

Synthesis, Structural Modification and Bioactivity Evaluation of Substituted Acridones as Potent Microtubule Affinity-Regulating Kinase 4 Inhibitors

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Table S1. Docking scores and interactions between MARK4 and synthesized acridones.

Compound	Binding score (Kcal/mol)	Hydrogen bonds	Other interacting residues
9a	-9.4	Ala135 (2.90 Å)	Ala83, Val70, Glu133, Val116, Met132, Ala195, Asn183, Glu182, Asp196, Gly63, Ile62, Gly138, Tyr134, Leu185
9b	-9.5	-	Ala135, Ala195, Ala83, Val116, Met132, Val70, Asp196, Lys85, Ala68, Lys69, Gly65, Gly63, Leu185, Glu139, Gly138, Ile62, Tyr134
9c	-10.0	Gly65 (3.09 Å)	Ala135, Ala195, Ala83, Glu133, Val116, Met132, Lys64, Gly63, Lys69, Lys85, Ala68, Val70, Asp196, Leu185, Glu139, Gly138, Ile62, Tyr134
9d	-9.5	Gly65 (3.08 Å)	Ala135, Ala195, Val116, Lys85, Ala83, Val70, Met132, Asp196, Ala68, Lys69, Lys64, Gly63, Leu185, Glu139, Gly138, Ile62, Tyr134
9e	-9.7	Gly65 (3.00 Å) Lys85 (3.07 Å)	Ala135, Ile62, Tyr134, Ala195, Ala83, Val116, Met132, Gly63, Val70, Ala68, Lys64, Lys69, Asp196, Lys85, Leu185, Glu139, Gly138
9f	-8.6	Ala135 (3.14 Å)	Ala135, Leu185, Gly138, Glu139, Glu182, Asn183, Asp196, Ala195, Val70, Val116, Ala83, Met132, Glu133, Lys85, Tyr134
9g	-9.5	-	Ala135, Leu185, Ala83, Glu133, Ala195, Val116, Met132, Gly63, Asp196, Lys64, Lys69, Gly65, Ala68, Lys85, Val70, Glu139, Gly138, Ile62, Tyr134
9h	-9.6	Gly65 (2.99 Å)	Ala135, Leu185, Ala83, Glu133, Ala195, Val116, Met132, Val70, Asp196, Lys69, Lys64, Ala68, Gly63, Glu139, Gly138, Ile62, Tyr134
9i	-9.9	Gly65 (3.08 Å)	Ala135, Ala195, Glu133, Ala83, Gly63, Met132, Val116, Lys85, Lys64, Asp196, Lys69, Ala68, Val70, Leu185, Glu139, Gly138, Ile62, Tyr134
10	-9.6	Ala135 (2.80 Å) Glu182 (2.01 Å) Asn183 (1.85 Å) Asp196 (2.75 Å)	Val70, Ala83, Glu133, Ala195, Met132, Val116, Gly63, Ile62, Gly138, Tyr134, Leu185
15a	-10.0	Ala135 (2.80 Å)	Val70, Ala83, Glu133, Val116, Ala195, Met132, Asn183, Glu182, Asp196, Gly65, Phe67, Ala68, Lys85, Gly63, Leu185, Ile62, Gly138, Tyr134
15b	-10.6	Ala135 (2.87 Å)	Ala83, Glu133, Val116, Val70, Ala195, Met132, Asn183, Glu182, Lys85, Ala68, Asn66, Gly65, Phe67, Ile87, Glu103, Gly198, Asp196, Gly63, Ile62, Leu185, Gly138, Tyr134
15c	-10.5	Ala135 (2.79 Å)	Ala83, Glu133, Val116, Val70, Ala195, Met132, Asn183, Glu182, Asp196, Lys85, Gly65, Ala68, Gly198, Glu103, Phe67, Gly63, Leu185, Ile62, Gly138, Tyr134
15d	-10.4	Ala135 (2.80 Å)	Ala83, Glu133, Val116, Val70, Ala195, Met132, Asn183, Glu182, Asp196, Lys85, Ala68, Gly65, Phe67, Gly198, Gly63, Leu185, Ile62, Gly138, Tyr134
15e	-10.3	Ala135 (2.80 Å)	Ala83, Glu133, Val116, Val70, Ala195, Met132, Asn183, Glu182, Asp196, Lys85, Gly65, Ala68, Phe67, Gly198, Gly63, Leu185, Ile62, Gly138, Tyr134
16a	-10.3	Ala135 (2.83 Å)	Val70, Glu133, Ala83, Leu185, Met132, Val116, Ala195, Gly63, Gly65, Lys64, Gly198, Asp178, Lys85, Glu182, Asp196, Tyr134, Gly138, Ile62
16c	-10.7	Ala135 (3.02 Å) Ala68 (3.66 Å)	Ala83, Val70, Glu133, Val116, Ala195, Gly63, Glu182, Asp196, Lys85, Phe67, Asn66, Ala68, Gly65, Ile62, Gly138, Tyr134, Leu185, Ala135
16b	-10.8	Ala135 (3.02 Å) Lys85 (3.24 Å)	Ala83, Glu133, Val116, Val70, Ala195, Gly63, Glu182, Gly198, Phe67, Gly65, Asn66, Asp196, Ala68, Ile62, Tyr134, Gly138, Leu185, Ala135
16d	-10.1	Ala135 (2.88 Å)	Val70, Ala83, Glu133, Val116, Ala195, Met132, Gly63, Gly65, Ala68, Glu182, Lys64, Asp196, Leu185, Gly138, Tyr134, Ile62
16e	-10.3	Ala135 (2.85 Å) Lys85 (3.36 Å) Asn66 (3.11 Å)	Ala83, Glu133, Ala195, Val116, Val70, Gly63, Met132, Ala68, Lys64, Gly65, Phe199, Asp178, Glu182, Asp196, Tyr134, Ile62, Gly138, Leu185
16f	-10.3	Ala135 (2.82 Å) Phe199 (3.38 Å)	Val70, Ala83, Glu133, Val116, Met132, Ala195, Gly63, Gly65, Lys64, Asp178, Gly198, Glu182, Asp196, Leu185, Tyr134, Gly138, Ile62
16g	-10.1	Ala135 (3.01 Å)	Ala83, Glu133, Val116, Ala195, Val70, Gly63, Glu182, Ala68, Gly65, Asn66, Phe67, Ser96, Leu92, Leu100, Ile87, Lys85, Asp196, Ile62, Gly138, Tyr134, Leu185, Ala135

Table S1 (Continued). Docking scores and interactions between MARK4 and synthesized acridones.

Compound	Binding score (Kcal/mol)	Hydrogen bonds	Other interacting residues
16h	-10.0	Ala135 (2.86 Å)	Val70, Ala83, Glu133, Val116, Ala195, Met132, Gly65, Ala68, Glu182, Asn183, Gly63, Asp196, Leu185, Gly138, Ile62, Tyr134
20	-9.9	Ala135 (3.80 Å) Asp196 (1.98 Å) Glu139 (2.62 Å)	Ala83, Glu133, Ala195, Val116, Glu182, Val70, Ala68, Lys85, Lys69, Gly65, Lys64, Glu139, Ile62, Gly63, Gly138, Tyr134, Leu185
23a	-10.5	Ala135 (2.85 Å) Asp196 (1.87 Å)	Ala83, Glu133, Val116, Met132, Ala195, Gly63, Glu139, Asp142, Lys64, Glu182, Gly138, Ala68, Lys85, Gly65, Lys69, Tyr134, Leu185, Ile62, Val70
23b	-10.6	Ala135 (2.80 Å) Asp196 (1.85 Å)	Leu185, Glu133, Ala83, Ala195, Met132, Val116, Glu182, Val70, Gly63, Lys85, Ala68, Lys69, Gly65, Lys64, Glu139, Asp142, Gly138, Tyr134, Ile62
23c	-10.3	Ala135 (2.87 Å) Asp196 (1.87 Å)	Ala83, Glu133, Val116, Met132, Ala195, Gly63, Glu139, Asp142, Lys64, Glu182, Gly138, Ala68, Lys85, Gly65, Lys69, Tyr134, Leu185, Ile62, Val70
23d	-10.4	Ala135 (2.85 Å) Asp196 (1.95 Å)	Ala83, Glu133, Val116, Met132, Ala195, Gly63, Glu139, Asp142, Ser136, Glu182, Lys64, Gly138, Ala68, Lys85, Gly65, Lys69, Leu185, Tyr134, Val70, Ile62, Ala135

Table S2. Druglikeness of synthesized acridones. (MW: Molecular Weight, MLogP: Lipophilicity, HBD: Hydrogen Bond Donor, HBA: Hydrogen Bond Acceptor, r.b.: rotatable bonds, TPSA: Topological Polar Surface Area)

Compound	MW (g/mol)	MLogP	HBD	HBA	r.b.	TPSA (Å ²)	Druglikeness	
							Lipinski	Veber
9a	299.37	3.78	0	1	2	22.00	Yes (0 violations)	Yes (0 violations)
9b	313.39	3.99	0	1	2	22.00	Yes (0 violations)	Yes (0 violations)
9c	367.36	4.58	0	4	3	22.00	Yes (1 violation)	Yes (0 violations)
9d	317.36	4.15	0	2	2	22.00	Yes (1 violation)	Yes (0 violations)
9e	335.35	4.53	0	3	2	22.00	Yes (1 violation)	Yes (0 violations)
9f	263.33	3.31	0	1	2	22.00	Yes (0 violations)	Yes (0 violations)
9g	355.47	4.63	0	1	3	22.00	Yes (1 violation)	Yes (0 violations)
9h	324.38	3.04	0	2	2	45.79	Yes (0 violations)	Yes (0 violations)
9i	344.36	2.63	0	3	3	67.82	Yes (0 violations)	Yes (0 violations)
10	314.38	3.16	1	1	2	48.02	Yes (0 violations)	Yes (0 violations)
15a	425.52	2.81	0	3	5	45.55	Yes (0 violations)	Yes (0 violations)
15b	481.63	3.59	0	3	6	45.55	Yes (0 violations)	Yes (0 violations)
15c	470.52	1.83	0	5	6	91.37	Yes (0 violations)	Yes (0 violations)
15d	450.53	2.13	0	4	5	69.34	Yes (0 violations)	Yes (0 violations)
15e	443.51	3.18	0	4	5	45.55	Yes (0 violations)	Yes (0 violations)
16a	473.95	3.07	0	3	5	62.62	Yes (0 violations)	Yes (0 violations)
16c	457.50	2.97	0	4	5	62.62	Yes (0 violations)	Yes (0 violations)
16b	457.50	2.97	0	4	5	62.62	Yes (0 violations)	Yes (0 violations)
16d	484.50	1.65	0	5	6	108.44	Yes (0 violations)	Yes (0 violations)
16e	510.54	1.71	0	5	7	108.44	Yes (1 violation)	Yes (0 violations)
16f	508.40	3.53	0	3	5	62.62	Yes (1 violation)	Yes (0 violations)
16g	575.50	4.10	0	9	7	62.62	Yes (1 violation)	Yes (0 violations)
16h	429.47	1.43	0	4	5	75.76	Yes (0 violations)	Yes (0 violations)
20	453.49	2.07	3	4	7	104.19	Yes (0 violations)	Yes (0 violations)
23a	542.63	3.07	3	3	9	95.99	Yes (1 violation)	Yes (0 violations)
23b	546.59	3.25	3	4	9	95.99	Yes (1 violation)	Yes (0 violations)
23c	563.05	3.34	3	3	9	95.99	Yes (1 violation)	Yes (0 violations)
23d	600.66	2.88	3	5	12	122.29	Yes (1 violation)	No (1 violation)

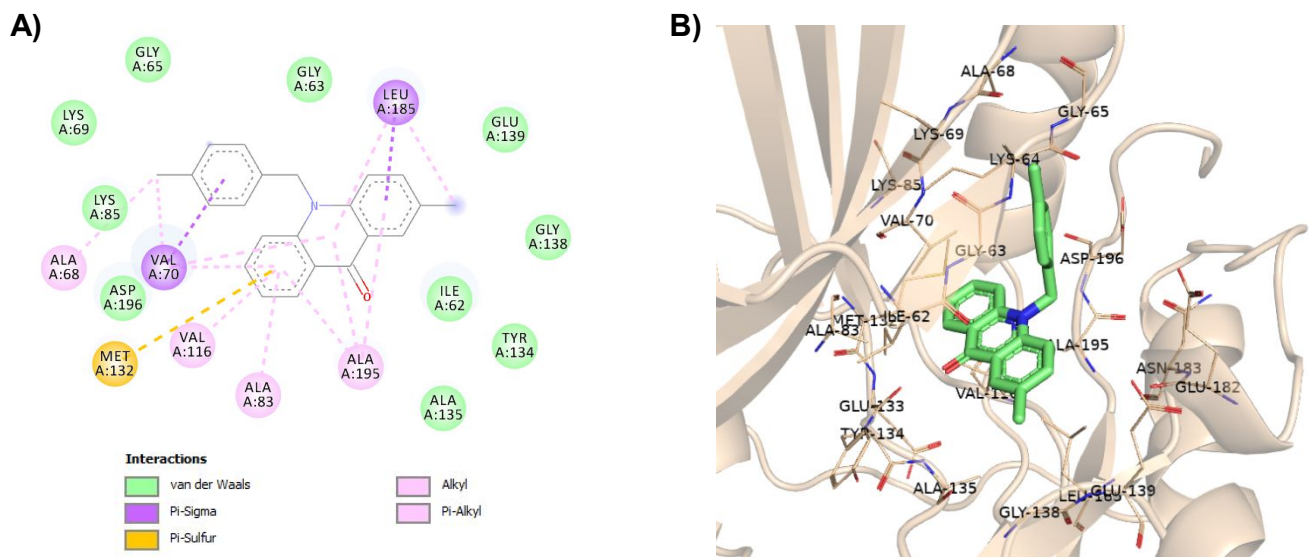


Figure S1. (A) 2D molecular docking model of compound **9b** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9b** in the active site of MARK4 (BIOVIA Discovery Studio).

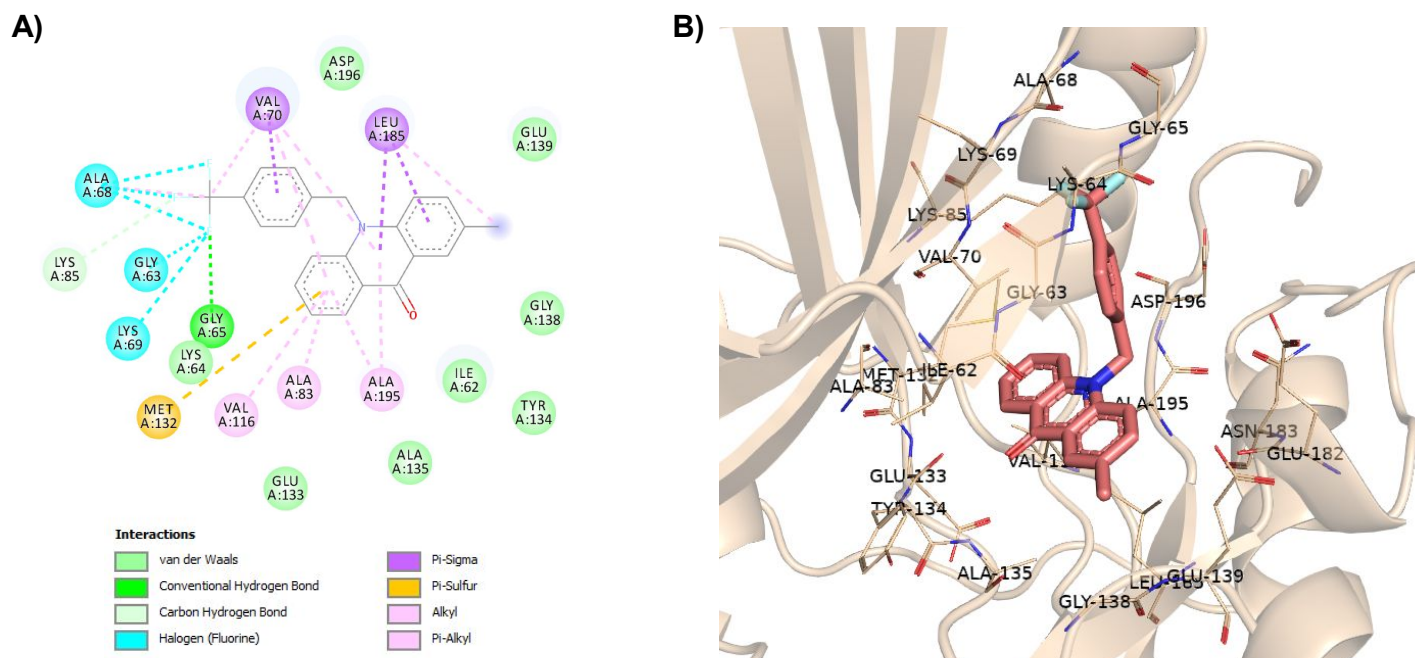


Figure S2. (A) 2D molecular docking model of compound **9c** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9c** in the active site of MARK4 (BIOVIA Discovery Studio).

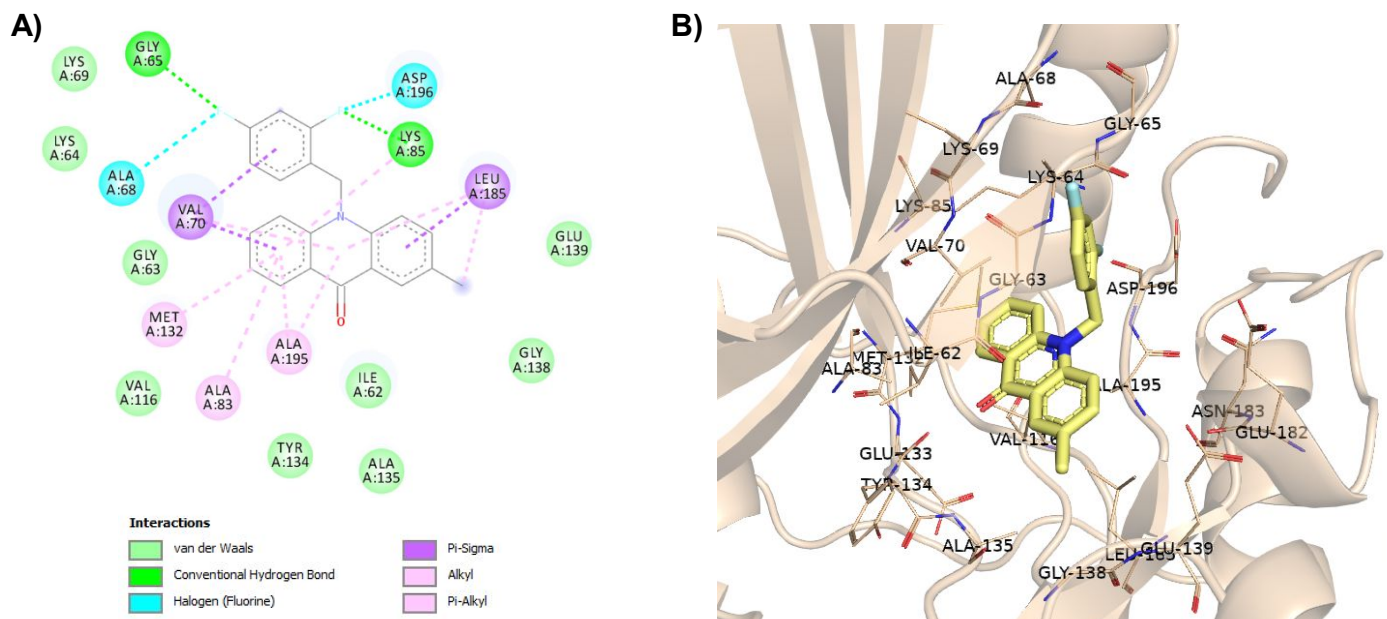


Figure S3. (A) 2D molecular docking model of compound **9e** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9e** in the active site of MARK4 (BIOVIA Discovery Studio).

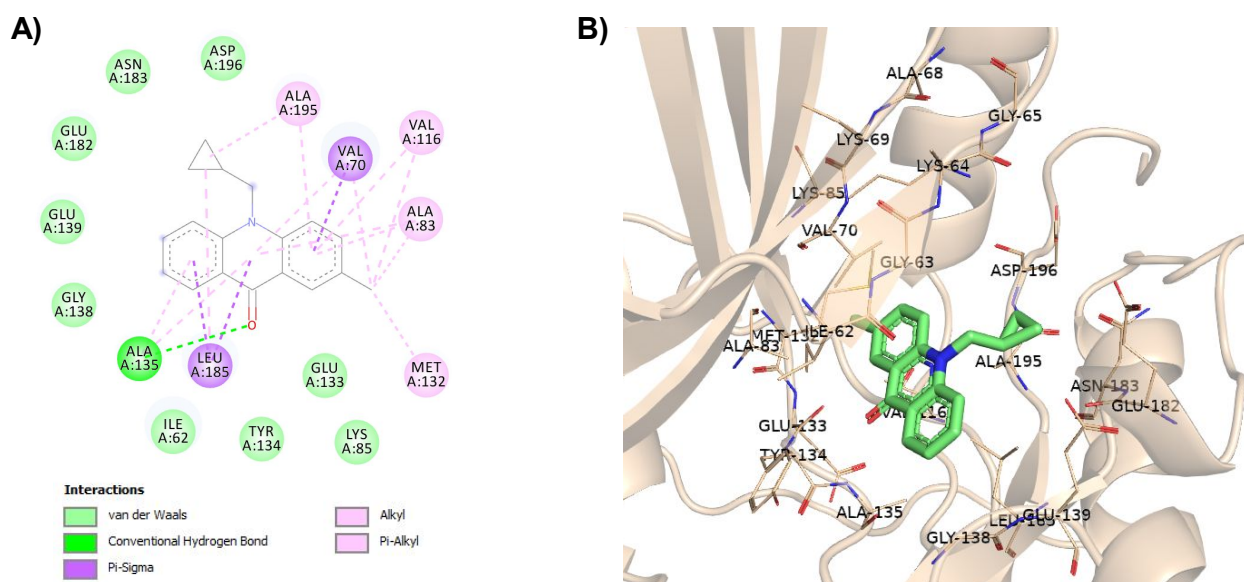


Figure S4. (A) 2D molecular docking model of compound **9f** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9f** in the active site of MARK4 (BIOVIA Discovery Studio).

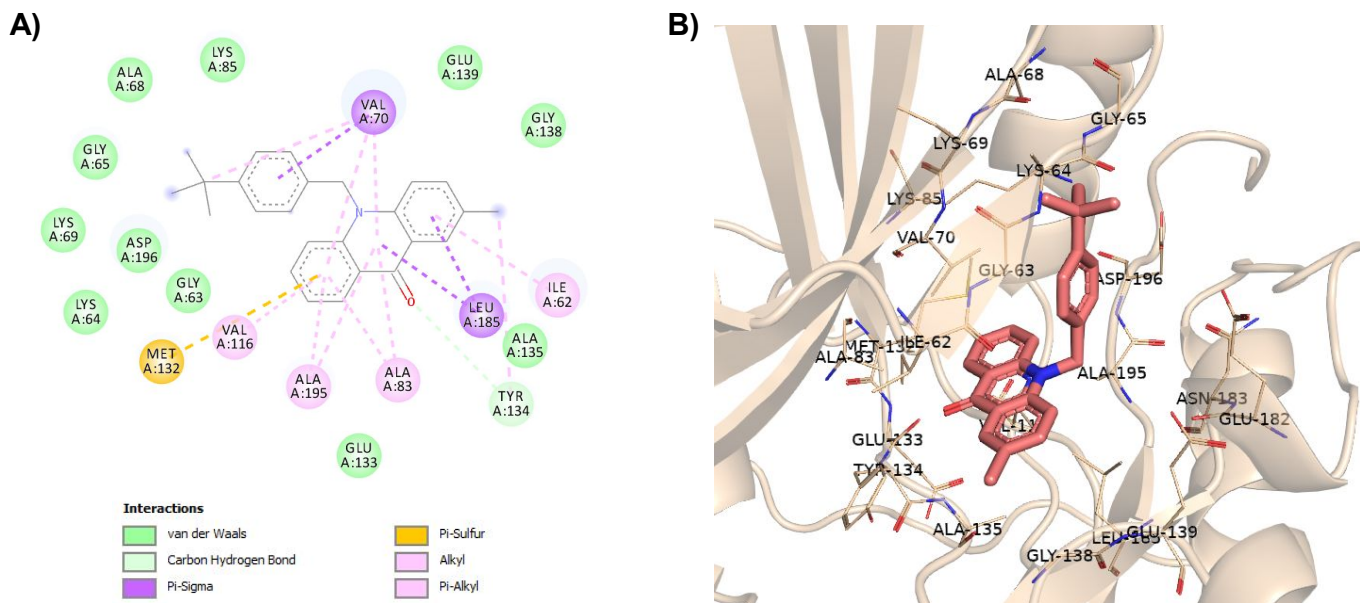


Figure S5. (A) 2D molecular docking model of compound **9g** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9g** in the active site of MARK4 (BIOVIA Discovery Studio).

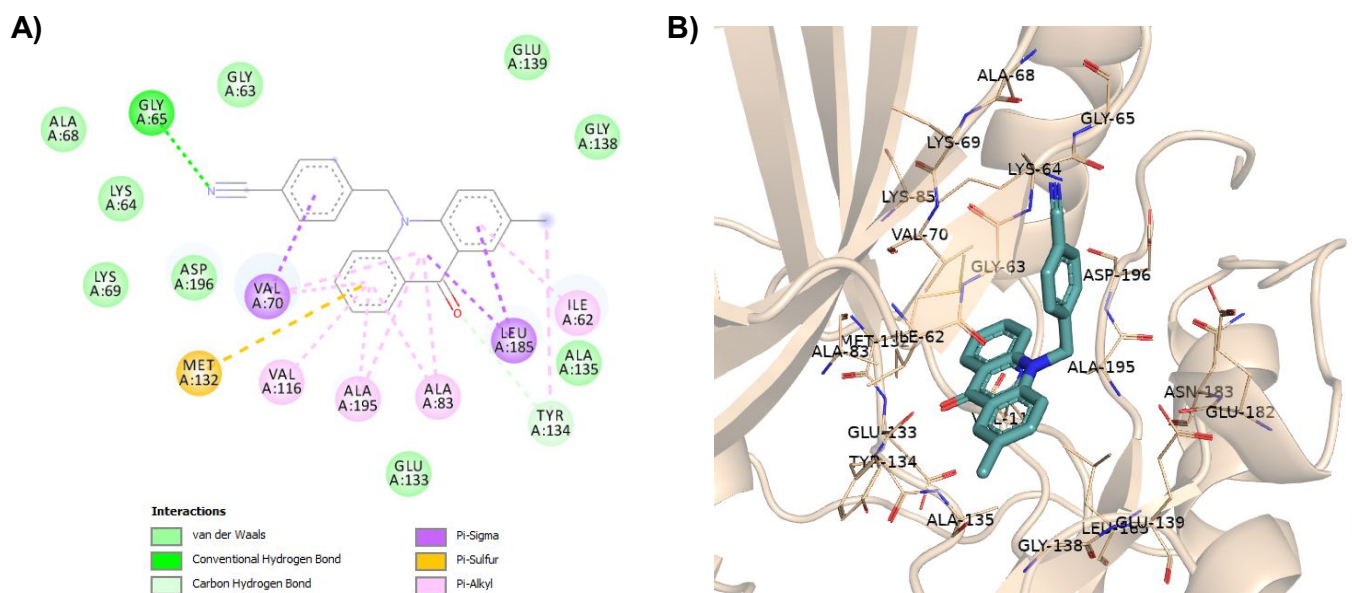


Figure S6. (A) 2D molecular docking model of compound **9h** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **9h** in the active site of MARK4 (BIOVIA Discovery Studio).

