

Supporting Information

Self-Masked Aldehyde Inhibitors: A Novel Strategy for Inhibiting Cysteine Proteases

Linfeng Li,[†] Bala C. Chenna,[†] Kai S. Yang,[‡] Taylor R. Cole,[†] Zachary T. Goodall,[†] Miriam Giardini,[§] Zahra Moghadamchargari,[‡] Elizabeth A. Hernandez,[†] Jana Gomez,[†] Claudia M. Calvet,[§] Jean A. Bernatchez,[§] Drake M. Mellott,[†] Jiyun Zhu,[†] Andrew Rademacher,[†] Diane Thomas,[§] Lauren R. Blankenship,[‡] Aleksandra Drelich,^{||} Arthur Laganowsky,[‡] Chien-Te K. Tseng,^{||} Wenshe R. Liu,^{†,‡} A. Joshua Wand,[†] Jorge Cruz-Reyes,[†] Jair L. Siqueira-Neto,[§] and Thomas D. Meek^{*,†}

[†]Department of Biochemistry and Biophysics, Texas A&M University, 300 Olsen Blvd, College Station, TX 77843, USA

[‡]Department of Chemistry, Texas A&M University, 580 Ross St, College Station, TX 77843, USA

[§]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, 9500 Gilman Dr, La Jolla, CA 92093, USA

^{||}Department of Microbiology and Immunology, University of Texas Medical Branch, 301 University Blvd, Galveston, TX 77555, USA

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Table S1. Kinetic parameters obtained from rapid dilution assays

Compound	k_{obs} ($\times 10^{-4} \text{ s}^{-1}$)	Residence time	Estimated k_d
		τ (s) ^a	($\times 10^{-4} \text{ s}^{-1}$) ^b
1	3.18 \pm 0.24	3141	2.89
2	30.2 \pm 1.9	331	27.5
6	67.4 \pm 4.8	148	61.3
7	54.3 \pm 3.5	184	49.4
8	62.4 \pm 2.5	160	56.8
9	32.1 \pm 1.3	312	29.2
10	53.1 \pm 5.7	188	48.3
11	3.71 \pm 0.21	2695	3.37
12	6.33 \pm 0.42	1580	5.75

^aResidence time $\tau = 1/k_{obs}$; ^b k_d values were estimated from k_{obs} based on eq. 3

Table S2. The details of peaks in ¹H-¹³C HSQC NMR

peak	¹ H (ppm)	¹³ C (ppm)	Width 1	Width 2	Volume
<i><u>12</u> only</i>					
A	5.34	90.84	192.6	31.4	40225129.1
B	5.13	90.80	192.59	26.24	52937692.9
<i><u>12</u> + cruzain</i>					
A'	6.13	76.25	137.58	49.49	5030193.12
B'	5.91	79.69	165.06	63.22	6245466.52
A (residual)	5.33	90.81	192.6	40.23	1725522.38

Table S3. Anti-CoV-2 activity of **18** on SARS-CoV-2 infected A549/ACE2 cells^a

Compound 18 (μM)	A549/ACE2 cells + CoV-2 infection + inhibitor	A549/ACE2 cells + CoV-2 infection + inhibitor	A549/ACE2 cells + CoV-2 infection no inhibitor	A549/ACE2 Cells no CoV-2 infection + inhibitor
20	Viable	Viable	CPE	Viable
10	Viable	Viable	CPE	Viable
5	CPE	Viable	CPE	Viable
2.5	CPE	CPE	CPE	Viable
1.25	CPE	CPE	CPE	Viable
0.625	CPE	CPE	CPE	Viable
0.313	CPE	CPE	CPE	Viable
0.156	CPE	CPE	CPE	Viable

^aViable cells or CPE: microscopic examination of treated cells indicated a majority of either fully viable cells, or a majority of cells which exhibited SARS-CoV-2-induced cytopathic effect (CPE).

Table S4. Statistic summary of co-crystal structure of 3CL^{pro} complexed with **18**.

3CL ^{pro} - 18	
Data collection	
Space group	I 1 2 1
Cell dimensions	
a, b, c (Å)	54.20, 80.74, 85.76
α, β, γ (°)	90.00, 97.12, 90.00
Resolution (Å)	48.25-1.70 (1.76-1.70)
R_{merge}	0.084 (1.632)
$\langle I/\sigma I \rangle$	1.18 (at 1.70Å)
CC _{1/2}	0.996 (0.475)
Completeness (%)	99.8 (99.3)
Redundancy	6.4 (5.6)
Refinement	
Resolution (Å)	48.25-1.70
No. Reflections	40267 (4001)
R_{work}/R_{free}	0.186/0.206
RMSD in bond lengths (Å)	0.008
RMSD in bond angles (°)	1.17
No. atoms	
Protein	2395
Ligand	40
Water	173
B factors	
Protein	41.6
Ligand	43.4
Water	44.9

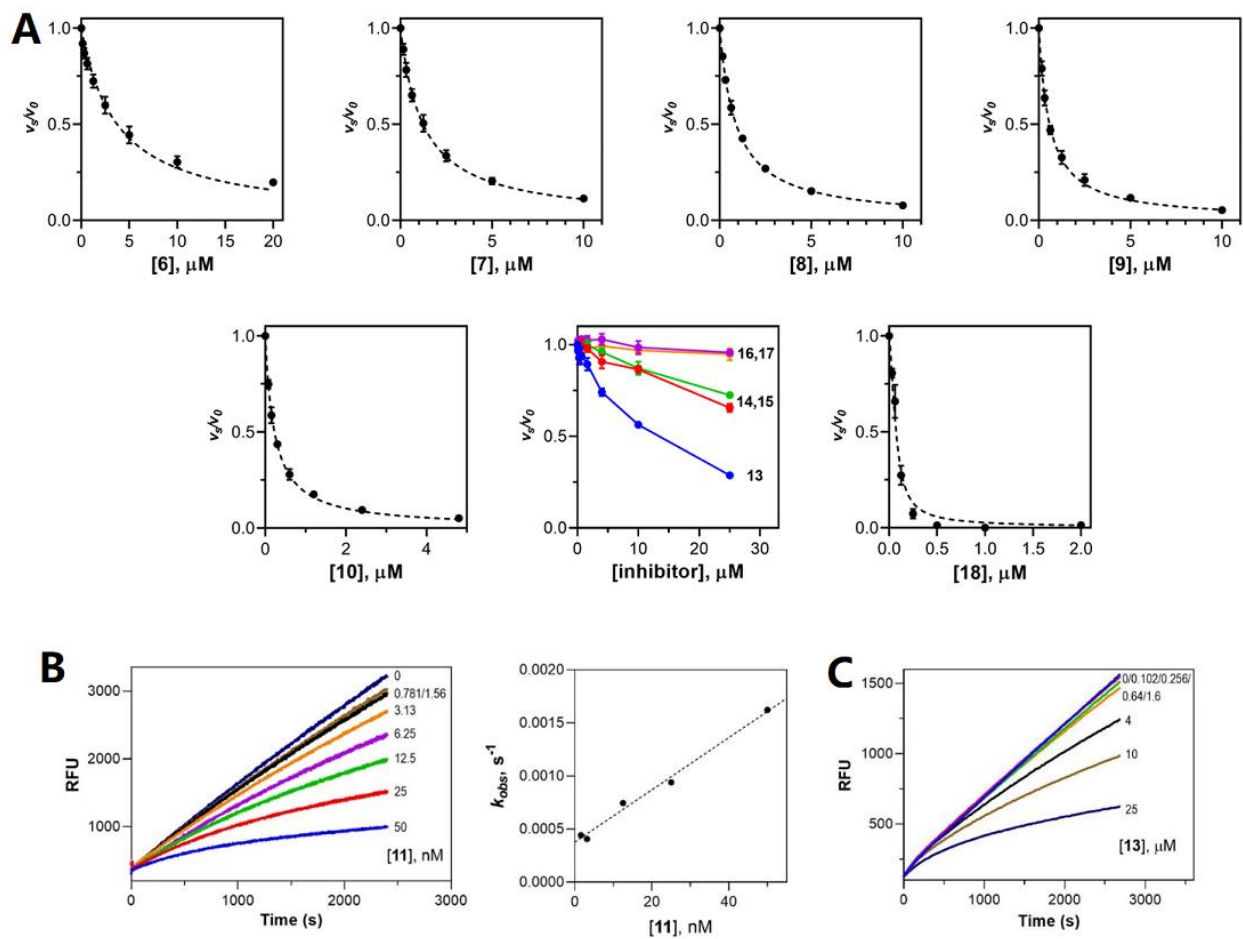


Figure S1. Kinetic data of cruzain inhibition by **6** – **11** and **13** – **17**, and 3CL^{PRO} inhibition by **18**. (A) Concentration-inhibition curves for SMAs and their prodrugs. (B) Time-courses of cruzain inhibition by free aldehyde **11**. The k_{obs} values were obtained by fitting progress curves to eq. 1. Replot of k_{obs} vs. [11] with the line drawn through data points from fitting to eq. 3 which afforded $k_A = (3.8 \pm 0.4) \times 10^{-4} \text{ s}^{-1}$. (C) Time-courses of cruzain inhibition by **13**.

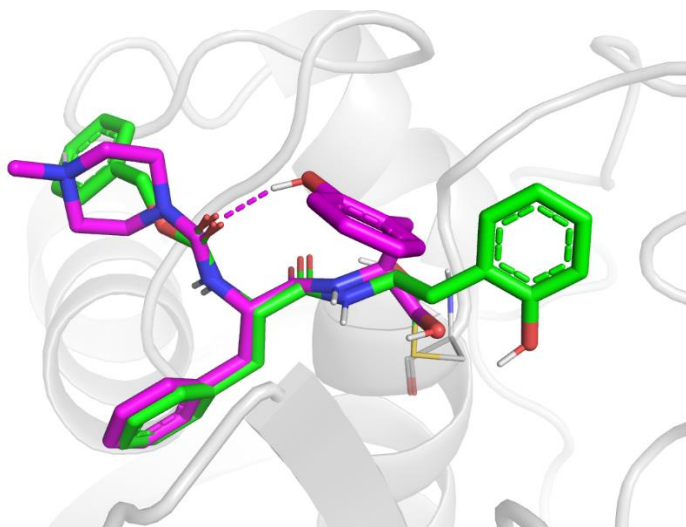


Figure S2. Compound **12** (magenta) was covalently docked to cruzain, and was superimposed with compound **2** (green). The intramolecular hydrogen bond between P₁ phenol and P₃ carbonyl group was drawn as magenta dashed lines.

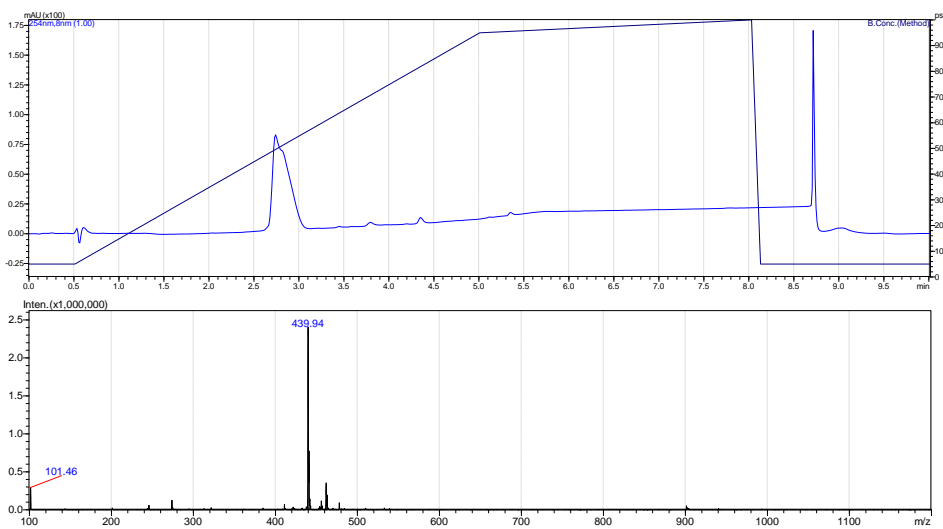


Figure S3. LC-MS of ¹³C-labeled **12**. Calculated m/z for molecular ion is 440.24 for hemiacetal and 458.25 for hydrate.

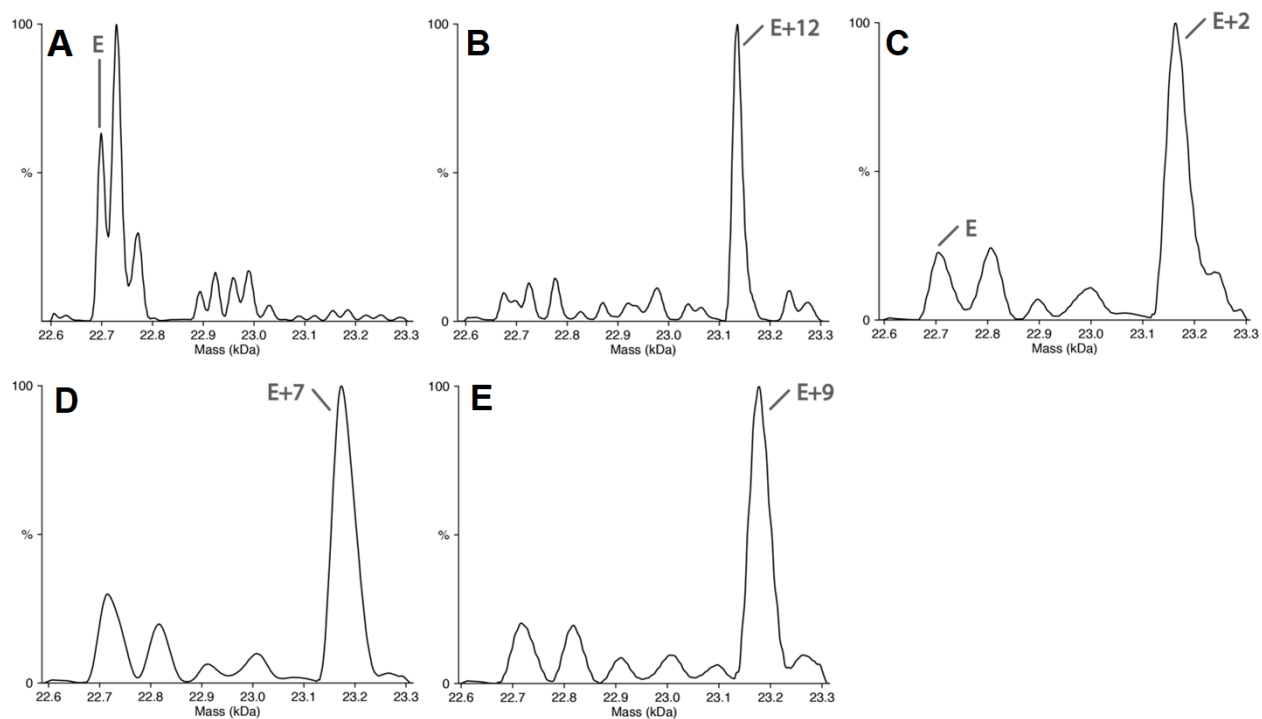


Figure S4. Native mass spectra of cruzain pre-incubated with selected SMAIs. The deconvoluted mass spectra are shown for 25 μM cruzain (A) alone or treated with 50 μM compounds (B) **12**, (C) **2**, (D) **7** and (E) **9**. The addition of compound **12** shows that compound is bound to apo-enzyme with a measured mass of 438.8 Da, consistent with the theoretical mass of **12** (438 Da).

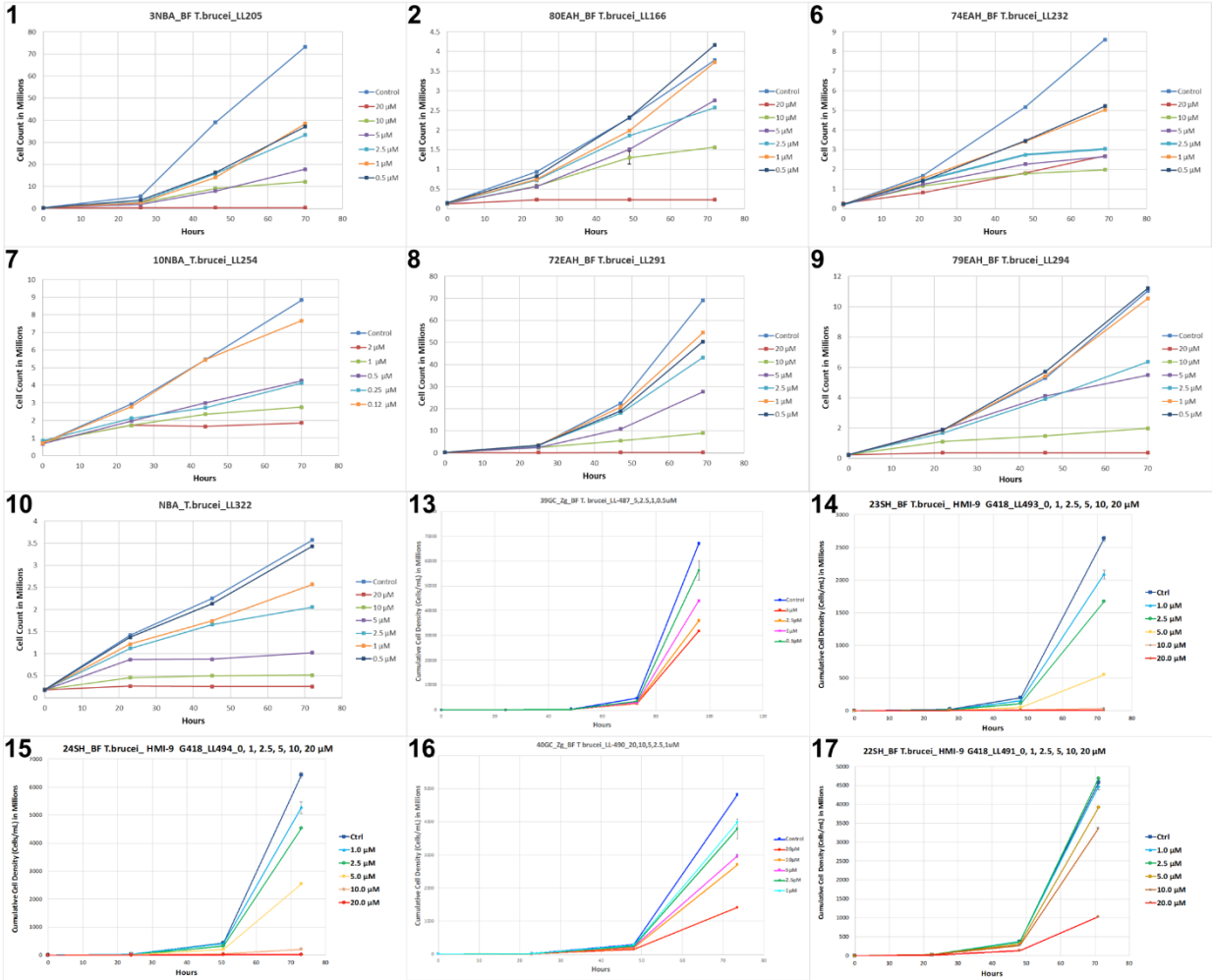


Figure S5. Growth curves for *T. brucei* BSFs treated with SMAIs and their prodrugs. Each diagram only represents one of the duplicate experiments.

