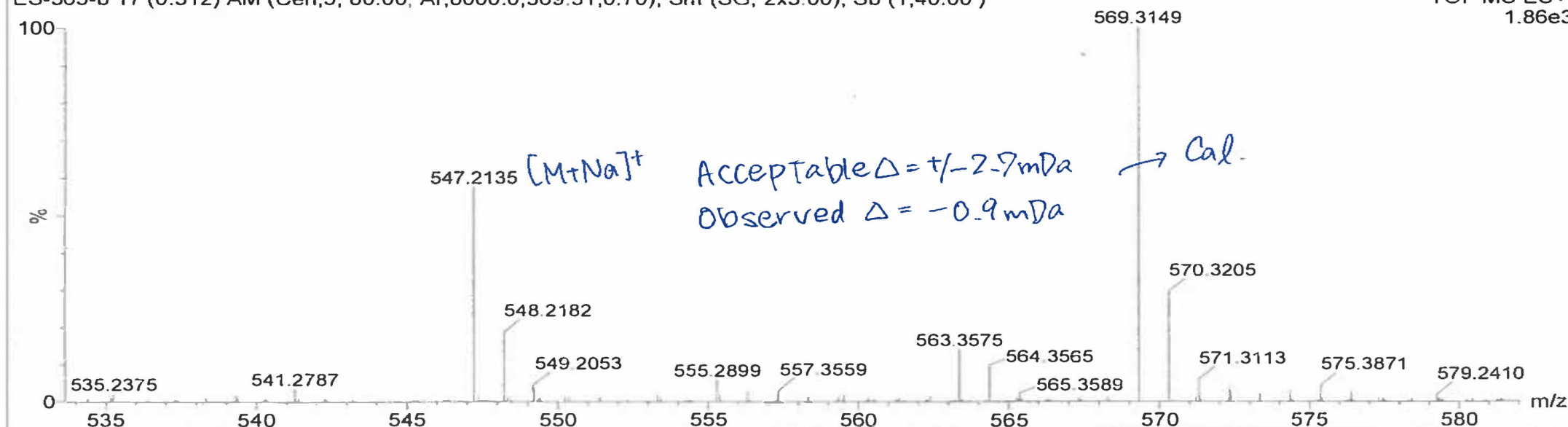
ES-365-b (0.019) Is (1.00,0.01) C<sub>31</sub>H<sub>32</sub>N<sub>4</sub>O<sub>2</sub>SNa  
547.2144

TOF MS ES+  
6.58e12



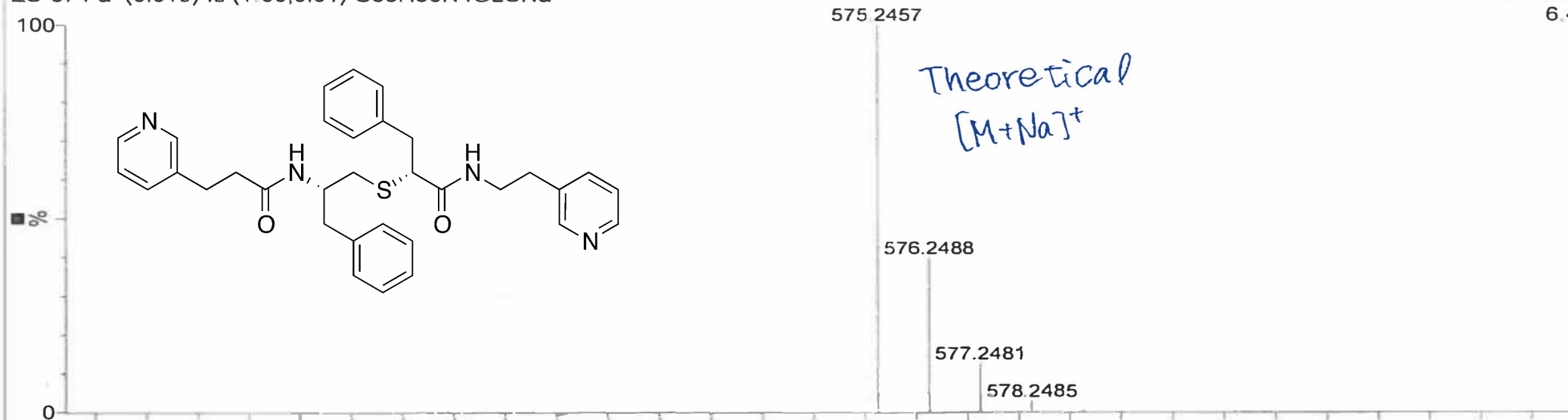
ES-365-b 17 (0.312) AM (Cen,5, 80.00, Ar,8000.0,569.31,0.70); Sm (SG, 2x3.00); Sb (1,40.00 )

TOF MS ES+  
1.86e3



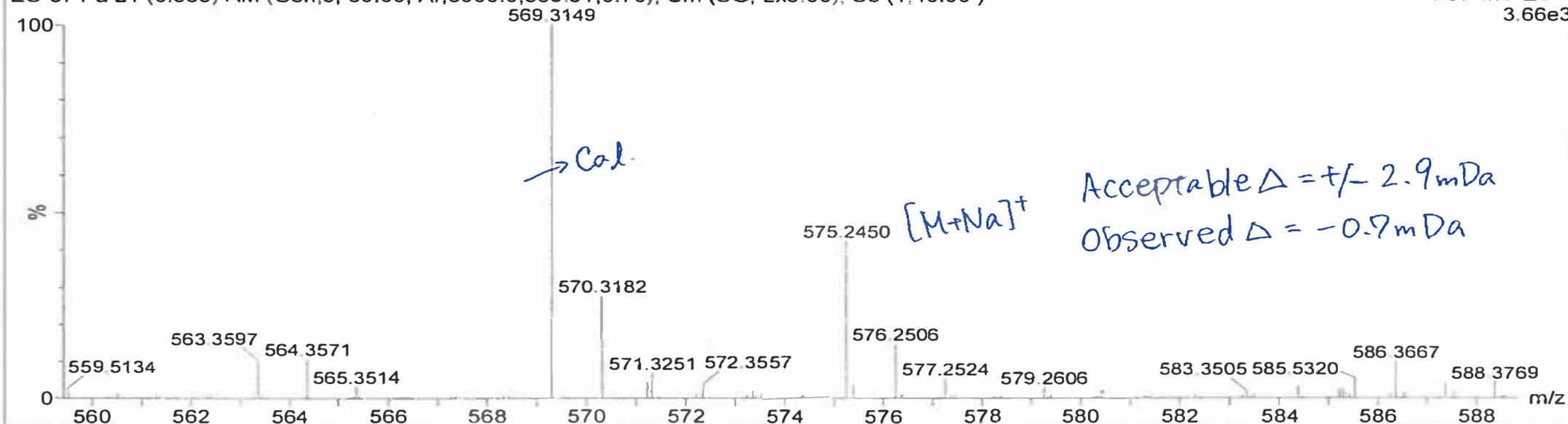
ES-374-a (0.019) Is (1.00,0.01) C<sub>33</sub>H<sub>36</sub>N<sub>4</sub>O<sub>2</sub>SNa