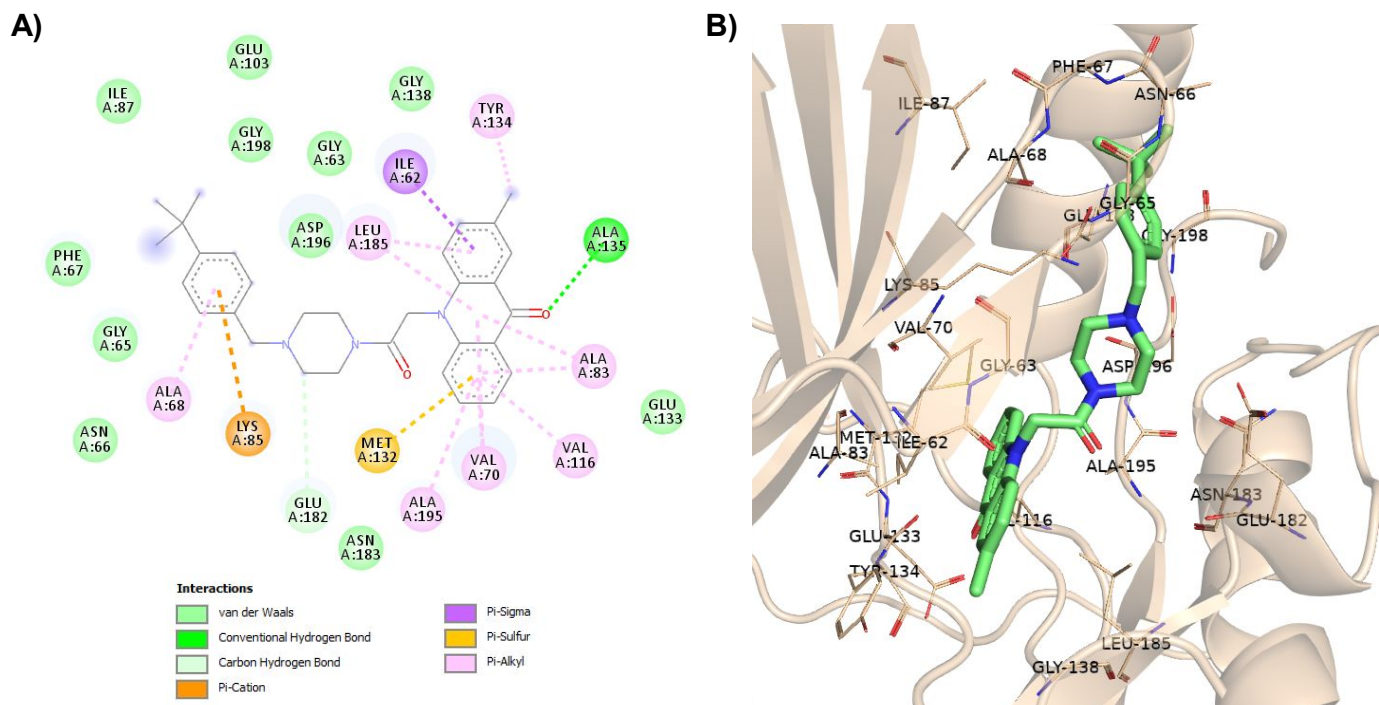


Figure S9. (A) 2D molecular docking model of compound **15b** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **15b** in the active site of MARK4 (BIOVIA Discovery Studio).

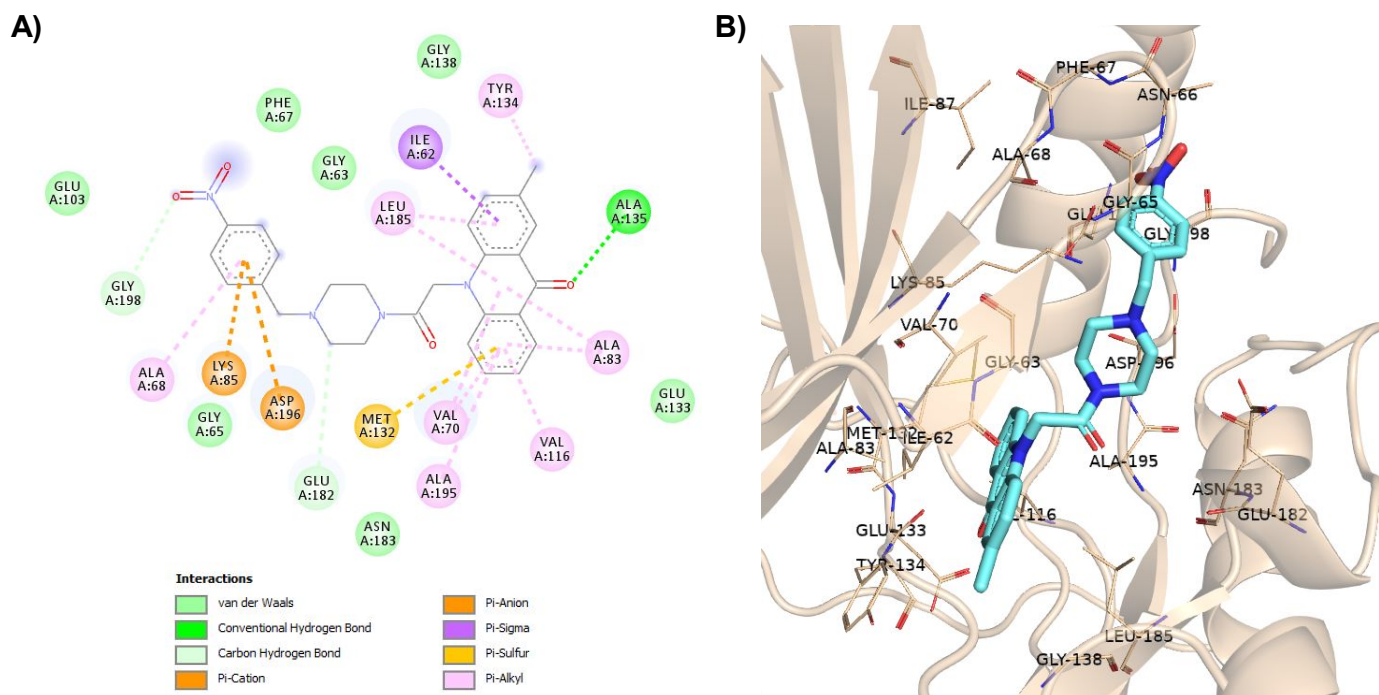


Figure S10. (A) 2D molecular docking model of compound **15c** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **15c** in the active site of MARK4 (BIOVIA Discovery Studio).

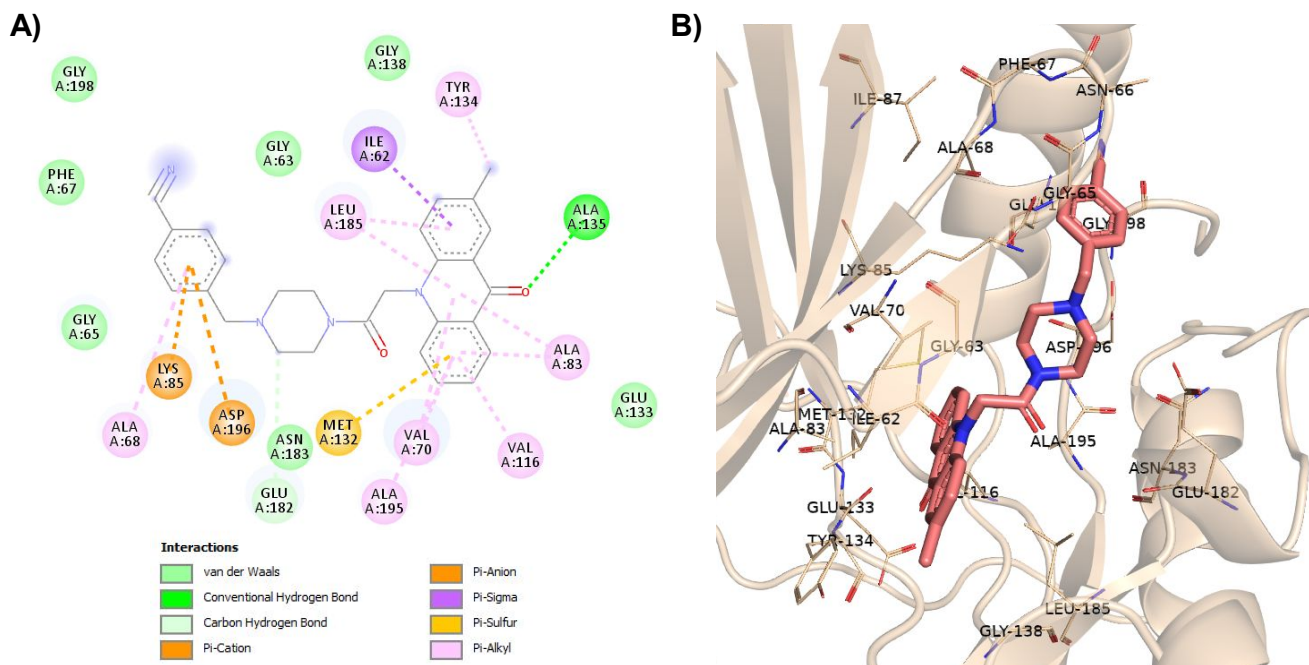


Figure S11. (A) 2D molecular docking model of compound **15d** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **15d** in the active site of MARK4 (BIOVIA Discovery Studio).

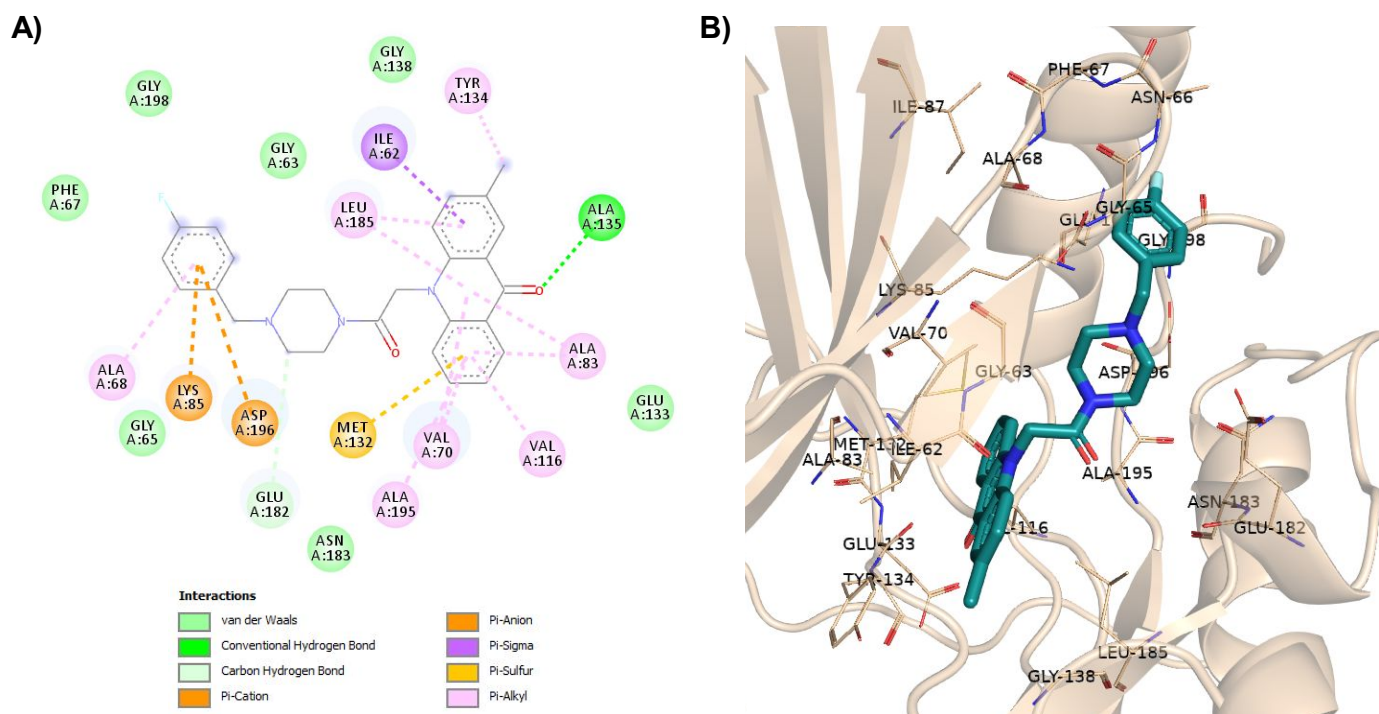


Figure S12. (A) 2D molecular docking model of compound **15e** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **15e** in the active site of MARK4 (BIOVIA Discovery Studio).

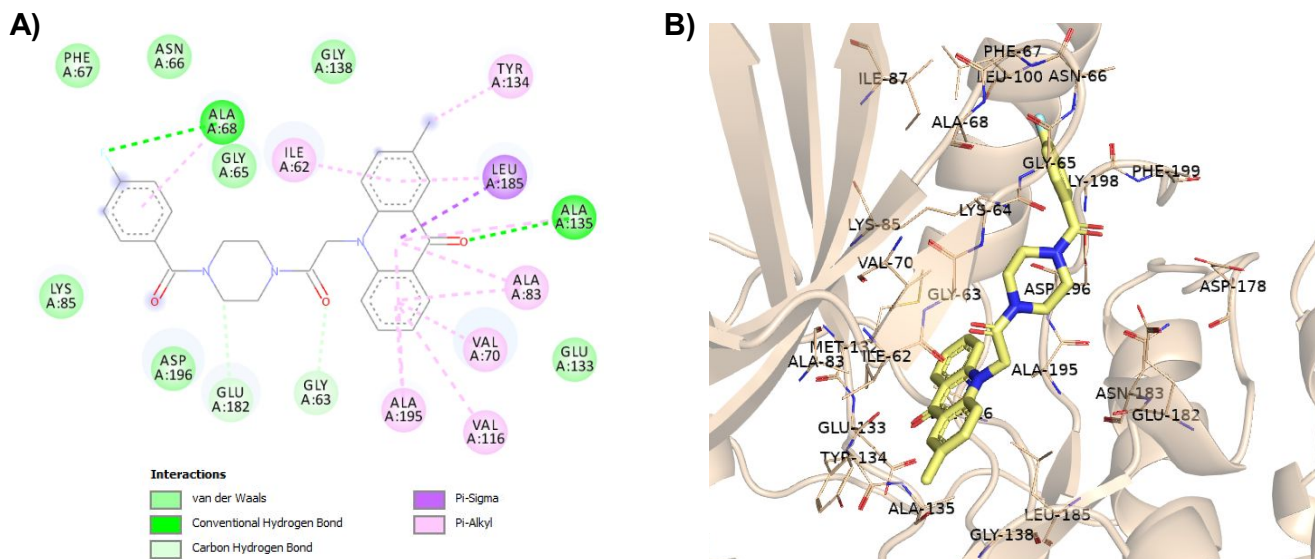


Figure S13. (A) 2D molecular docking model of compound **16c** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16c** in the active site of MARK4 (BIOVIA Discovery Studio).

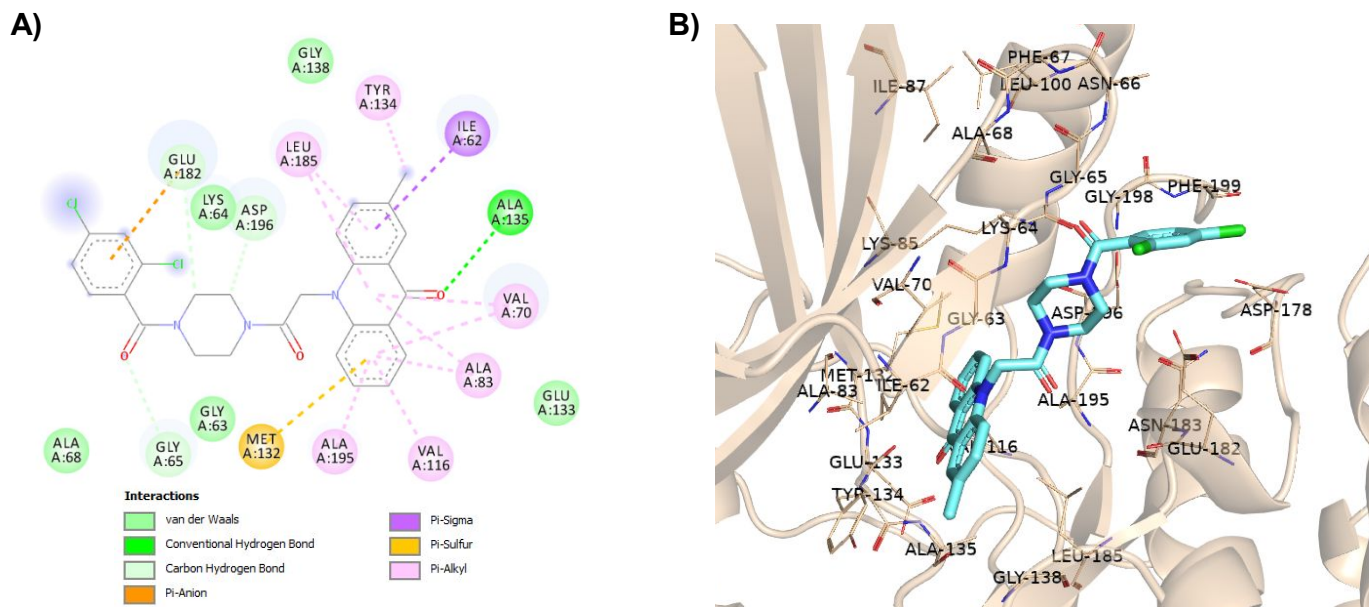


Figure S14. (A) 2D molecular docking model of compound **16d** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16d** in the active site of MARK4 (BIOVIA Discovery Studio).

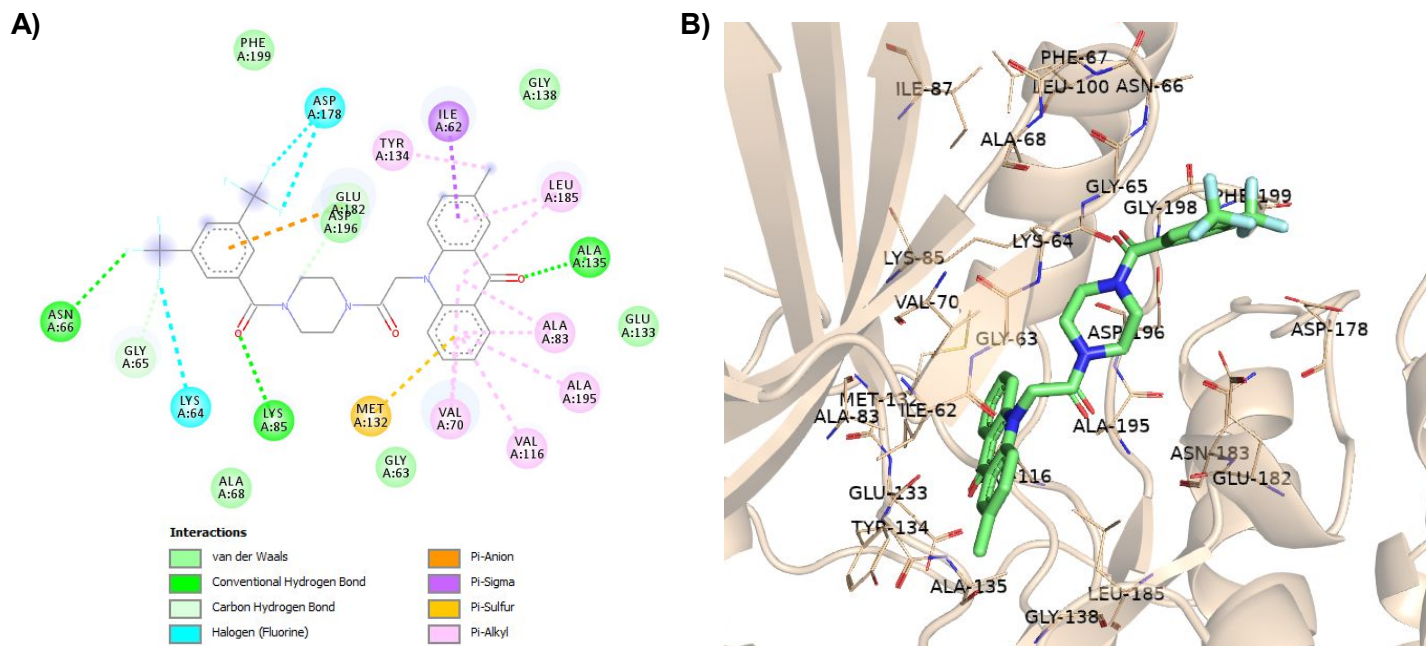


Figure S15. (A) 2D molecular docking model of compound **16e** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16e** in the active site of MARK4 (BIOVIA Discovery Studio).

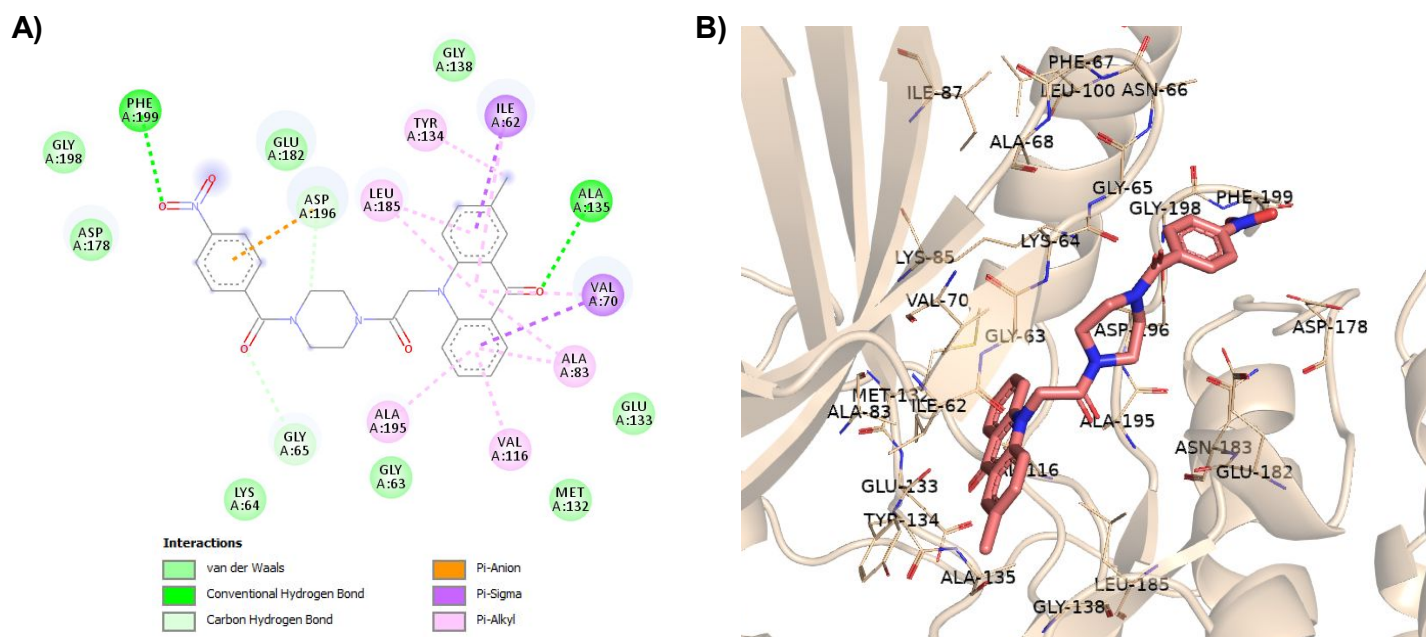


Figure S16. (A) 2D molecular docking model of compound **16f** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16f** in the active site of MARK4 (BIOVIA Discovery Studio).

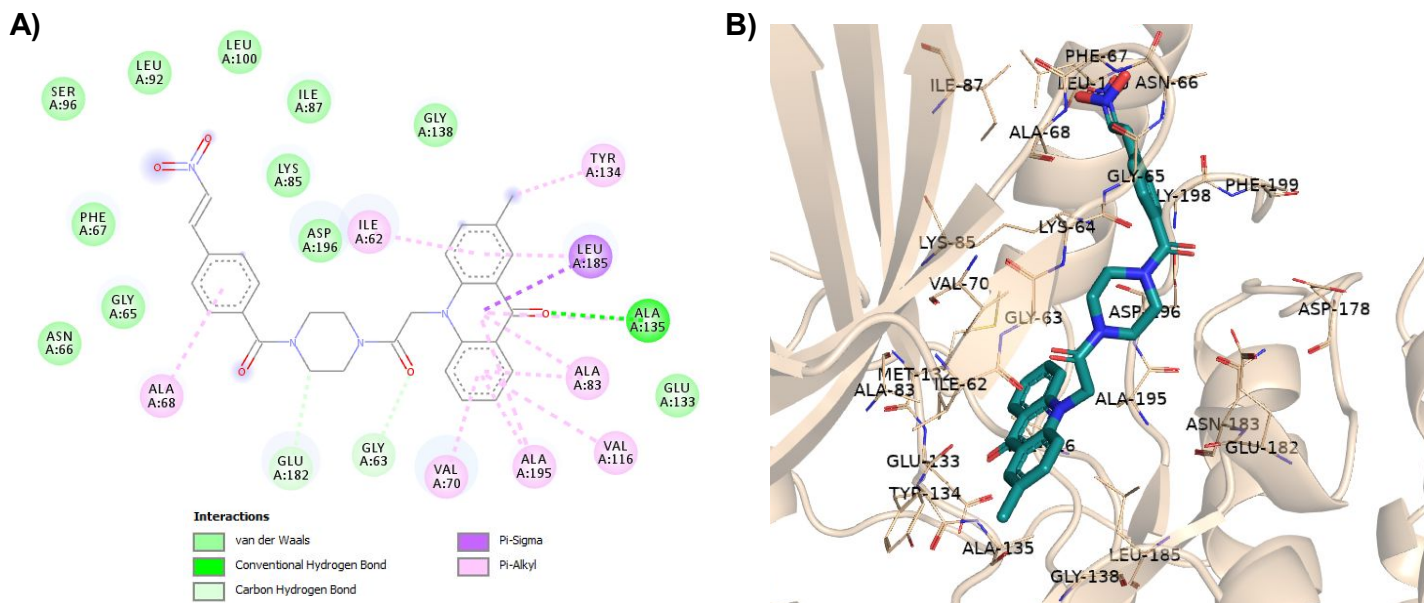


Figure S17. (A) 2D molecular docking model of compound **16g** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16g** in the active site of MARK4 (BIOVIA Discovery Studio).