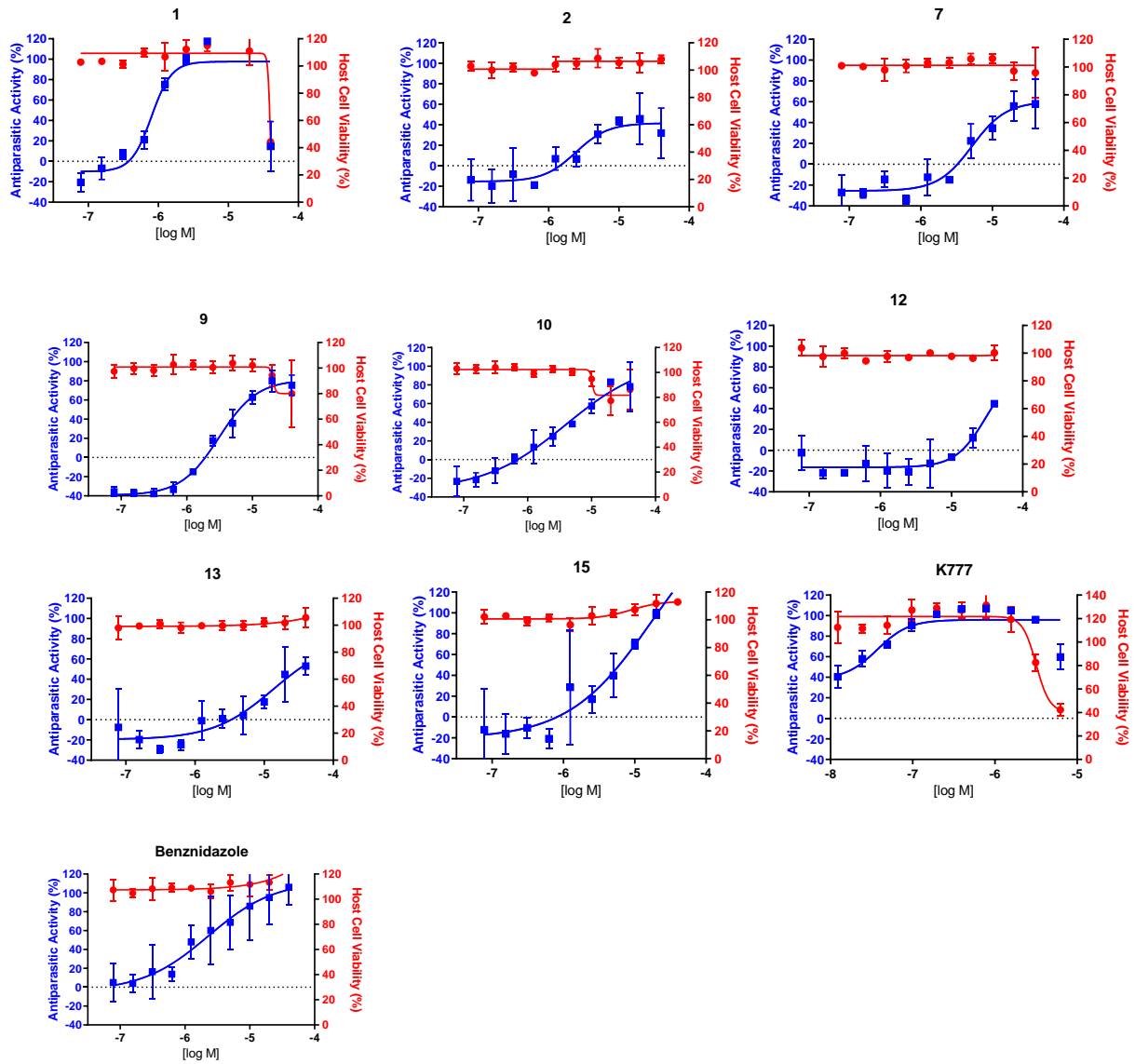
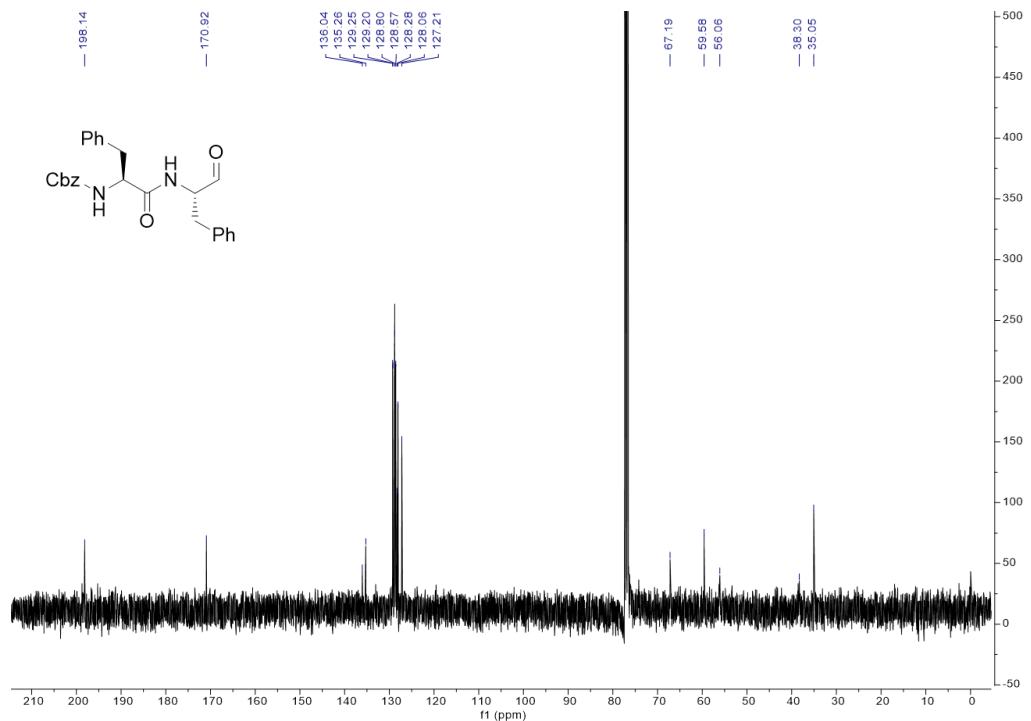
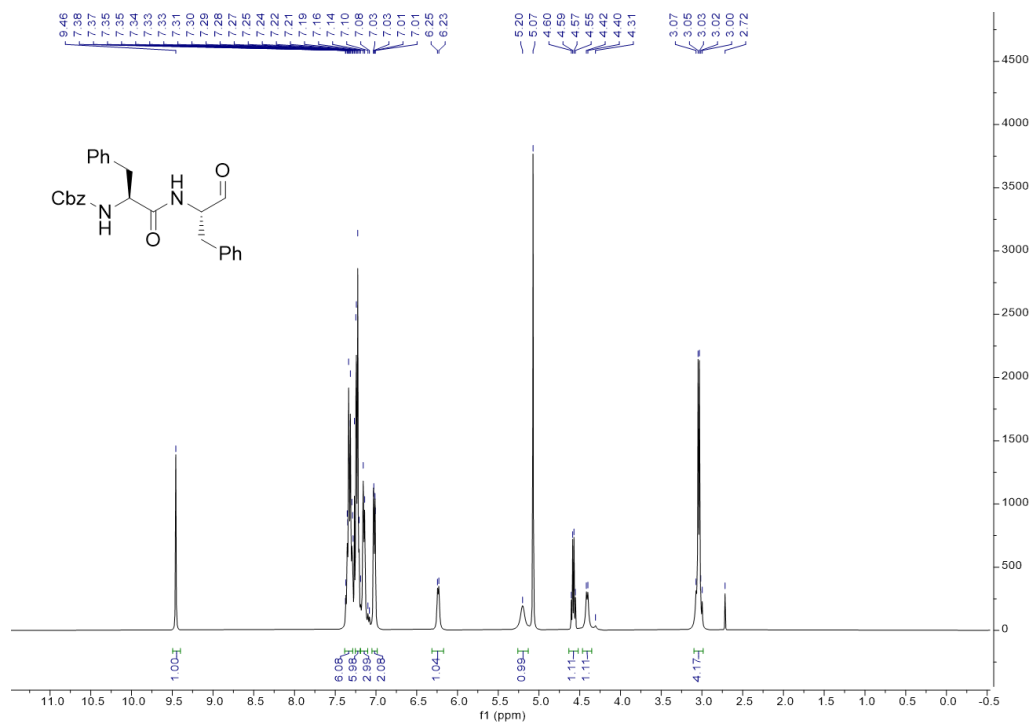


Figure S6. Cell viability of *T. cruzi*-infected murine cardiomyoblasts in presence of 1, 2, 7, 9, 10, 12, 13, 15, K777, and benznidazole.

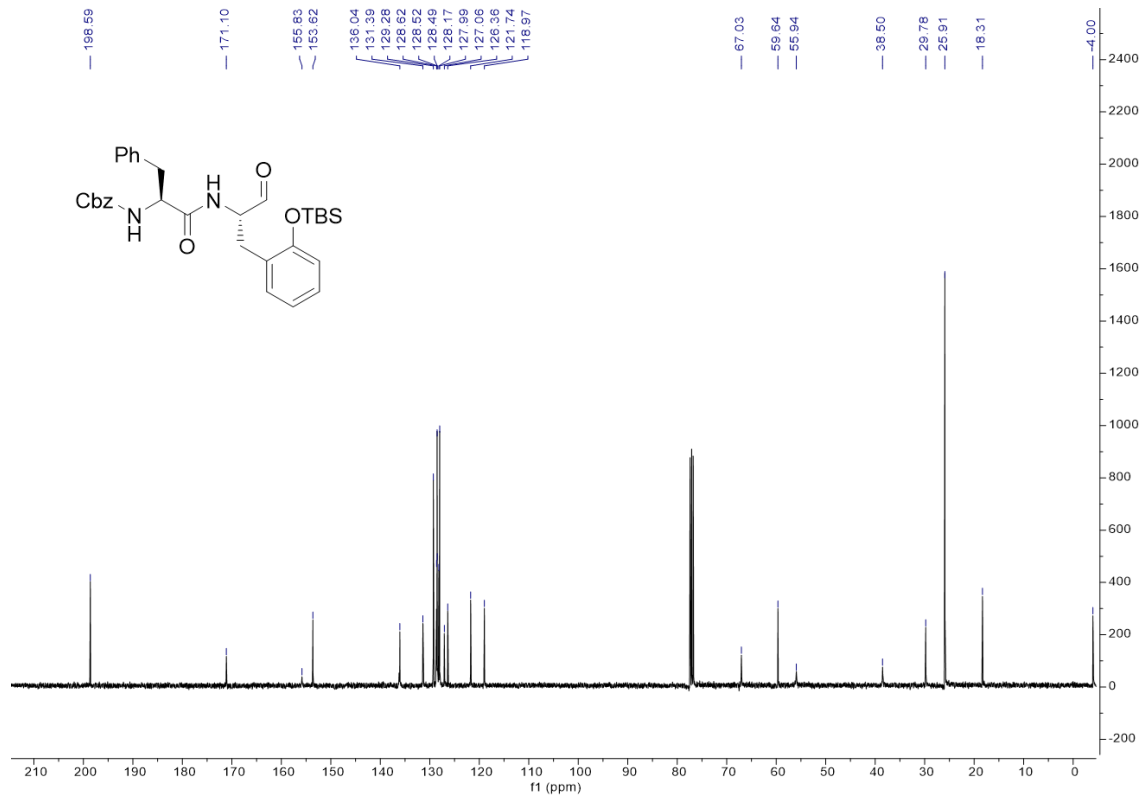
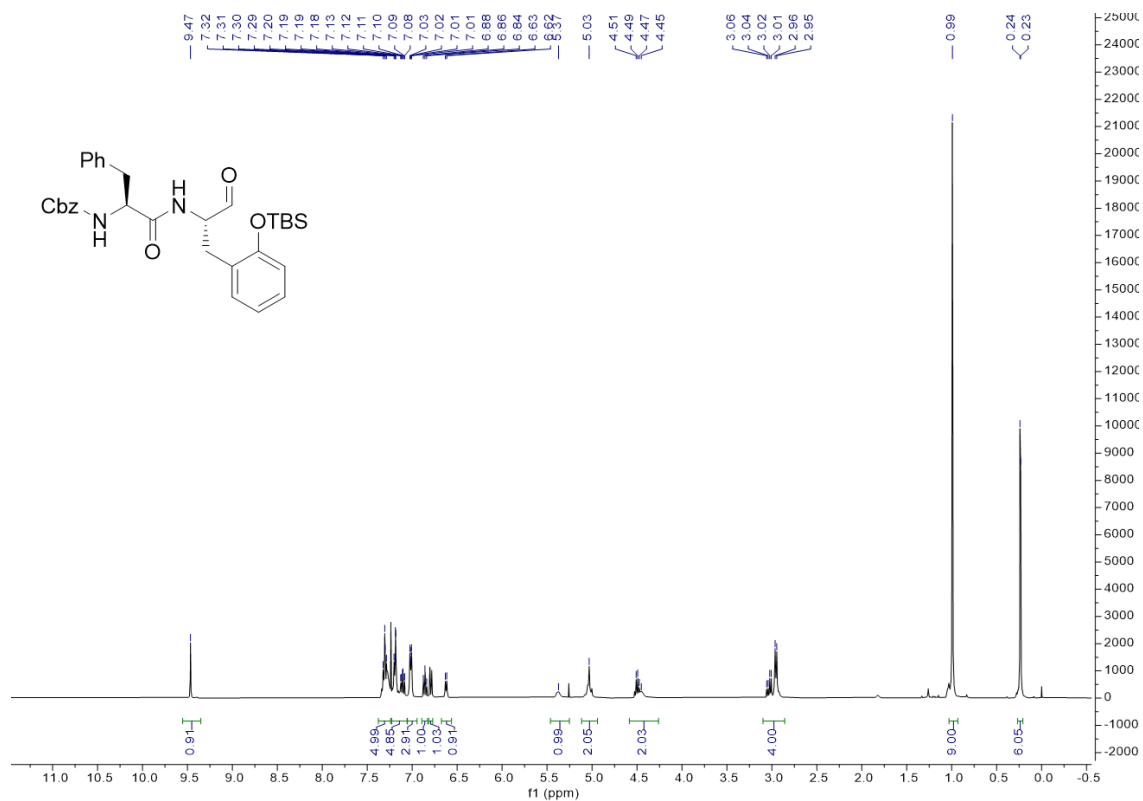
NMR spectra

(Note: The presence of lactol anomers in many SMAIs led to complicated splitting/overlapping and low-quality NMR spectra; therefore, the NMR spectra of corresponding precursors (the second last products) were provided.)