TOF MS ES+  
6.43e12



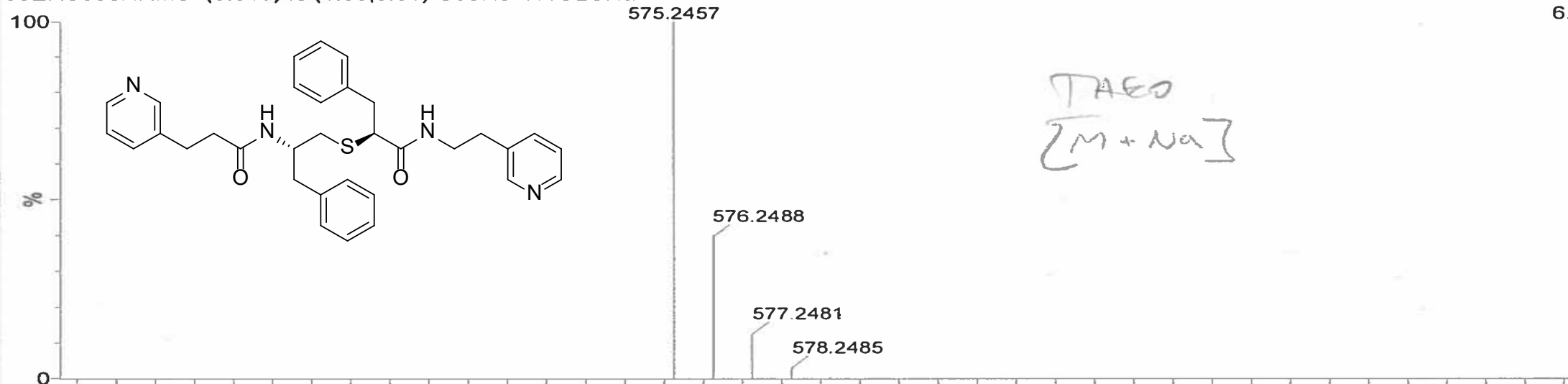
ES-374-a 21 (0.385) AM (Cen,5, 80.00, Ar,8000.0,569.31,0.70); Sm (SG, 2x3.00); Sb (1.40.00)

TOF MS ES+  
3.66e3



05ERS058HRMS (0.019) Is (1.00,0.01) C<sub>33</sub>H<sub>36</sub>N<sub>4</sub>O<sub>2</sub>SNa

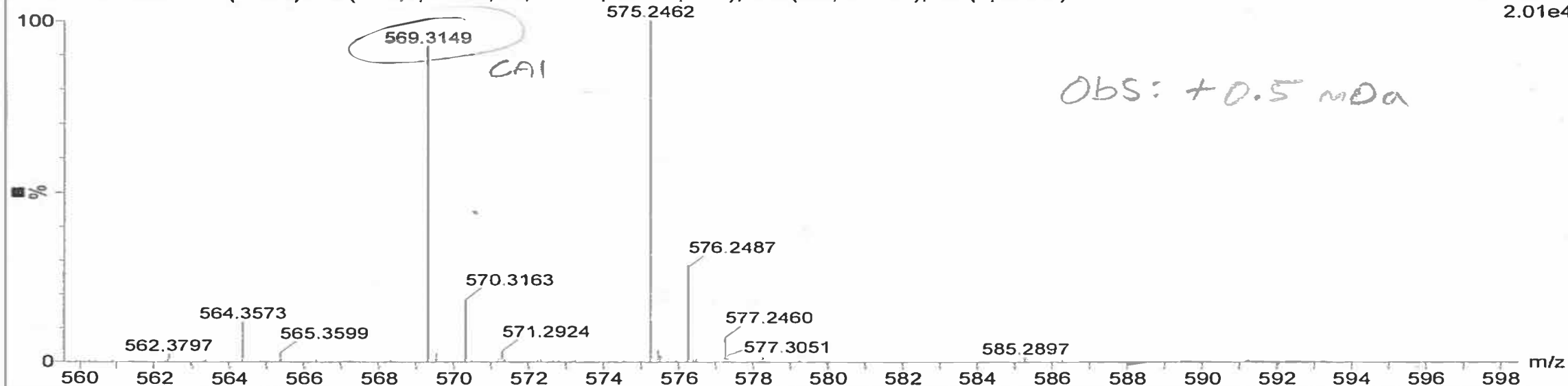
TOF MS ES+  
6.43e12



TAED  
[M+Na]