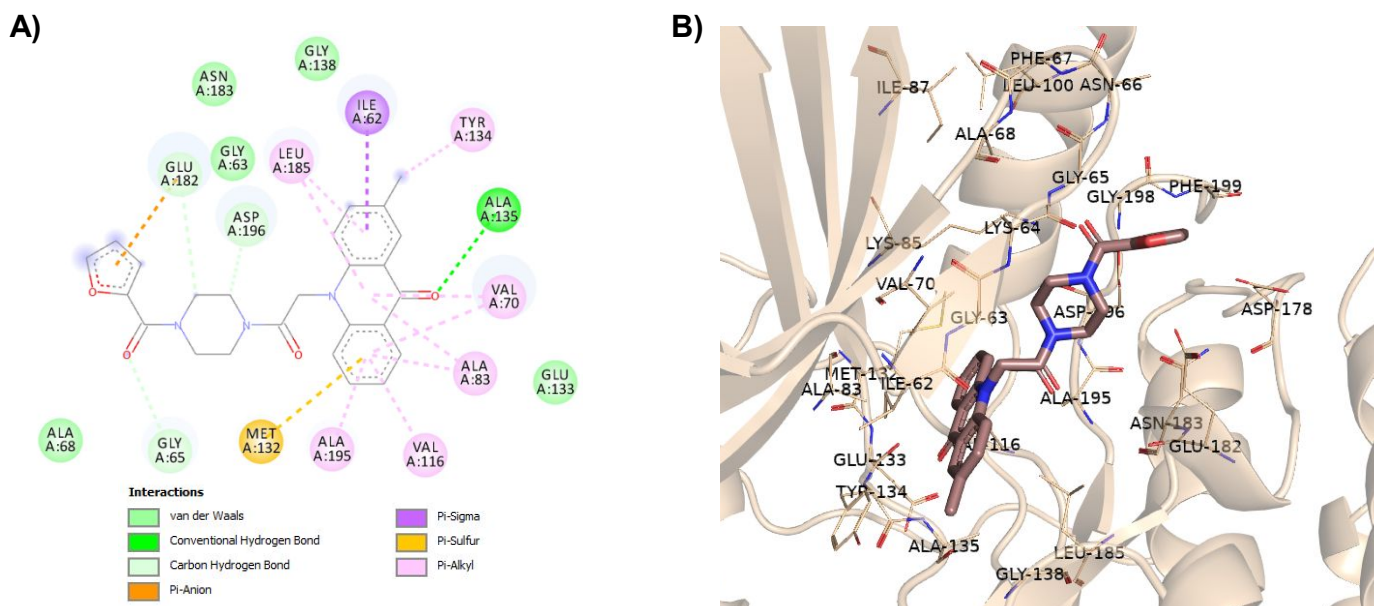


Figure S18. (A) 2D molecular docking model of compound **16h** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **16h** in the active site of MARK4 (BIOVIA Discovery Studio).

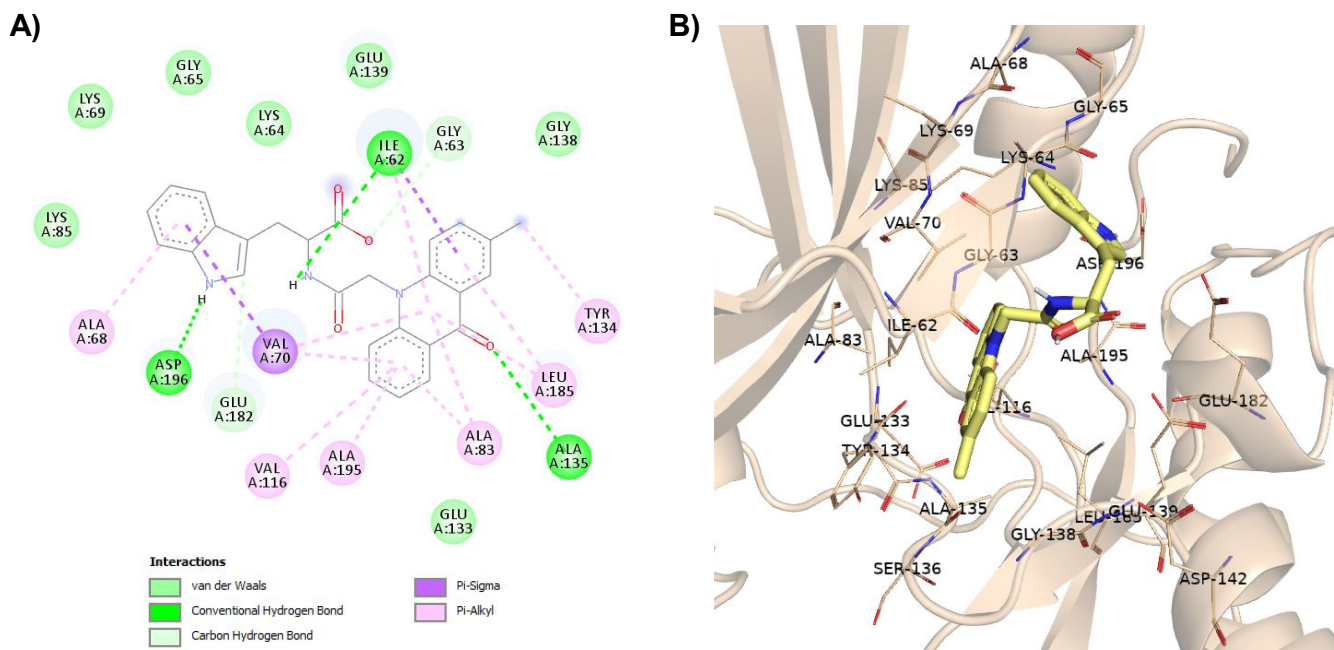


Figure S19. (A) 2D molecular docking model of compound **20** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **20** in the active site of MARK4 (BIOVIA Discovery Studio).

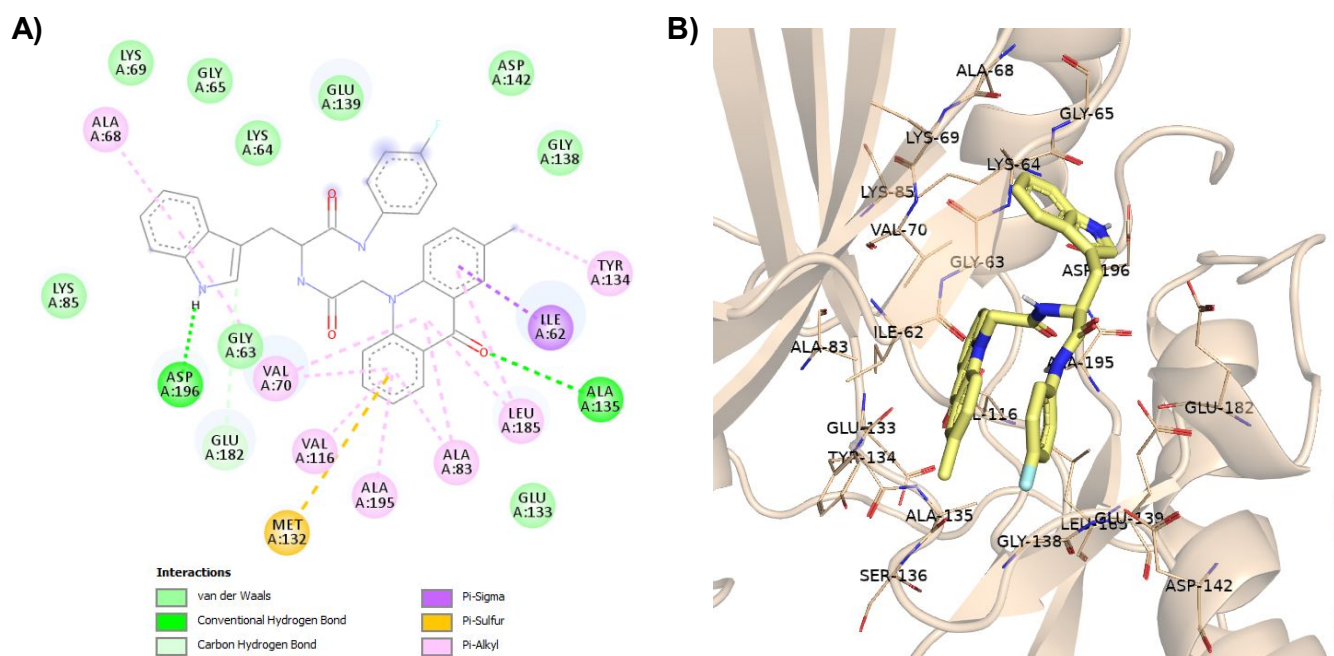
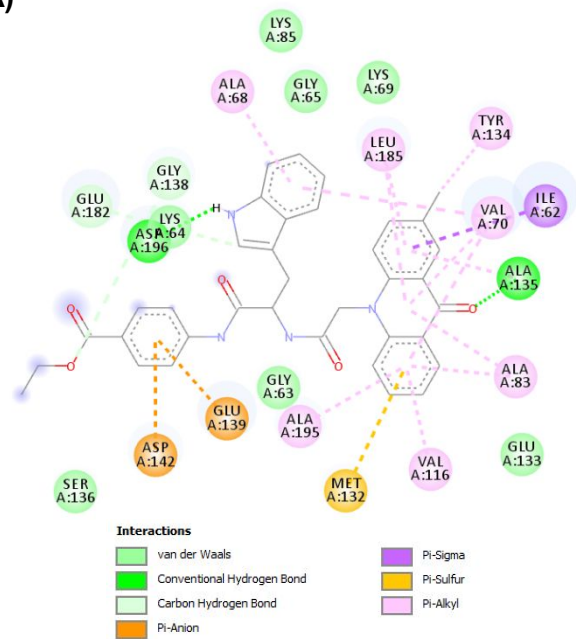


Figure S20. (A) 2D molecular docking model of compound **23b** in the active site of MARK4 (PDB code: 5ES1). **(B)** 3D model of the interaction between compound **23b** in the active site of MARK4 (BIOVIA Discovery Studio).

A)



B)

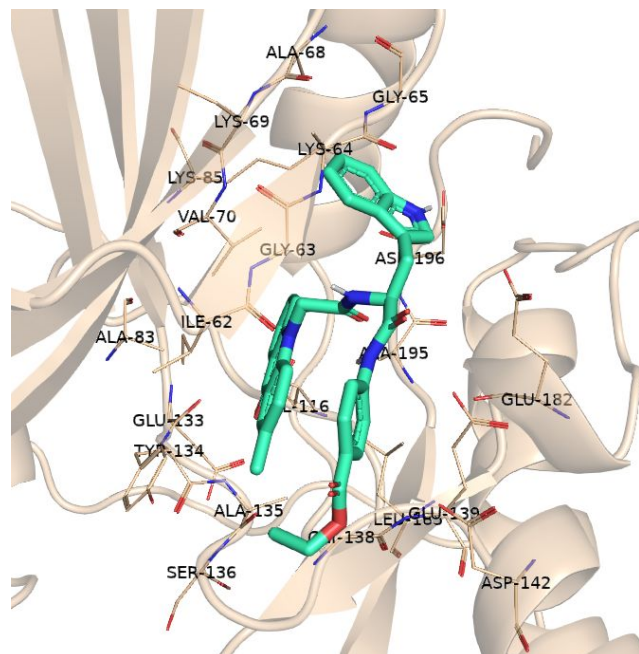


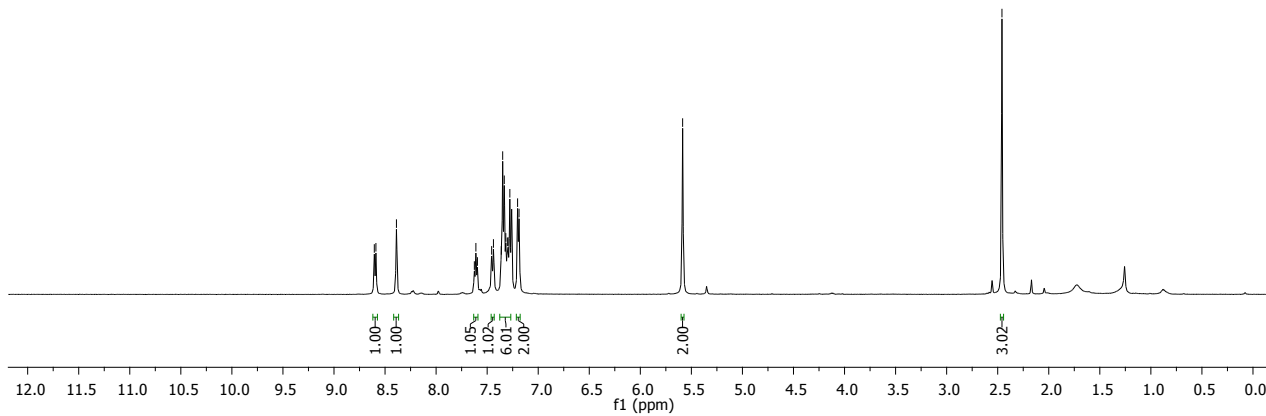
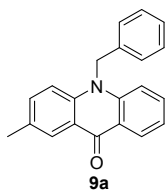
Figure S21. (A) 2D molecular docking model of compound **23d** in the active site of MARK4 (PDB code: 5E51). **(B)** 3D model of the interaction between compound **23d** in the active site of MARK4 (BIOVIA Discovery Studio).

acr04

8.61
8.39
8.29
7.63
7.61
7.60
7.46
7.44
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7.32
7.30
7.28
7.20
7.19

5.59

2.46



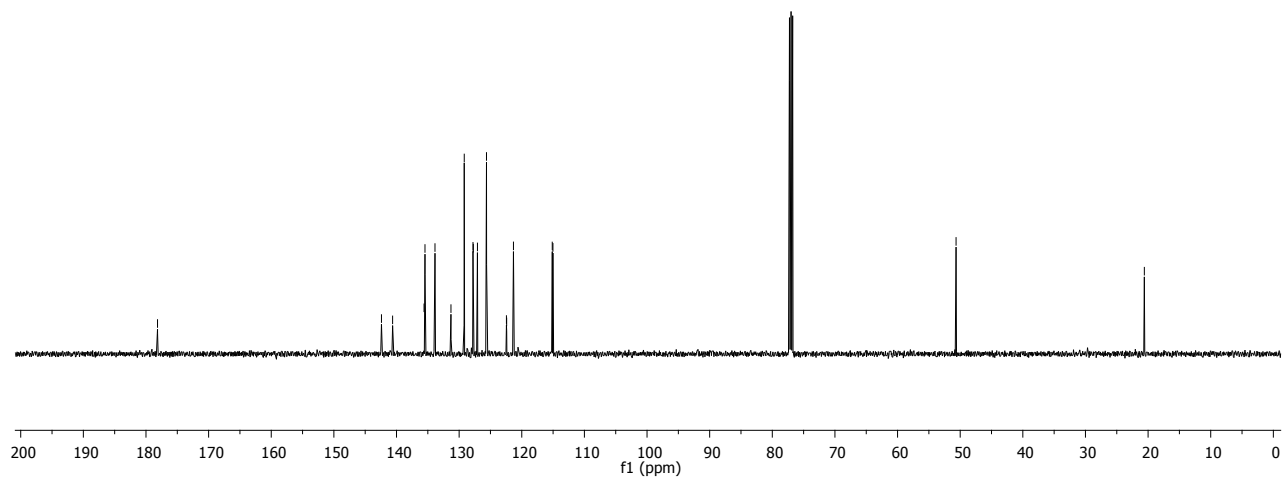
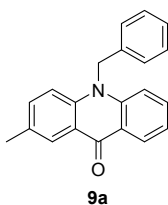
acr04 carbon

178.16

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115.13
115.02

50.66

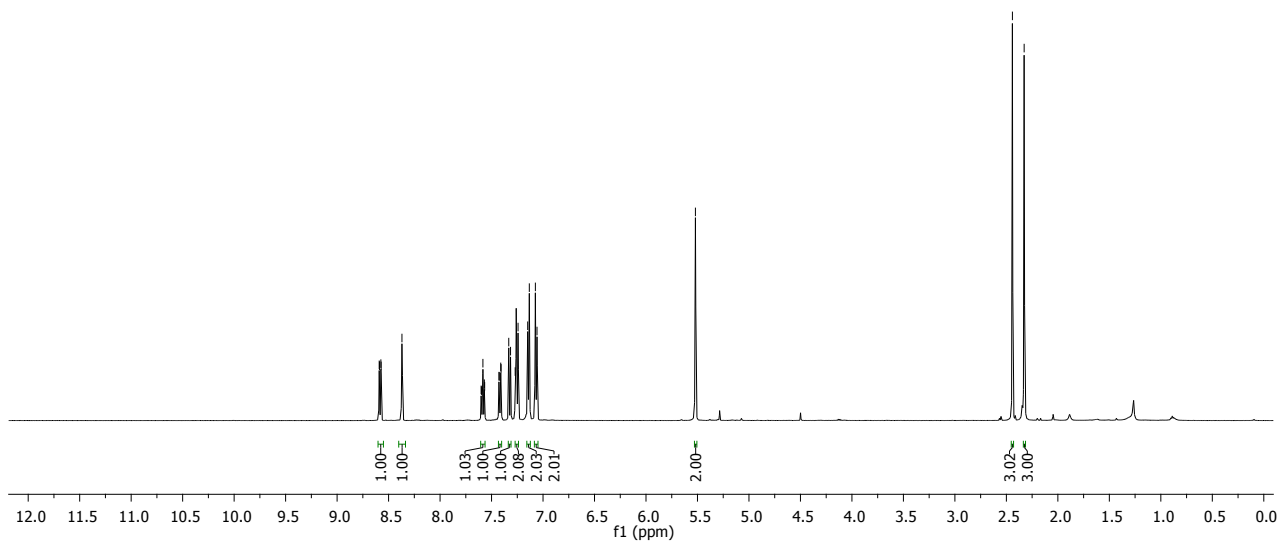
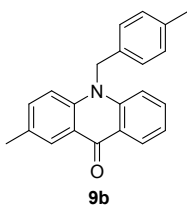
20.60



acr05

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7.07
7.06
5.52

2.44
2.33



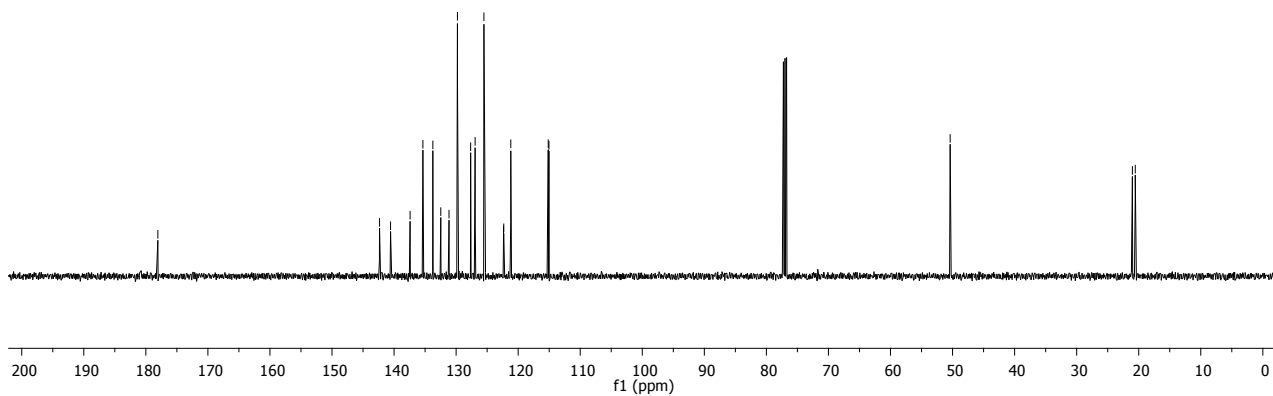
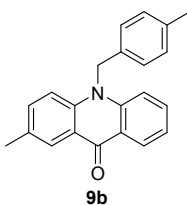
acr05 carbon

178.06

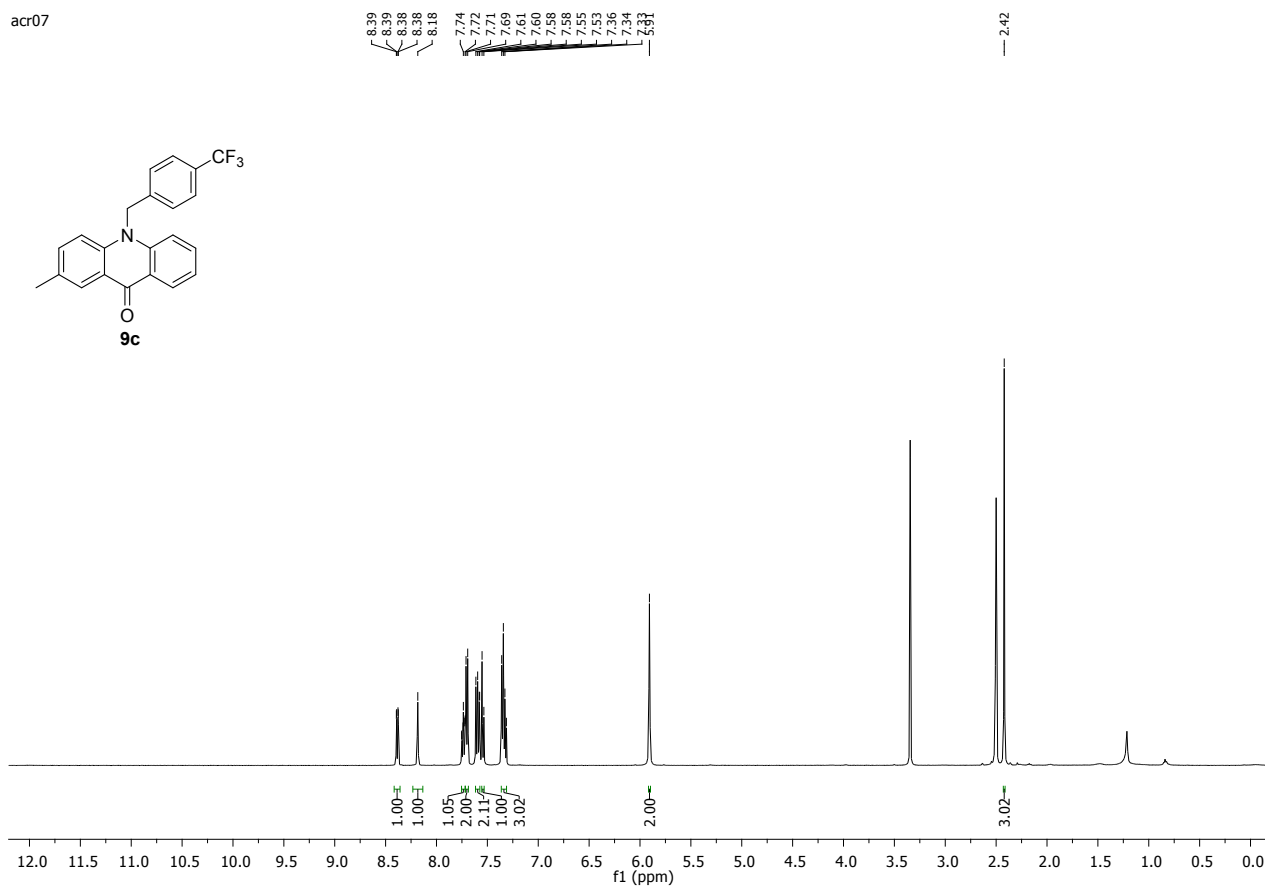
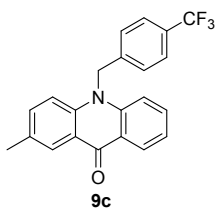
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122.32
121.19
115.16
115.04

50.38

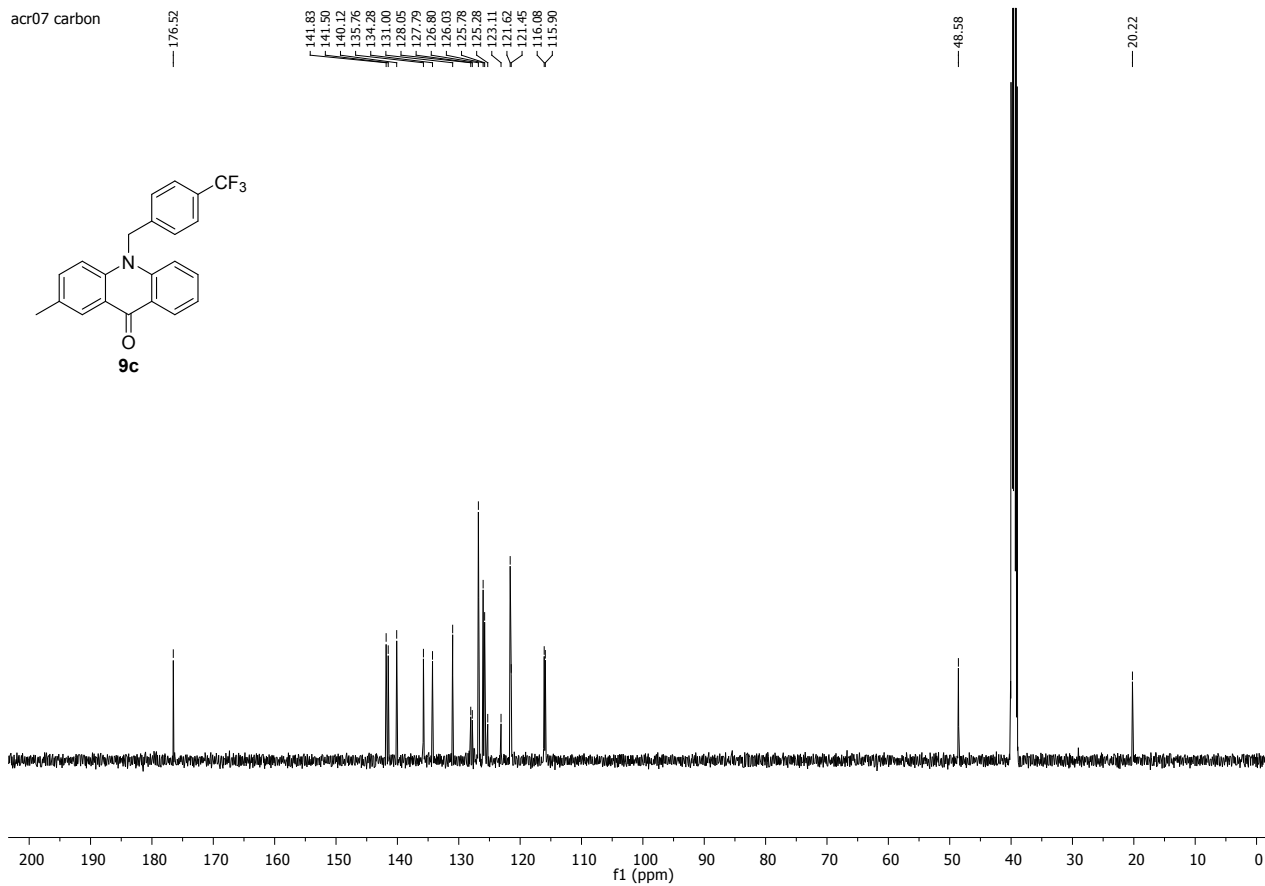
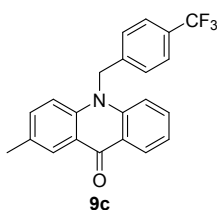
21.02
20.56



acr07



acr07 carbon

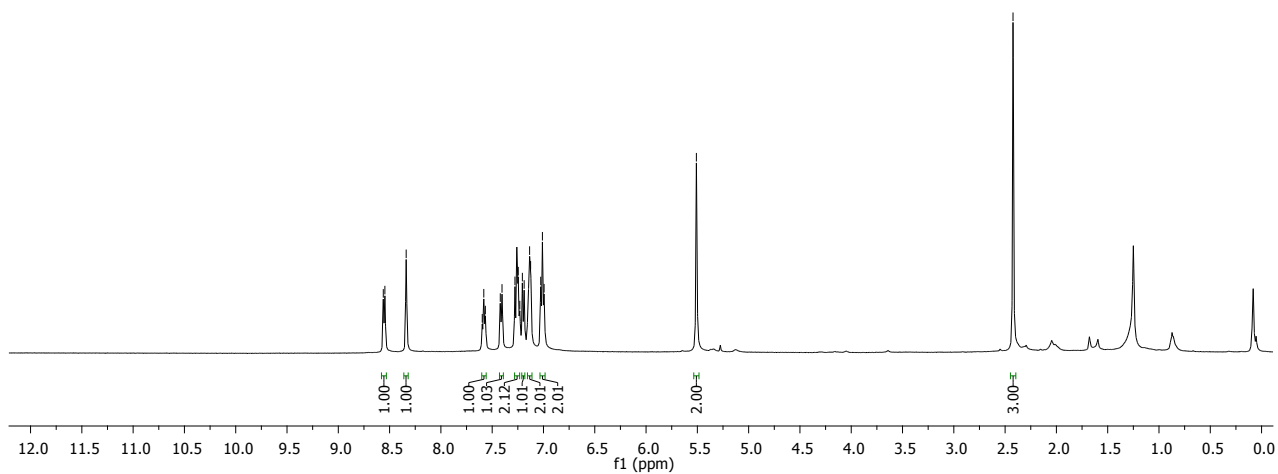
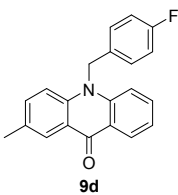


acr08

8.56
8.55
8.34
7.60
7.58
7.57
7.42
7.40
7.28
7.25
7.23
7.21
7.19
7.13
7.03
7.01
6.99