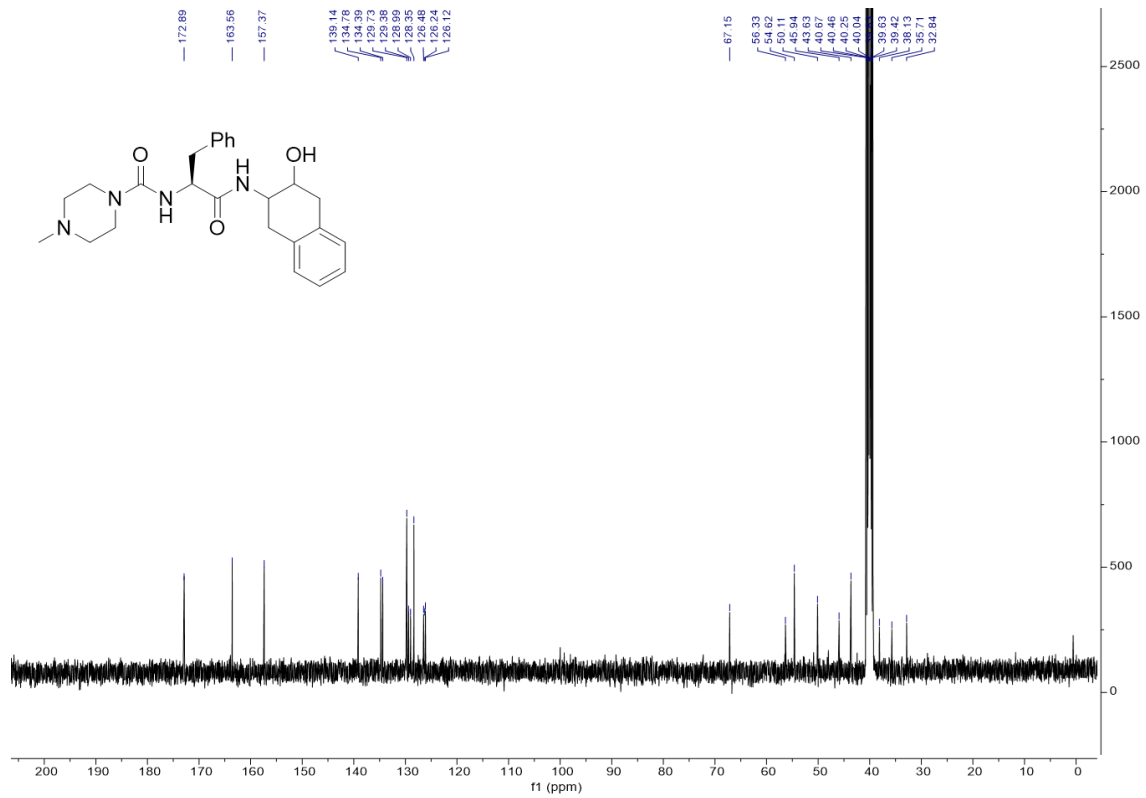
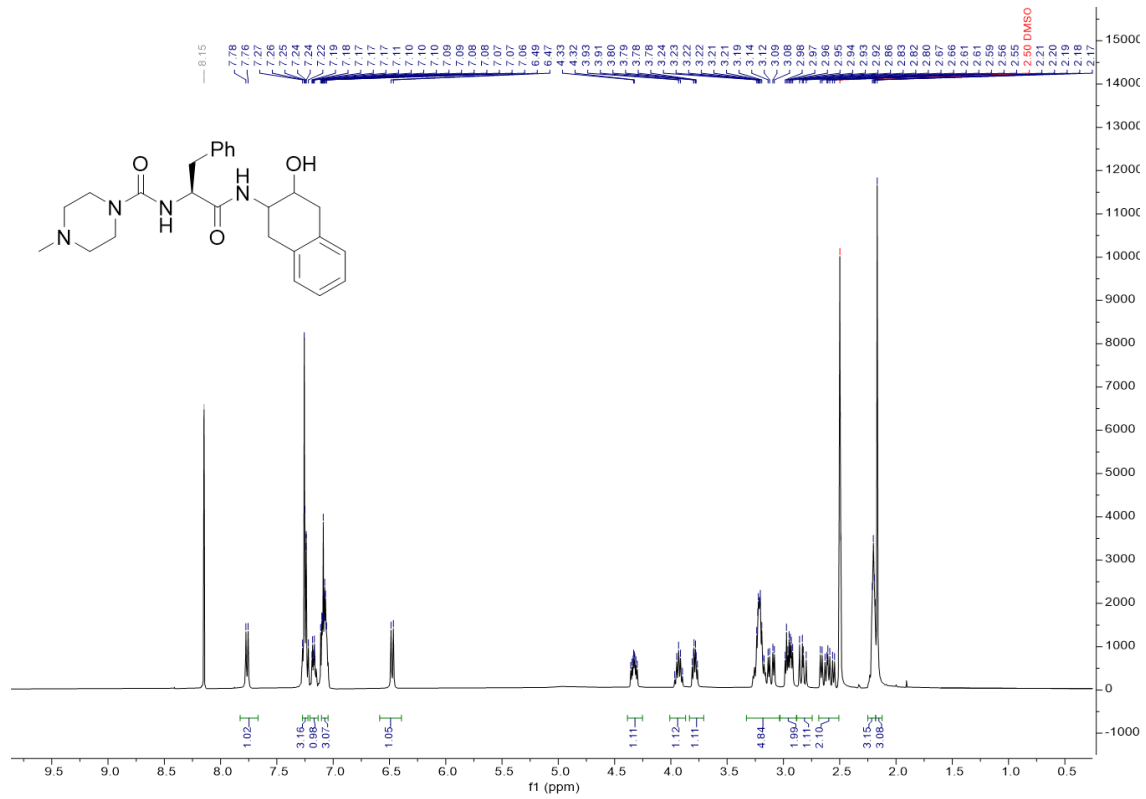
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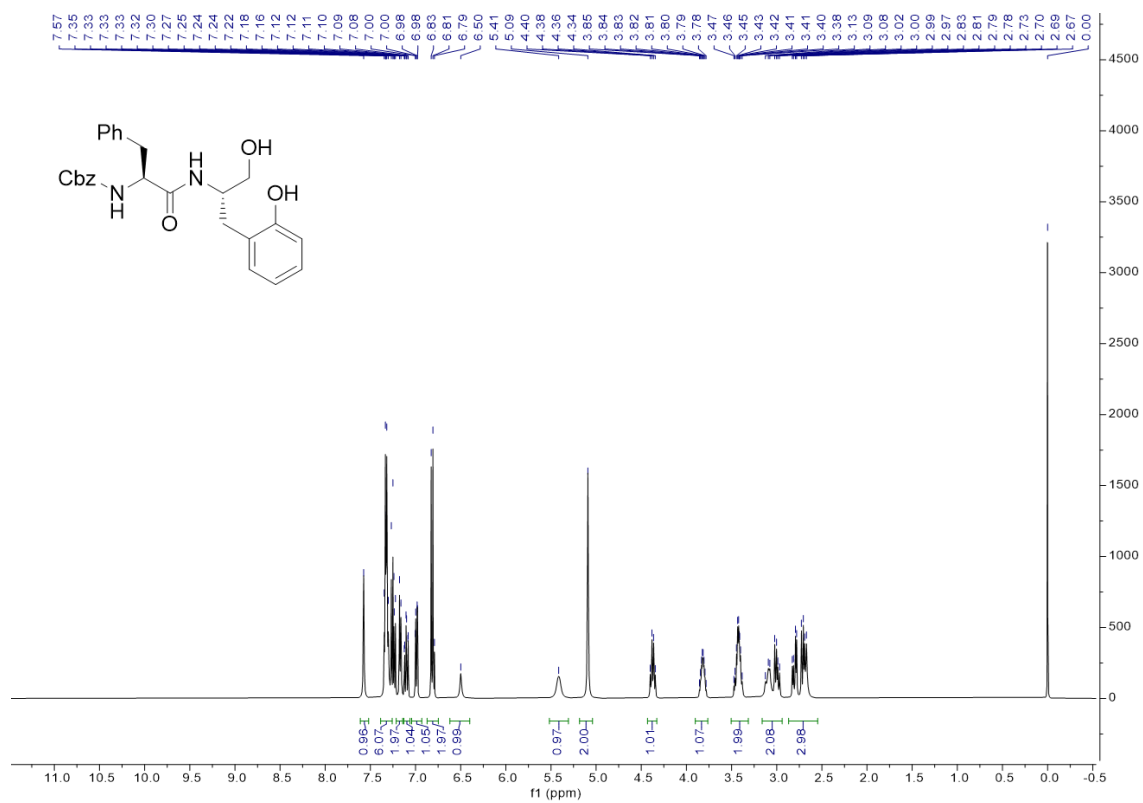
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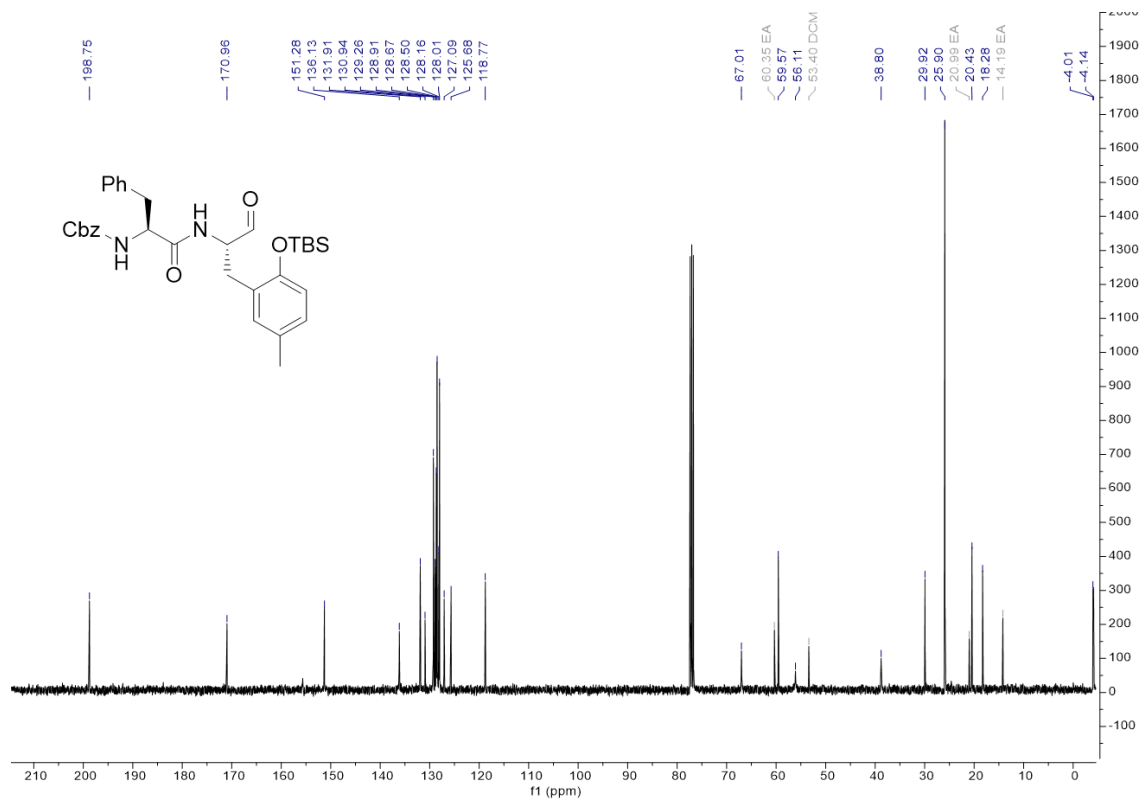
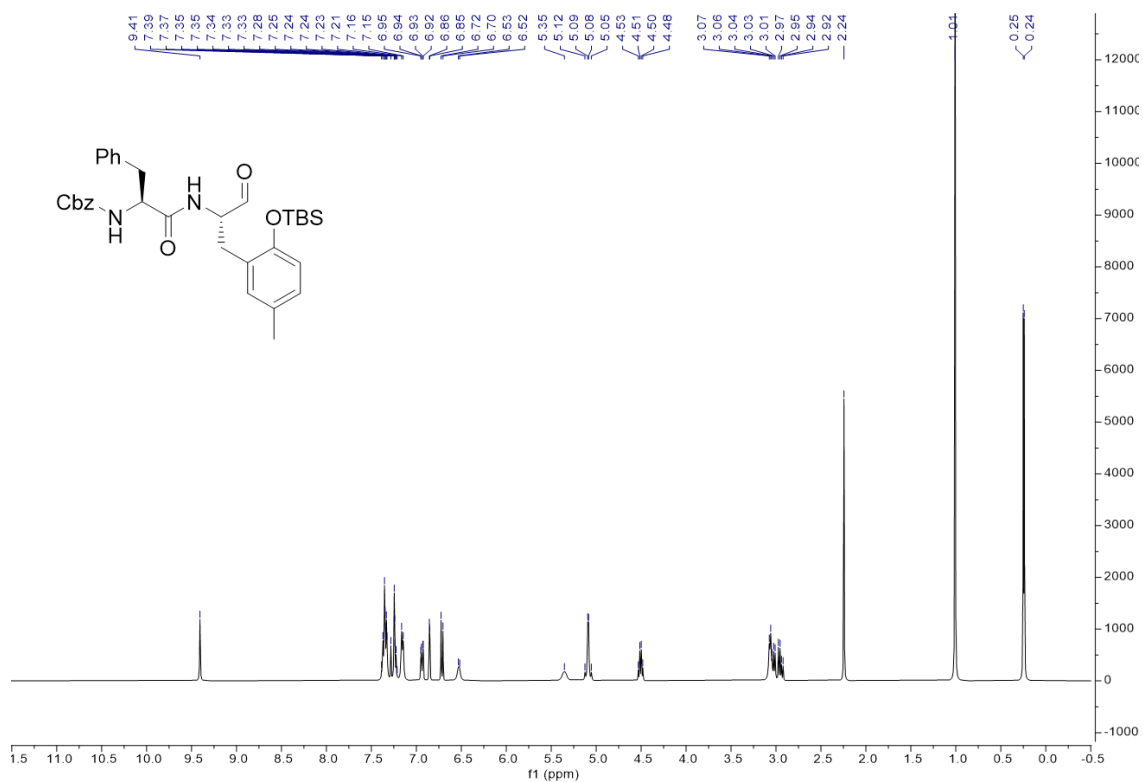
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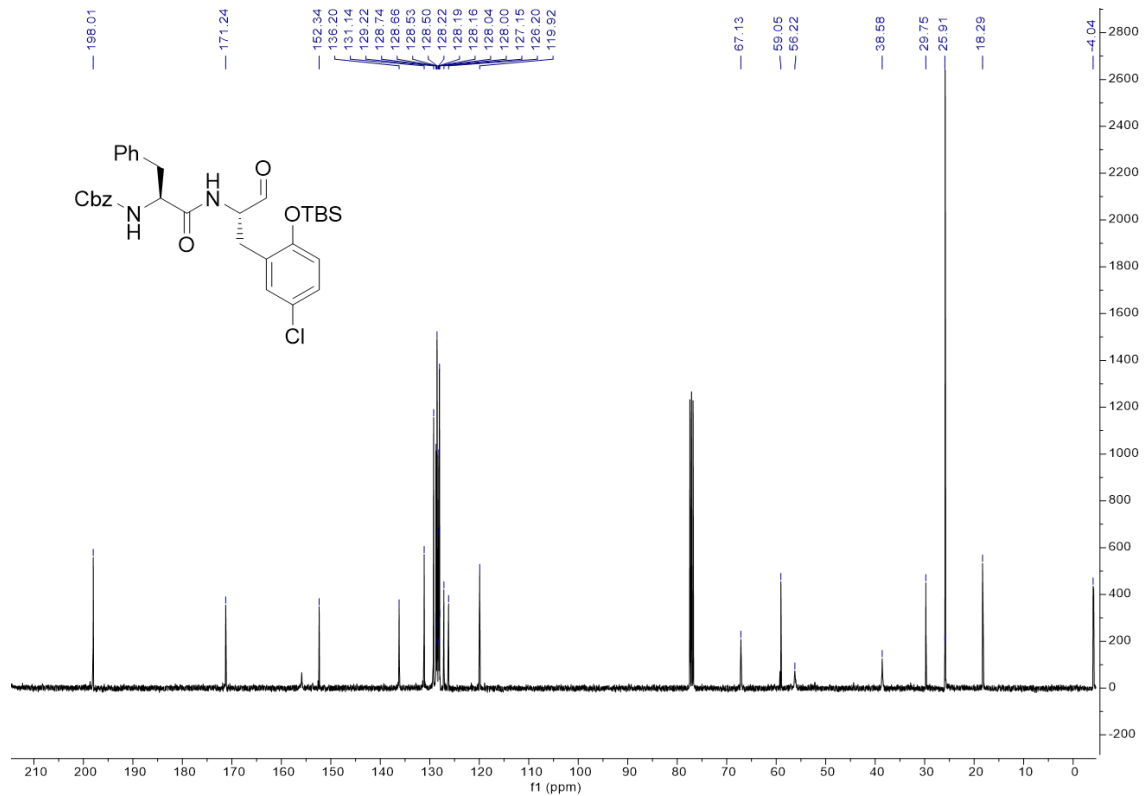
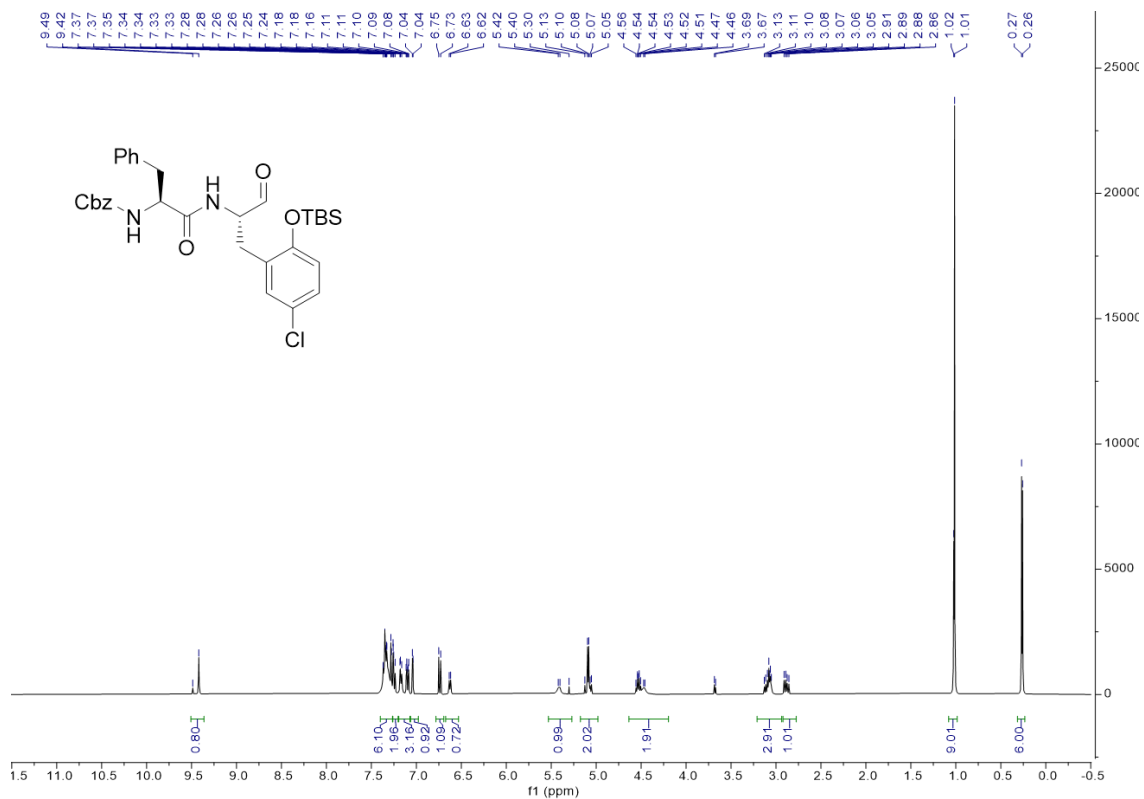
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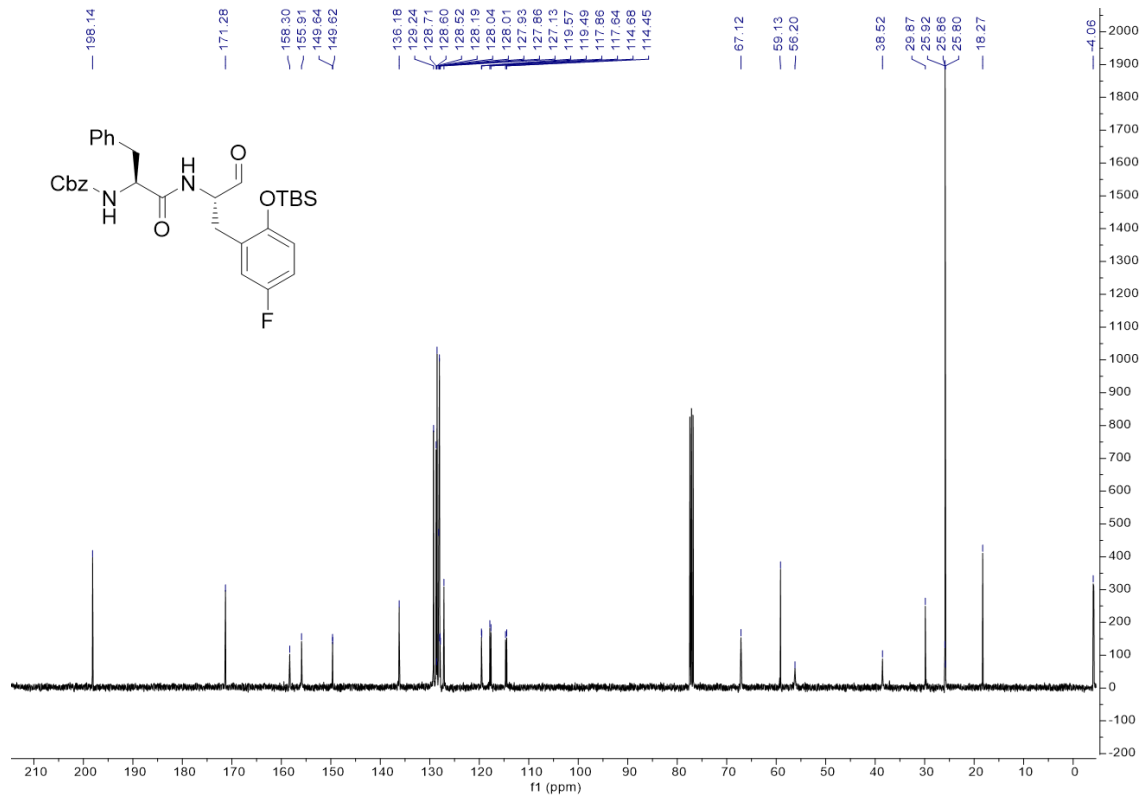
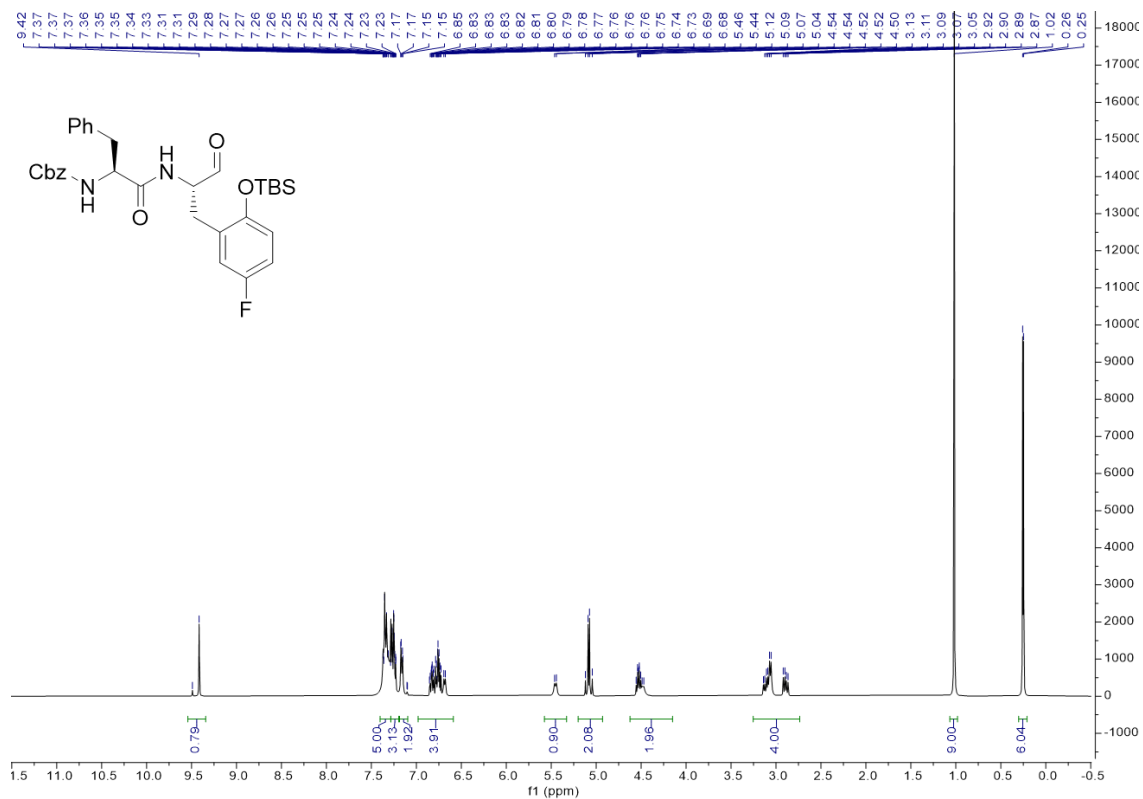
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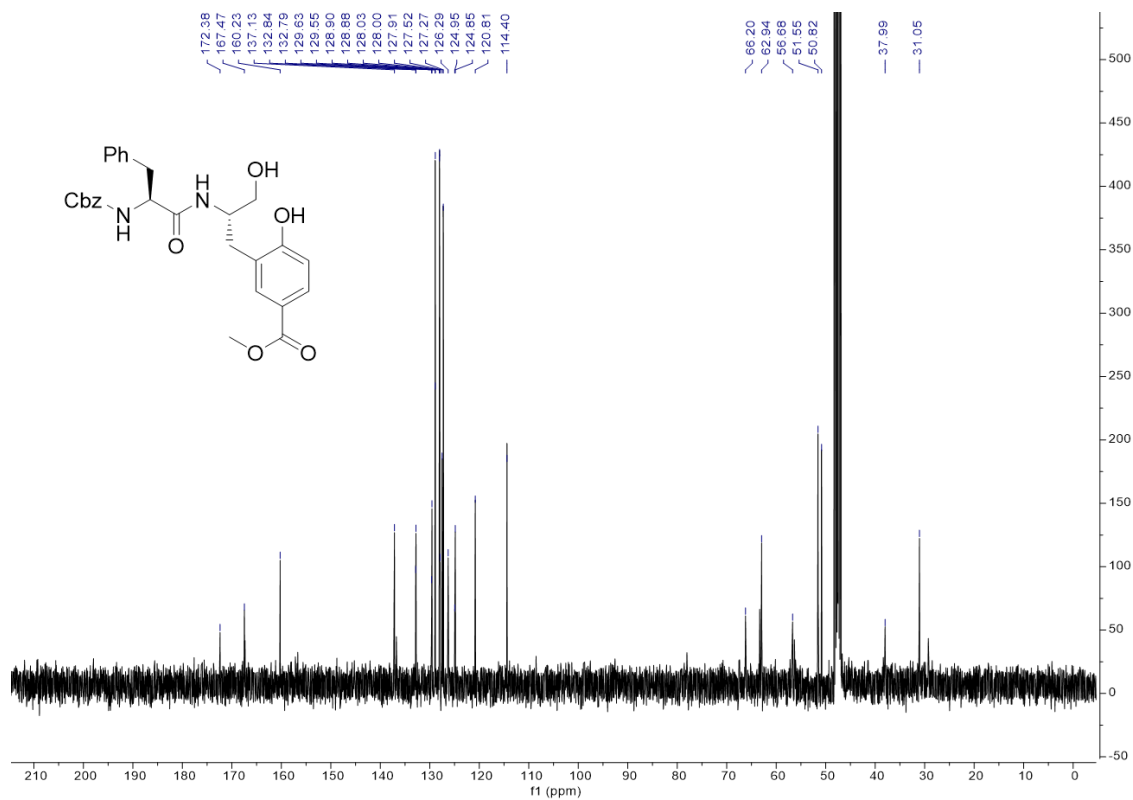
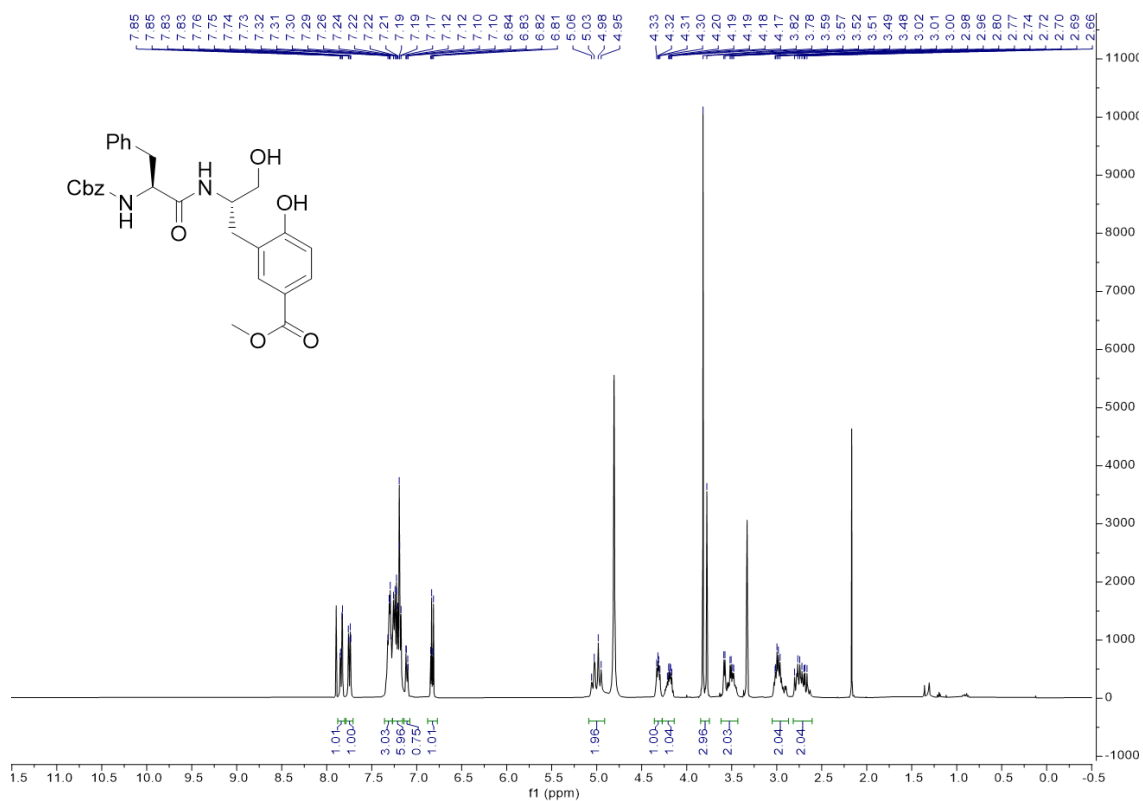
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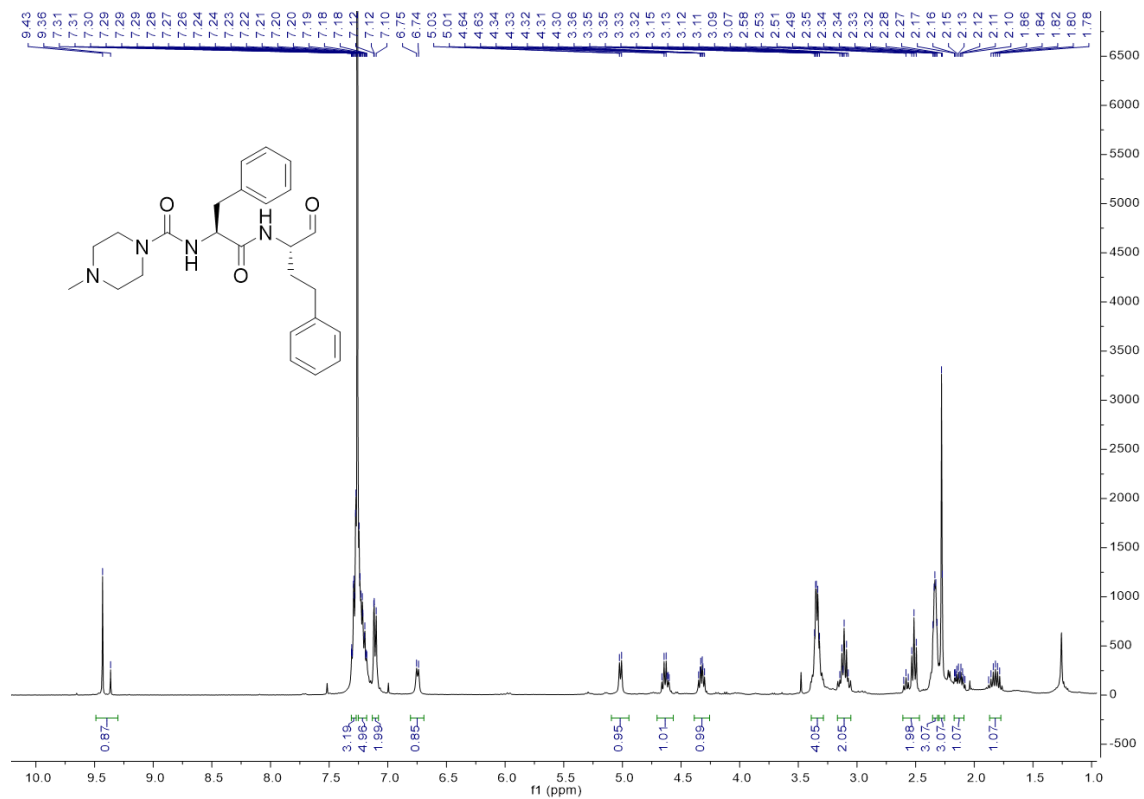
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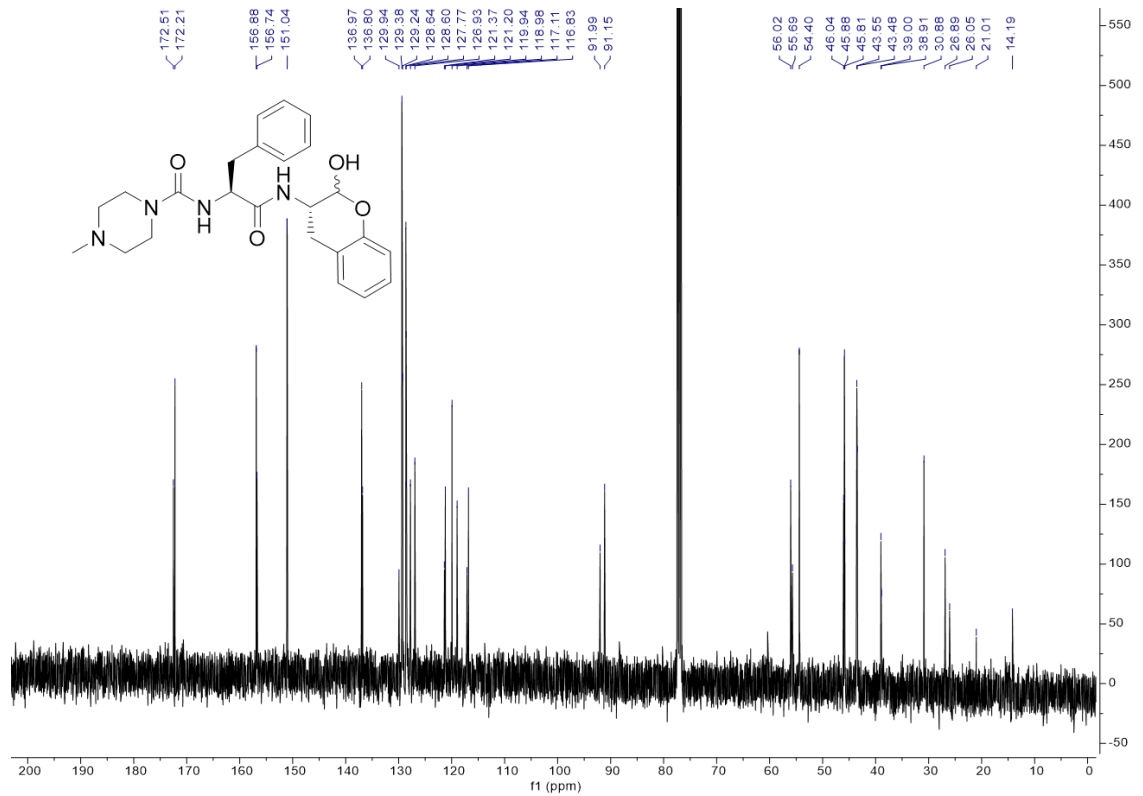
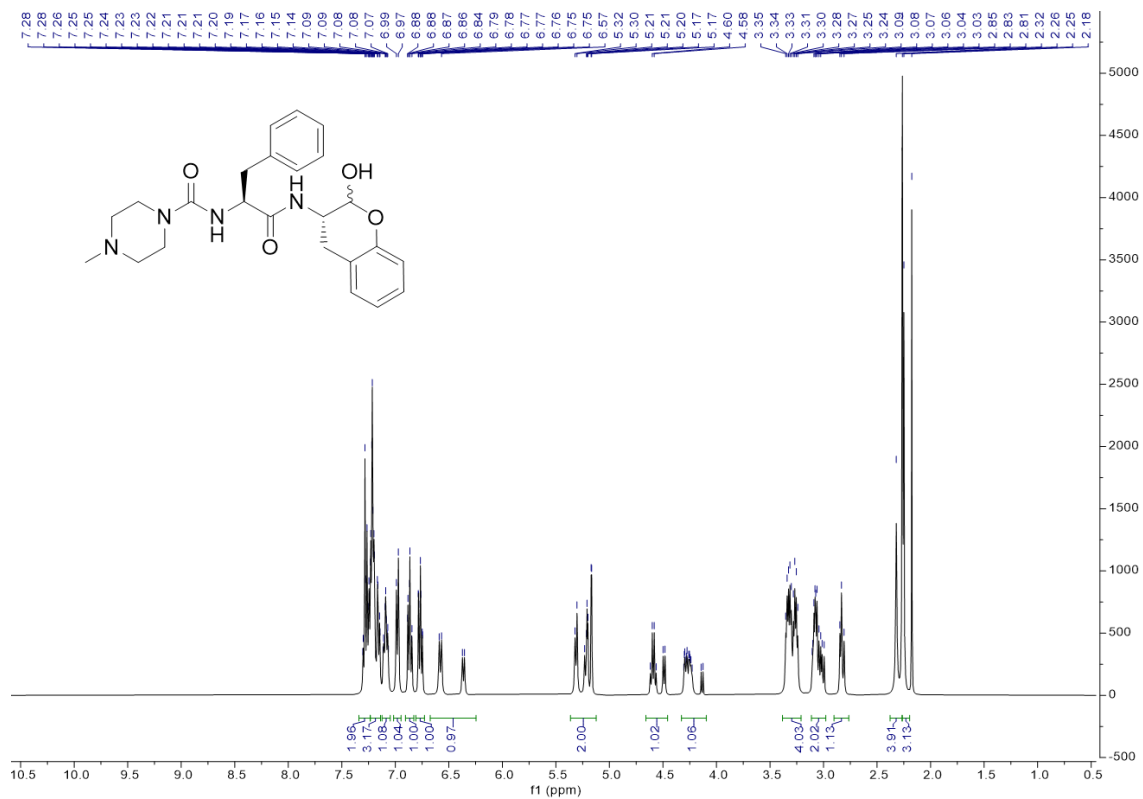