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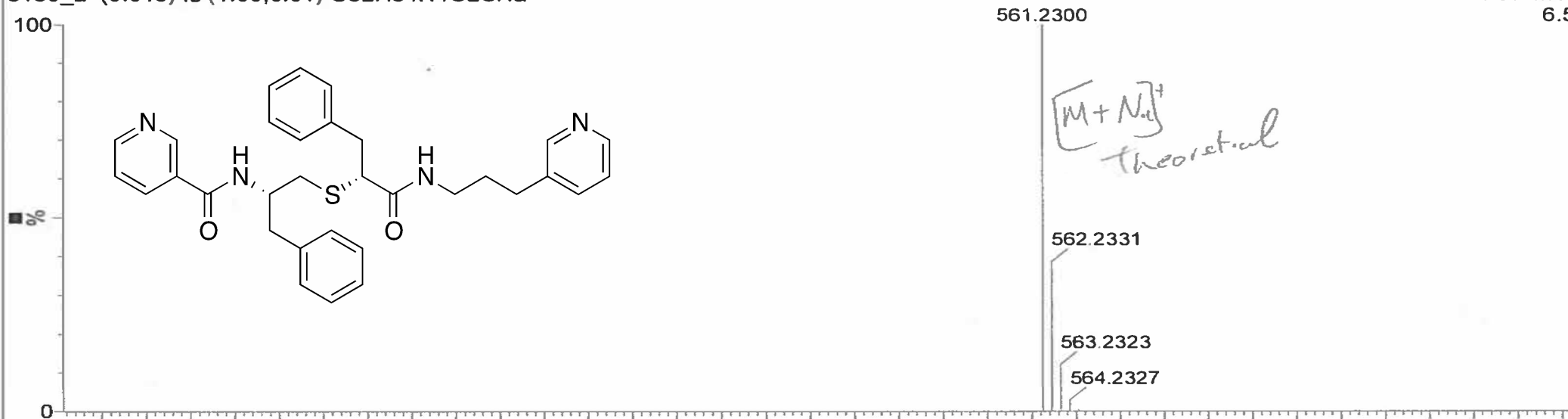
TOF MS ES+  
2.01e4



Obs: +0.5 mDa

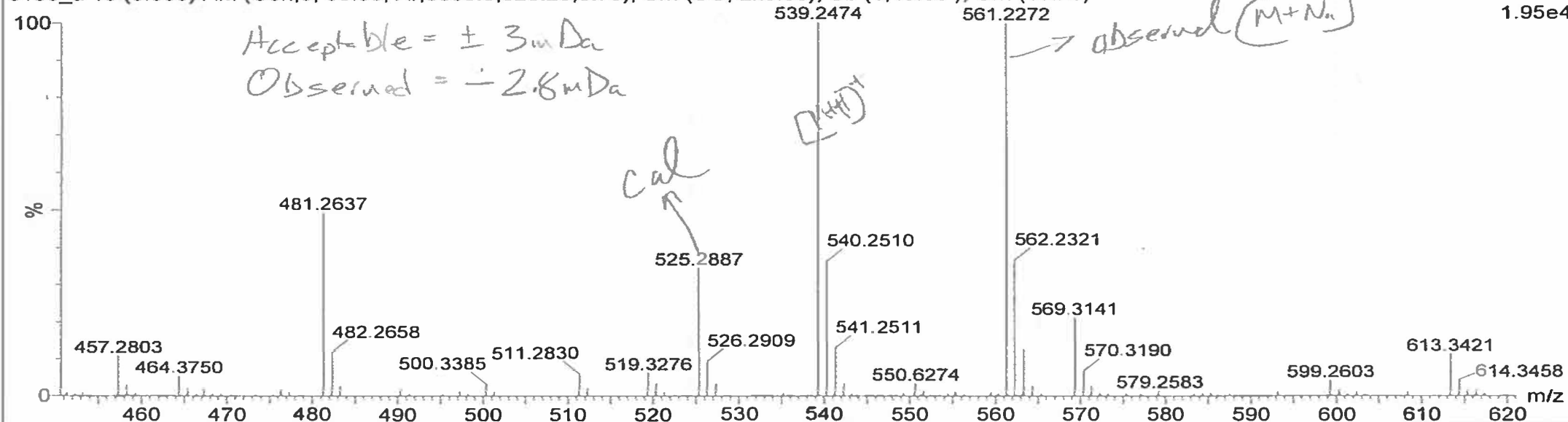
3130\_a (0.019) Is (1.00,0.01) C<sub>32</sub>H<sub>34</sub>N<sub>4</sub>O<sub>2</sub>SNa

TOF MS ES+  
6.51e12



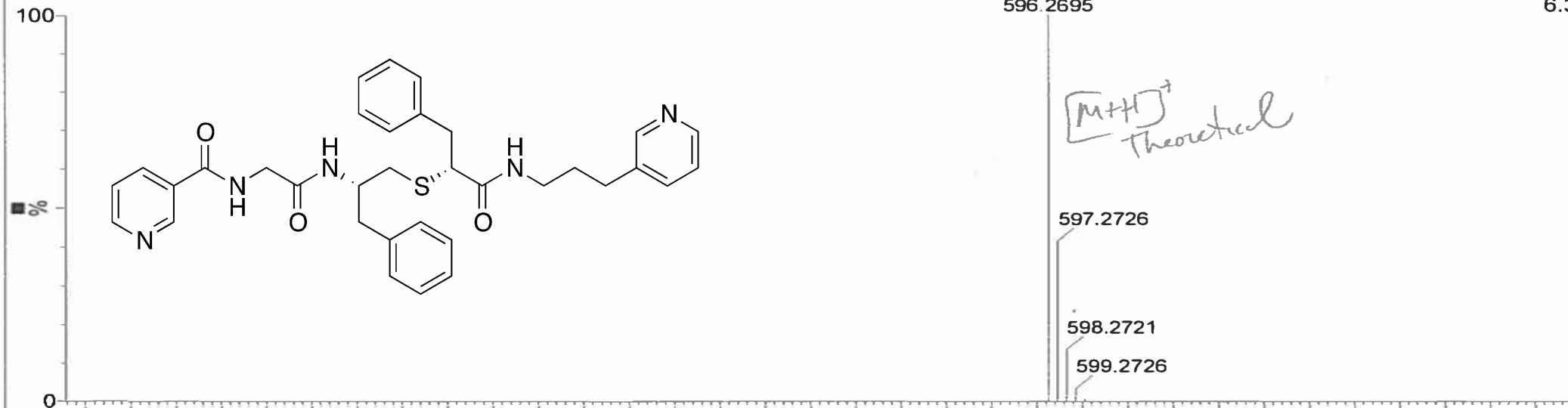
3130\_a 18 (0.330) AM (Cen,5, 80.00, Ar,8000.0,525.29,0.70); Sm (SG, 2x3.00); Sb (1,40.00 ); Cm (15:26)