5.51

2.42



acr08 carbon

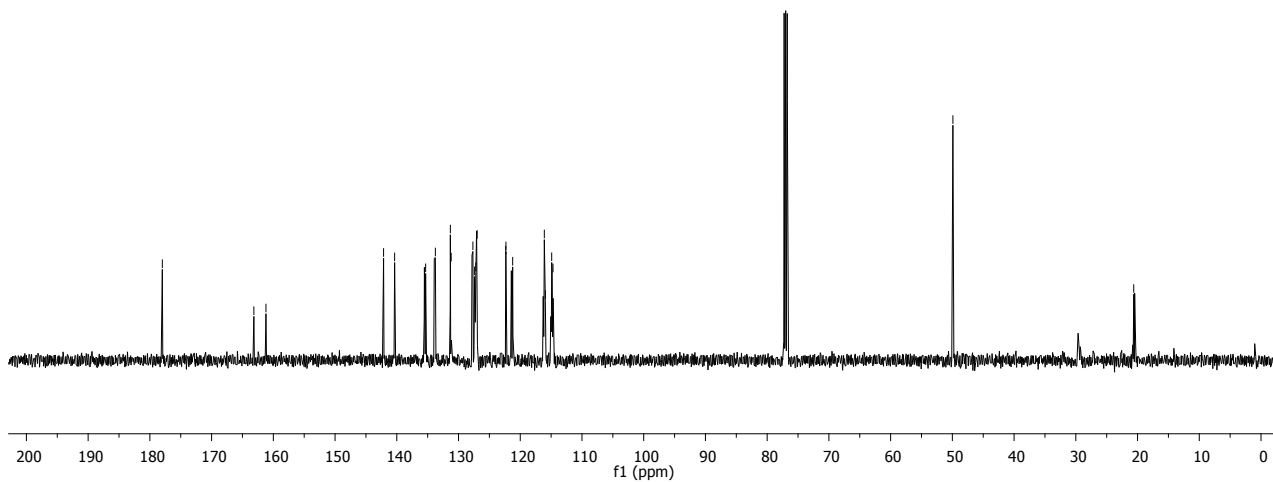
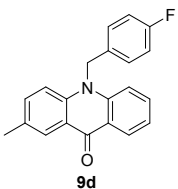
177.98

163.15
161.19

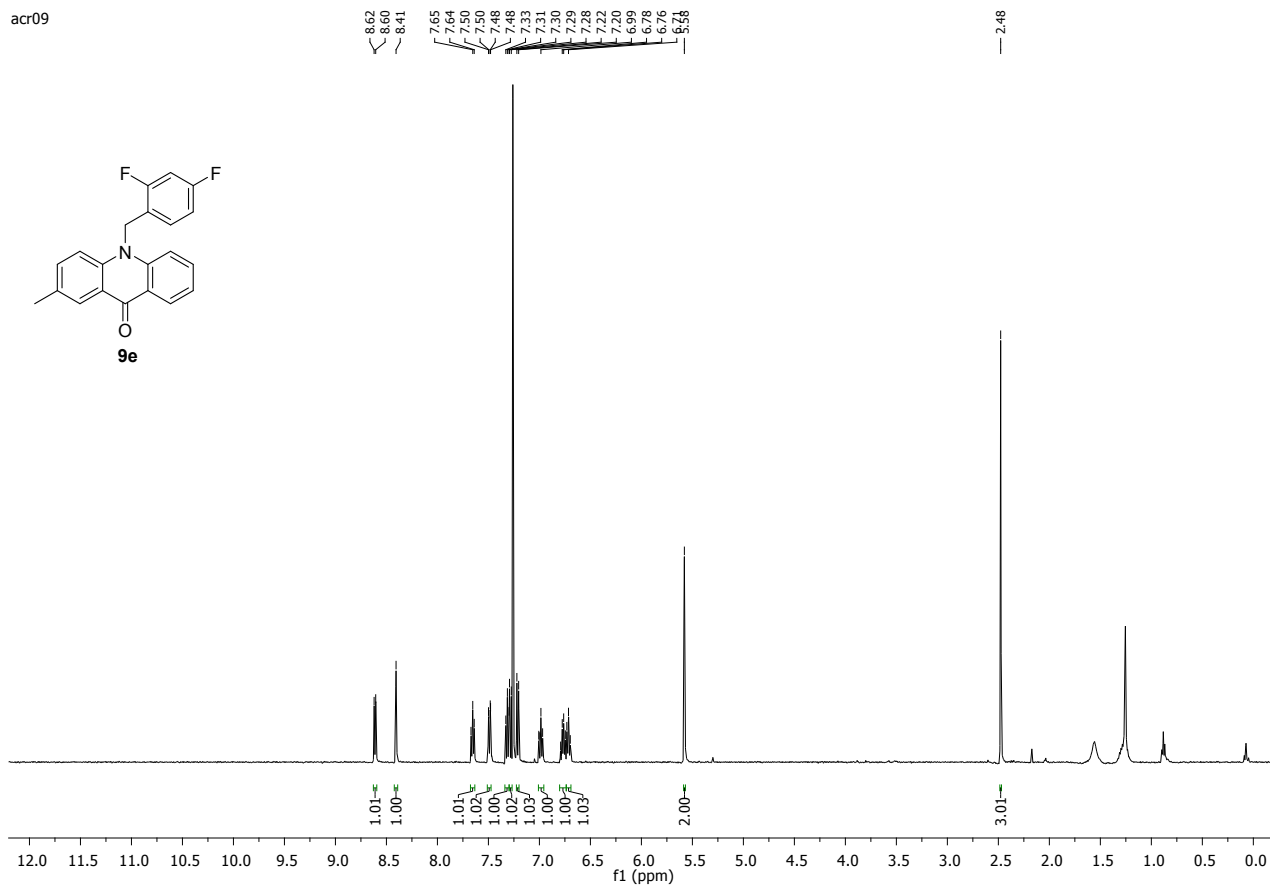
142.14
140.35
133.75
131.32
131.19
127.67
126.98
122.35
122.32
118.10
115.94
114.90
114.70

49.91

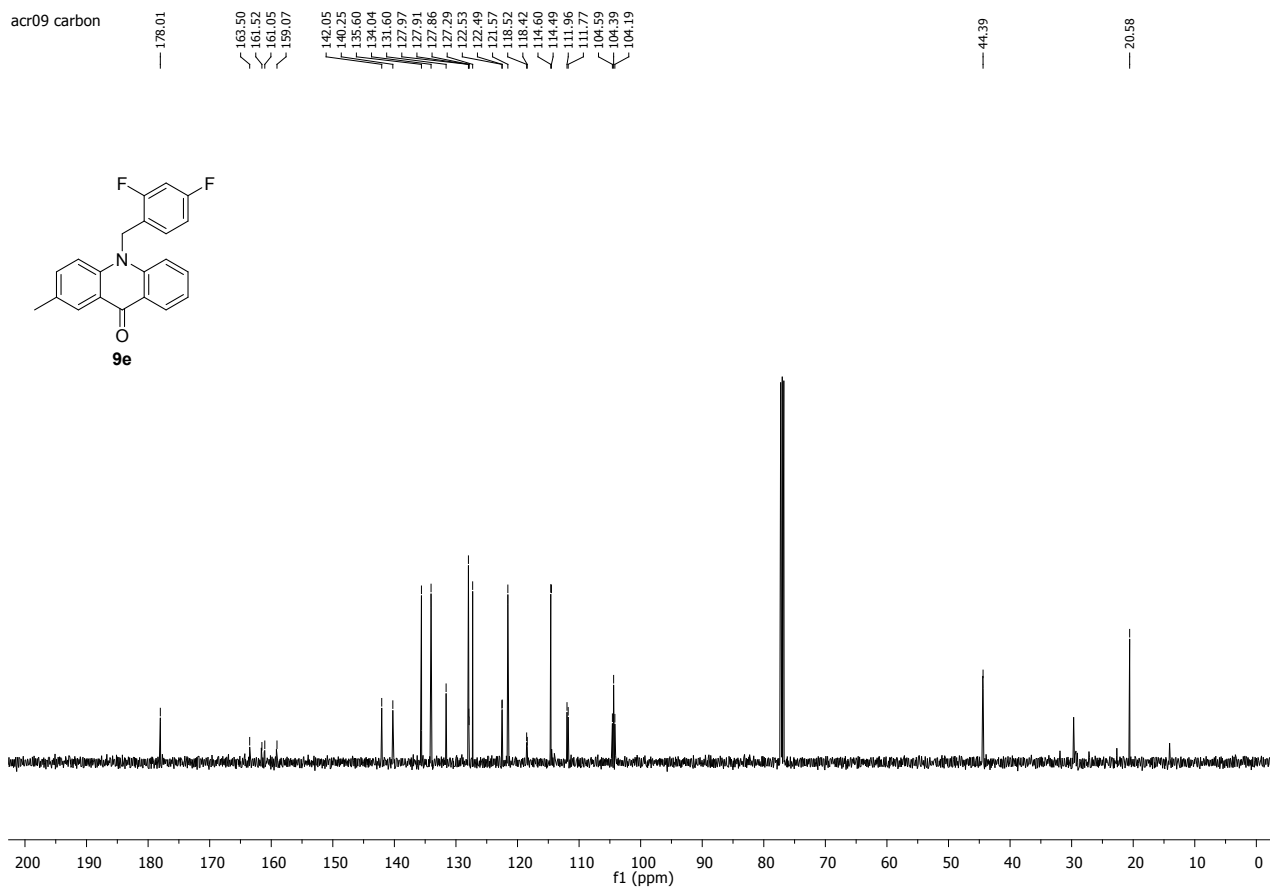
20.62



acr09

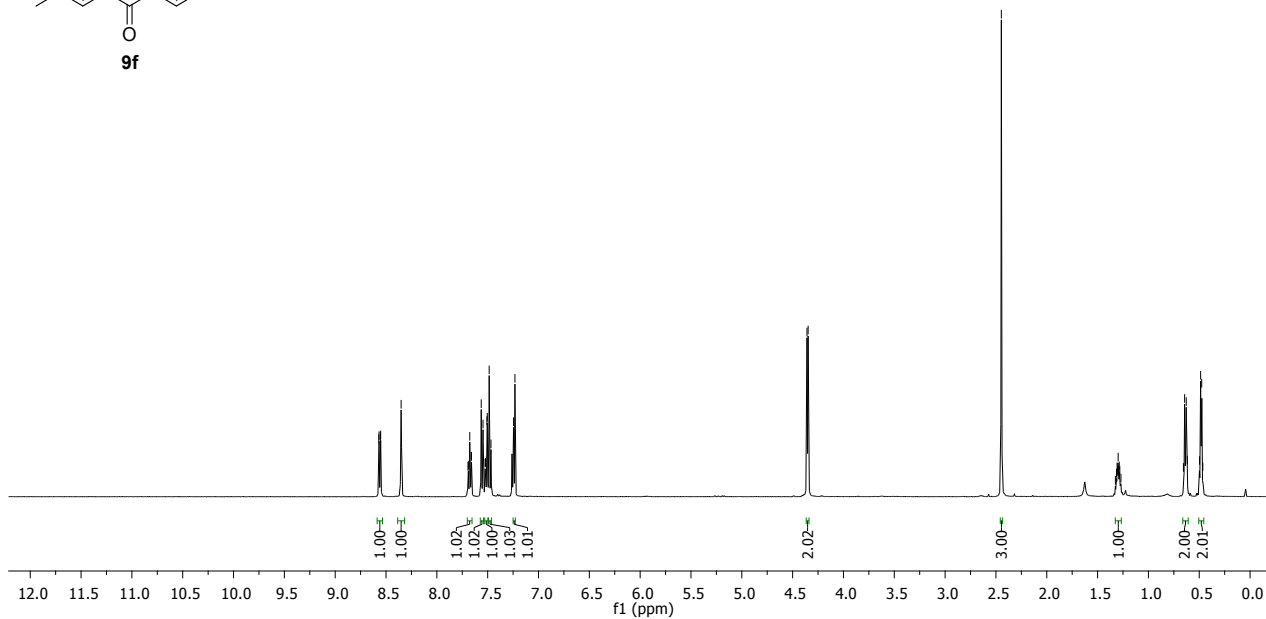
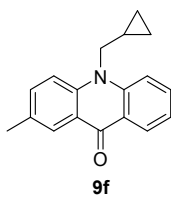


acr09 carbon



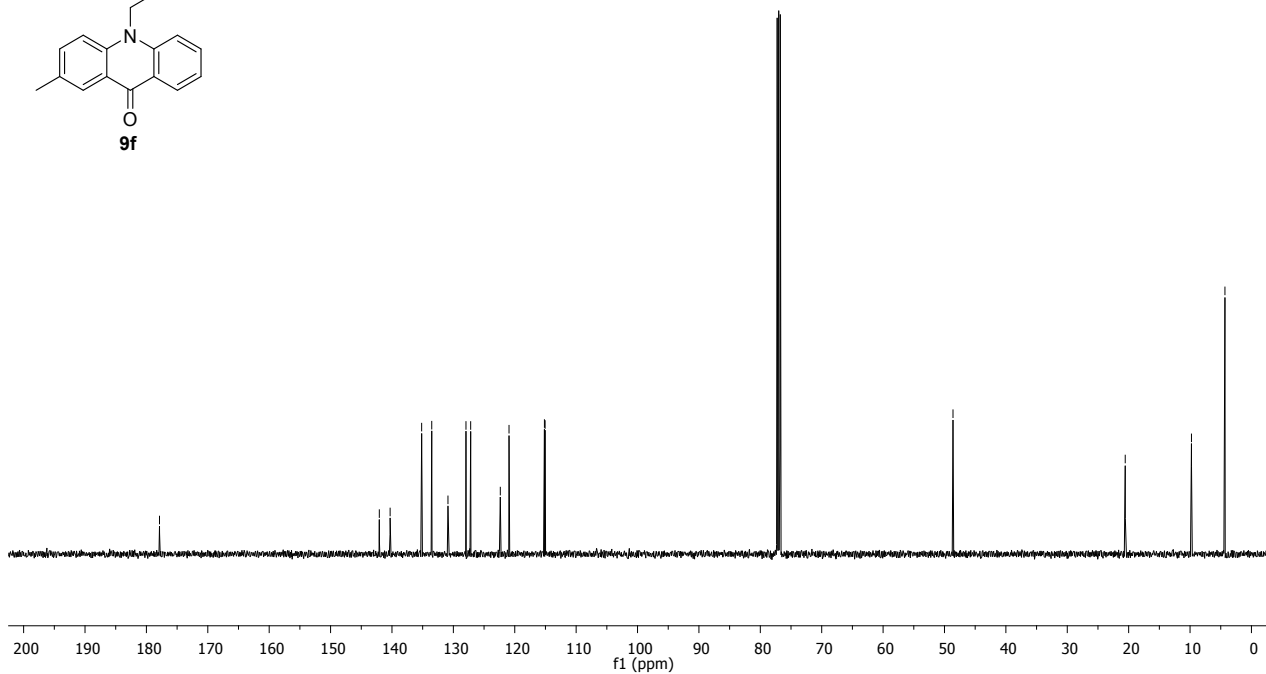
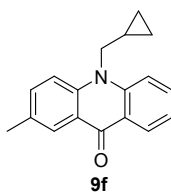
acr10

8.57 8.57 8.56 8.55 8.35 7.89 7.88 7.66 7.56 7.55 7.53 7.52 7.51 7.50 7.49 7.47 7.25 7.23 4.36 4.35 2.45 1.32 1.31 1.30 1.29 1.28 1.27 0.64 0.63 0.50 0.49 0.48 0.47

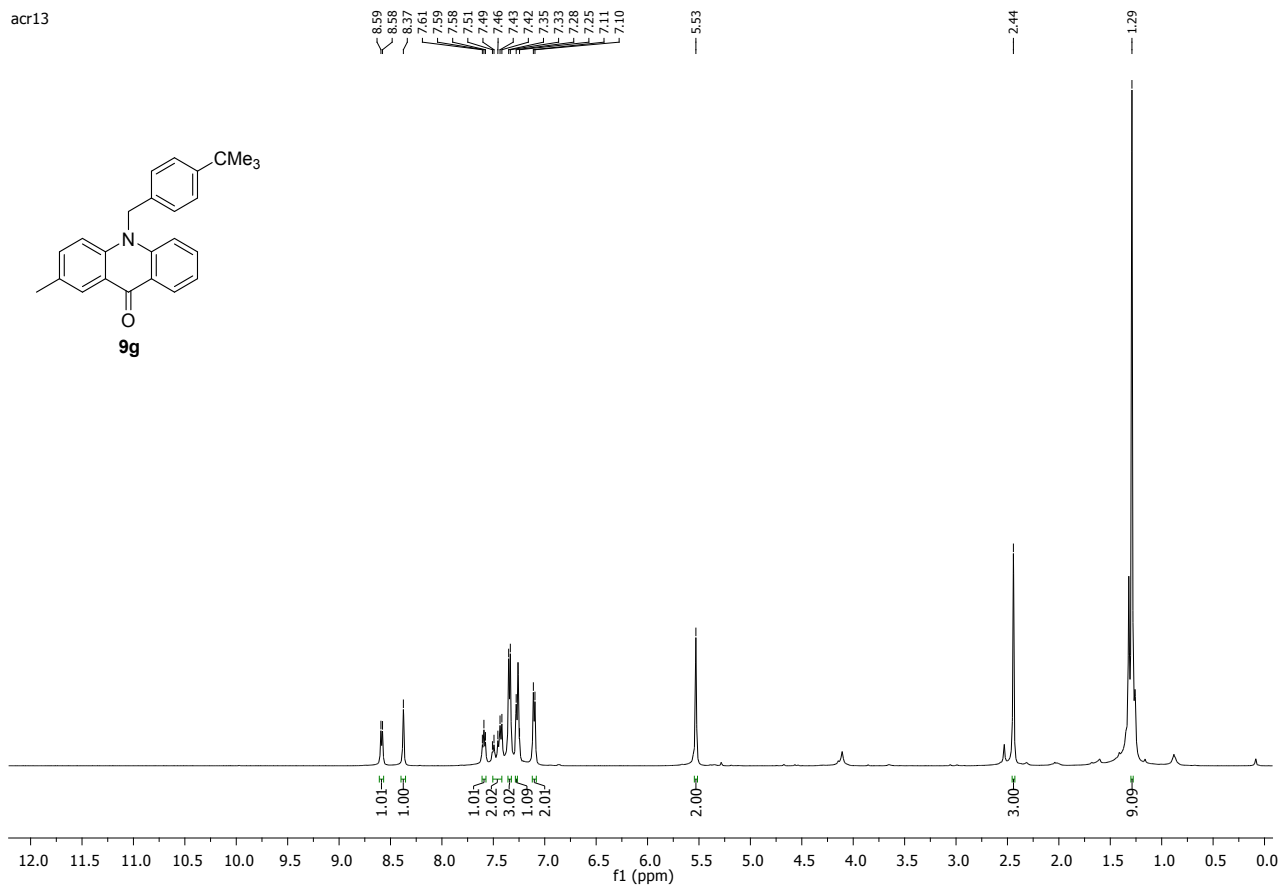


acr10 carbon

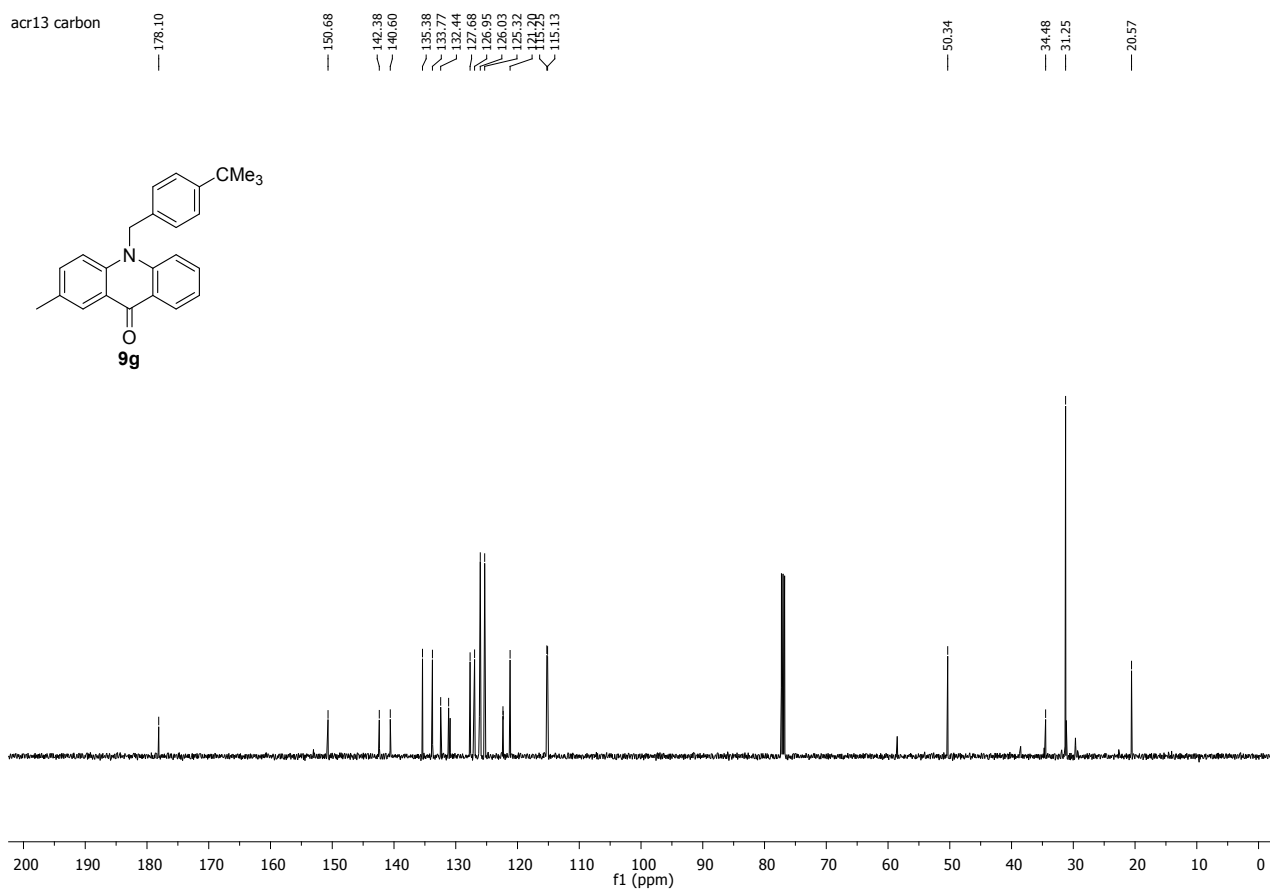
177.87 142.06 140.30 135.16 133.52 130.88 127.98 127.35 120.93 115.17 115.06 48.61 20.56 9.77 4.32