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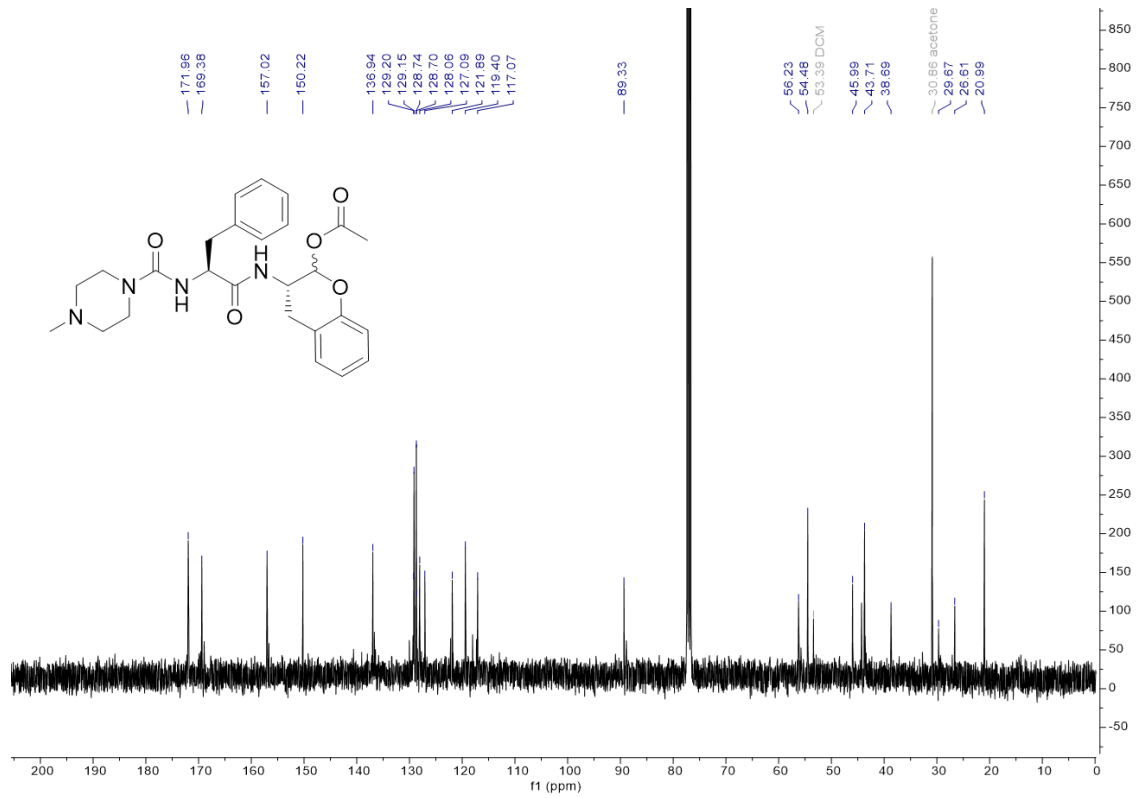
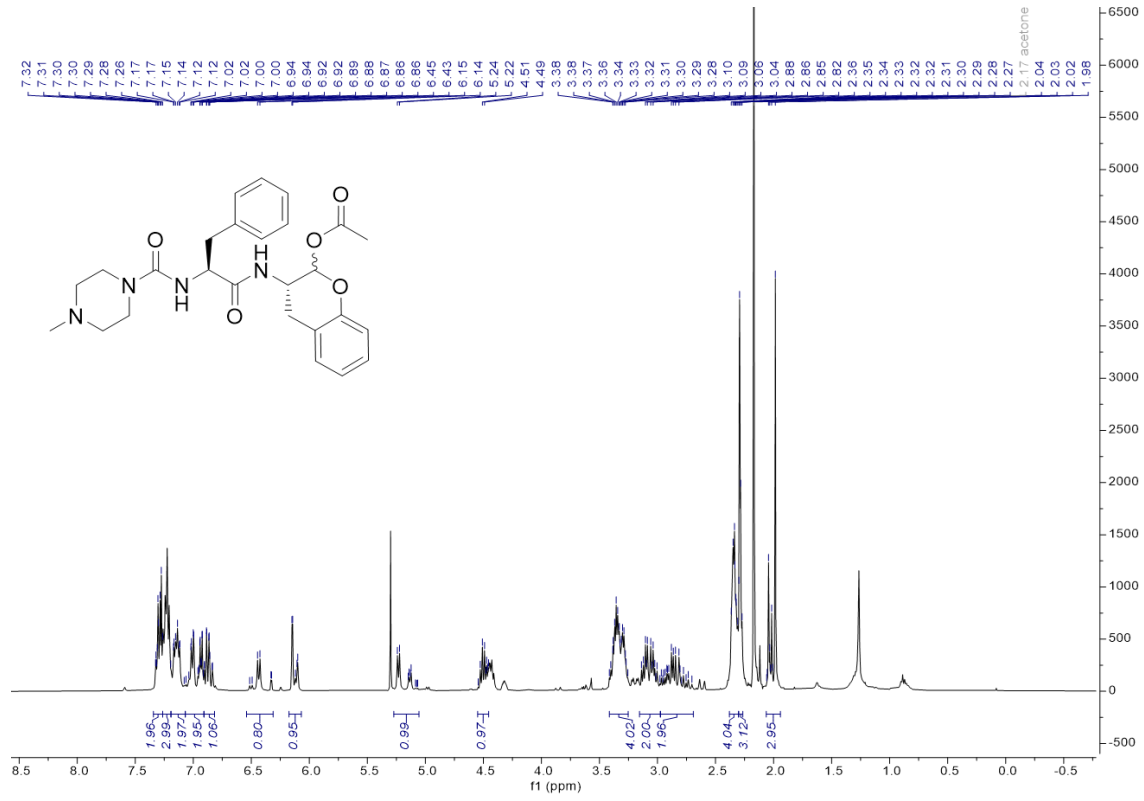
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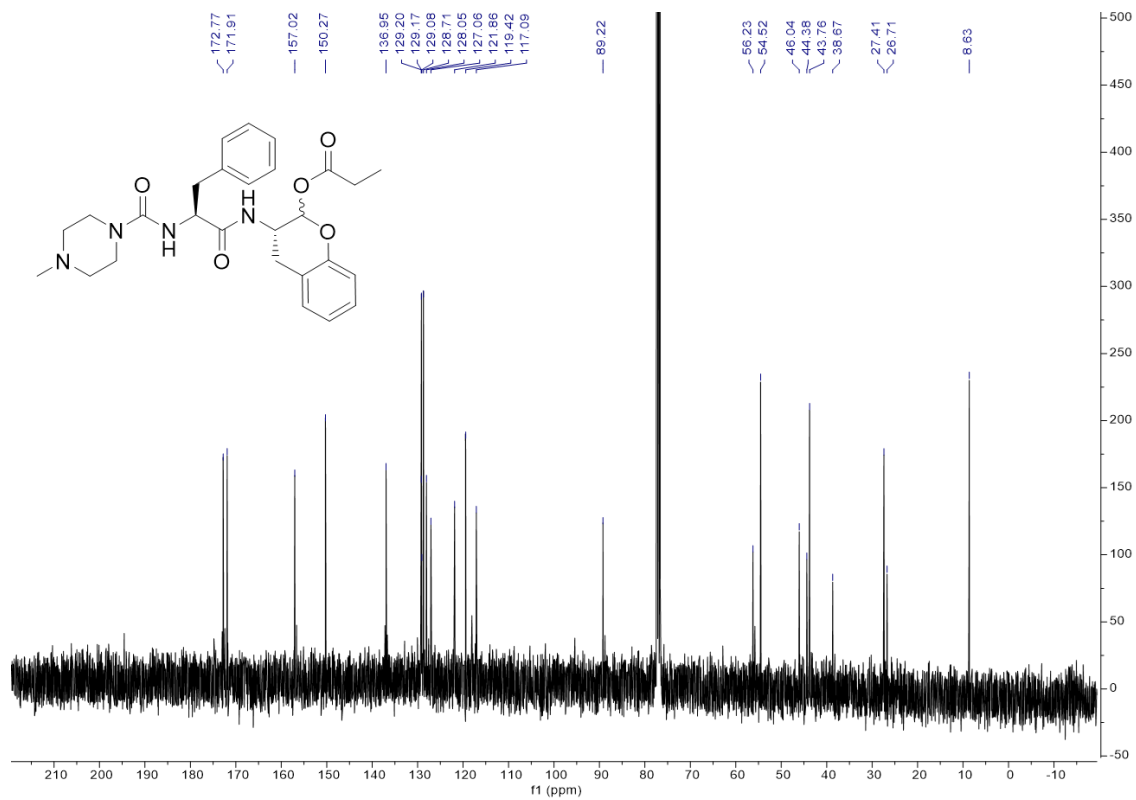
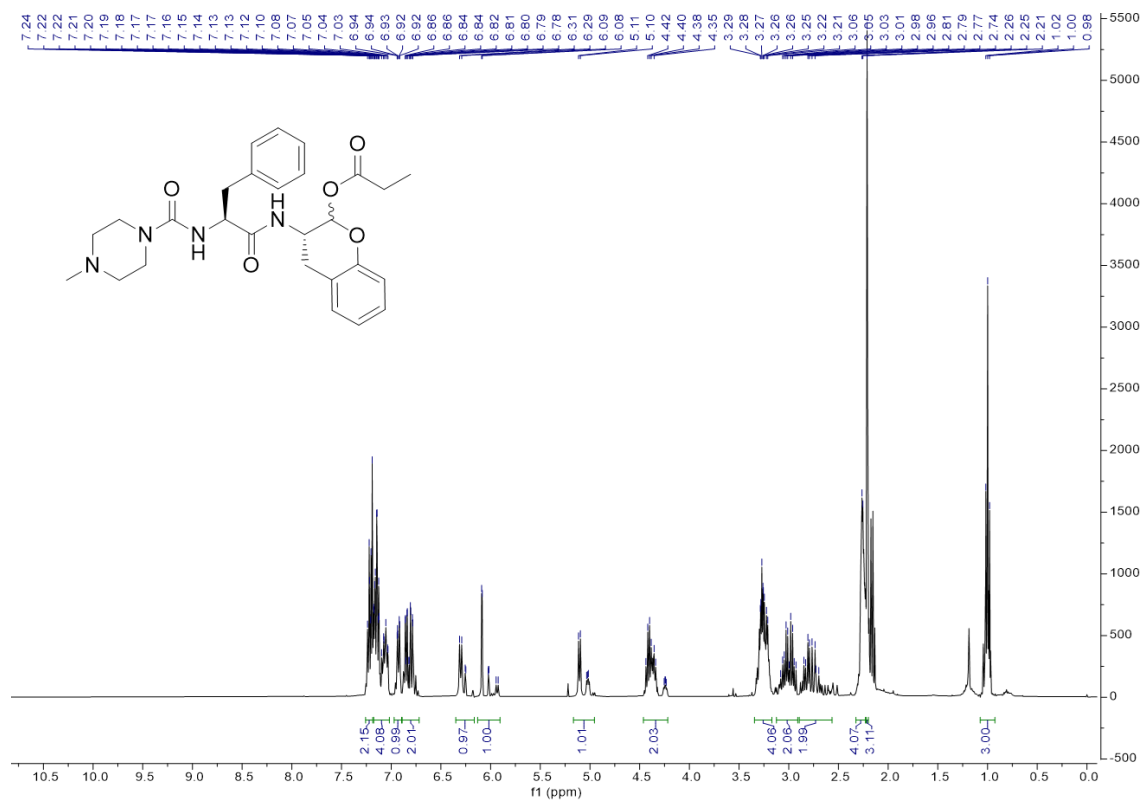
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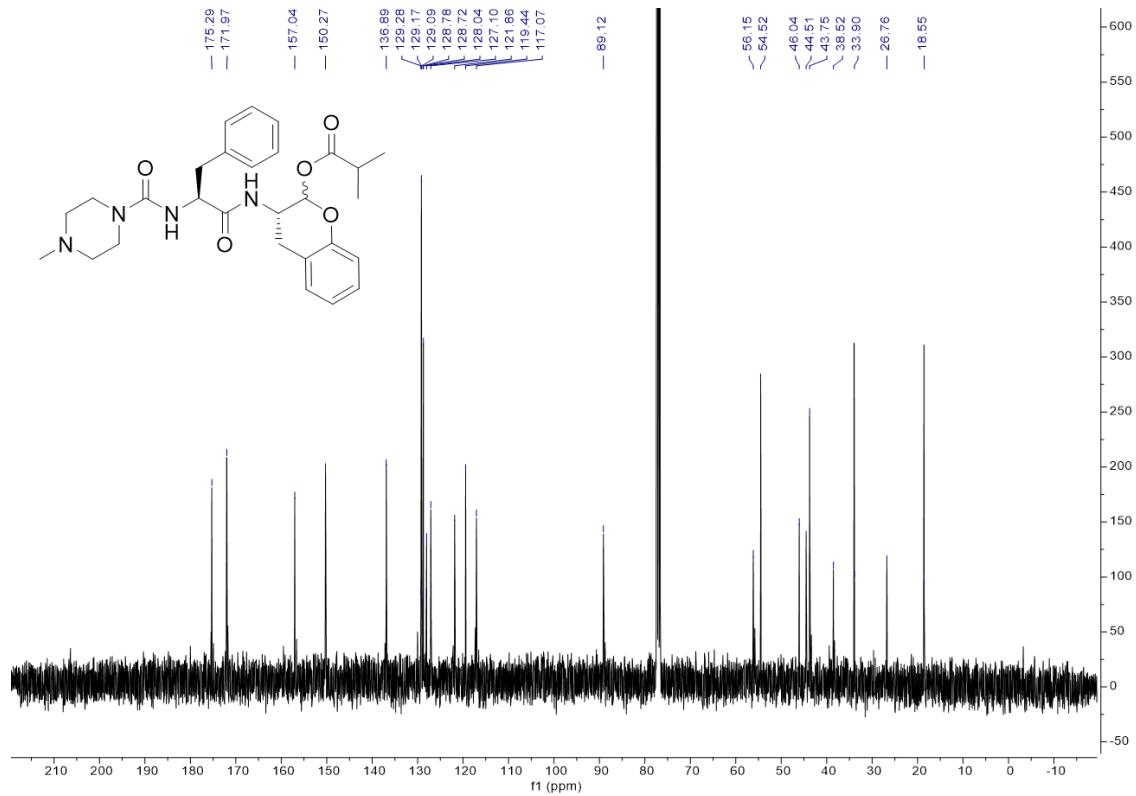
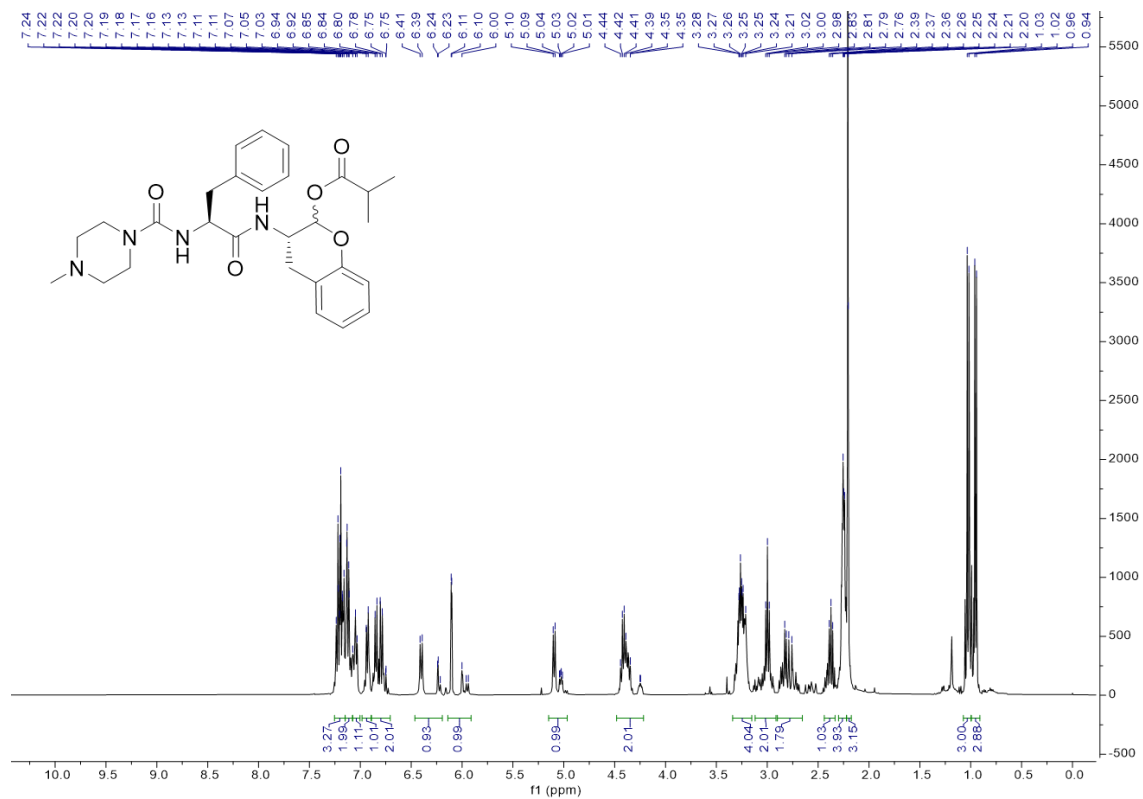
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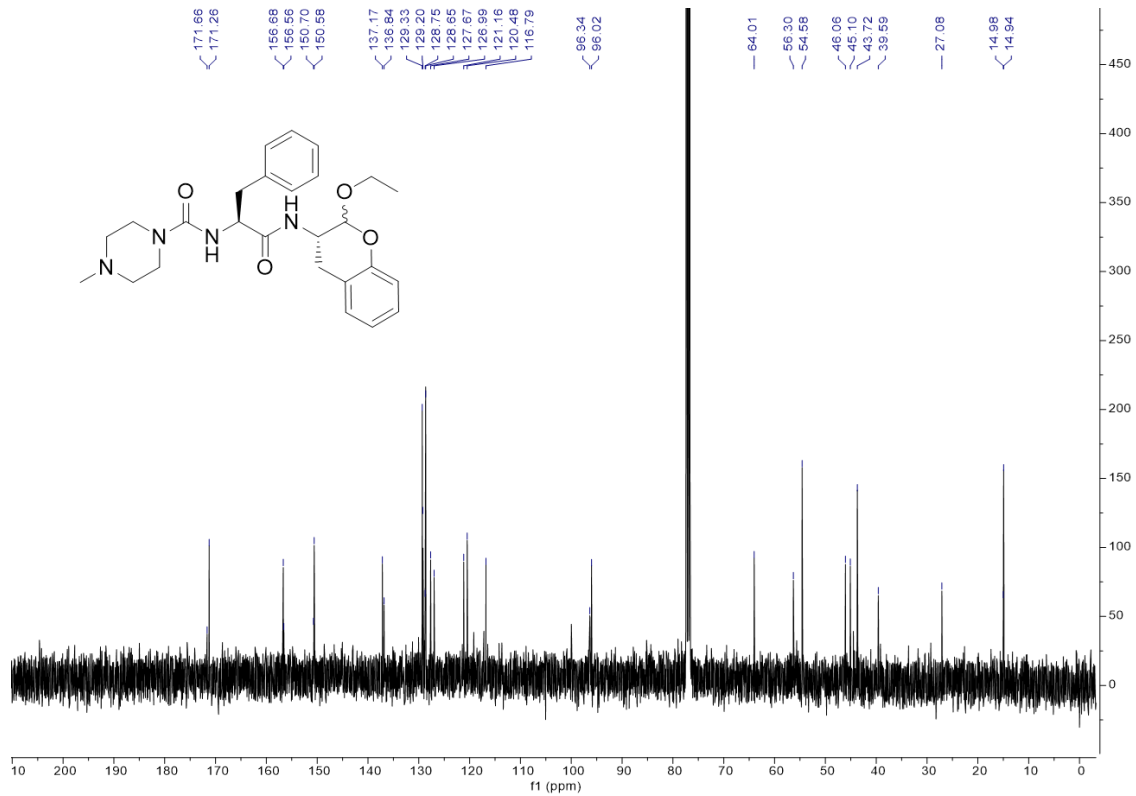
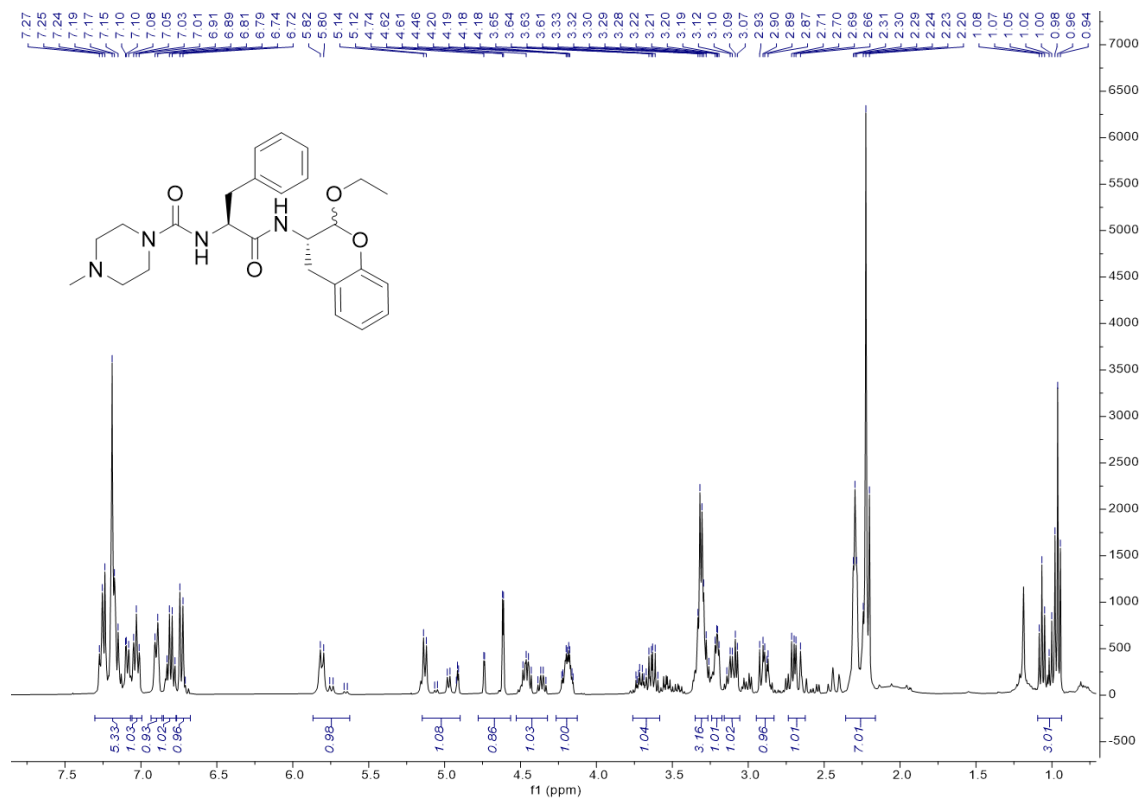
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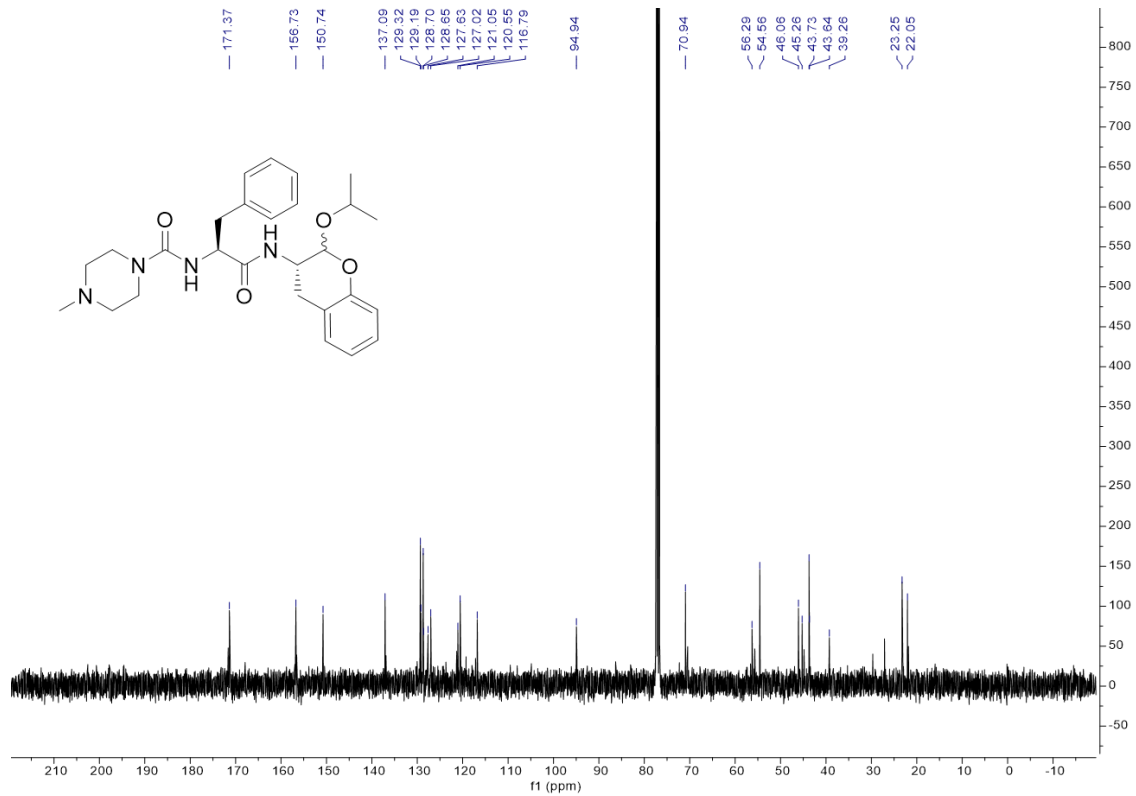
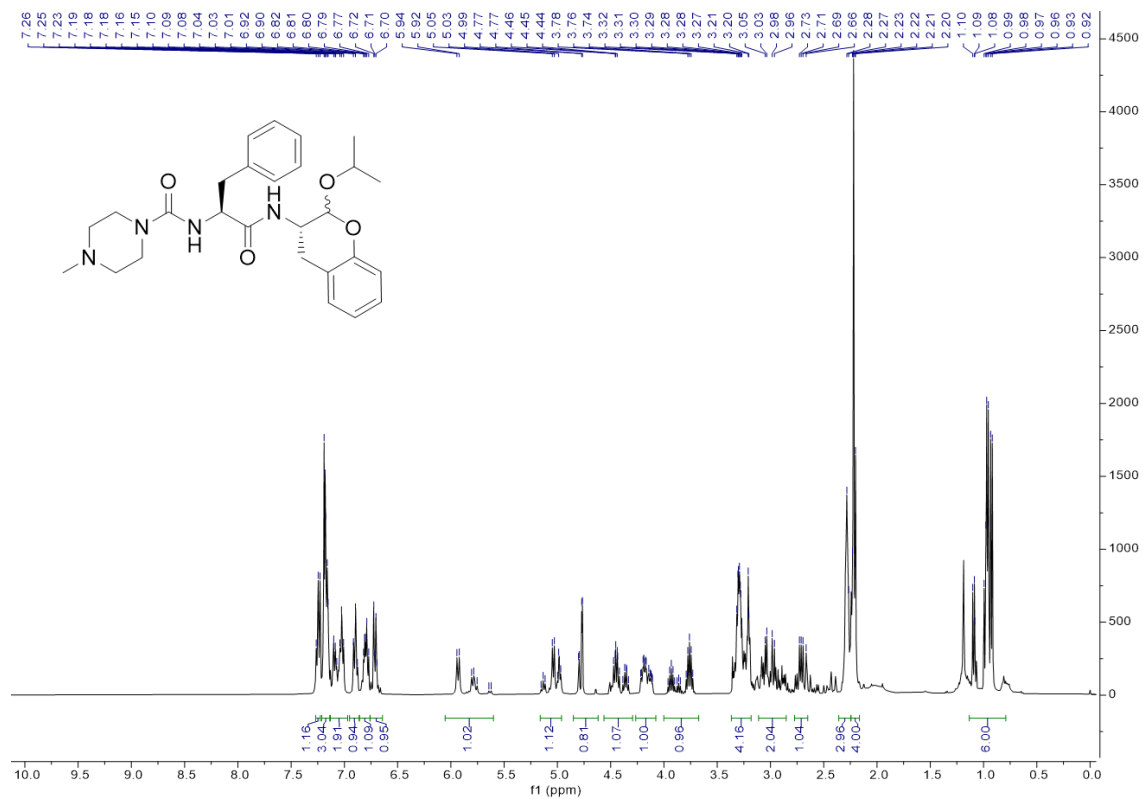
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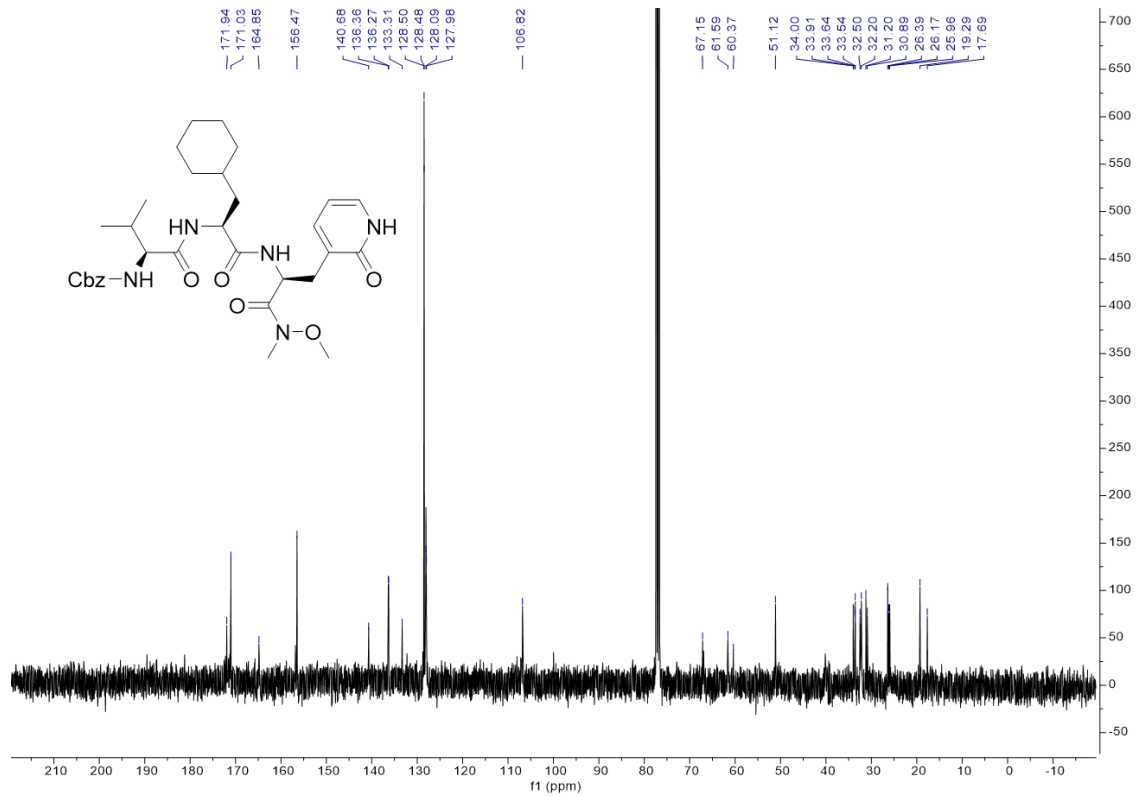
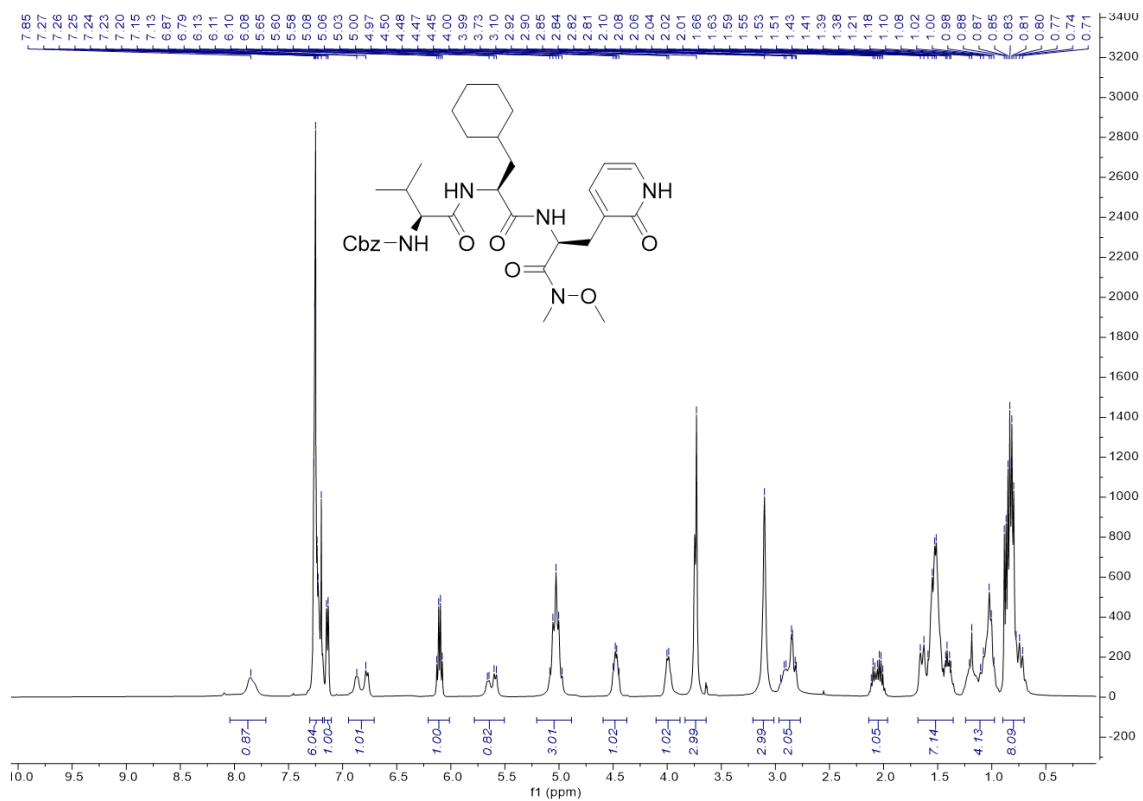
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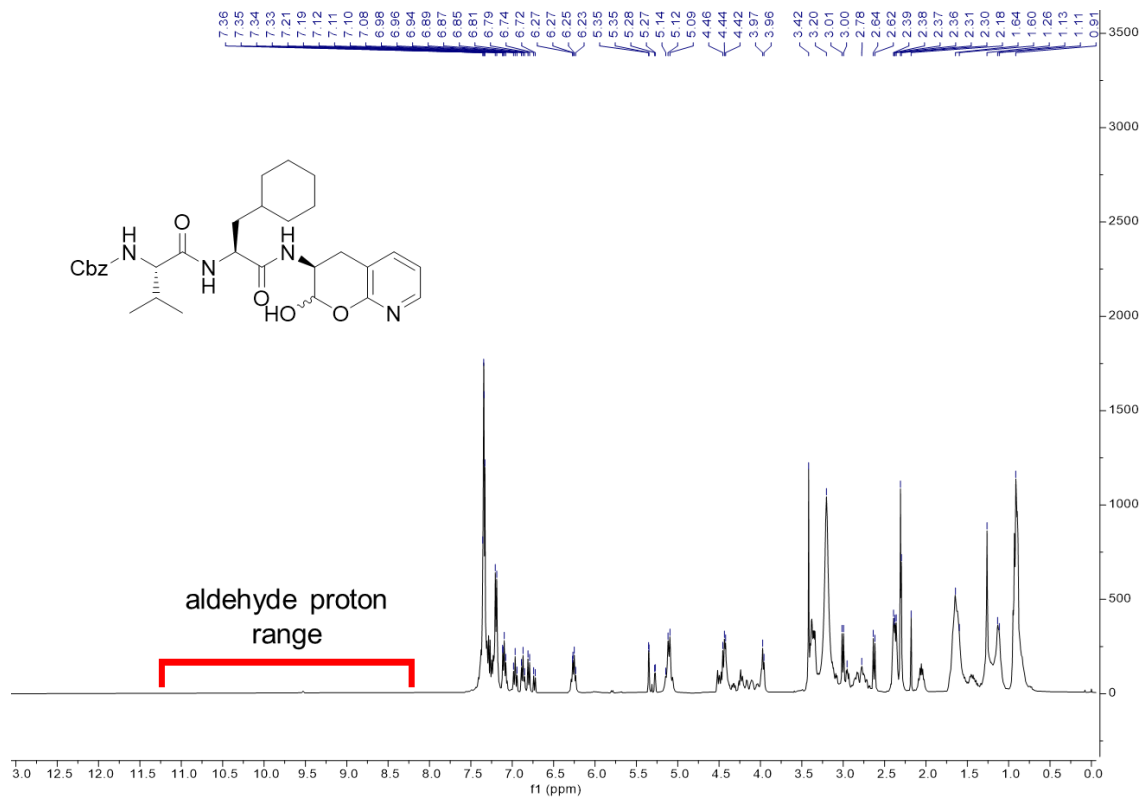