TOF MS ES+  
1.95e4



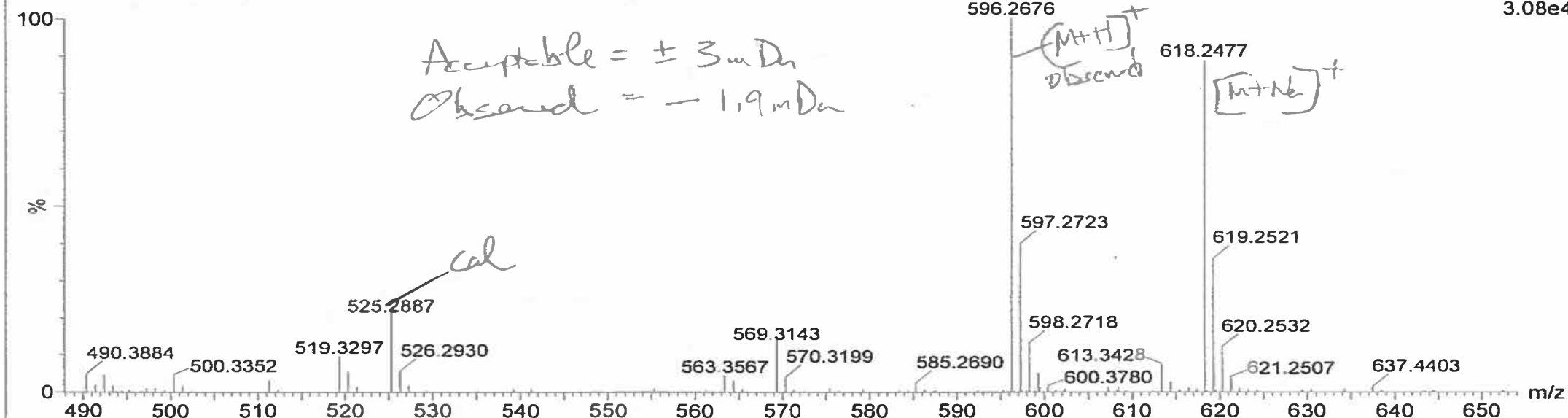
3138\_a (0.019) Is (1.00,0.01) C<sub>34</sub>H<sub>38</sub>N<sub>5</sub>O<sub>3</sub>S

TOF MS ES+  
6.32e12

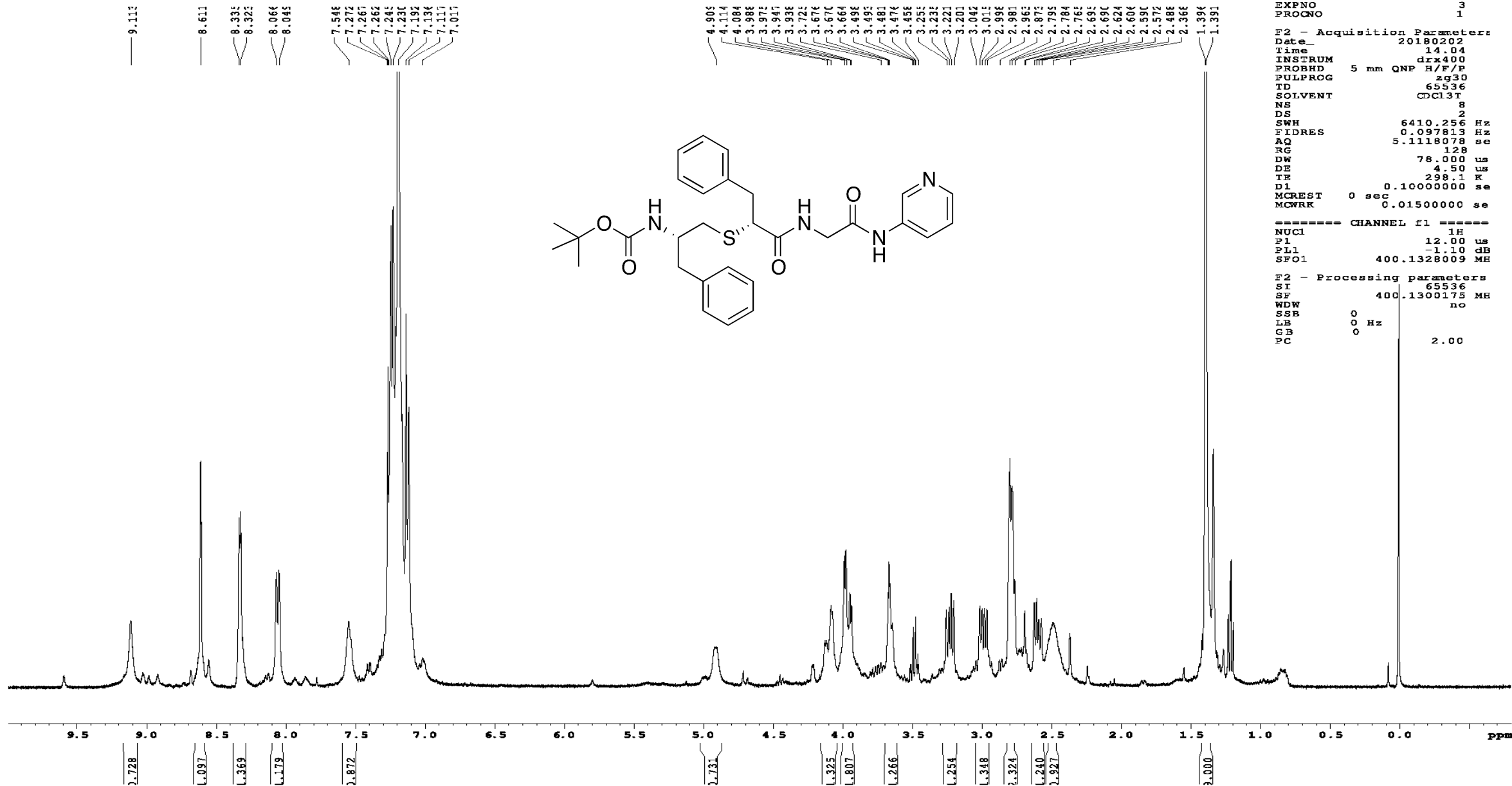


3138\_a 24 (0.440) AM (Cen,5, 80.00, Ar,8000.0,525.29,0.70); Sm (SG, 2x3.00); Sb (1,40.00 ); Cm (11:36)