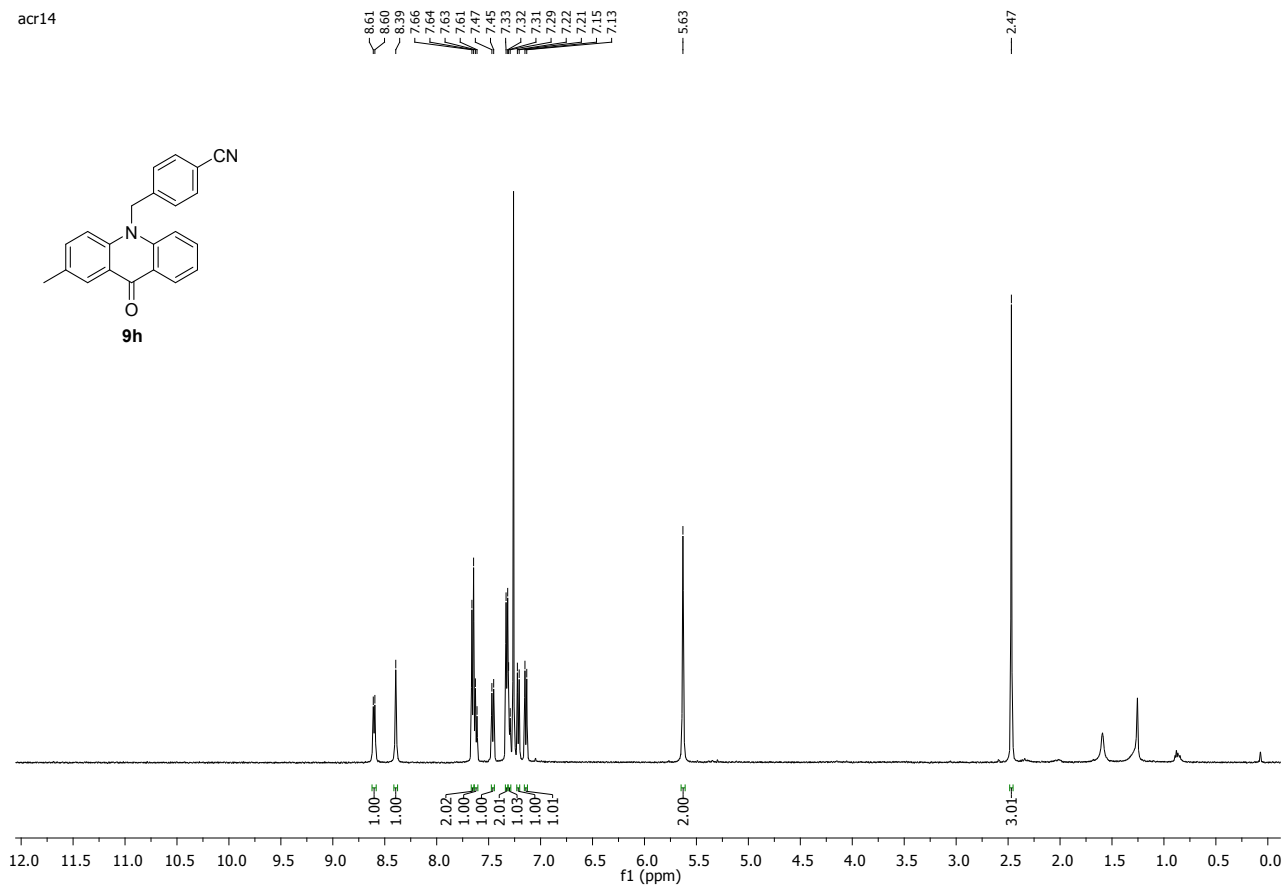
acr13



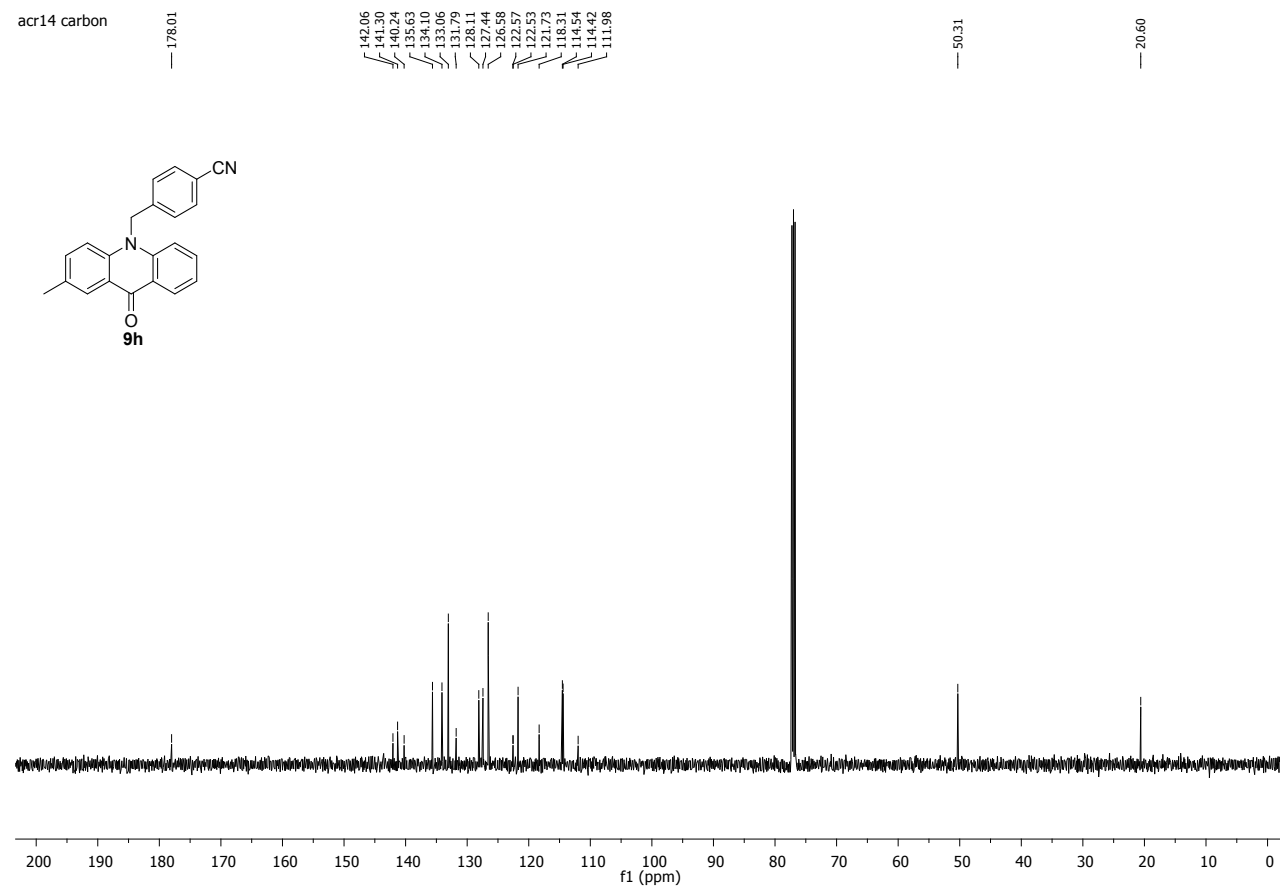
acr13 carbon



acr14



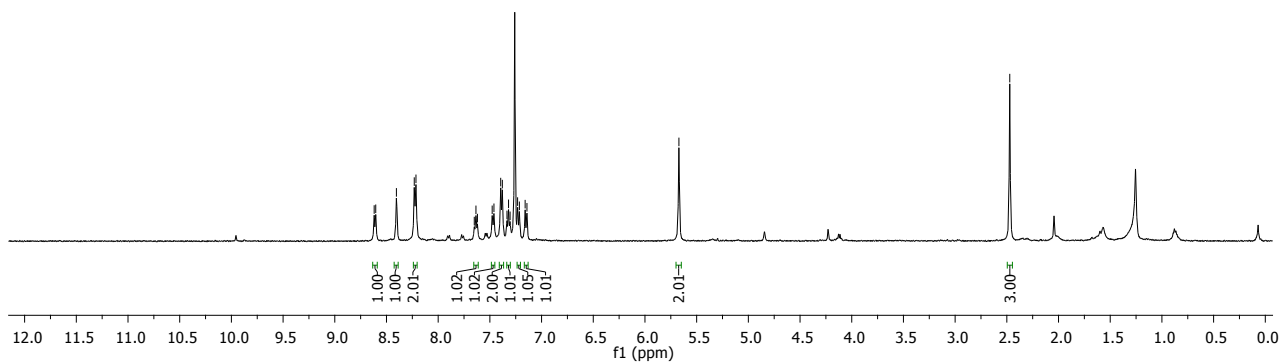
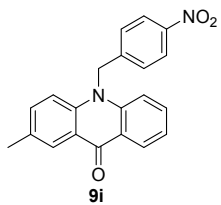
acr14 carbon



acr15

8.62
8.60
8.40
8.23
8.21
7.65
7.63
7.62
7.48
7.46
7.40
7.38
7.33
7.22
7.20
7.16
7.14
5.67

2.47



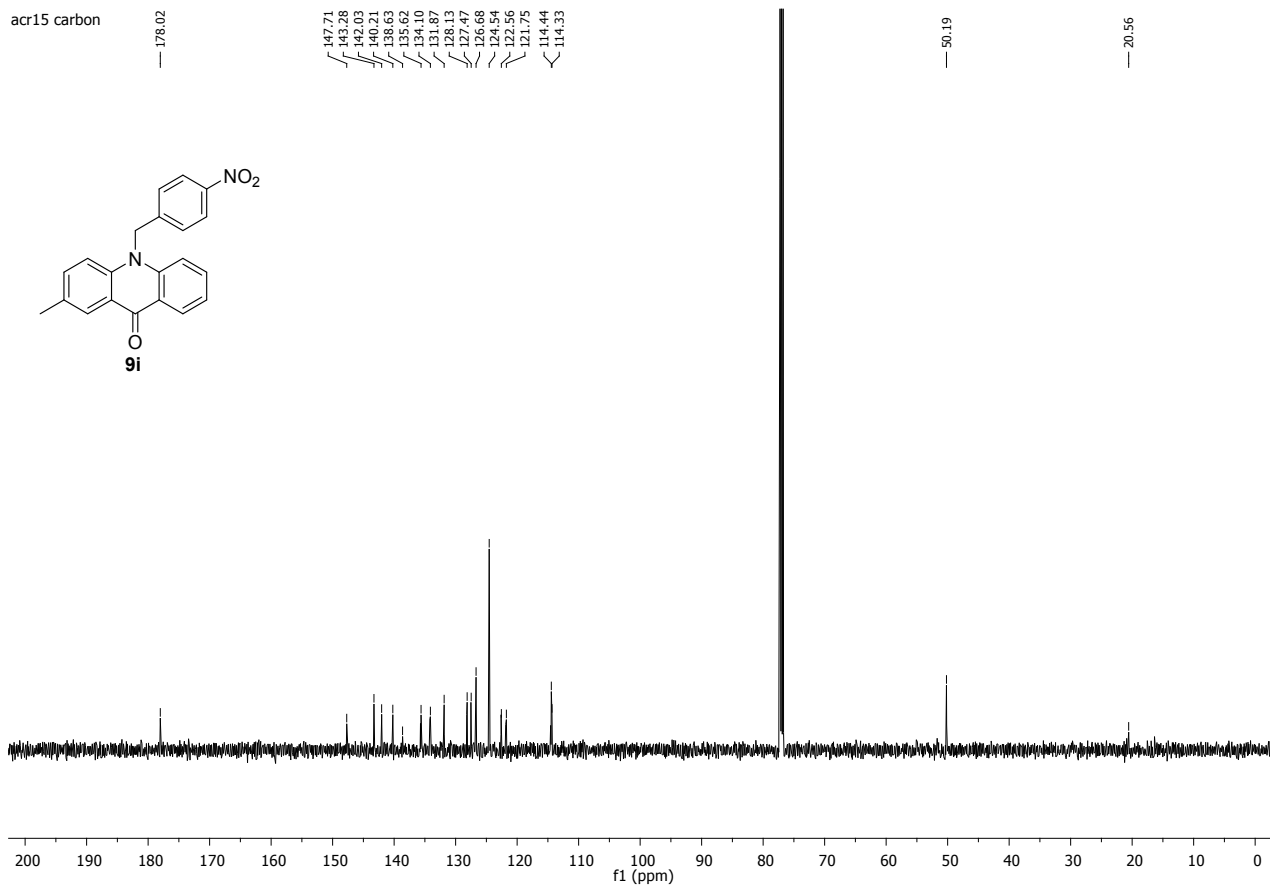
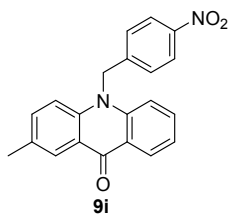
acr15 carbon

178.02

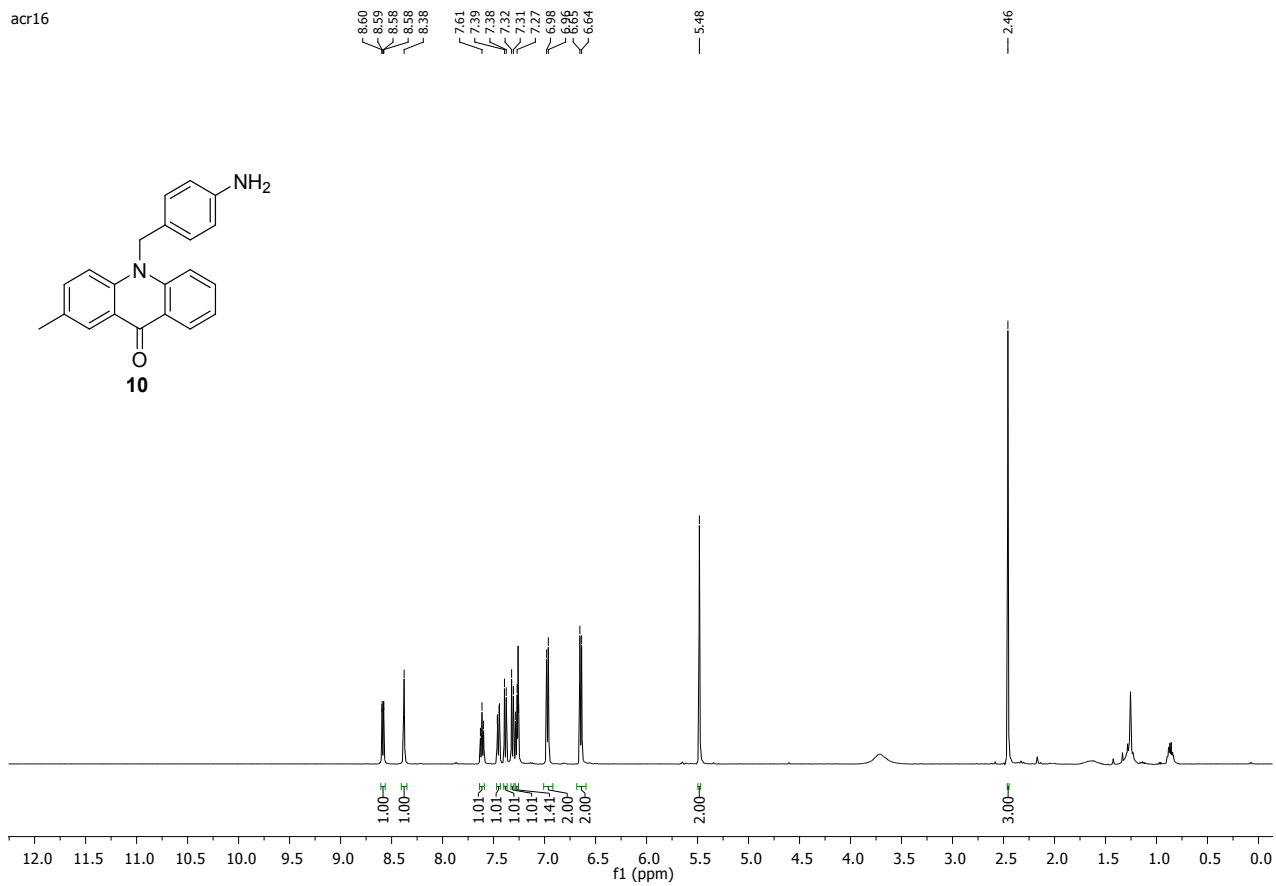
147.71
143.28
142.03
140.21
138.63
135.62
134.10
131.67
129.47
127.68
124.94
122.56
121.75
114.44
114.33

50.19

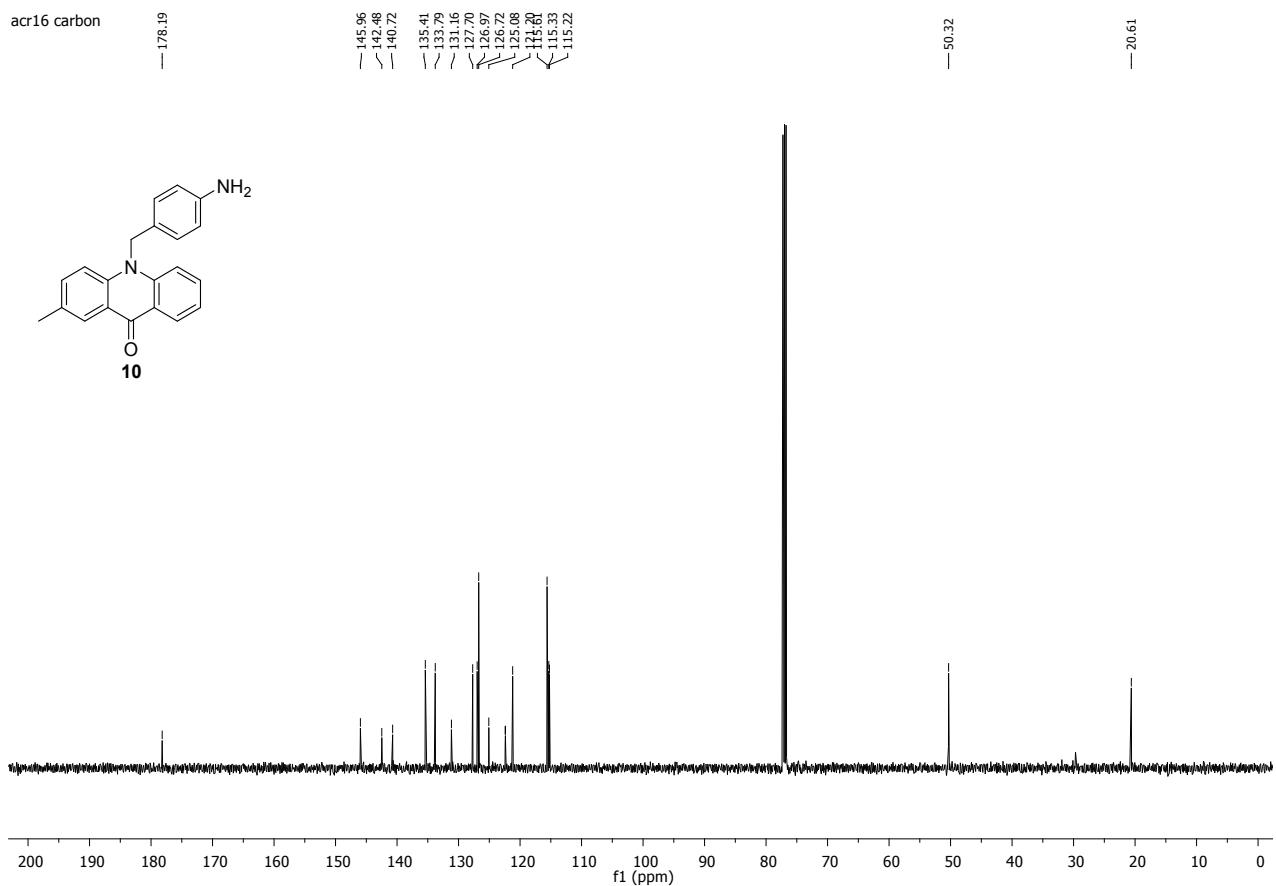
20.56



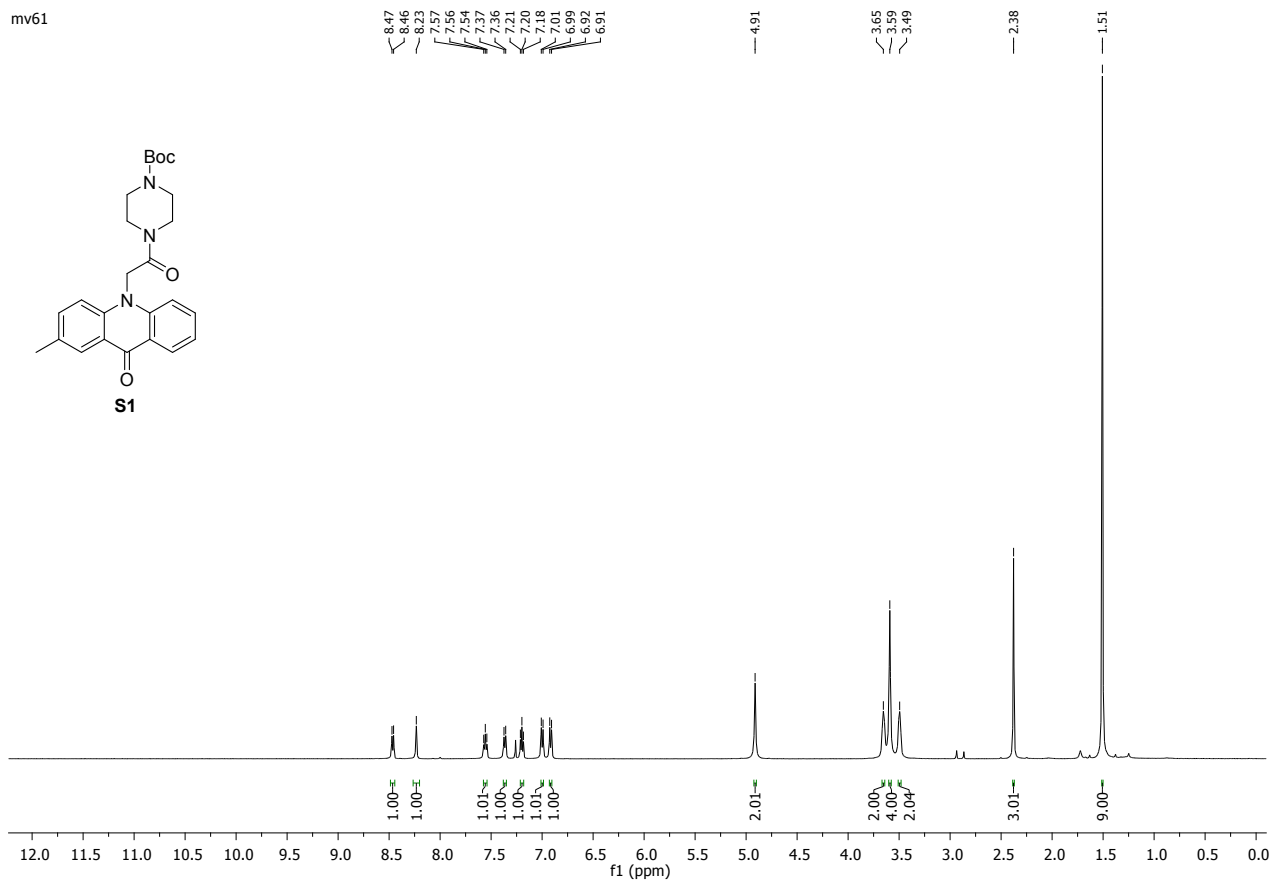
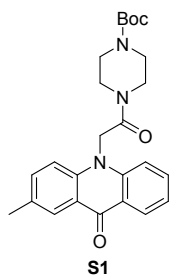
acr16



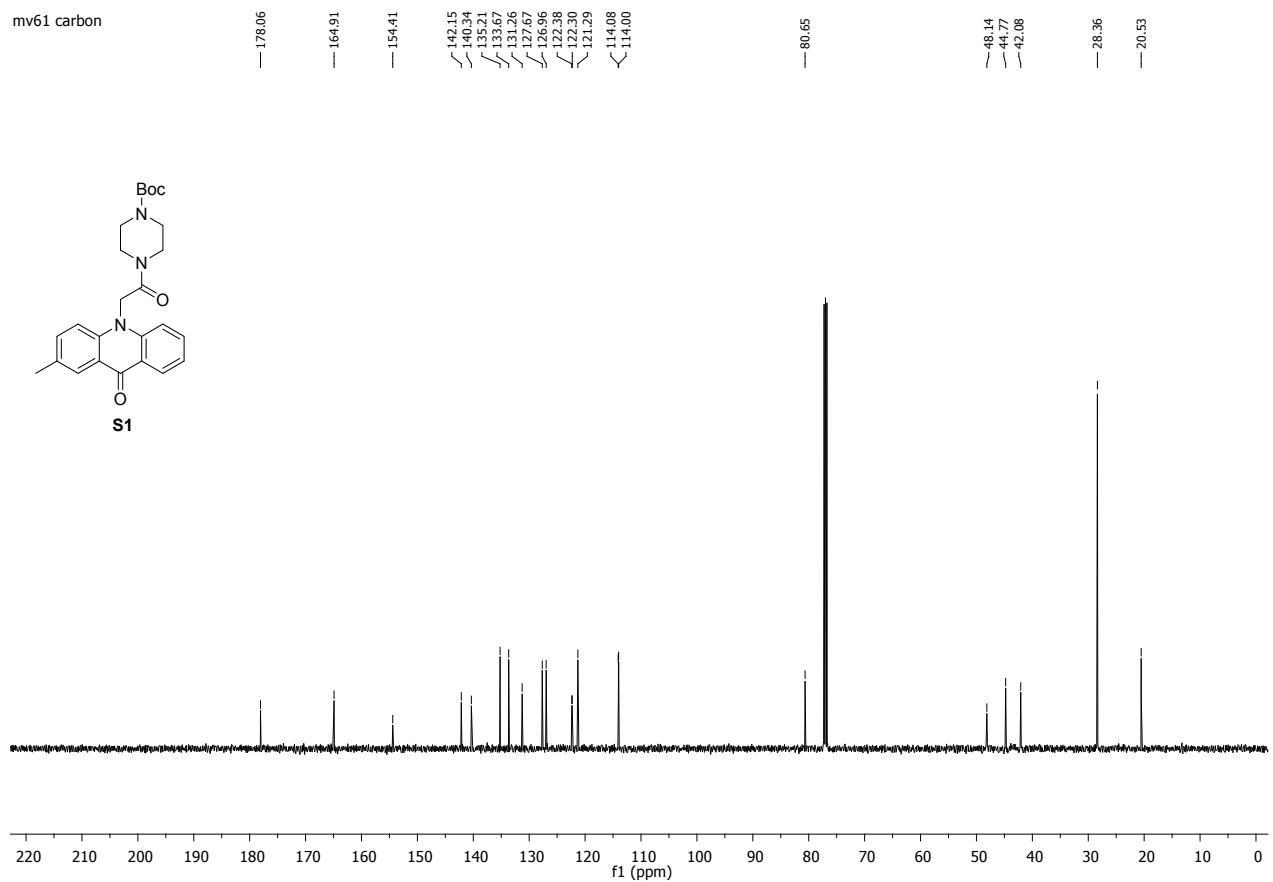
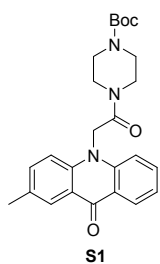
acr16 carbon