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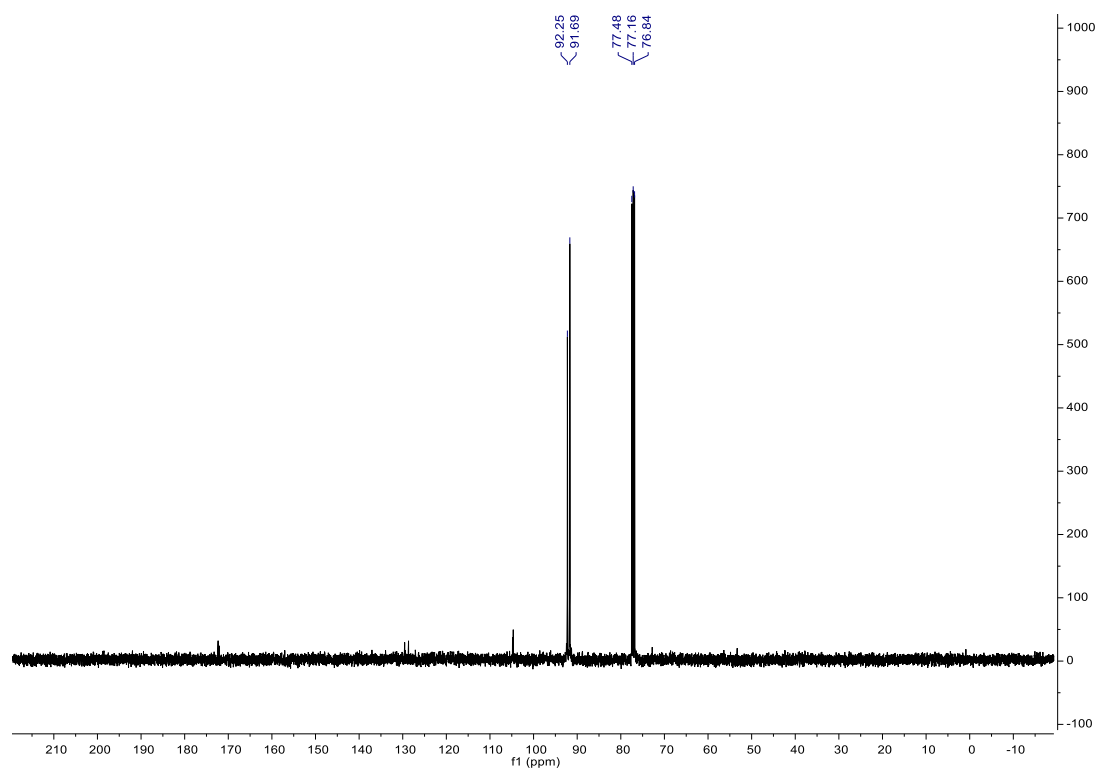