TOF MS ES+  
3.08e4



<sup>1</sup>H spectrum



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PROCNO 1

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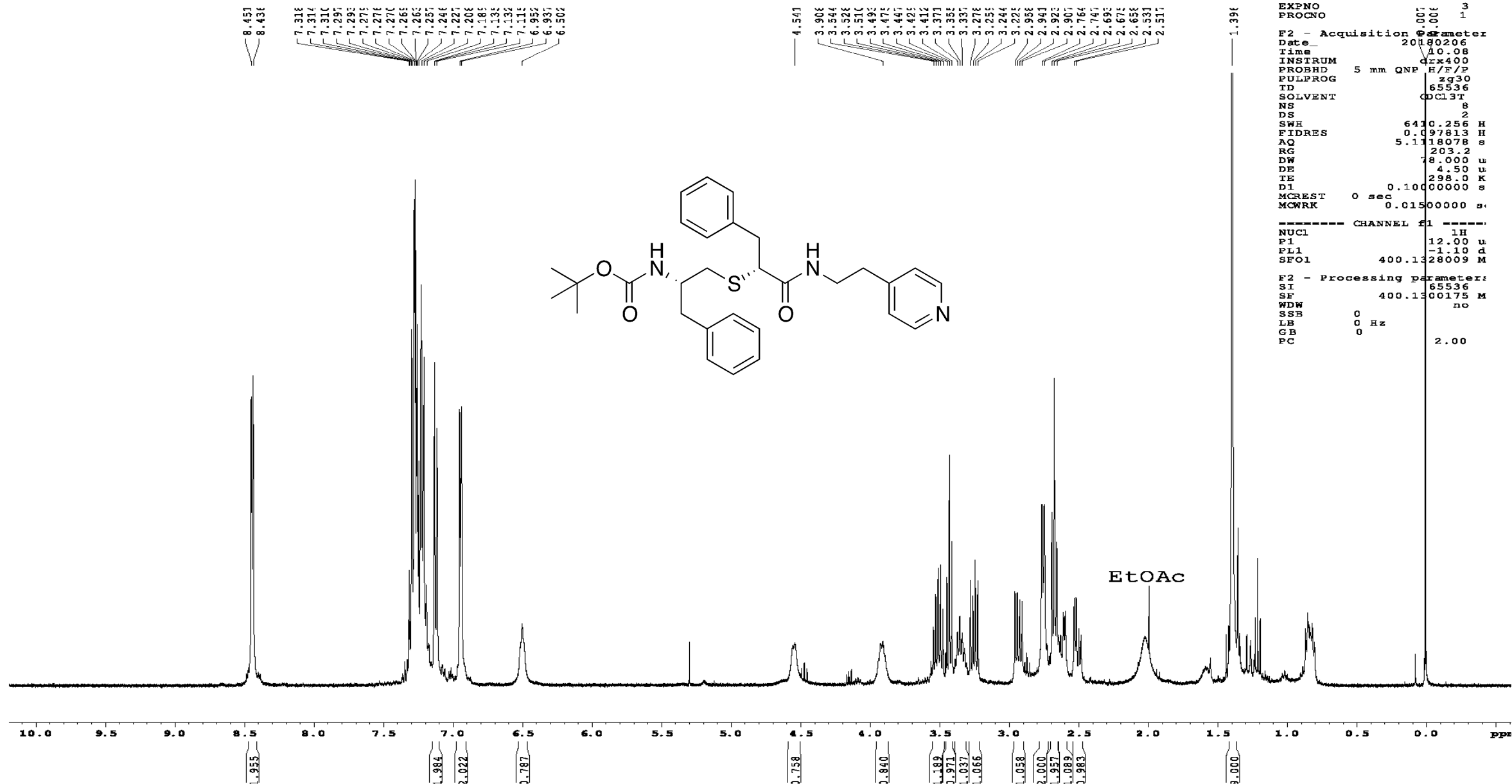
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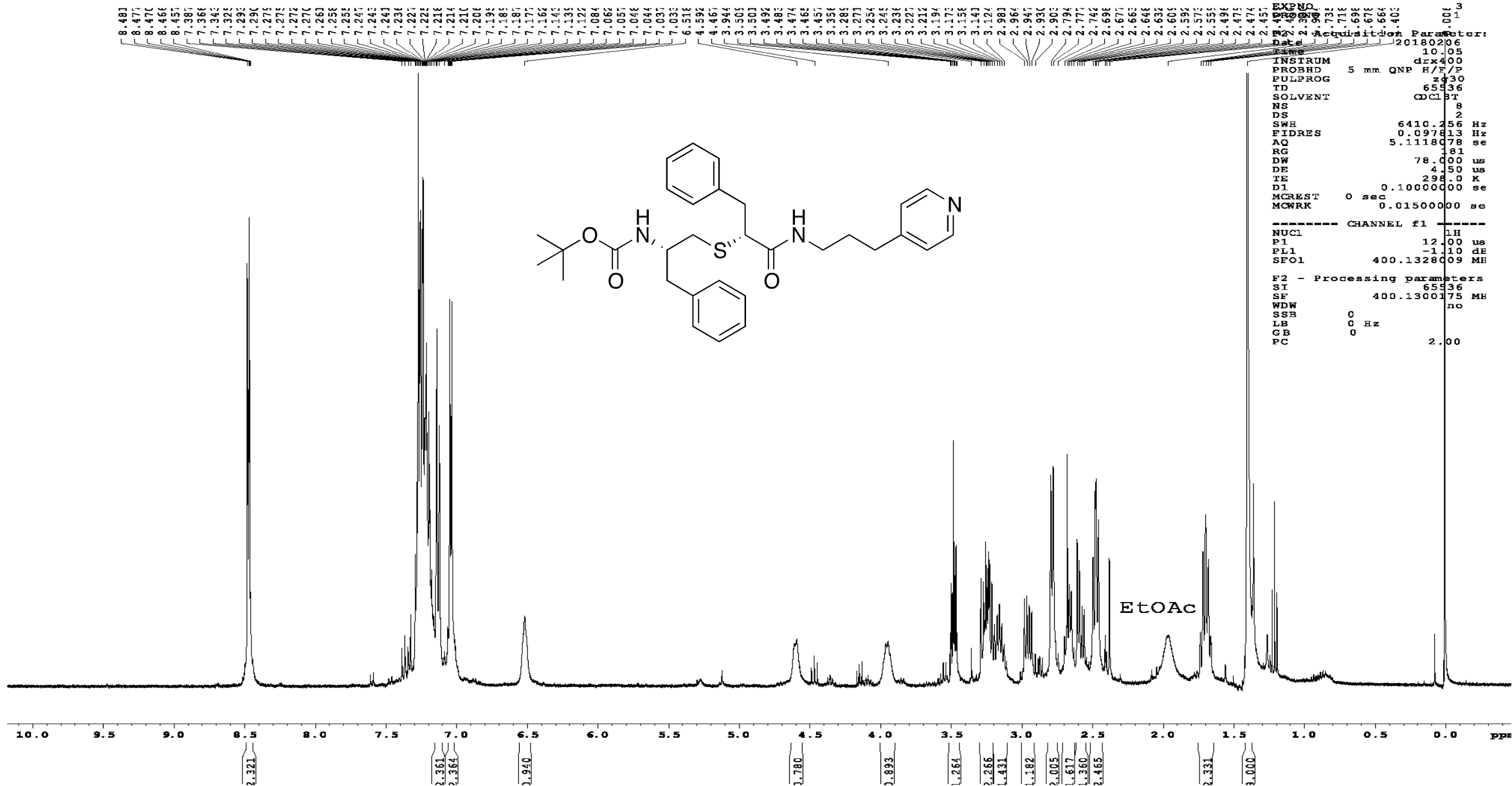
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1H spectrum