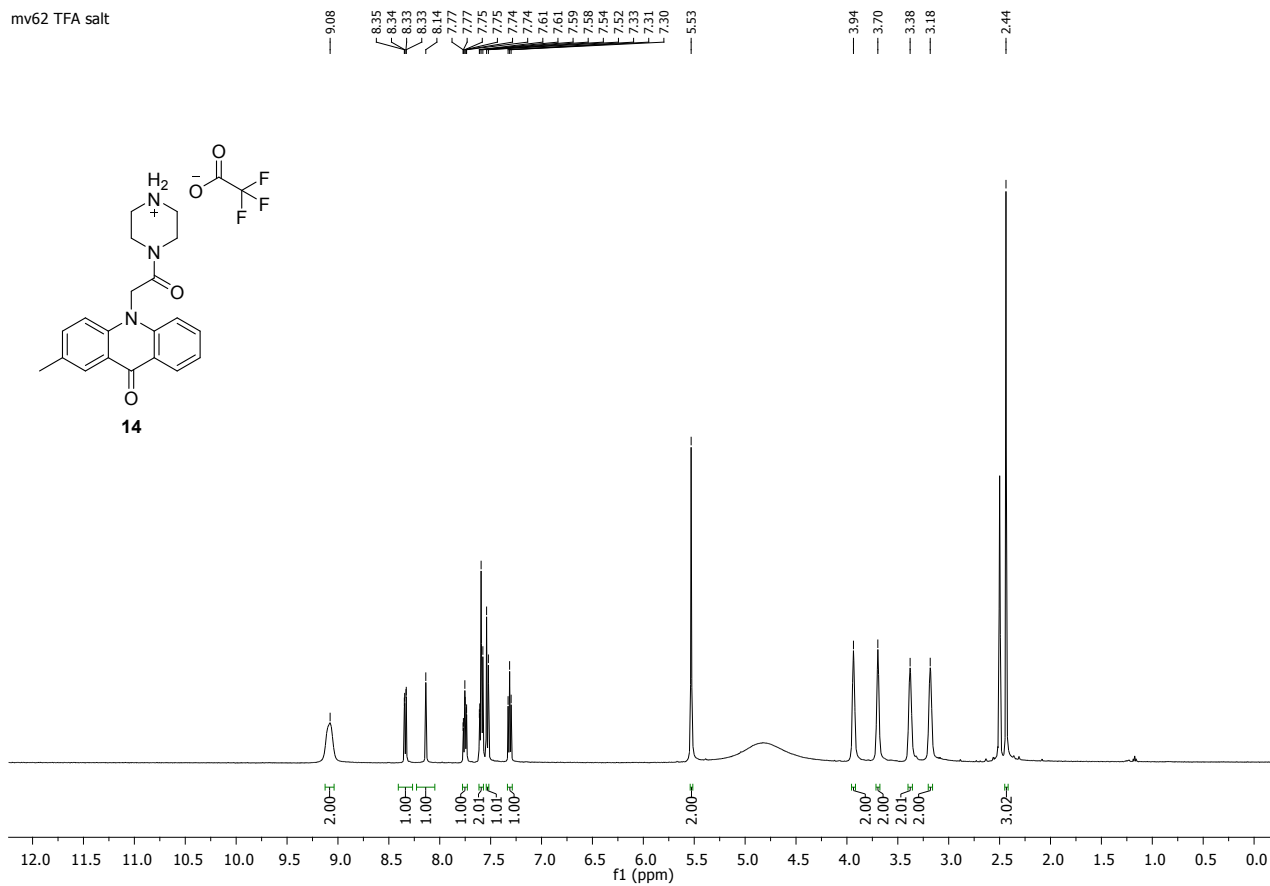
mv61



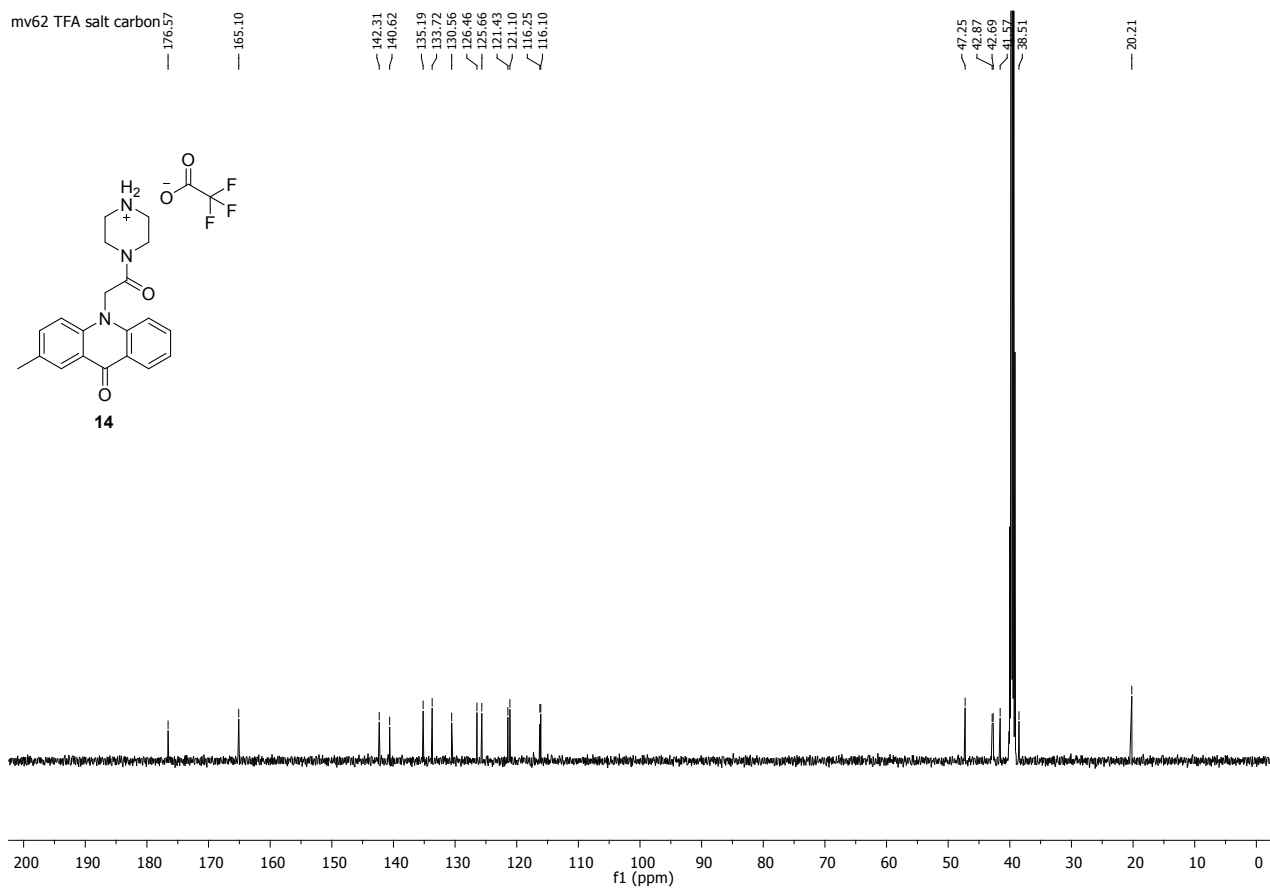
mv61 carbon



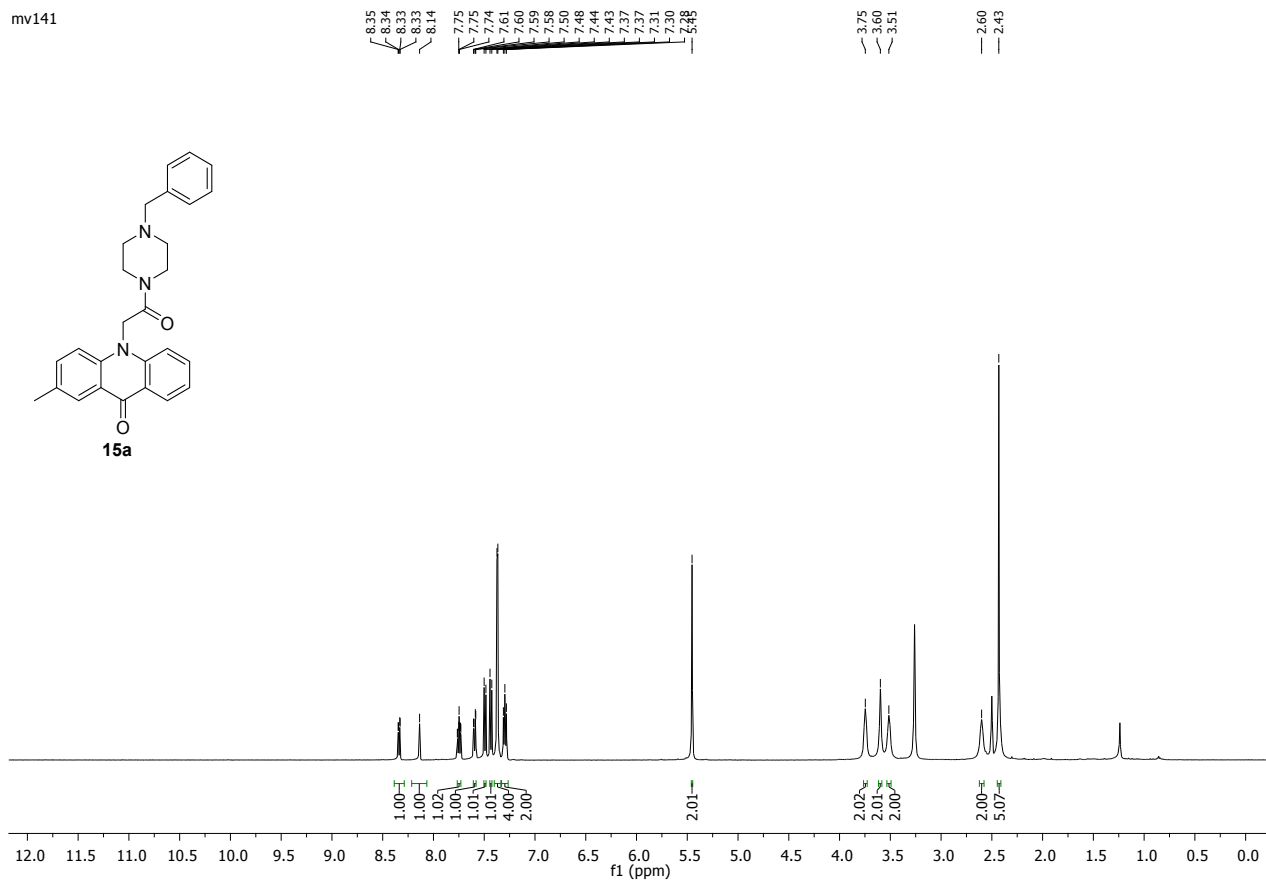
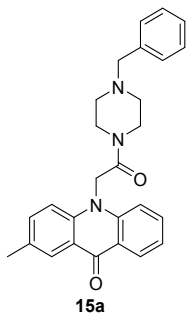
mv62 TFA salt



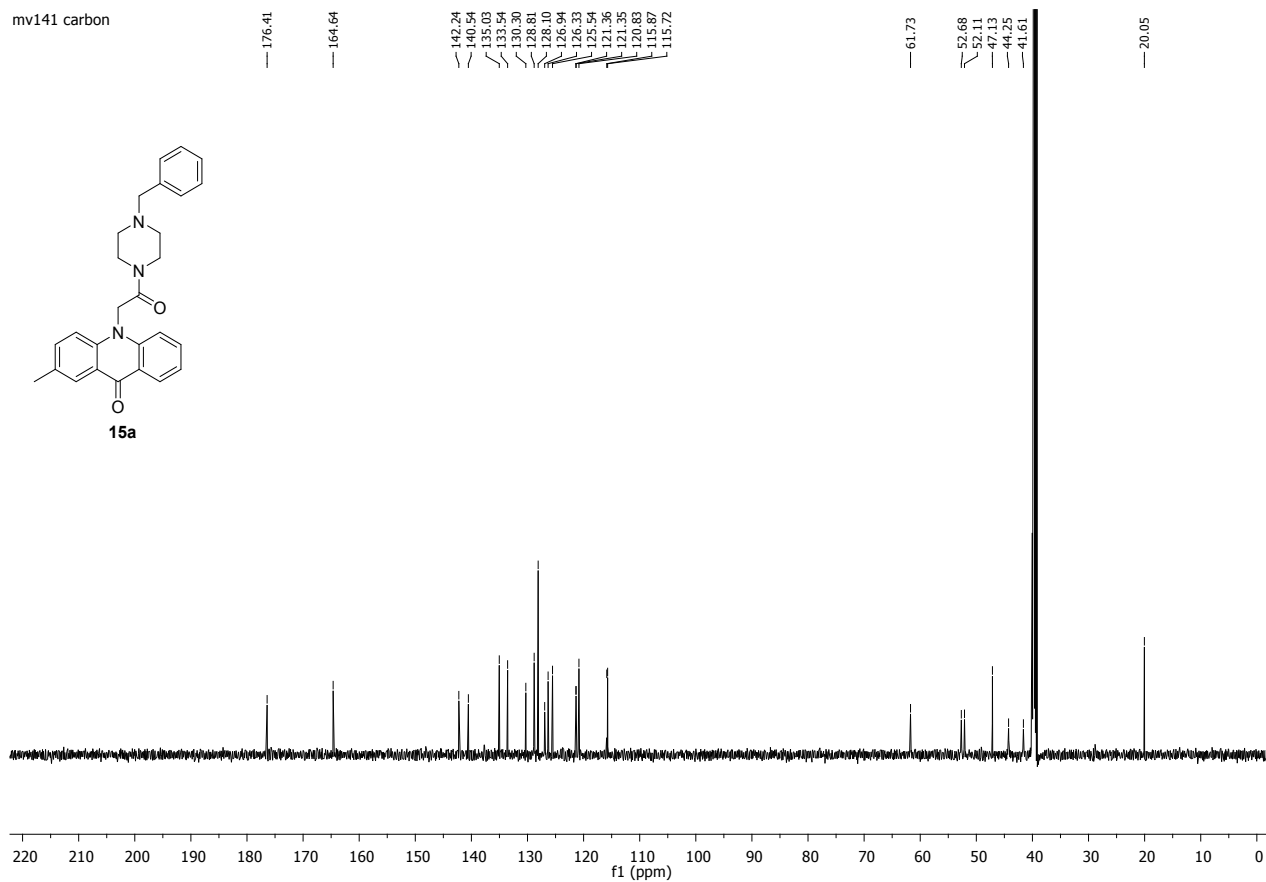
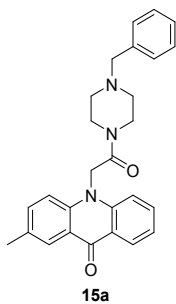
mv62 TFA salt carbon