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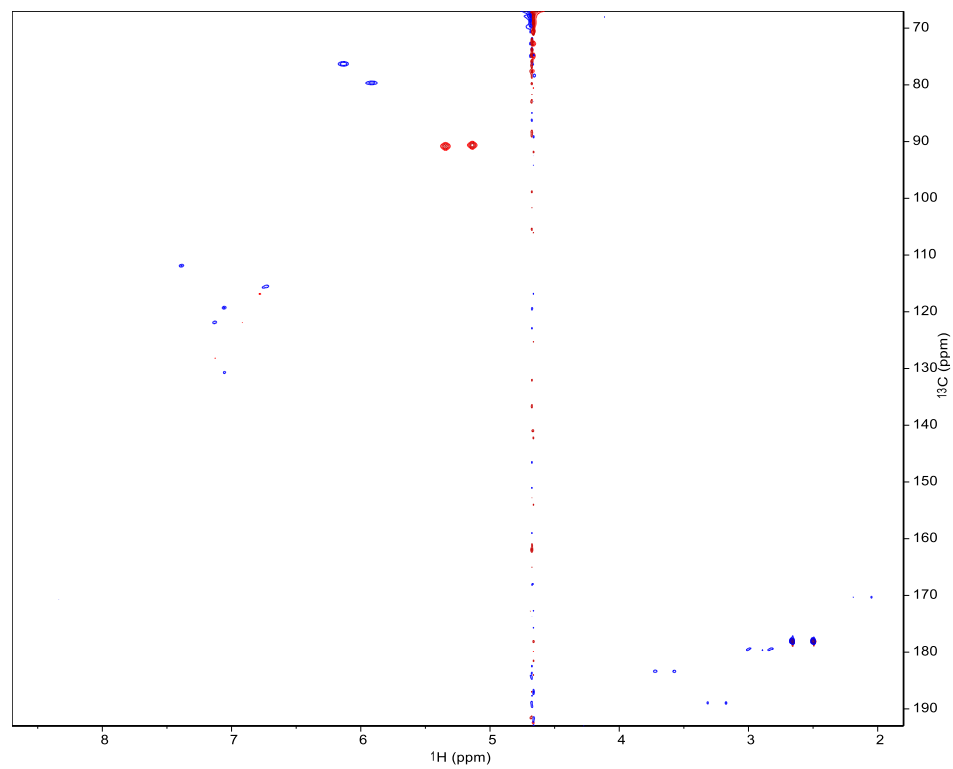