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DS 2  
SWH 6410.256 H  
FIDRES 0.097813 H  
AQ 5.1118078 s  
RG 203.2  
DW 78.000 u  
DE 4.50 u  
TE 298.0 K  
D1 0.1000000 s  
MCREST 0 sec  
MCWRK 0.01500000 s  
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PL1 -1.10 d  
SFO1 400.1328009 M  
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SF 400.1300175 M  
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1H spectrum



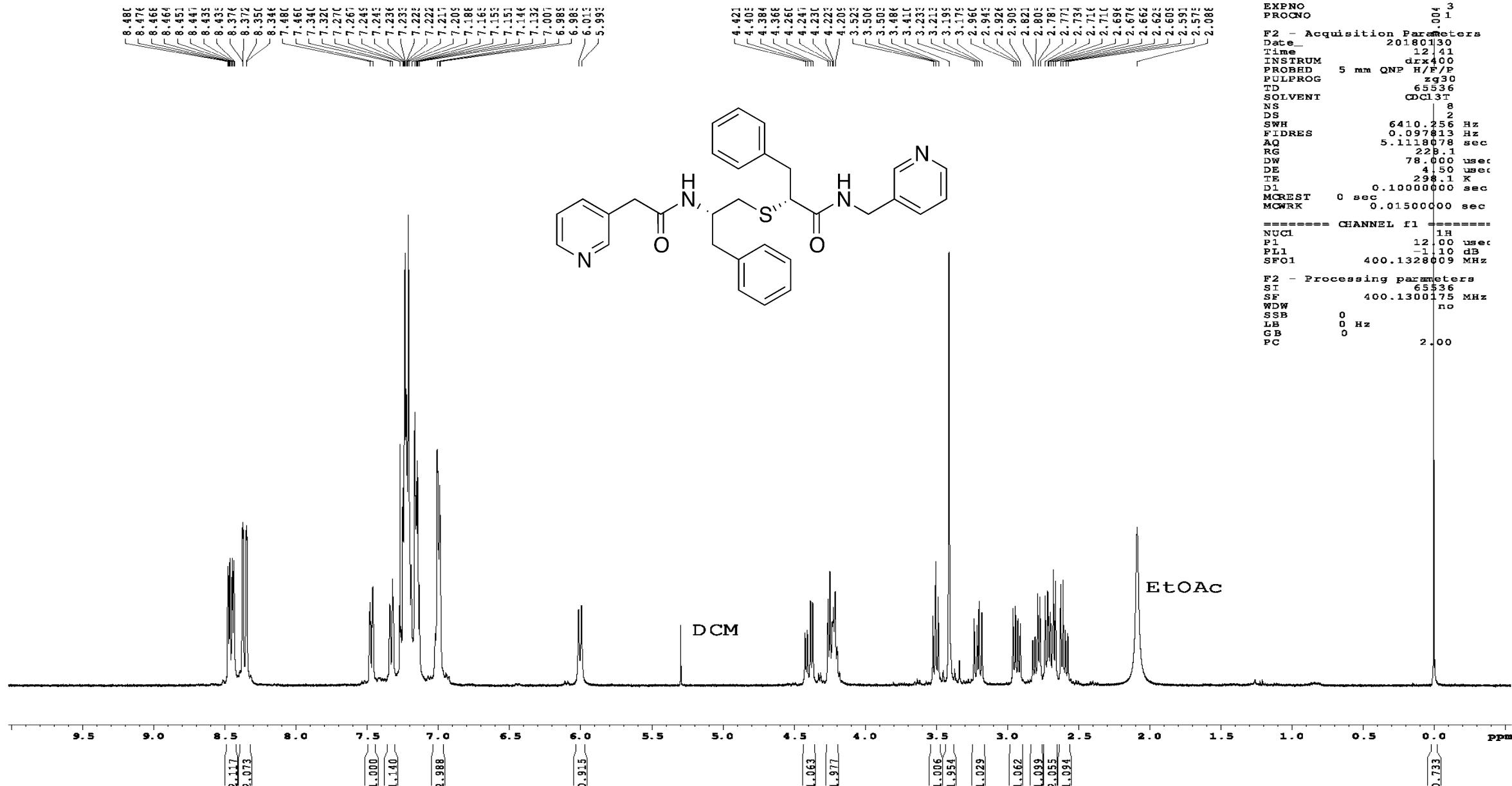
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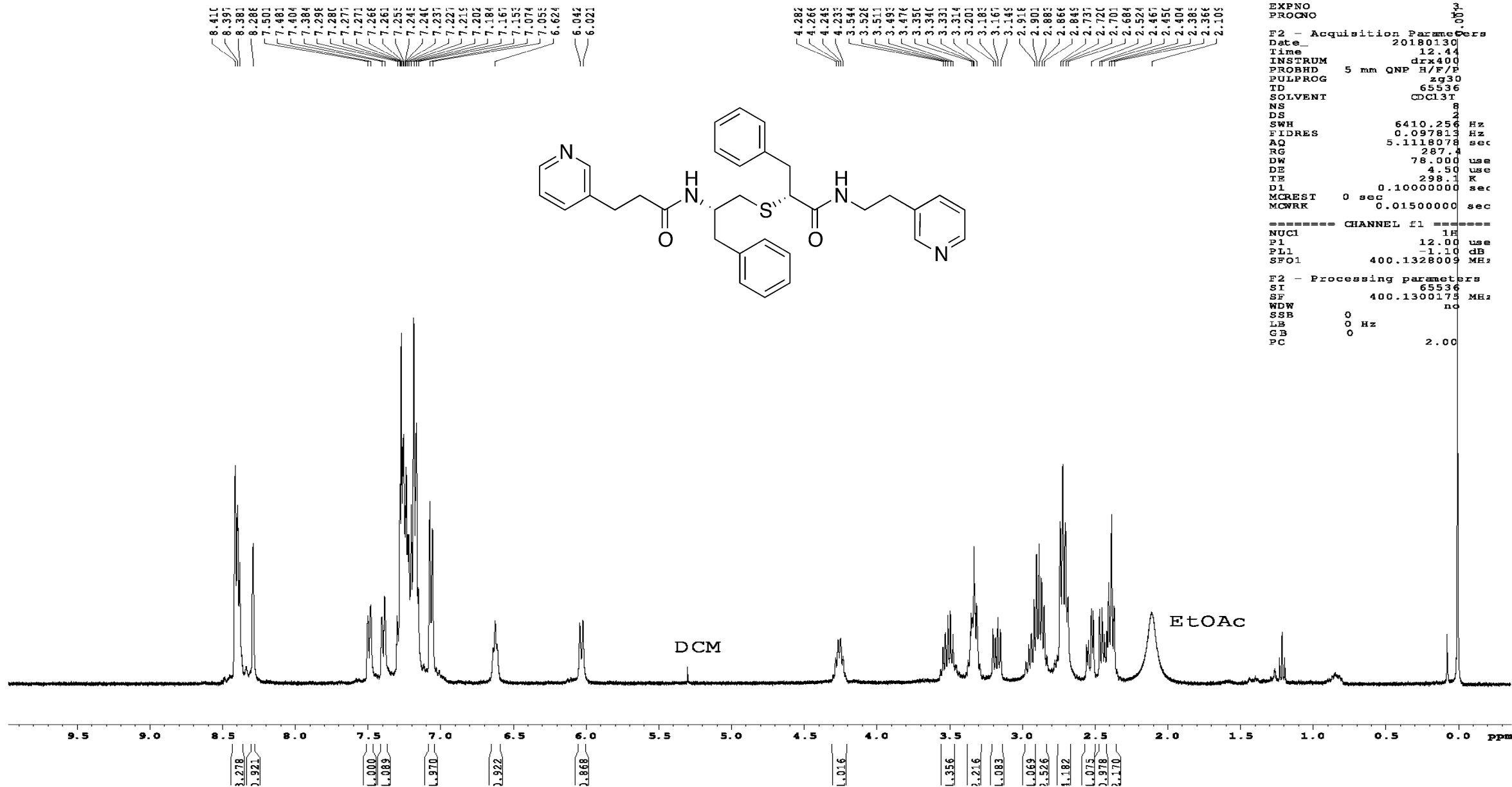