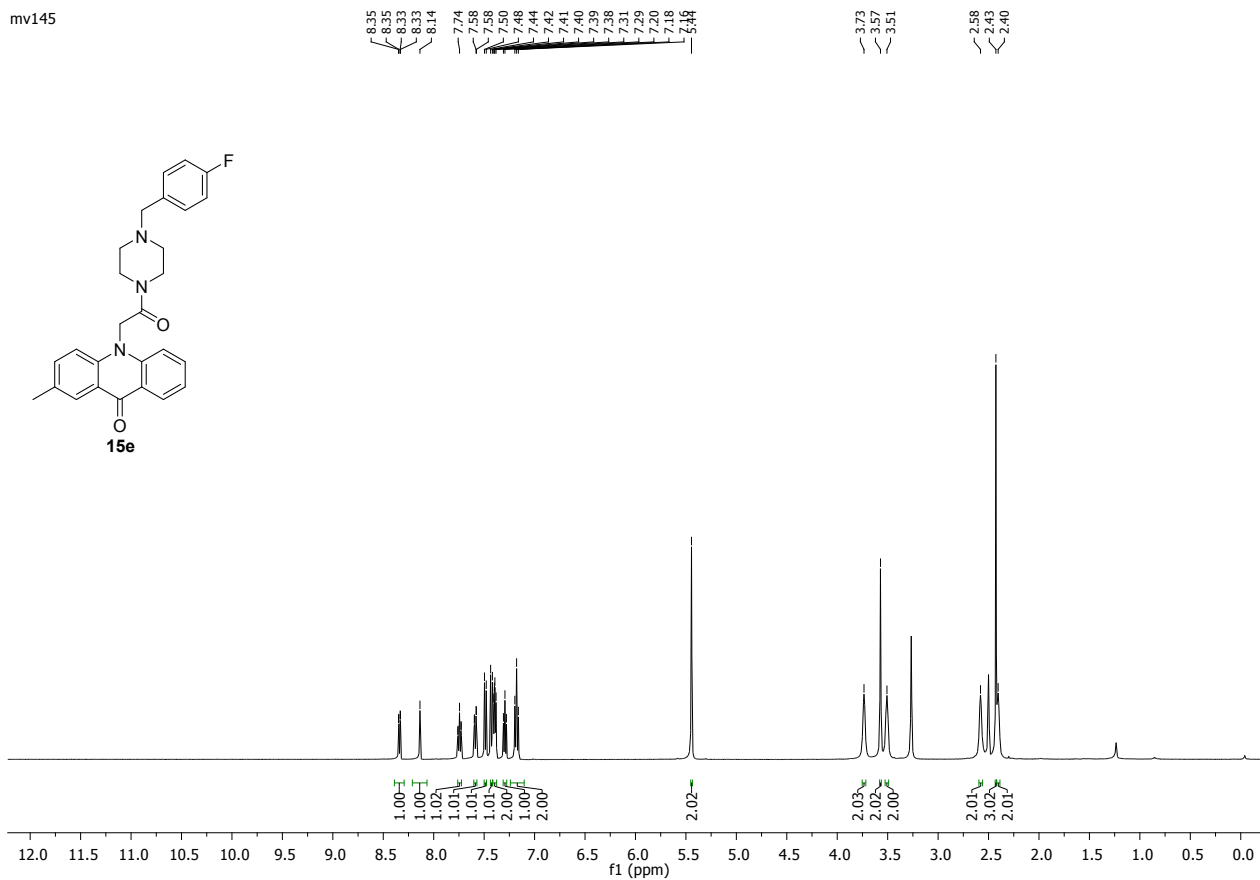
mv141



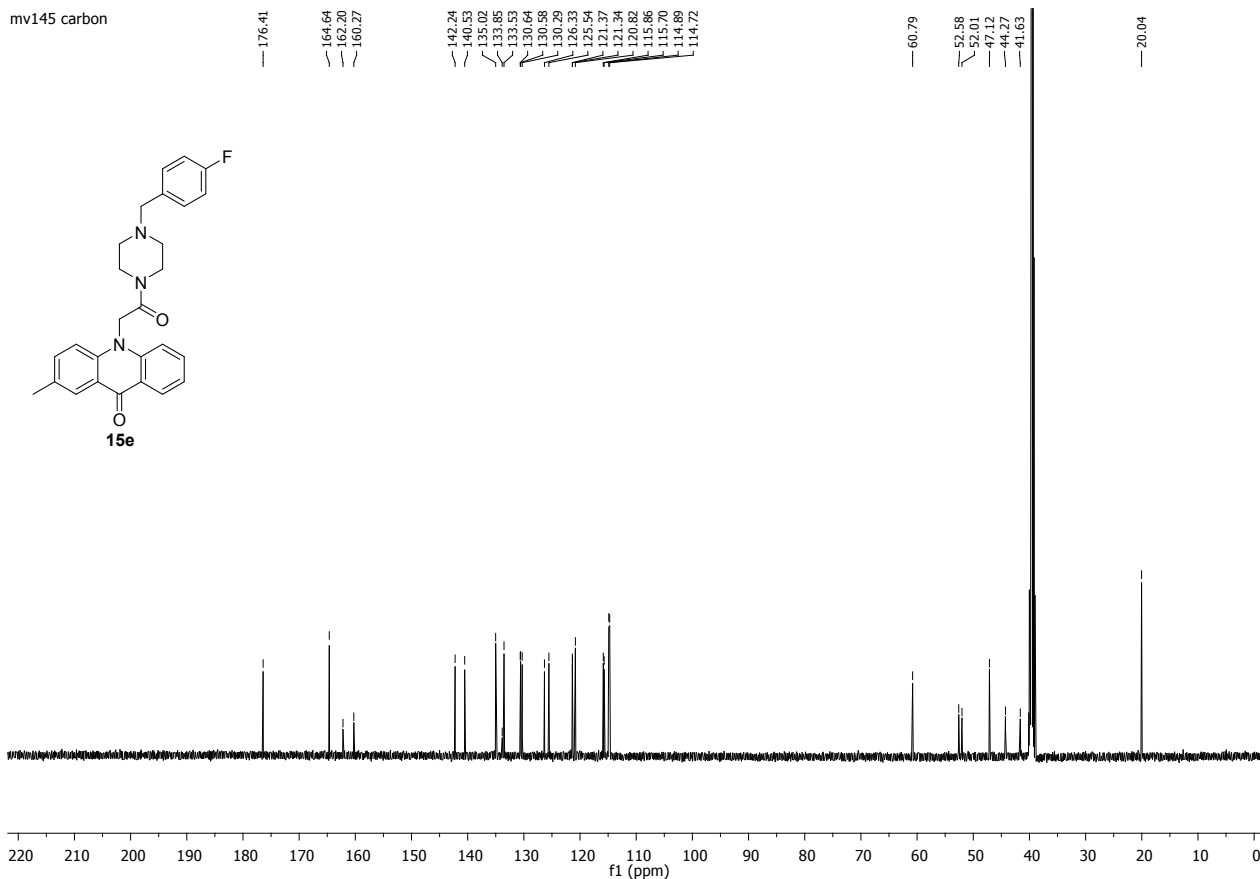
mv141 carbon



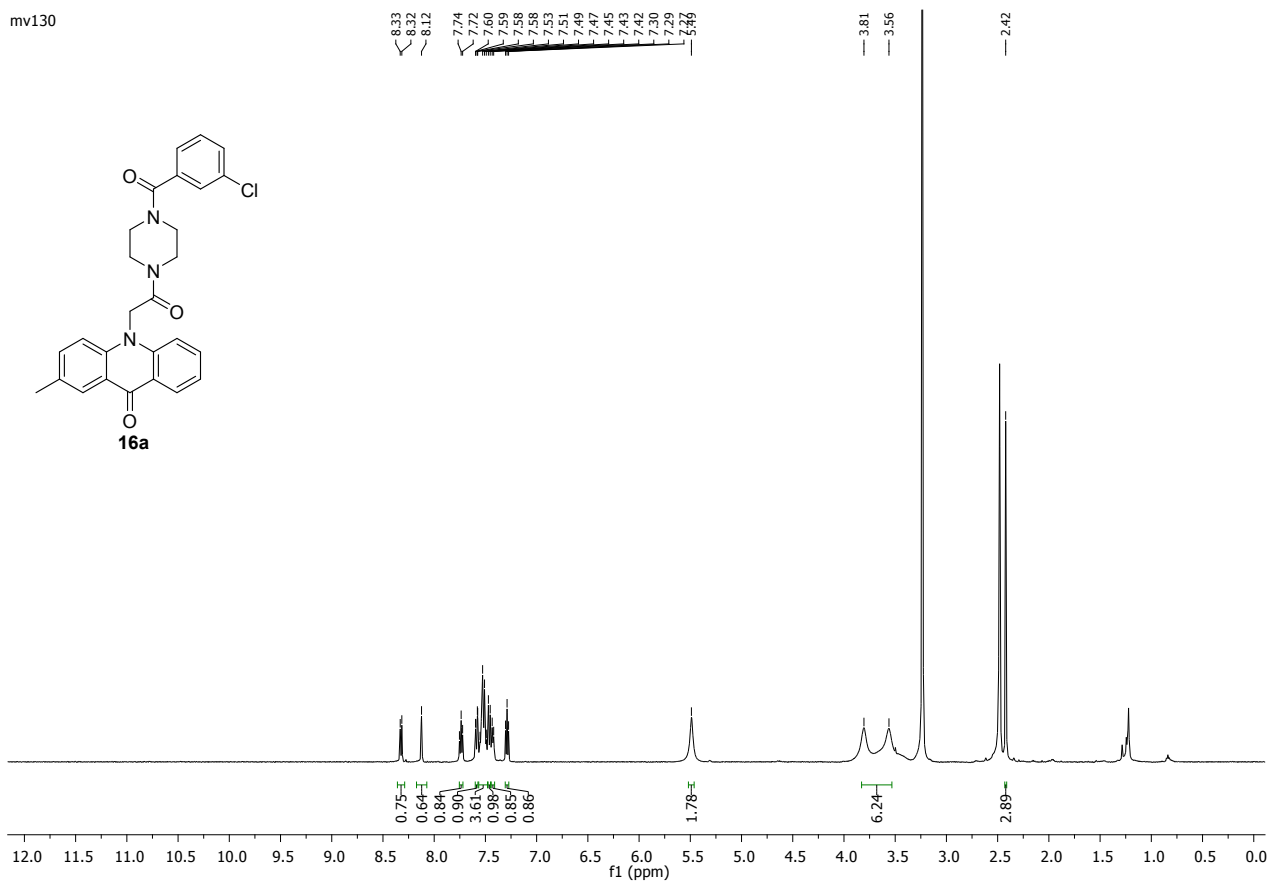
mv145



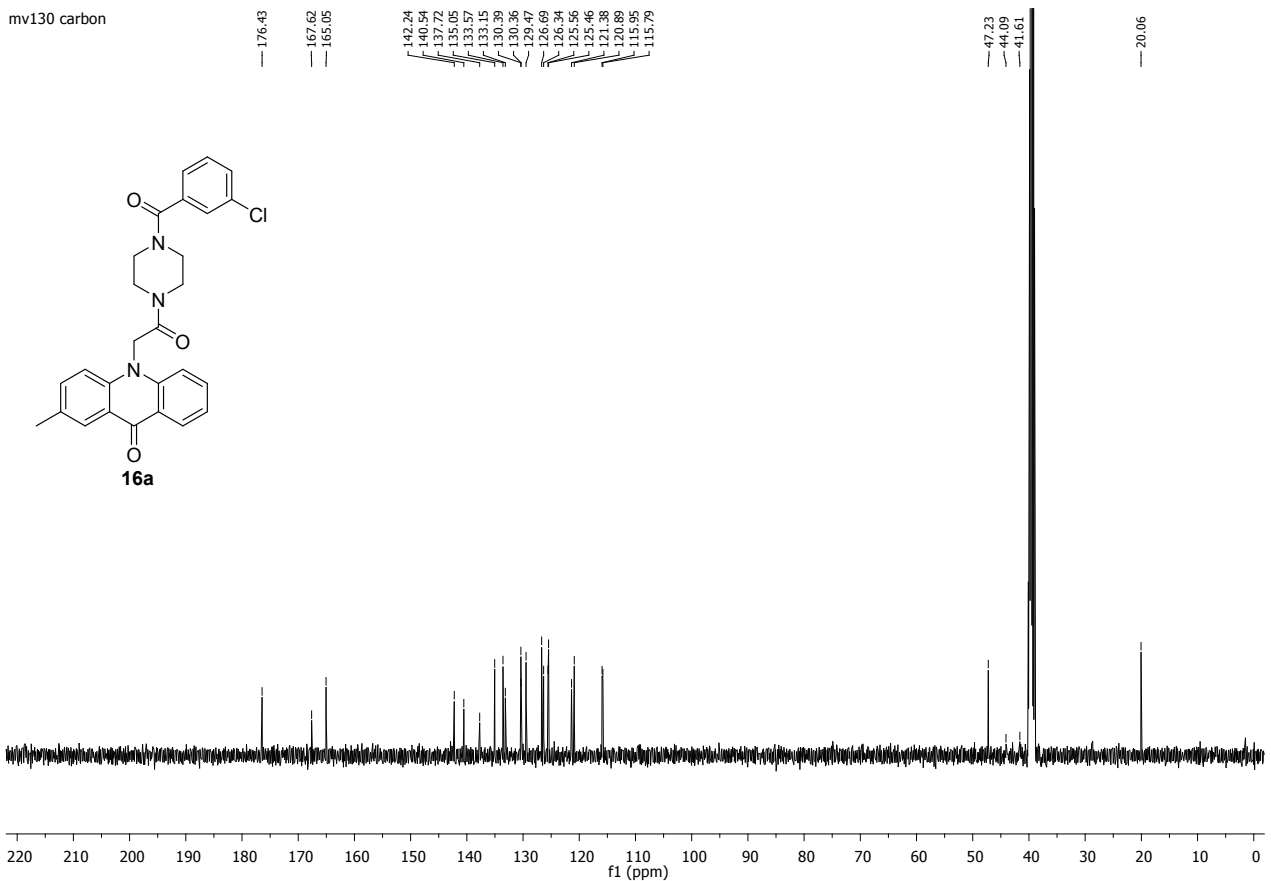
mv145 carbon



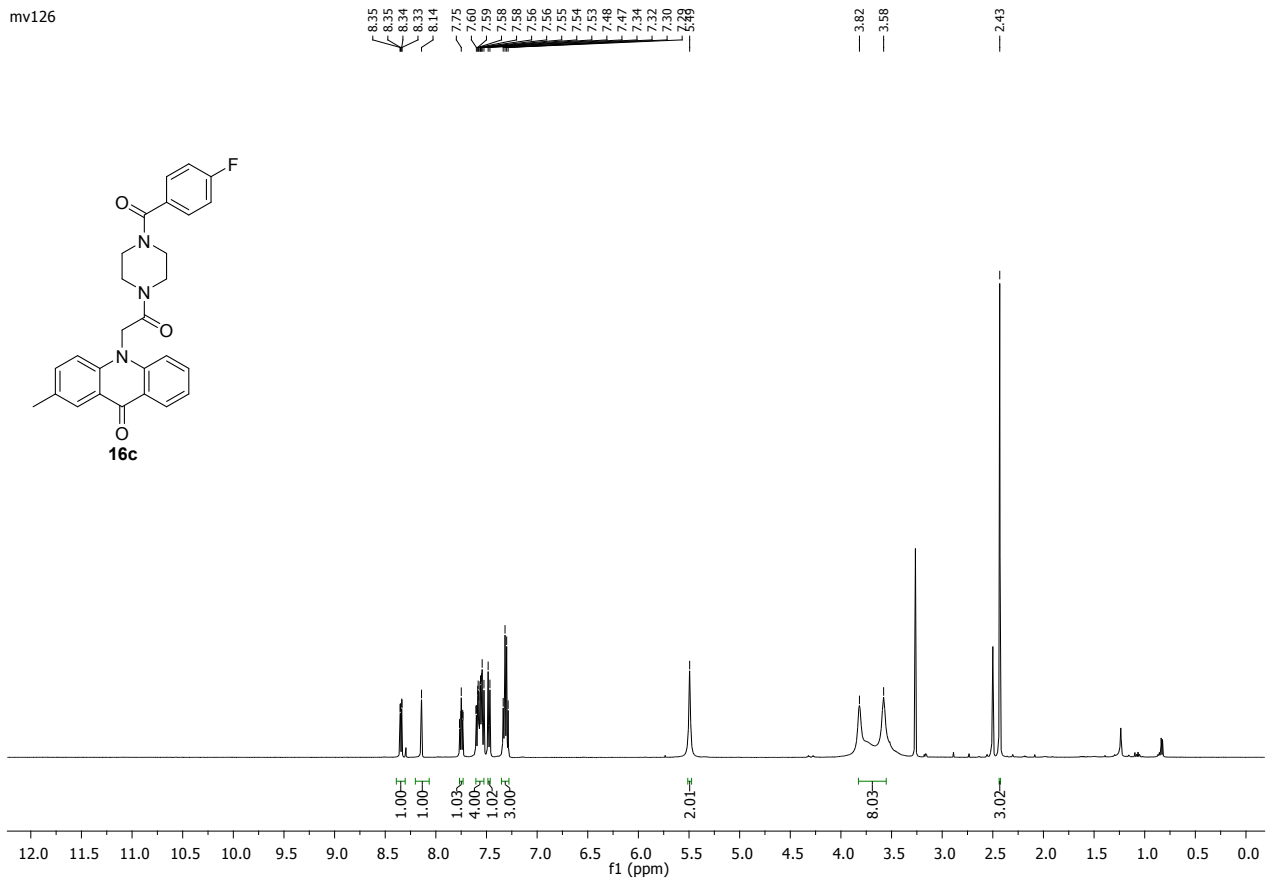
mv130



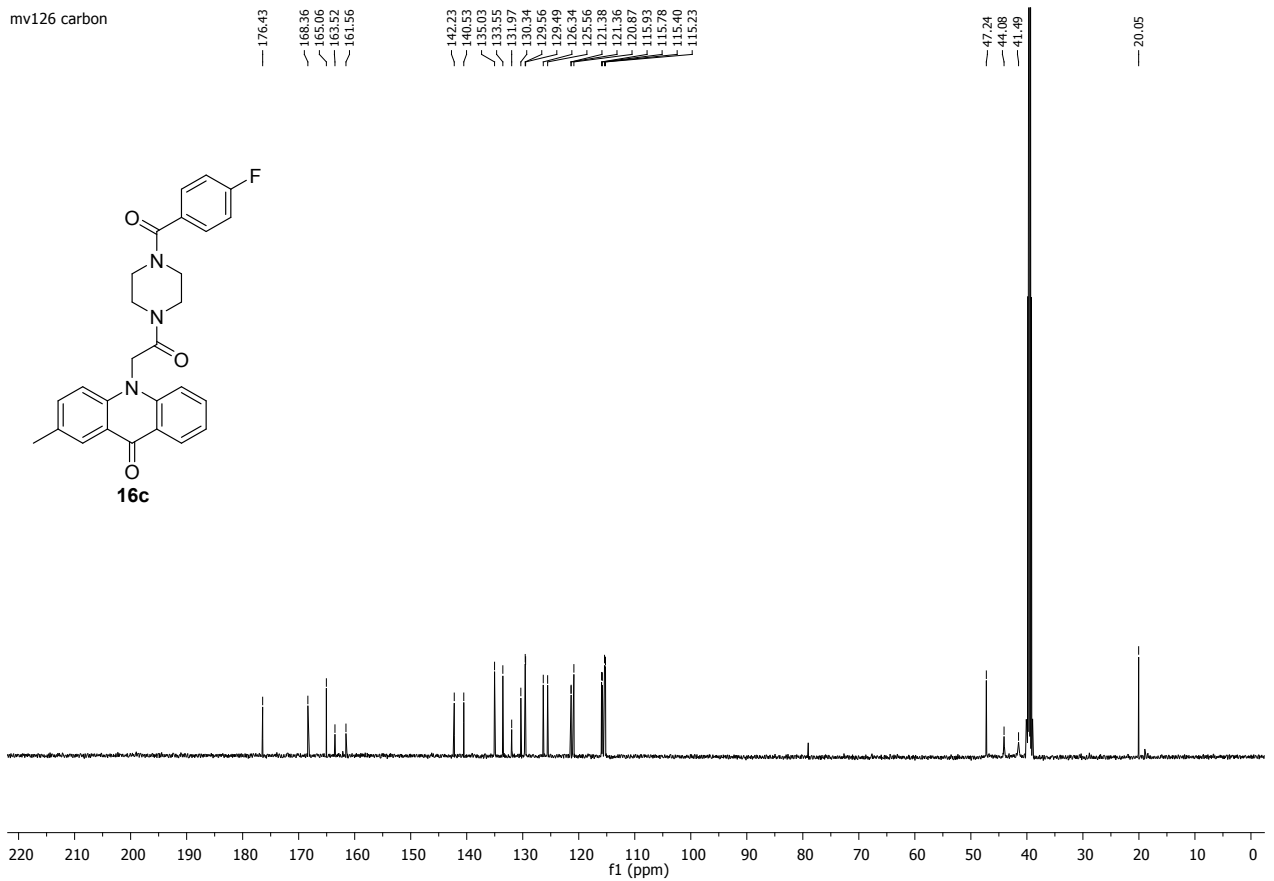
mv130 carbon



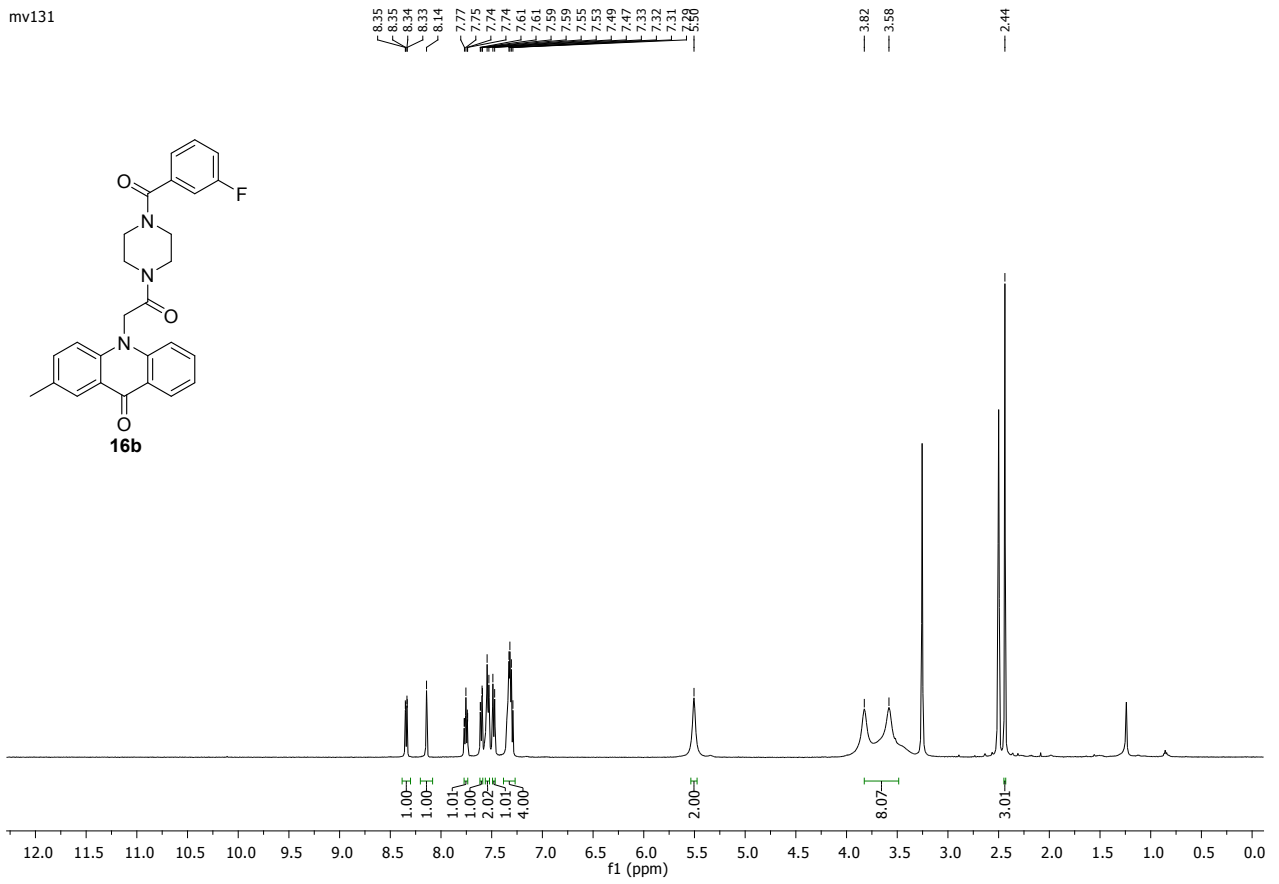
mv126



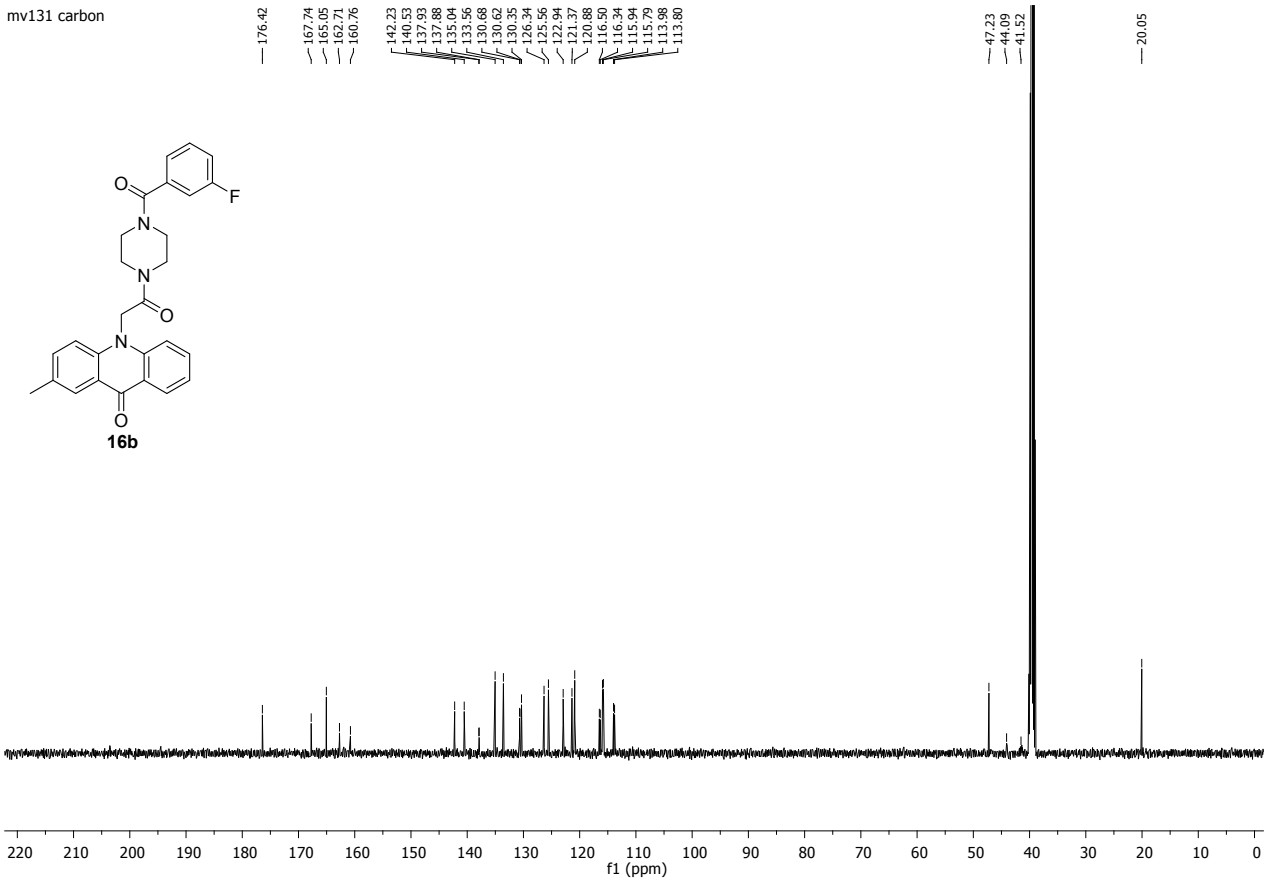
mv126 carbon



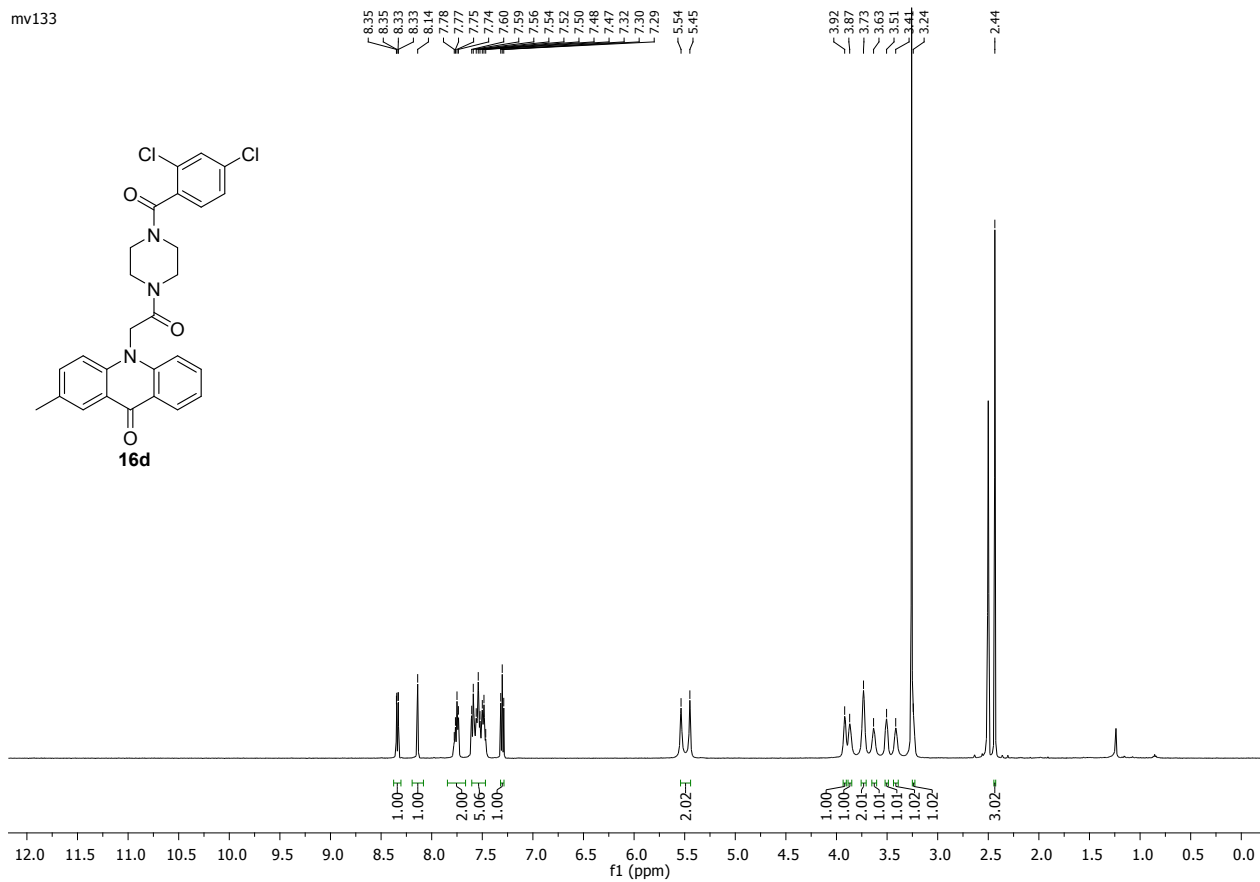
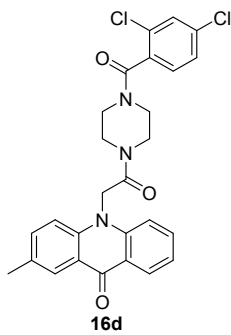
mv131



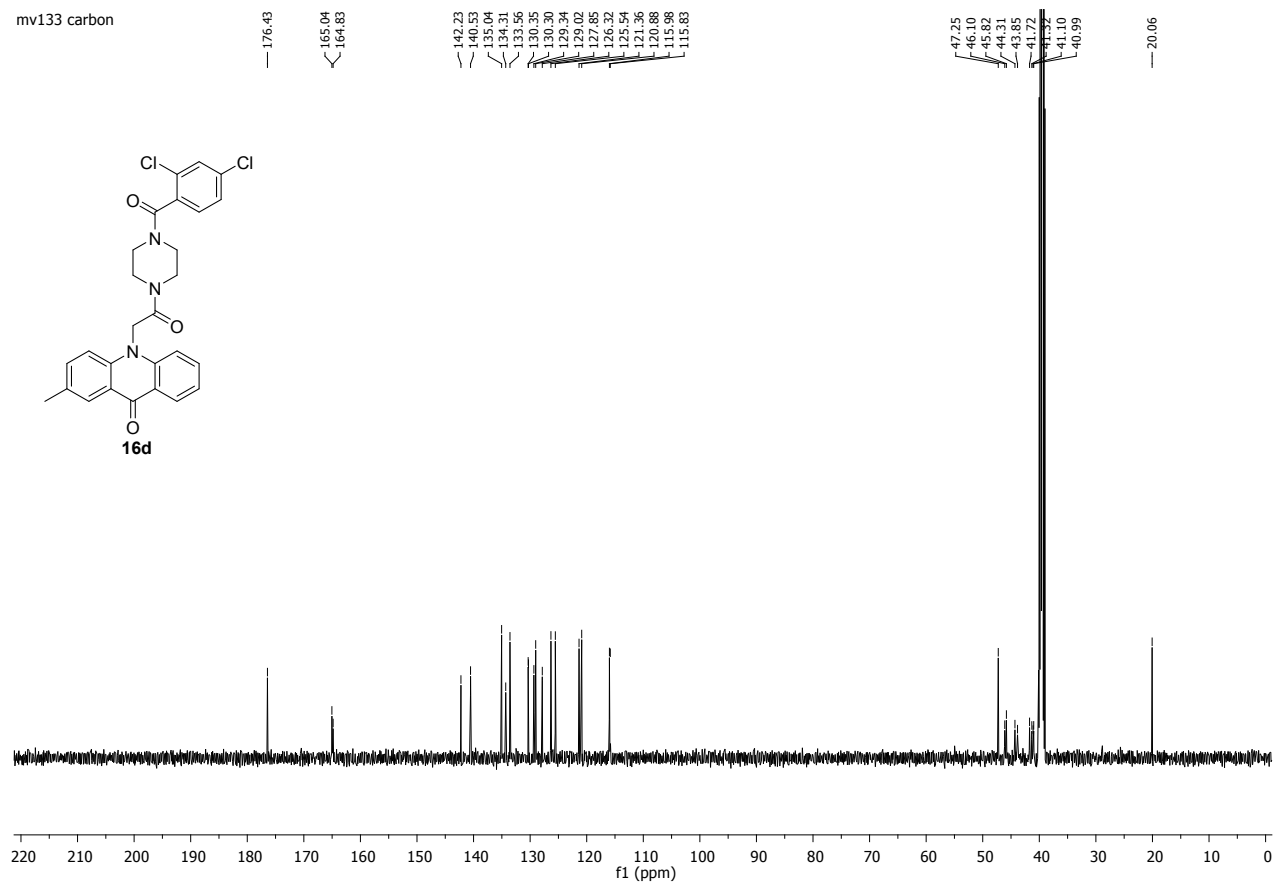
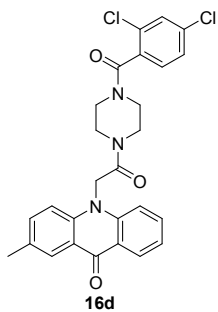
mv131 carbon