^{13}C -labeled **12** in chloroform- d_3 :

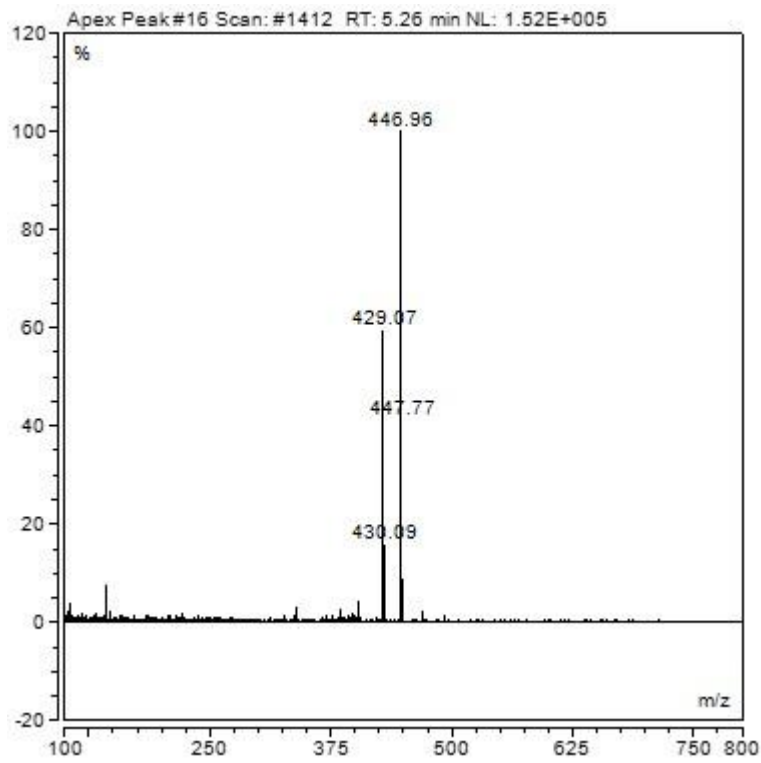
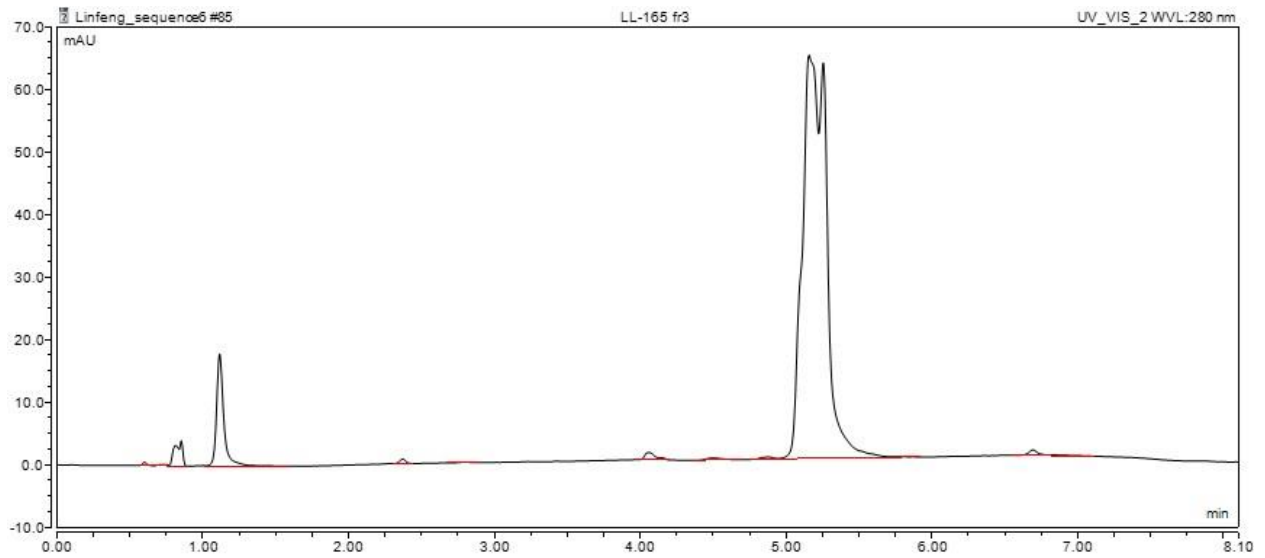


^1H - ^{13}C HSQC NMR of ^{13}C -labeled **12** with and without cruzain in buffer (full view):

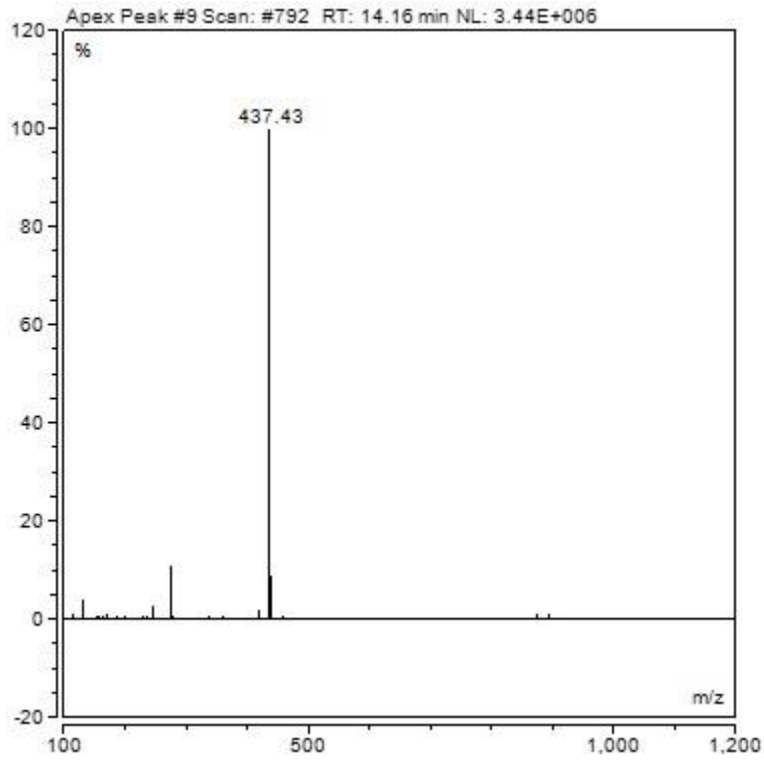
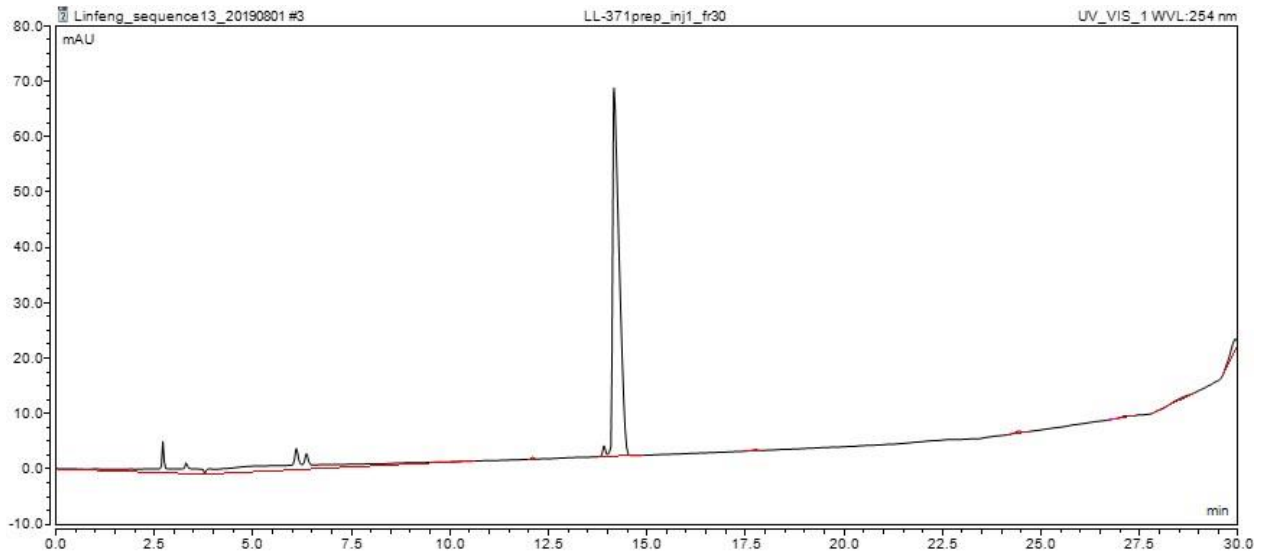


HPLC traces and MS data

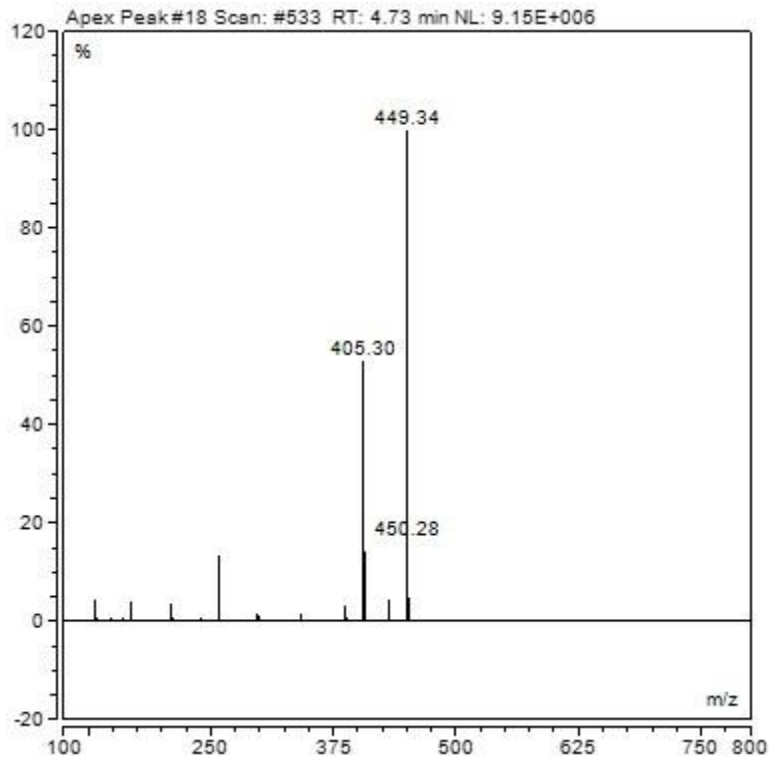
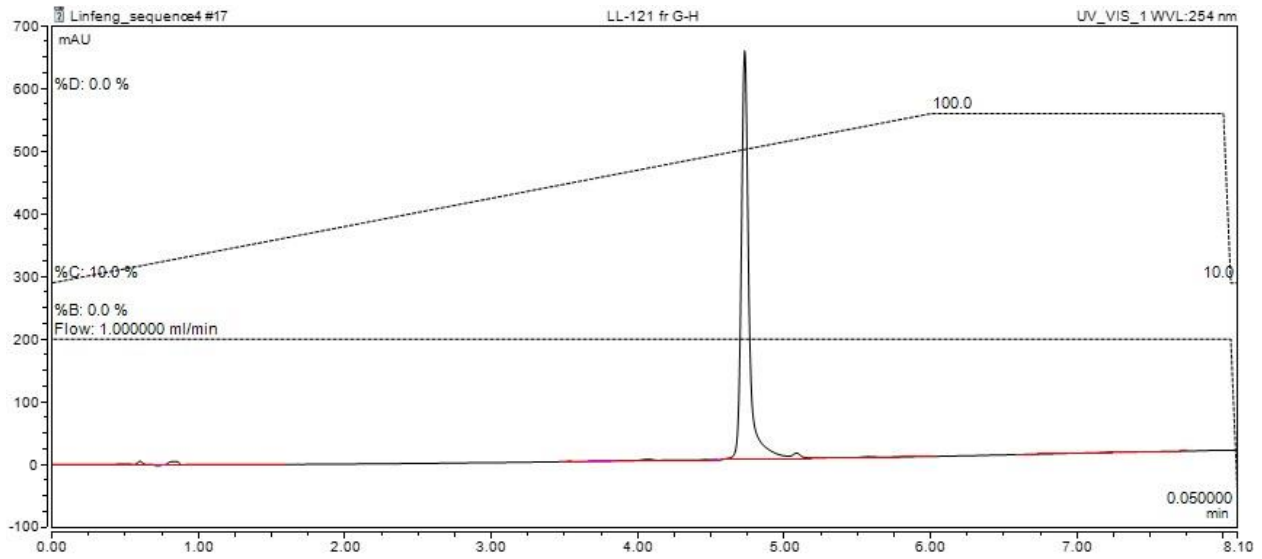
2: exact mass = 446.18