<sup>1</sup>H spectrum



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RG 228.1  
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<sup>1</sup>H spectrum

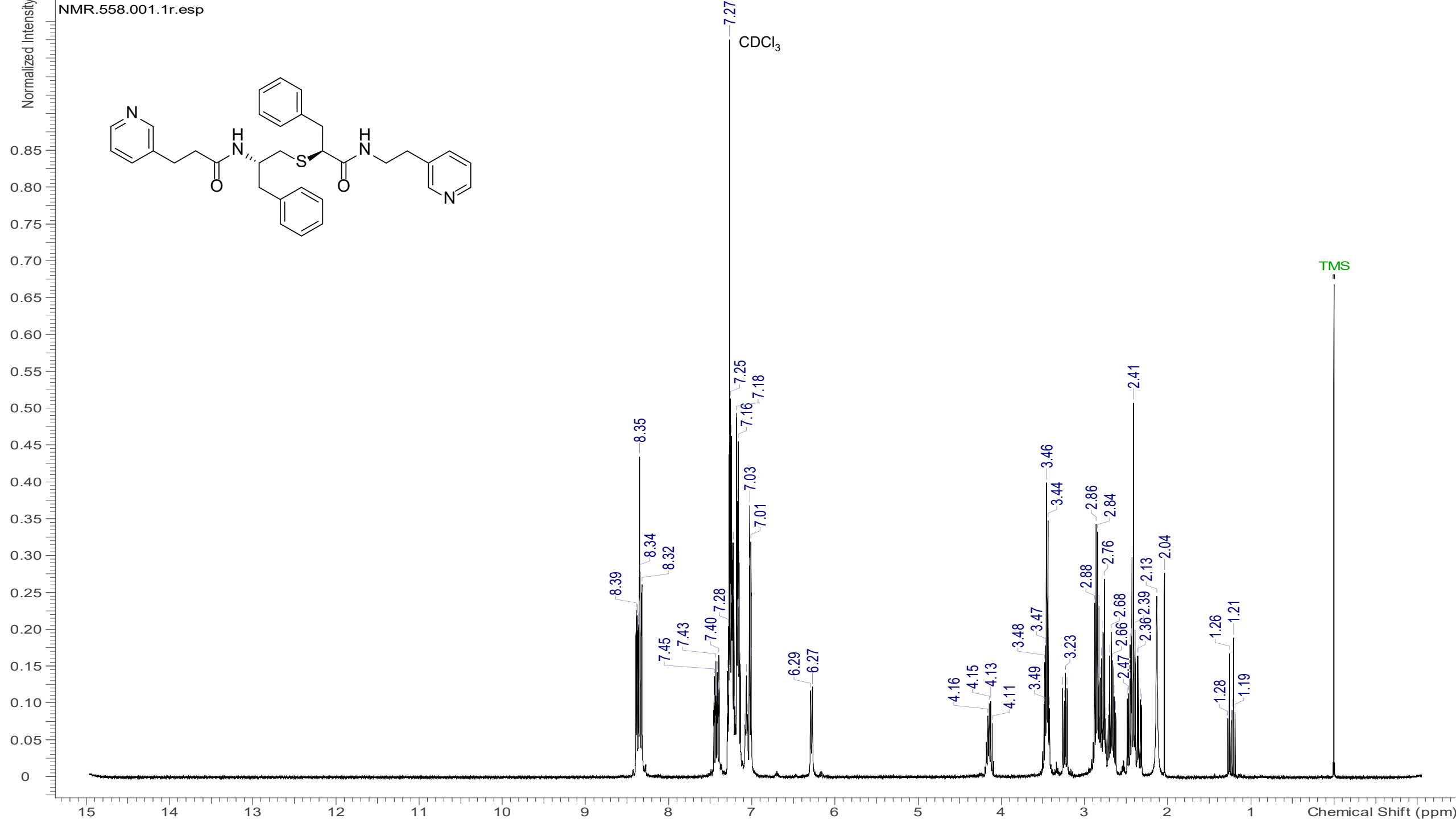


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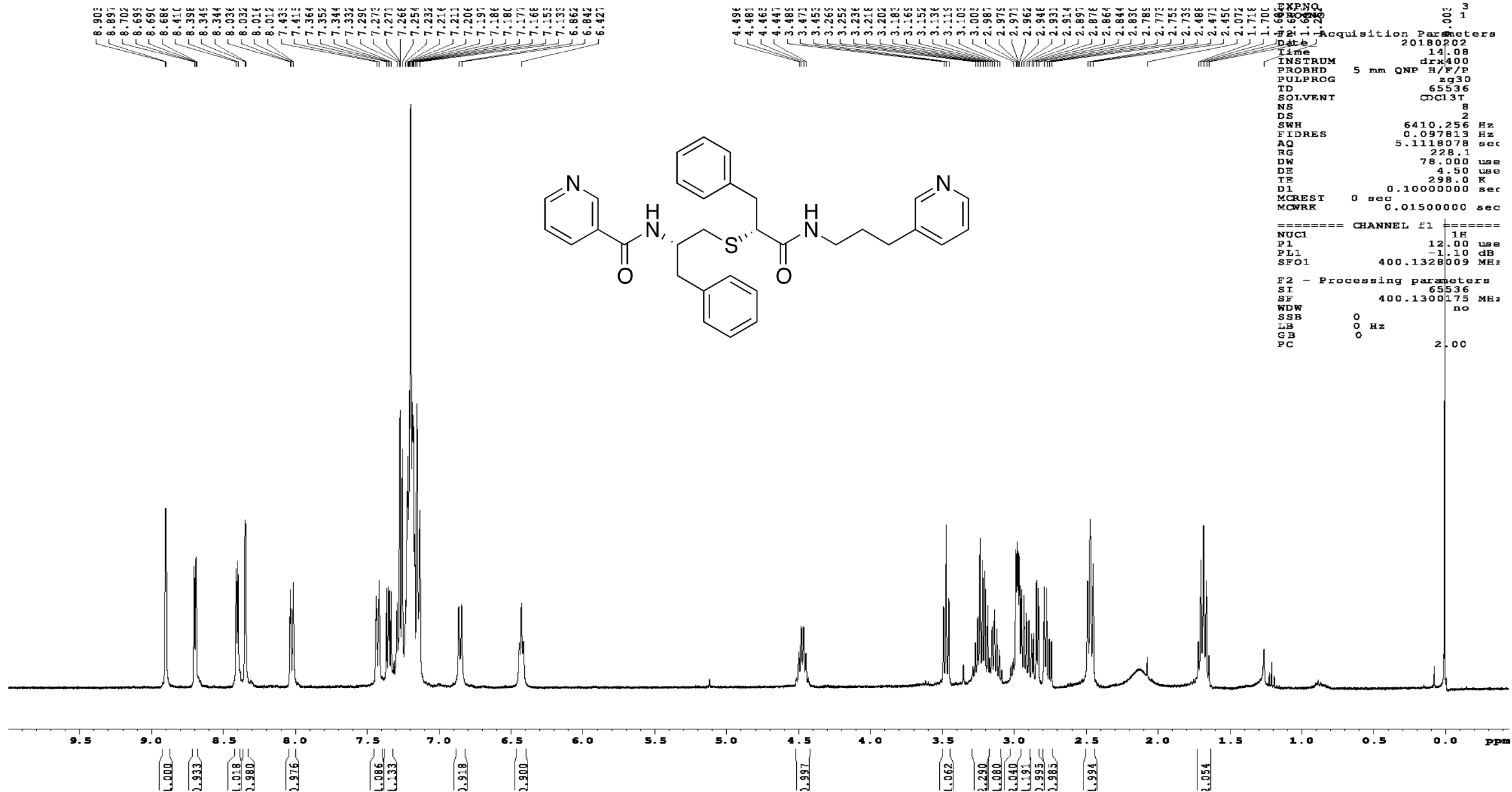
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F2 - Processing parameters
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<sup>1</sup>H spectrum



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PULPROG zgpg30  
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SOLVENT CDCl3  
NS 8  
DS 2  
SWH 6410.256 Hz  
FIDRES 0.097813 Hz  
AQ 5.1118078 sec  
RG 228.1  
DW 76.000 use  
DE 4.50 use  
TE 298.0 K  
D1 0.10000000 sec  
MCREST 0 sec  
MCWRK 0.01500000 sec

===== CHANNEL f1 =====  
NUC1 1H  
P1 12.00 use  
PL1 -1.10 dB  
SFO1 400.1328009 MHz

F2 - Processing parameters  
SI 65536  
SF 400.1300175 MHz  
WDW no  
SSB 0  
LB 0 Hz  
GB 0  
PC 2.00

<sup>1</sup>H spectrum