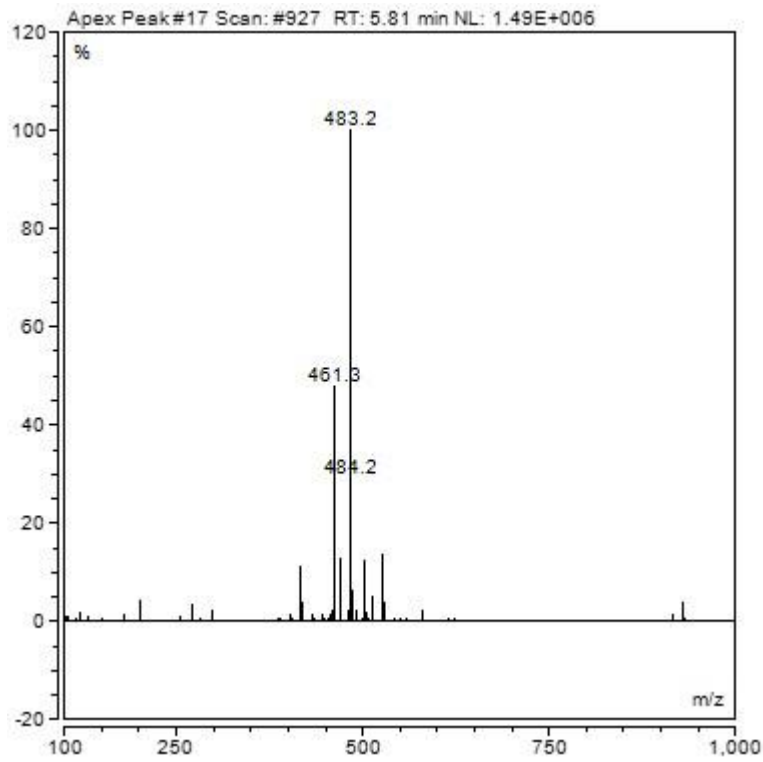
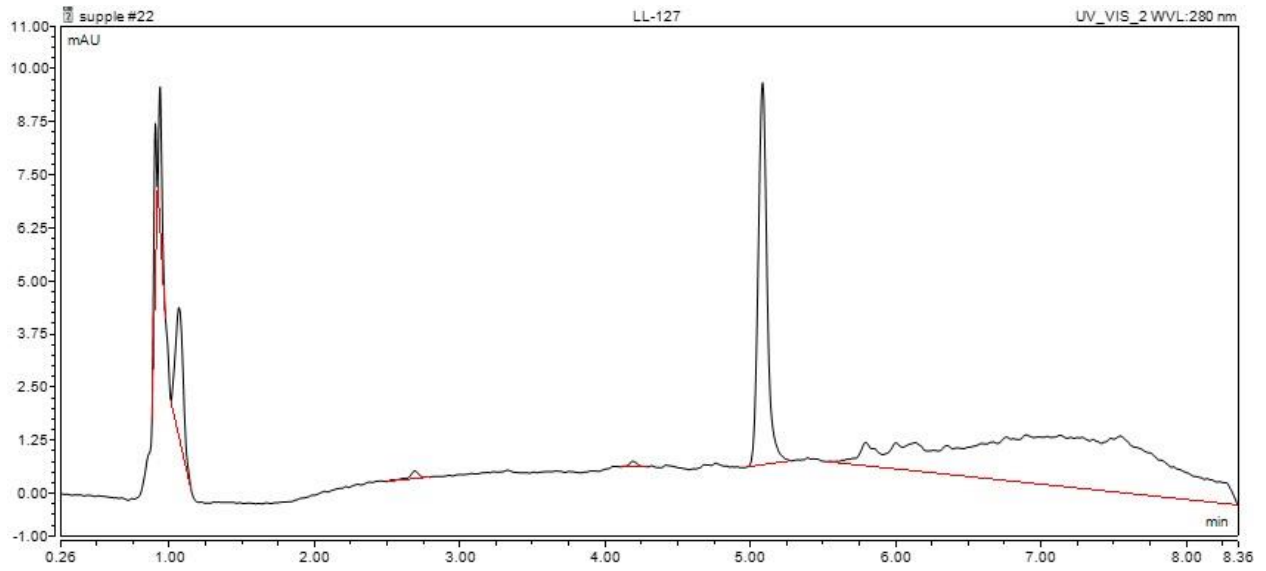
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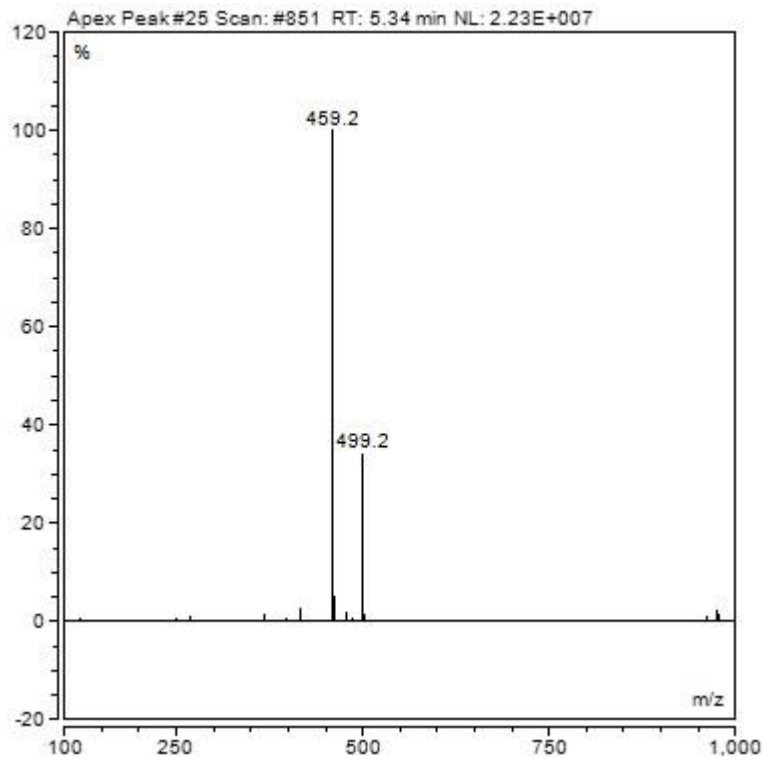
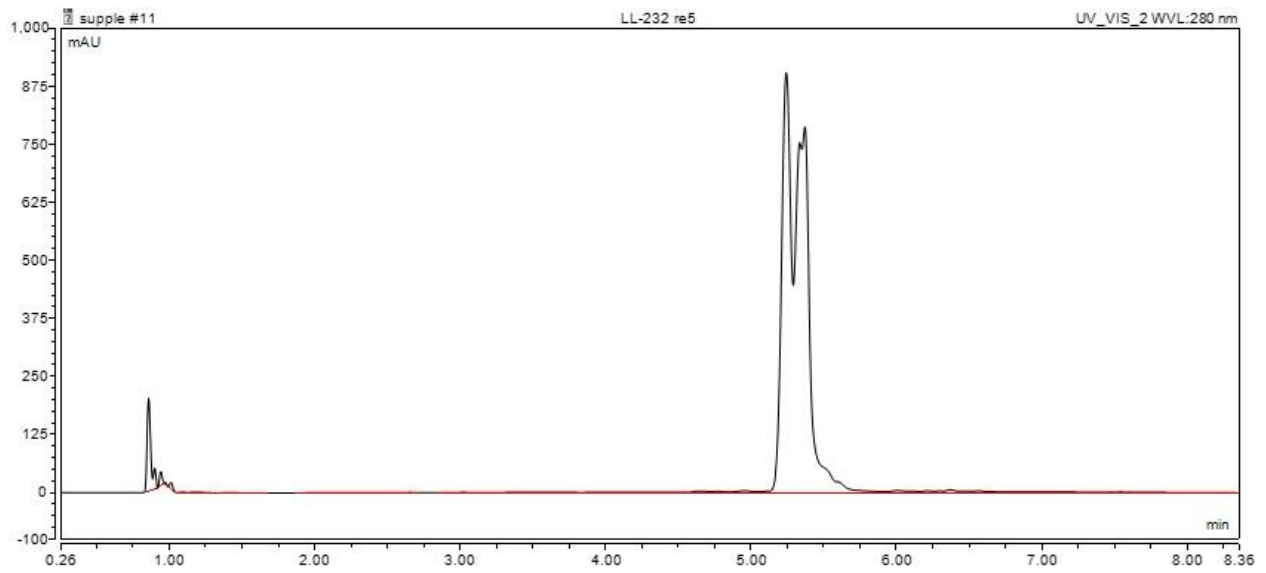
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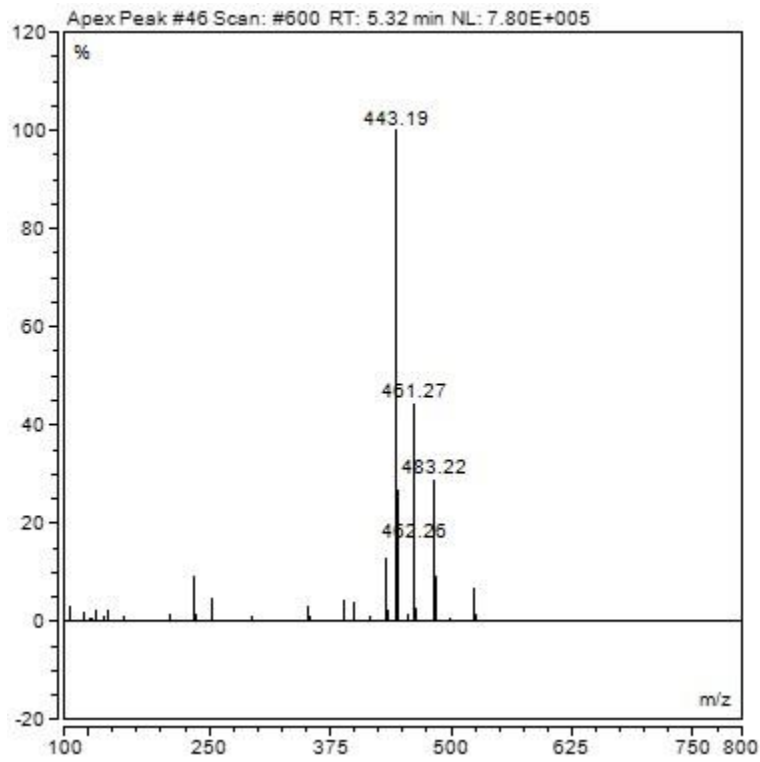
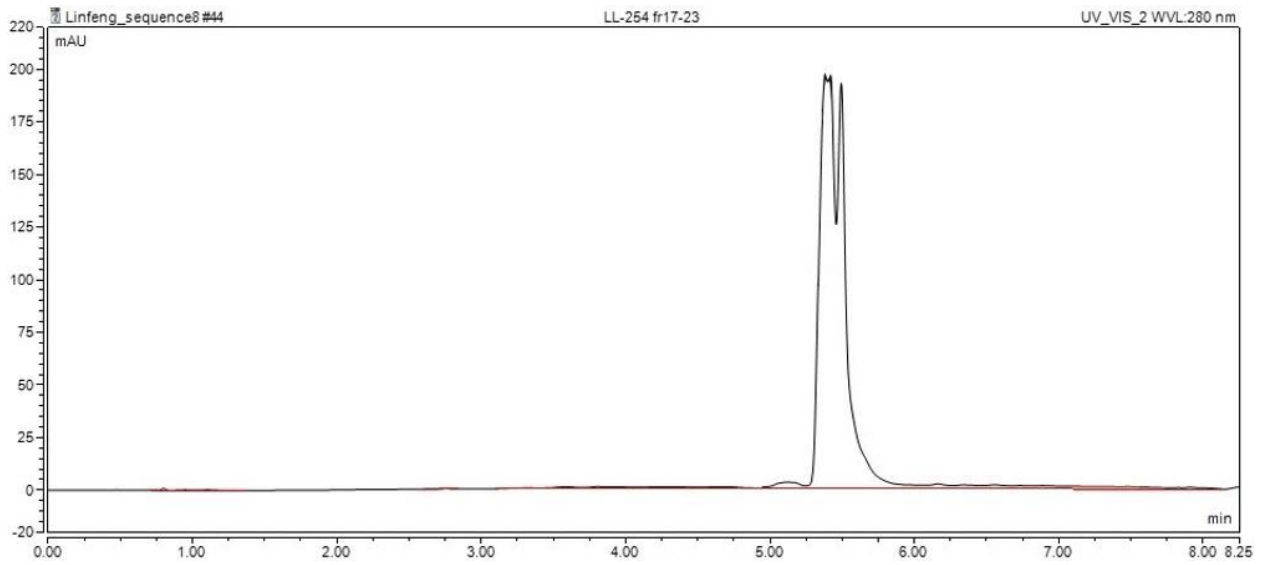
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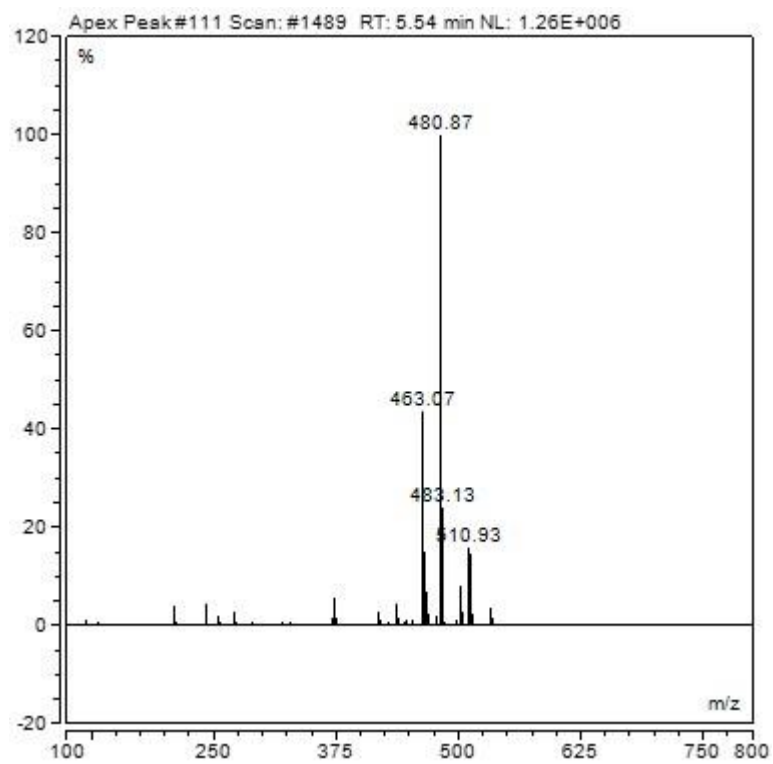
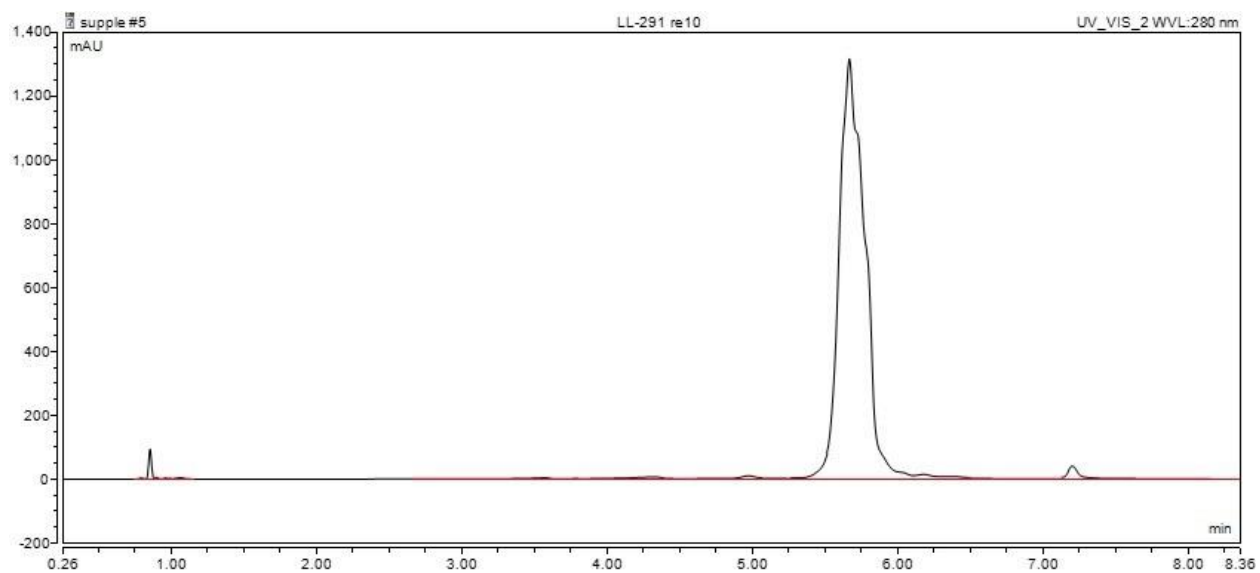
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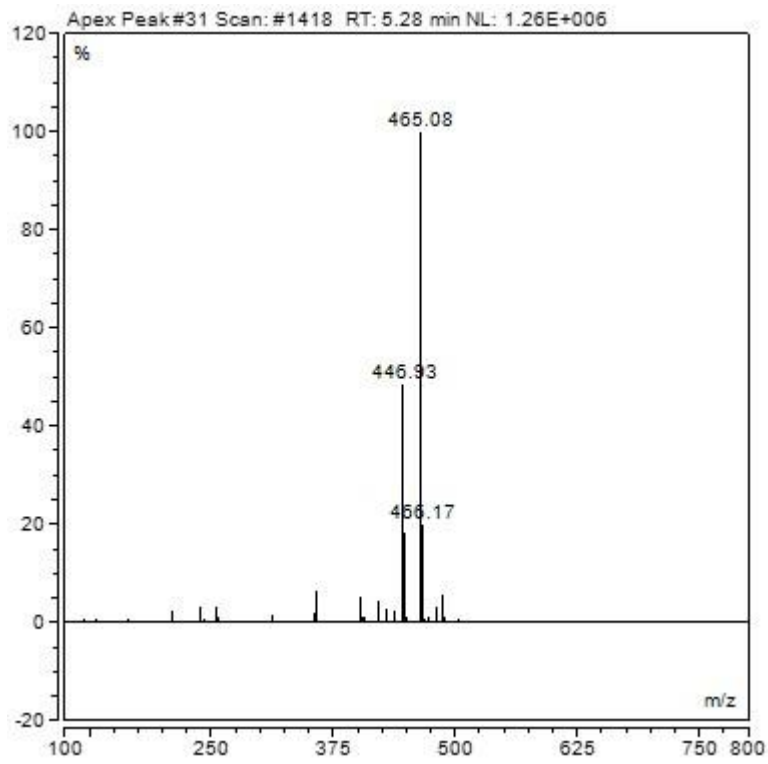
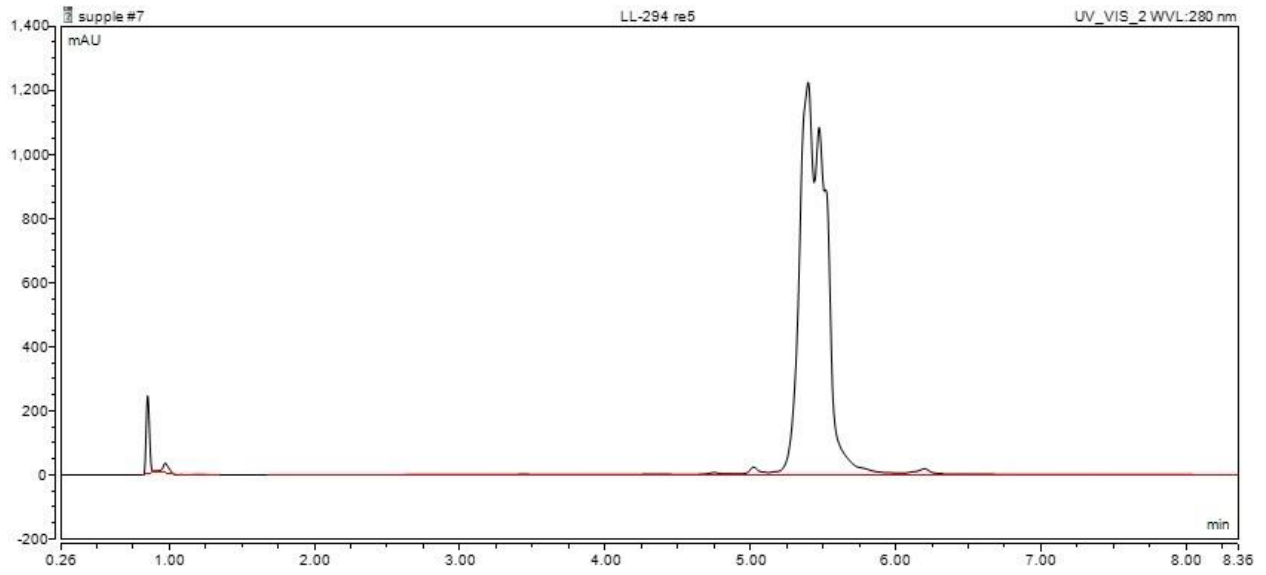
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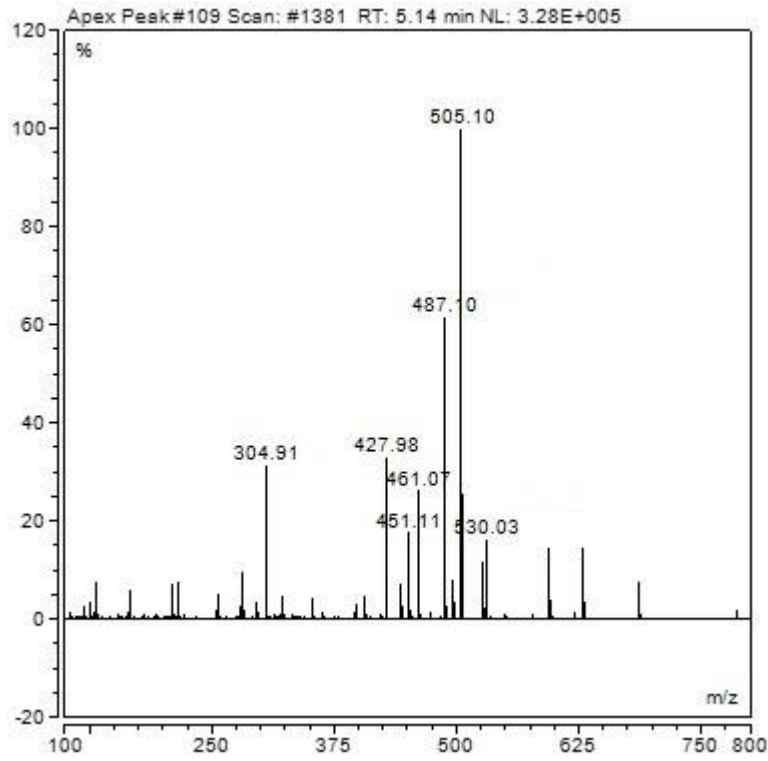
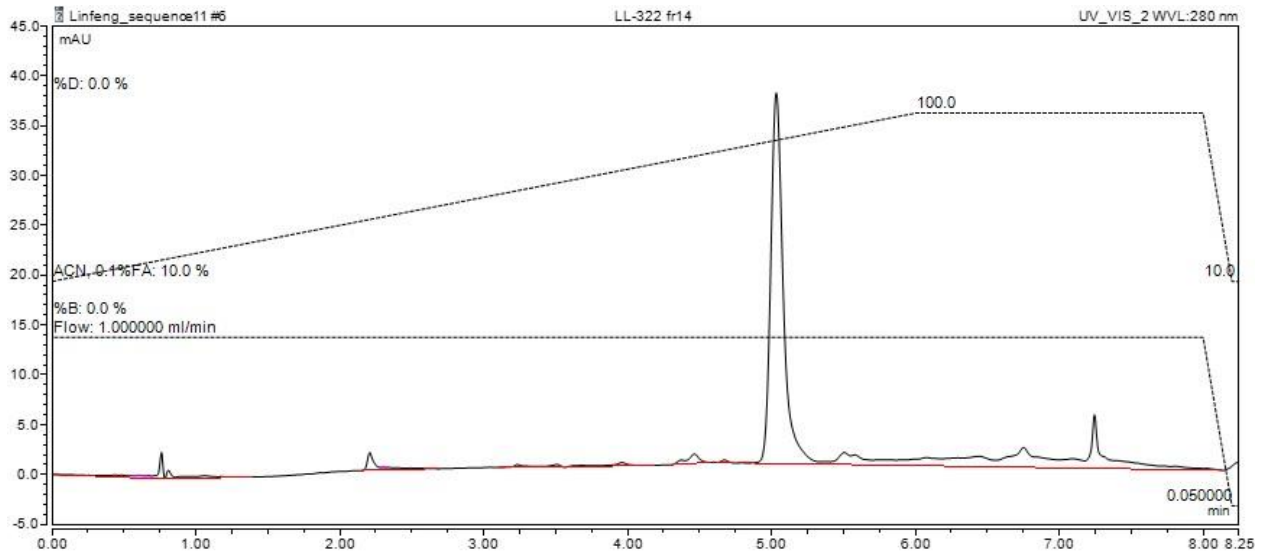
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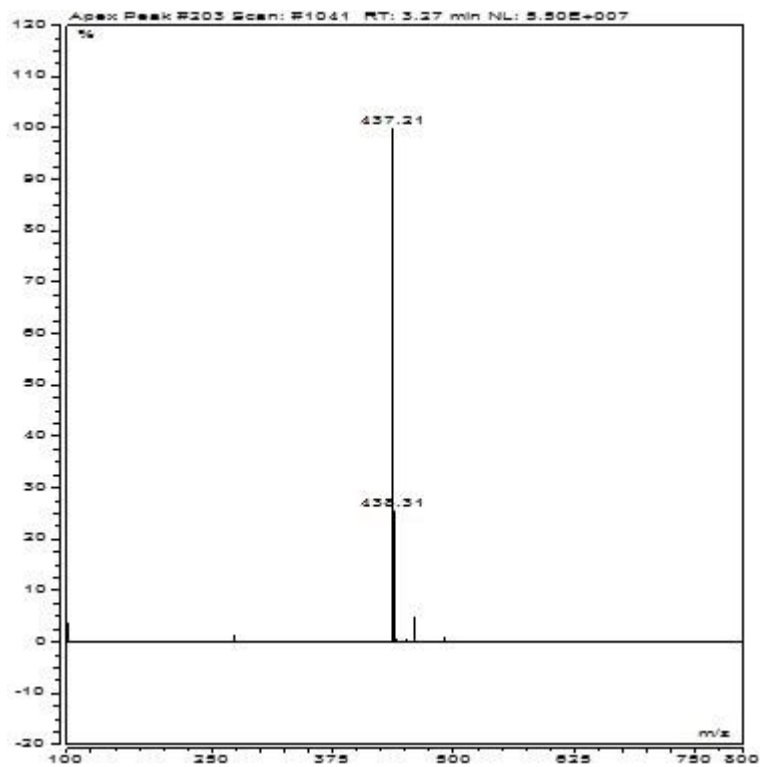
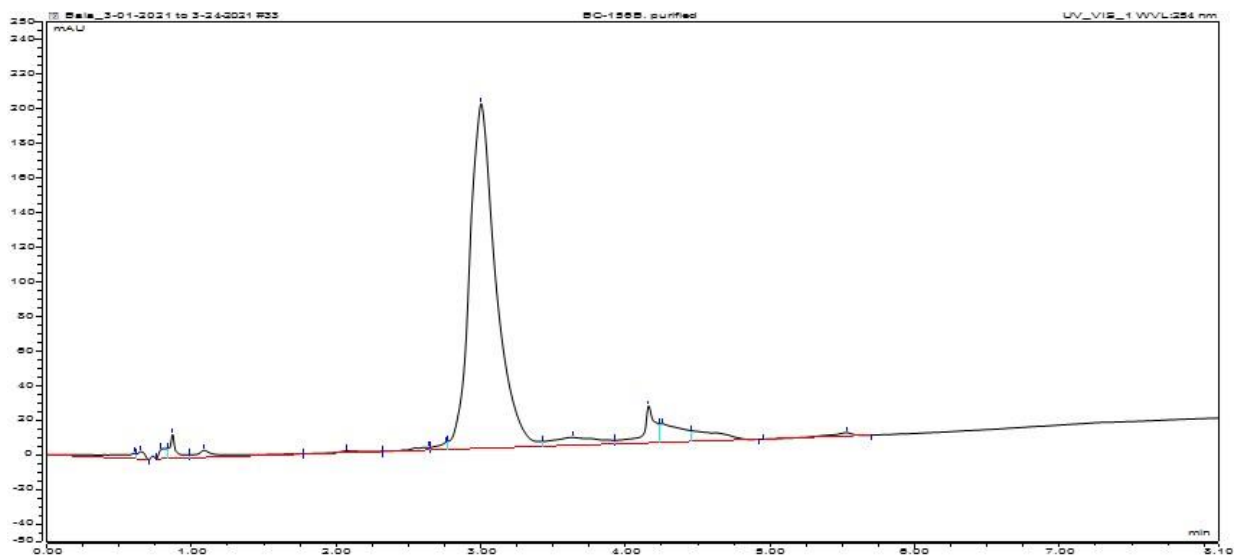
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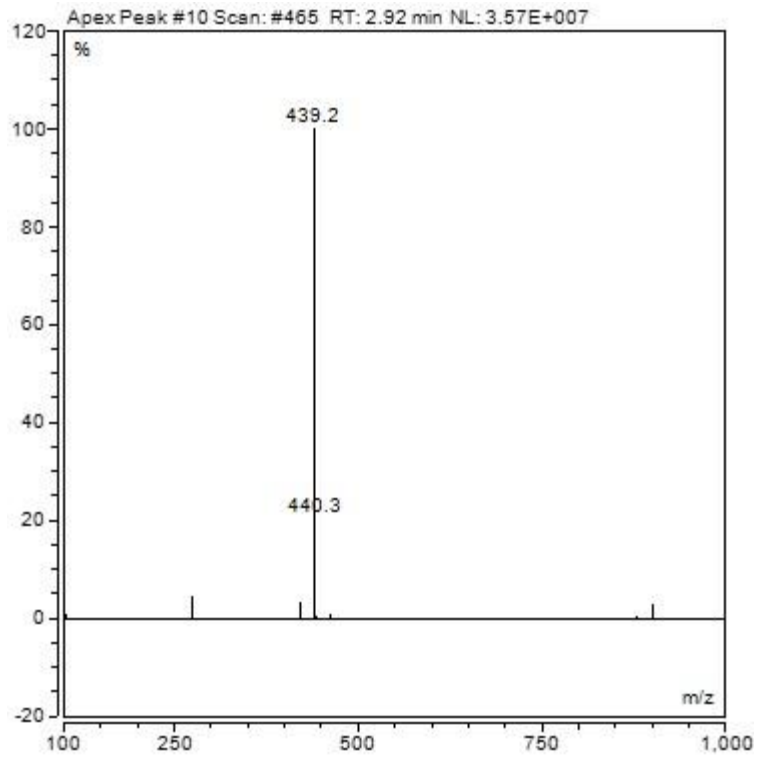
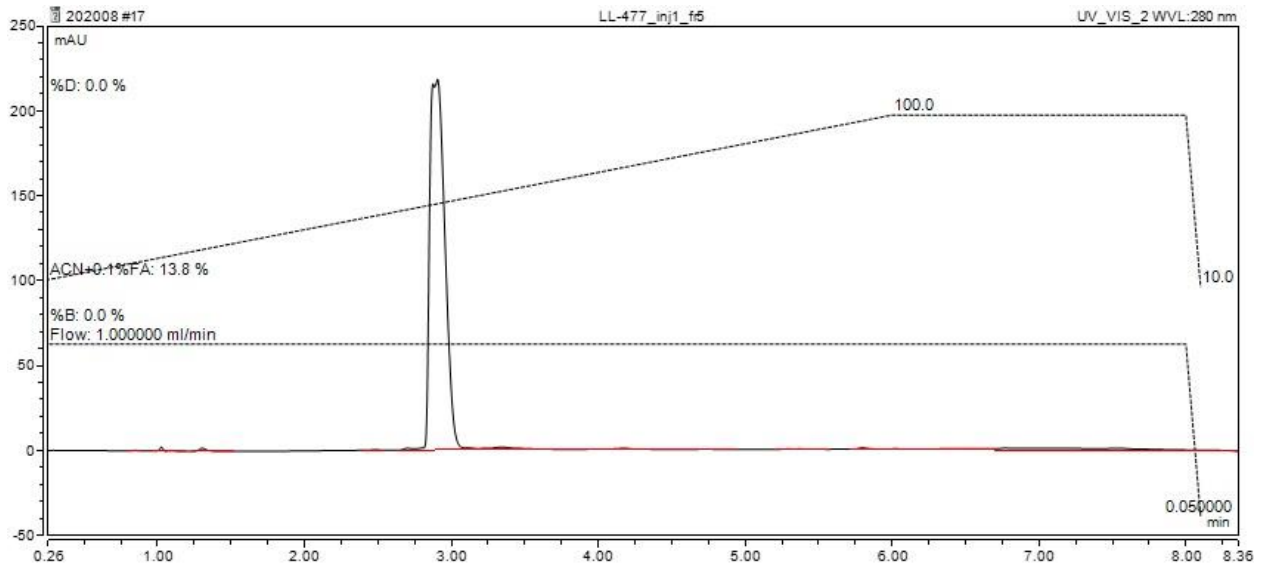
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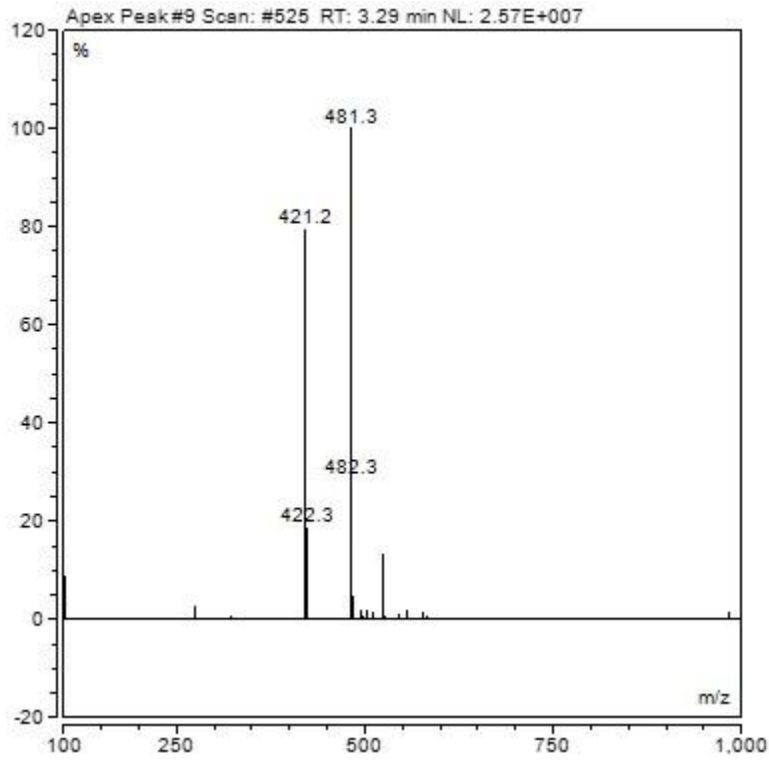
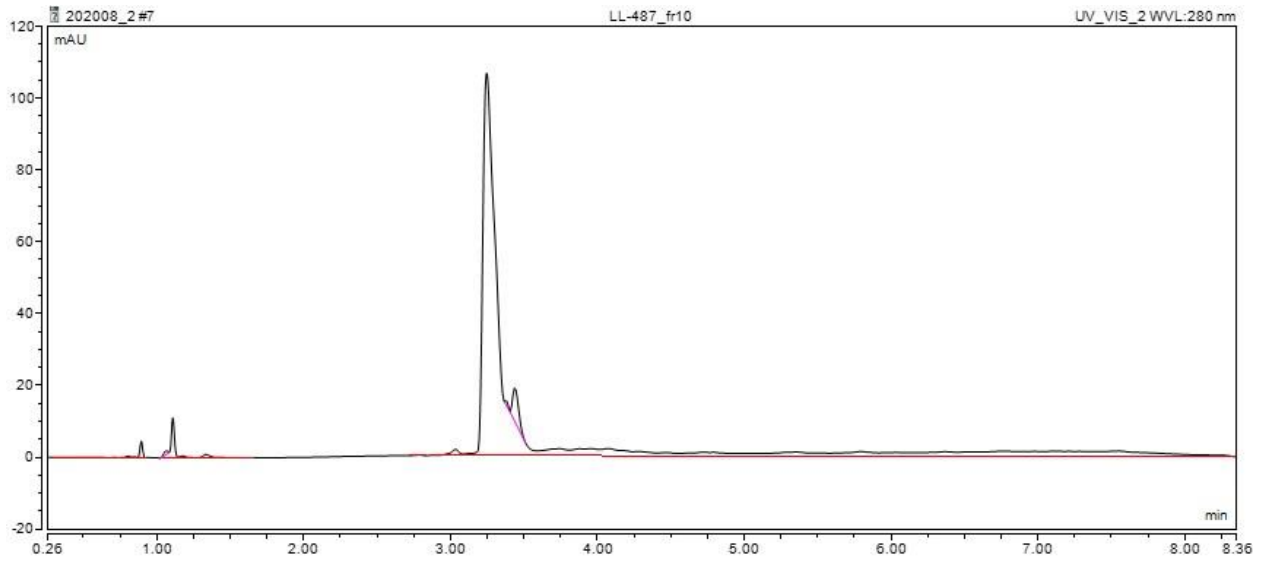
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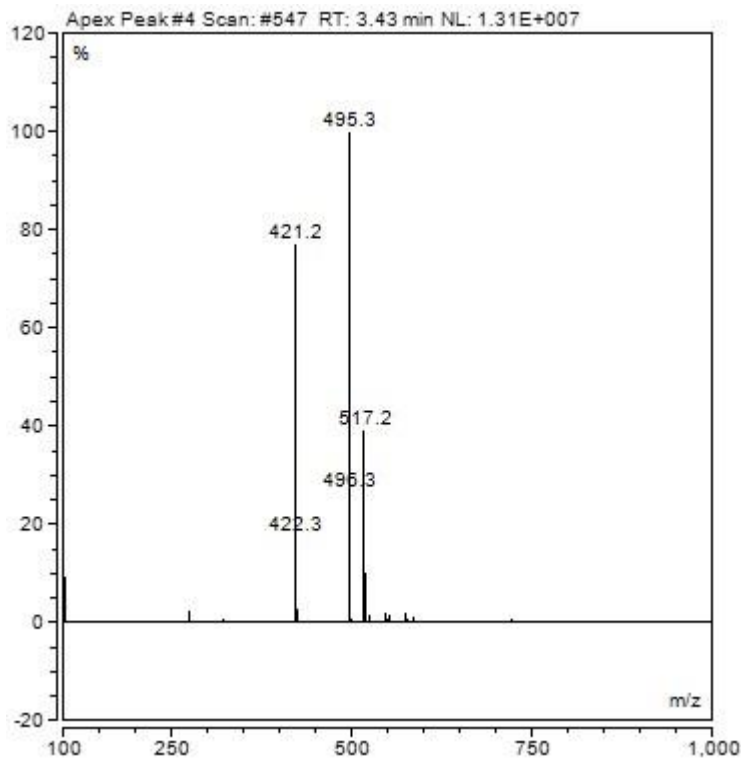
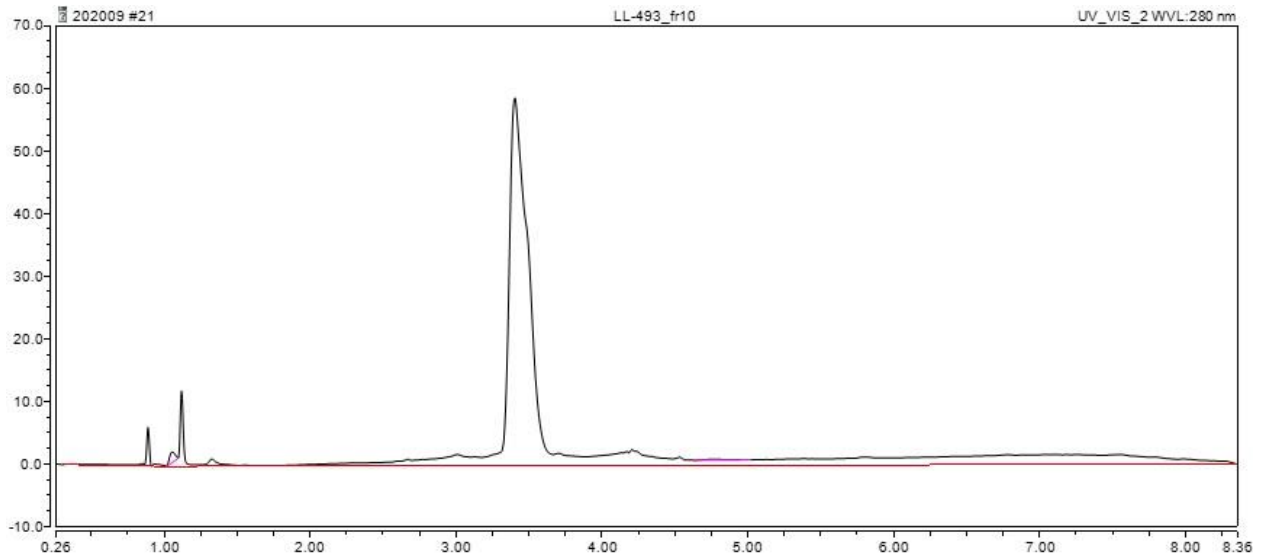
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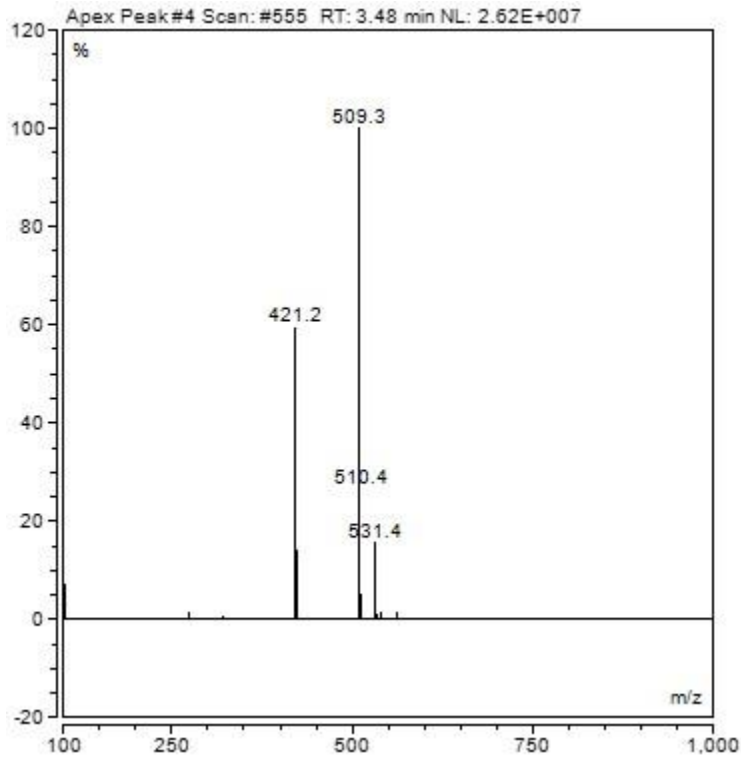
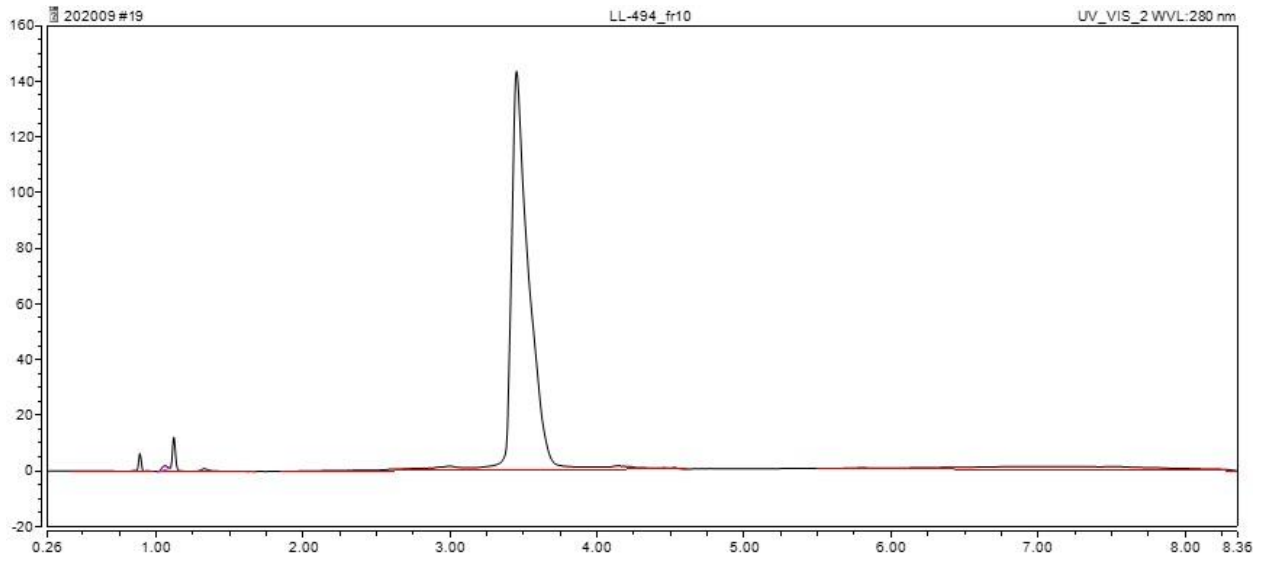
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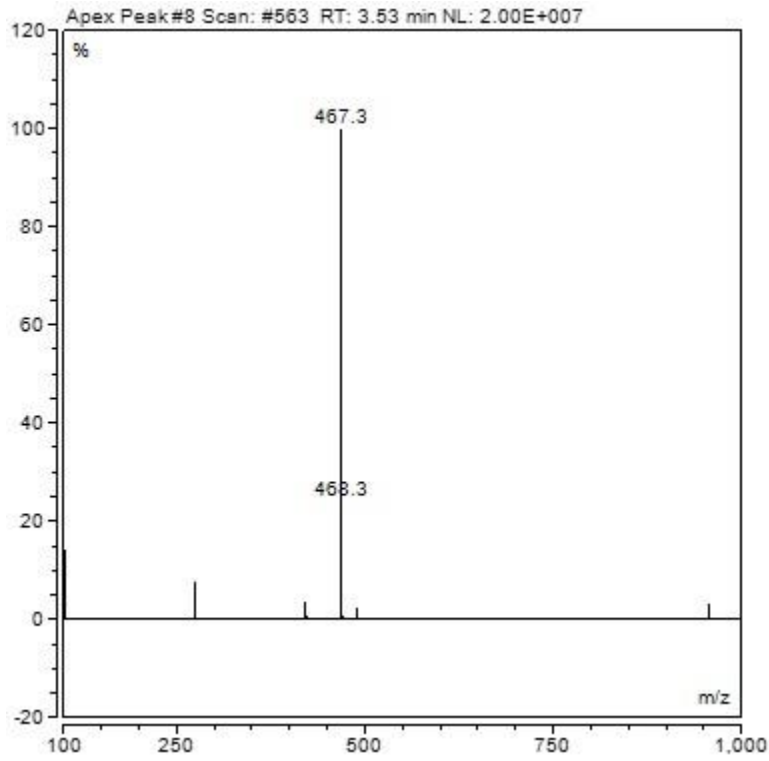
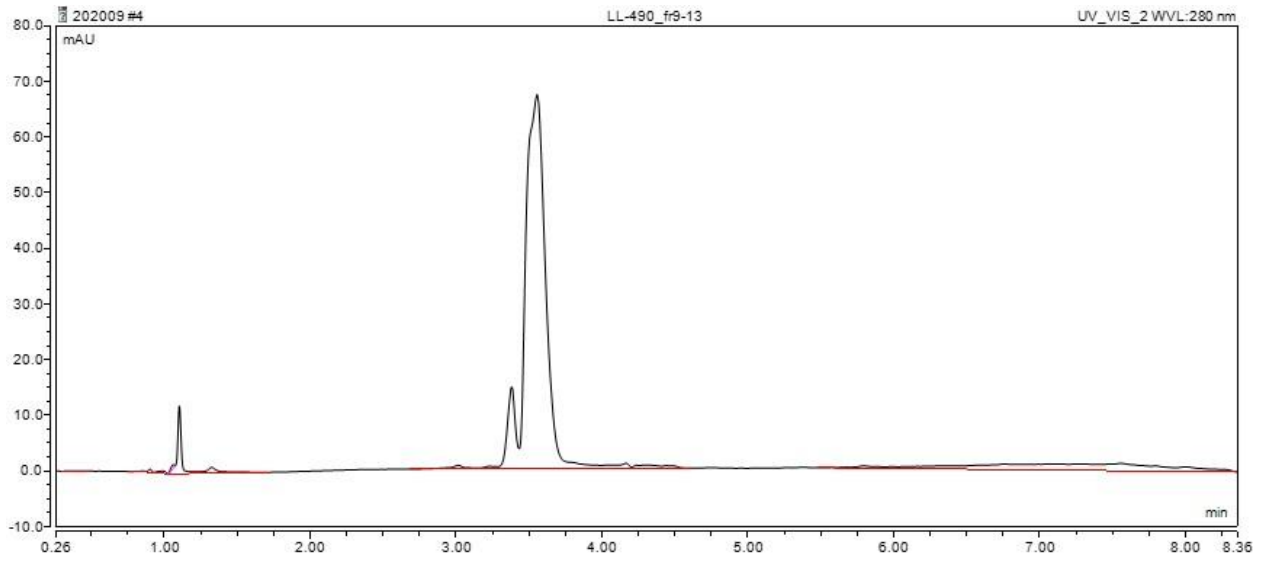
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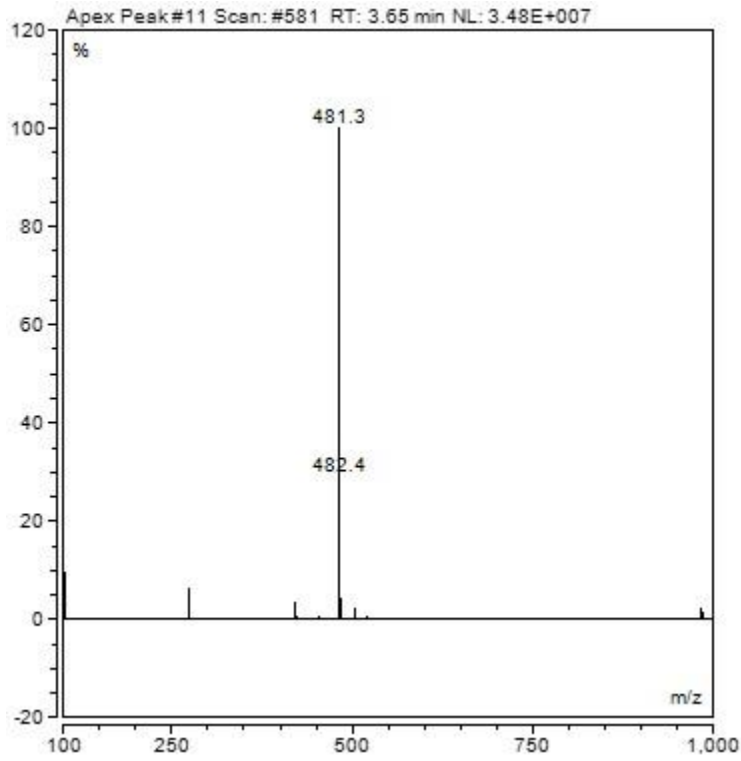
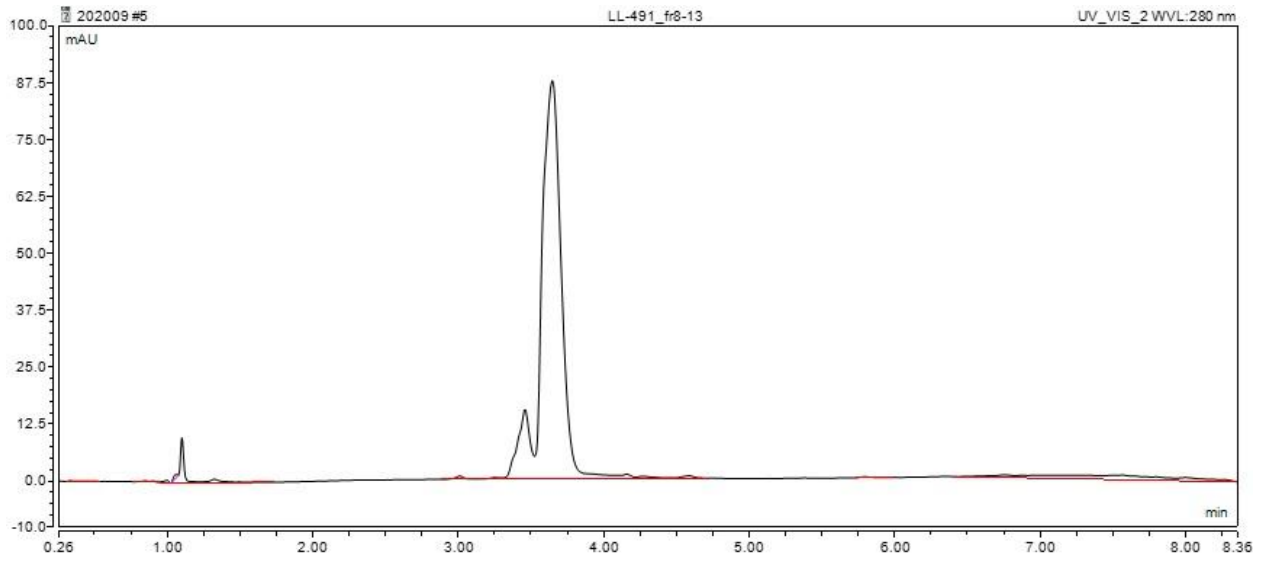
15: exact mass = 508.27



16: exact mass = 466.26



17: exact mass = 480.27



18: exact mass = 552.29