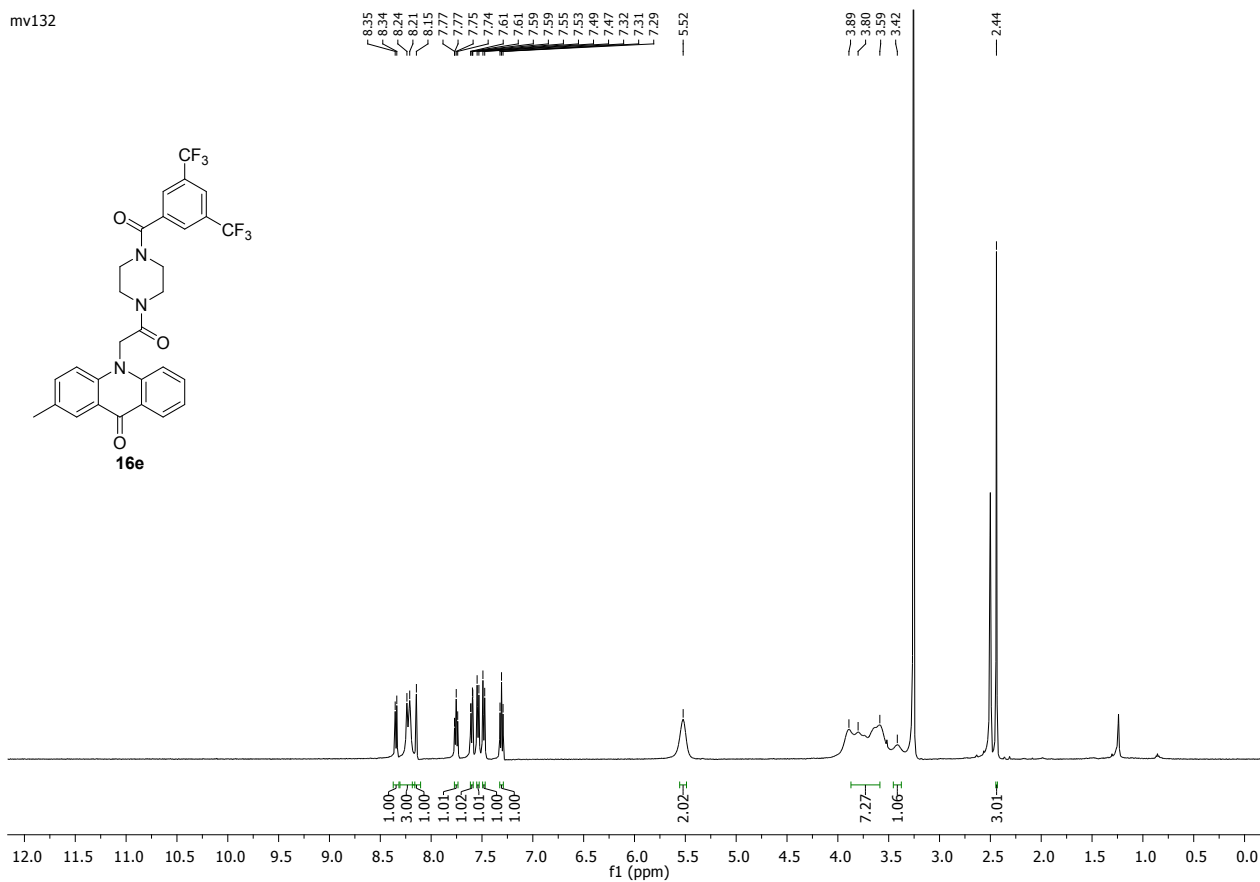
mv133



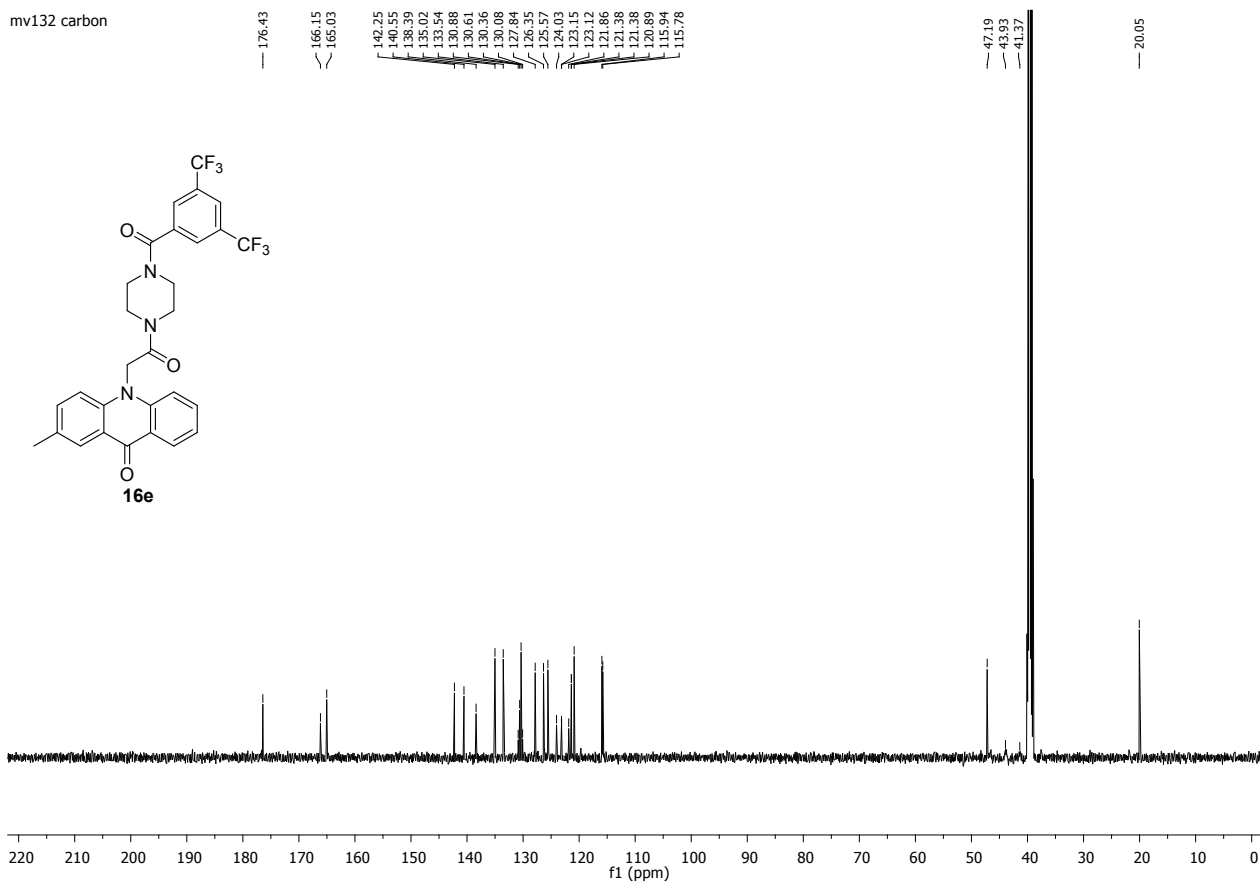
mv133 carbon



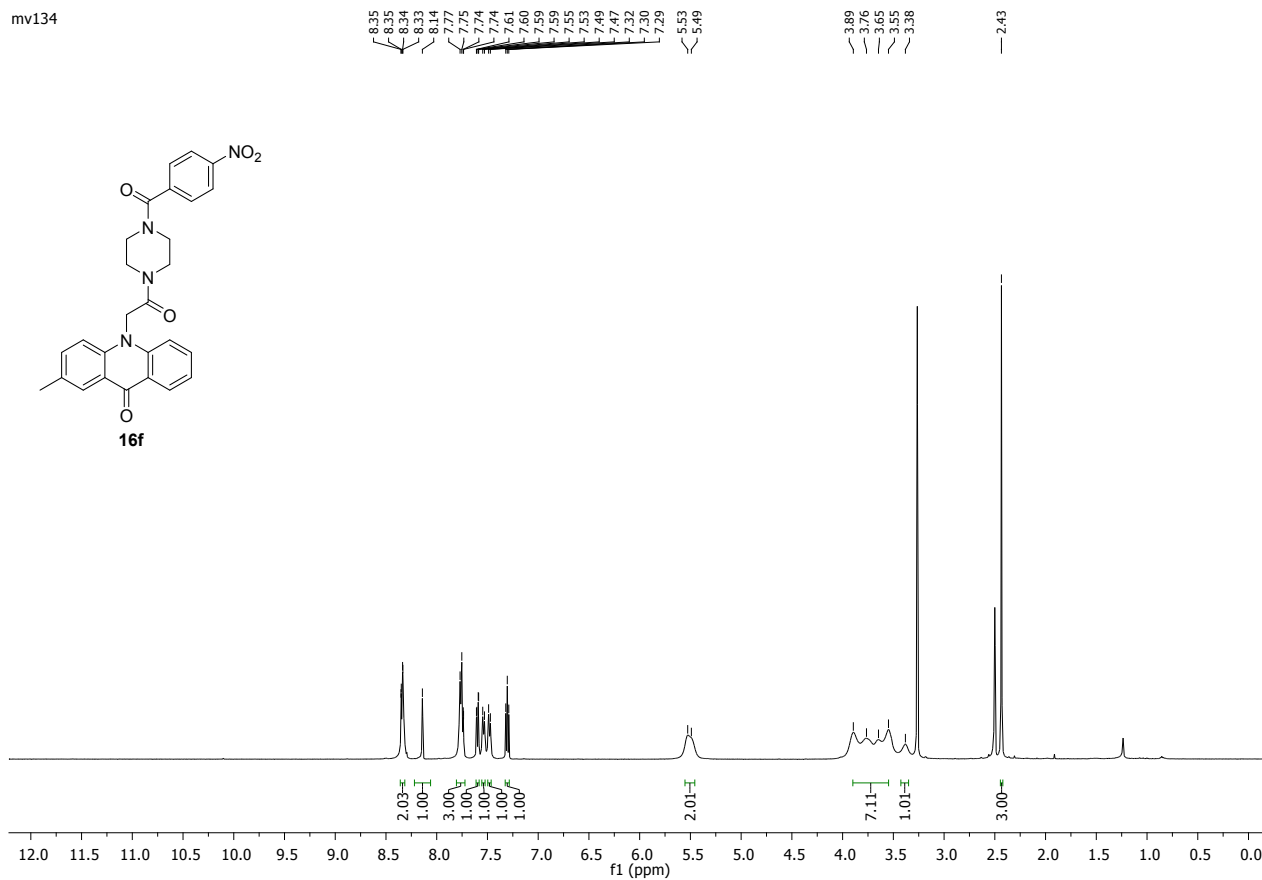
mv132



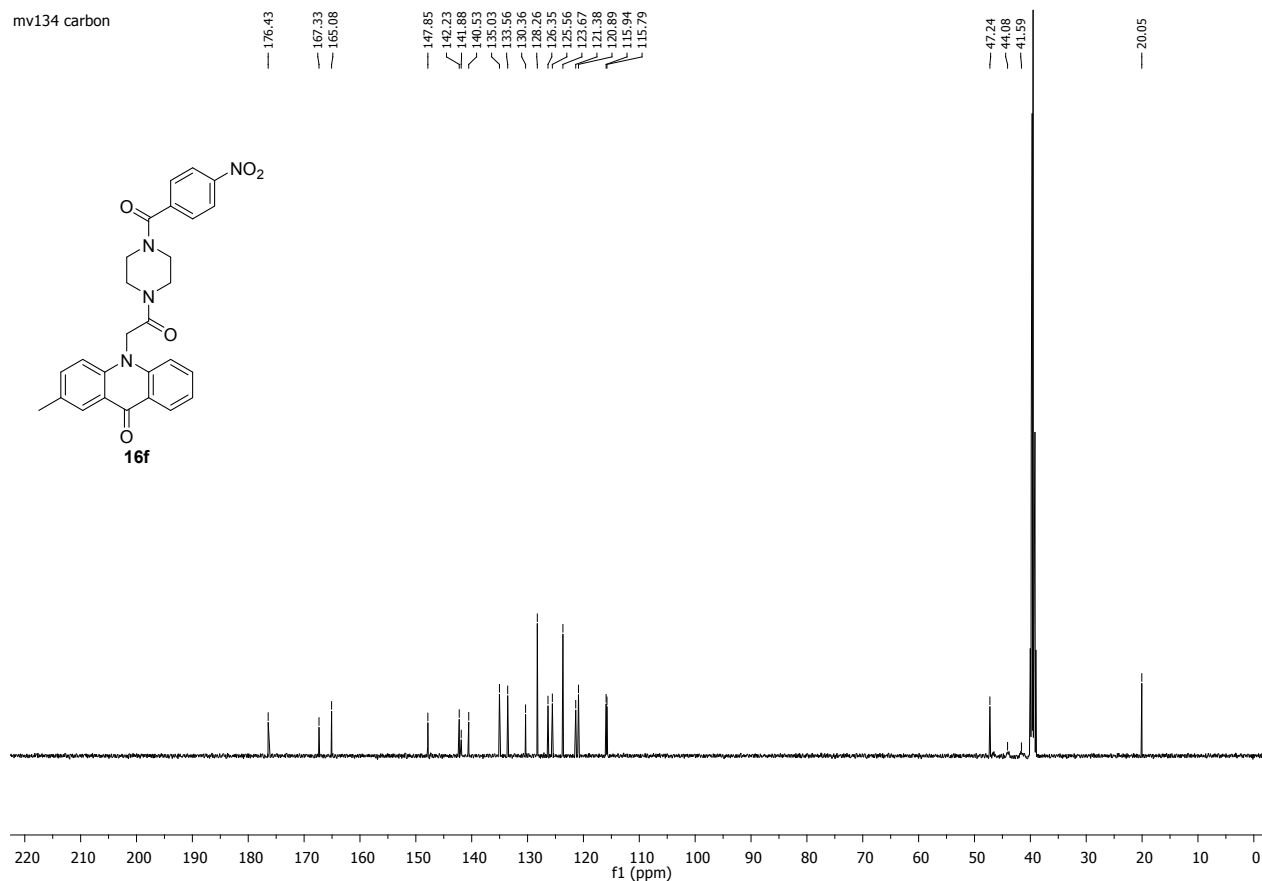
mv132 carbon



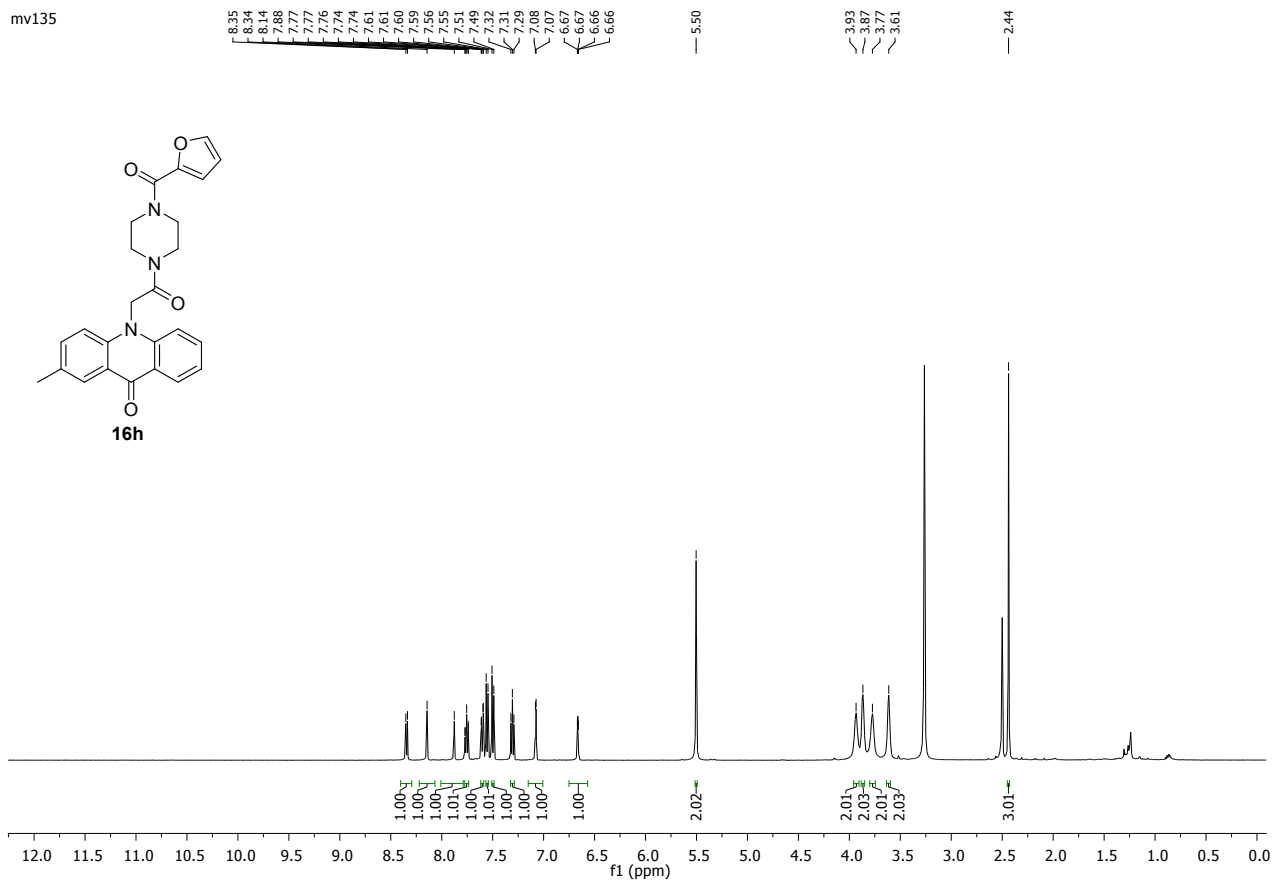
mv134



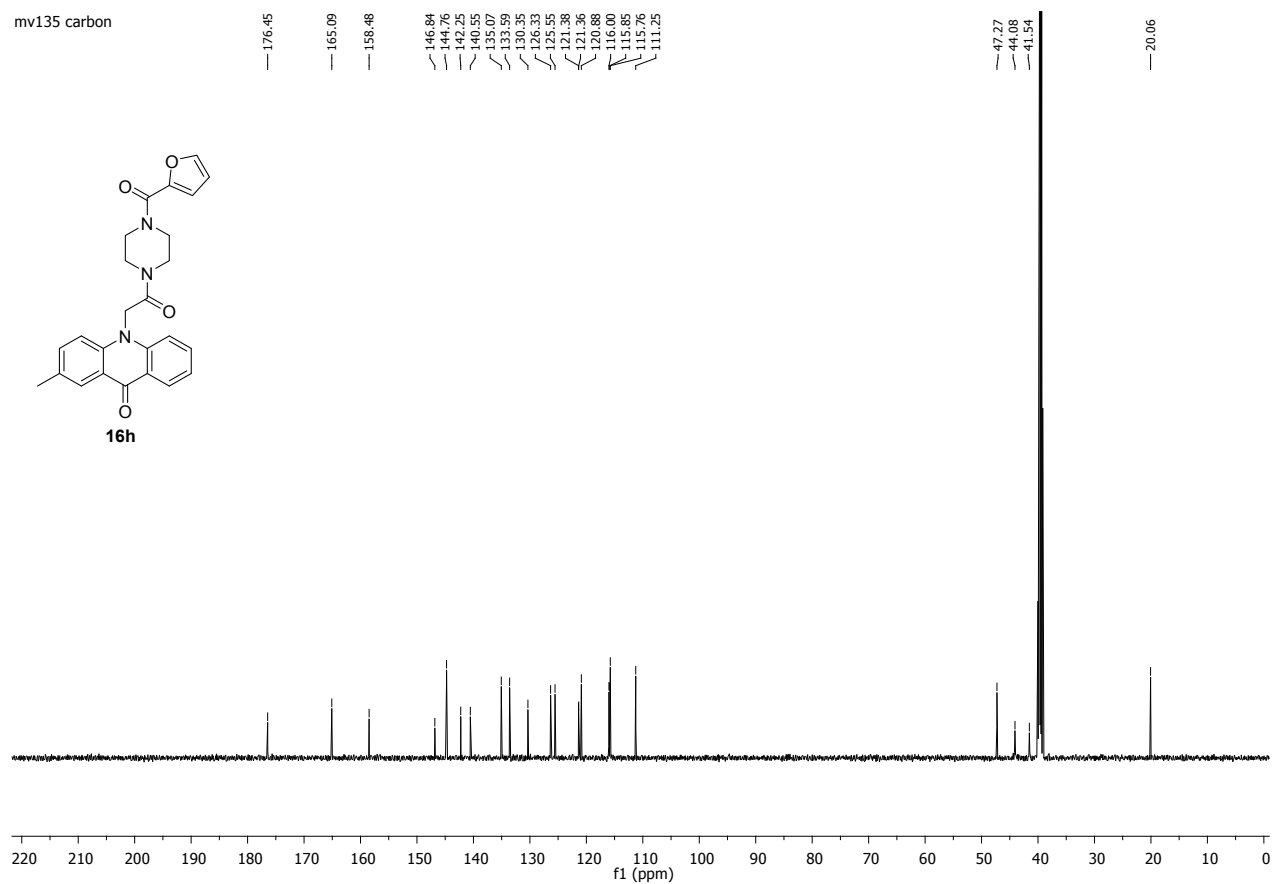
mv134 carbon



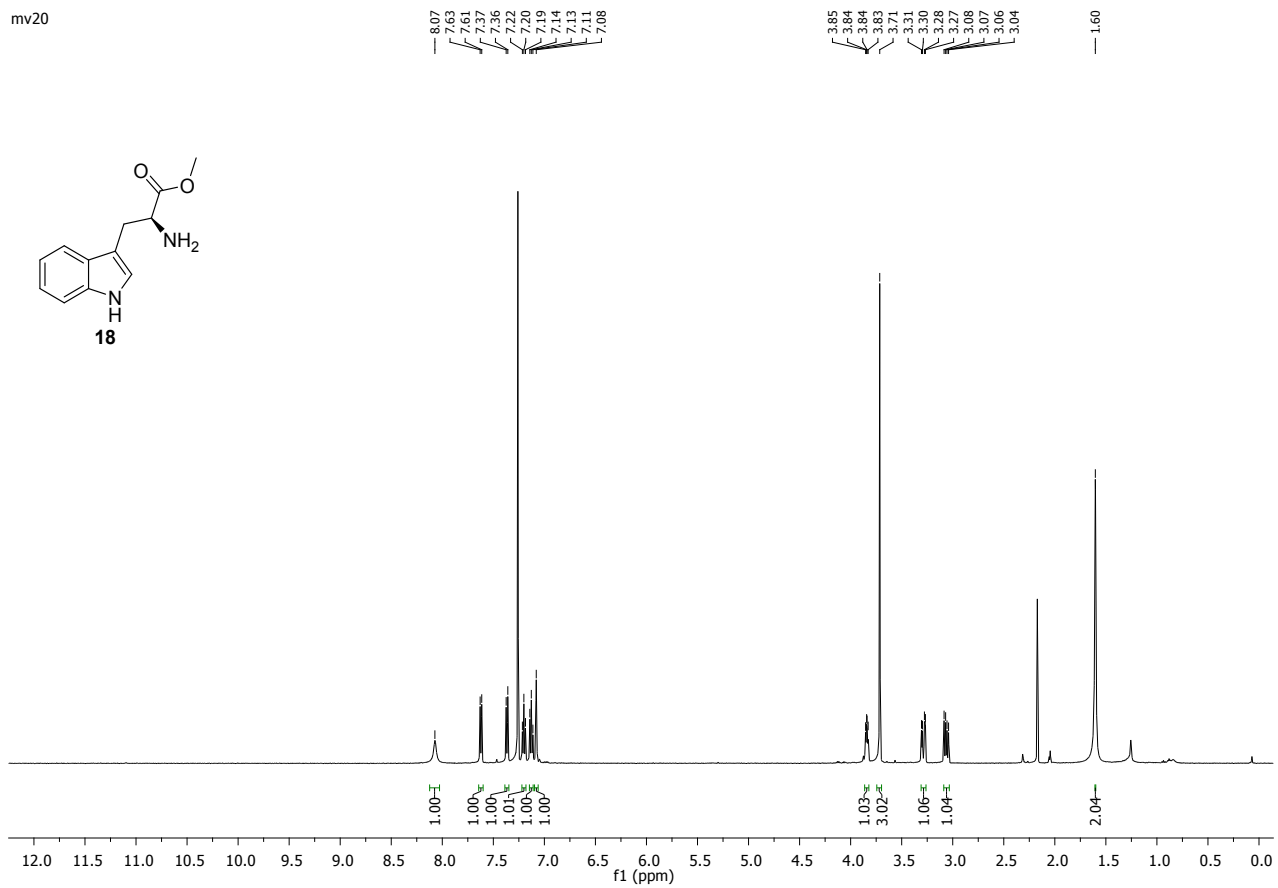
mv135



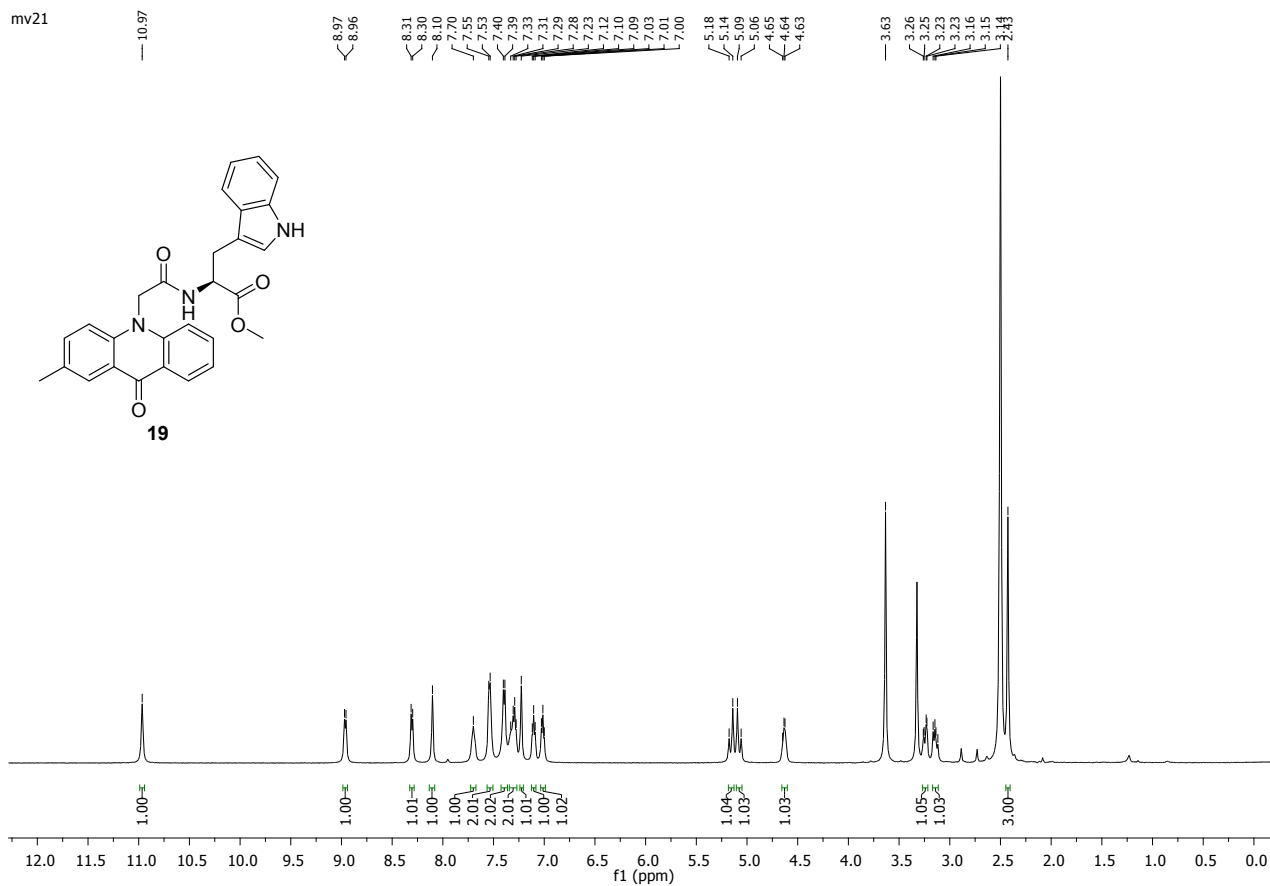
mv135 carbon



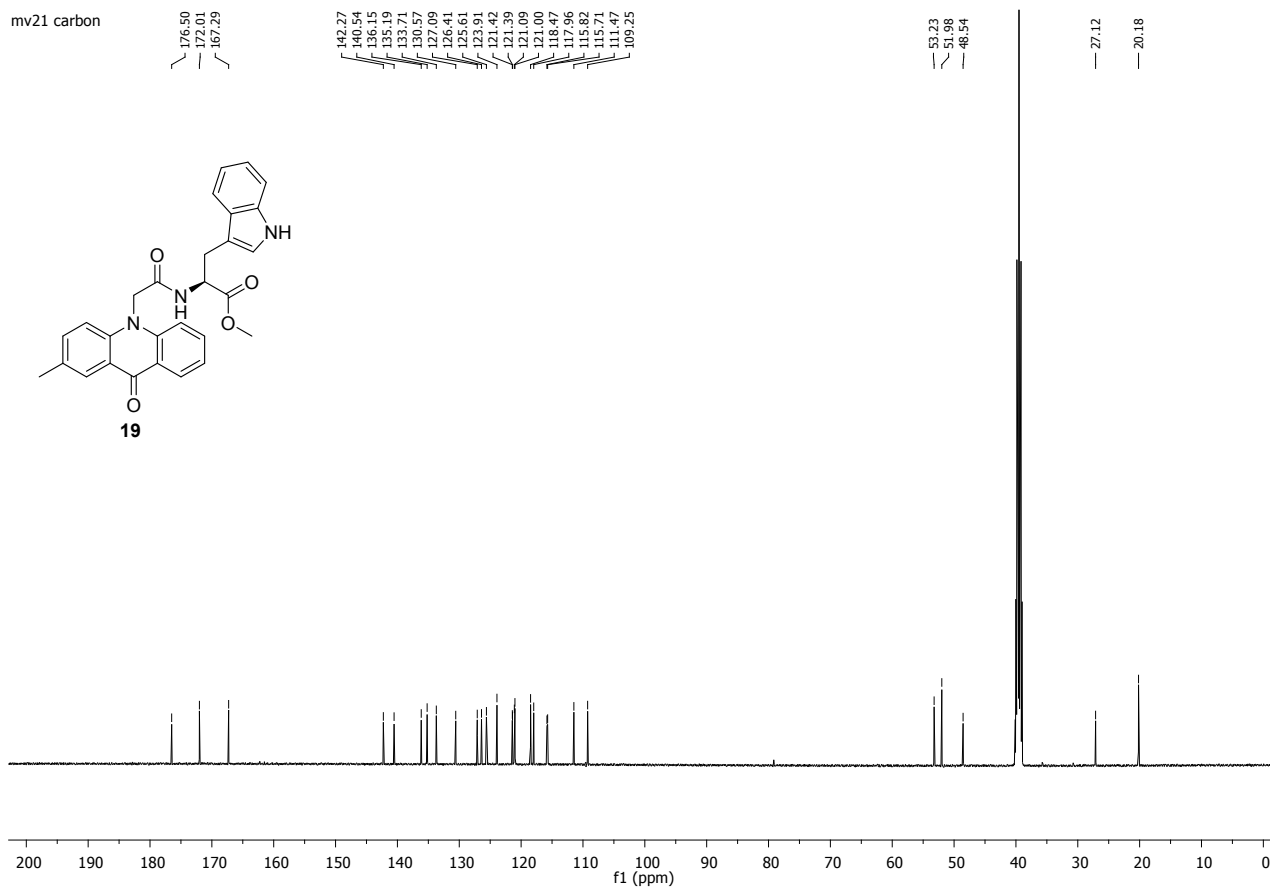
mv20



mv21



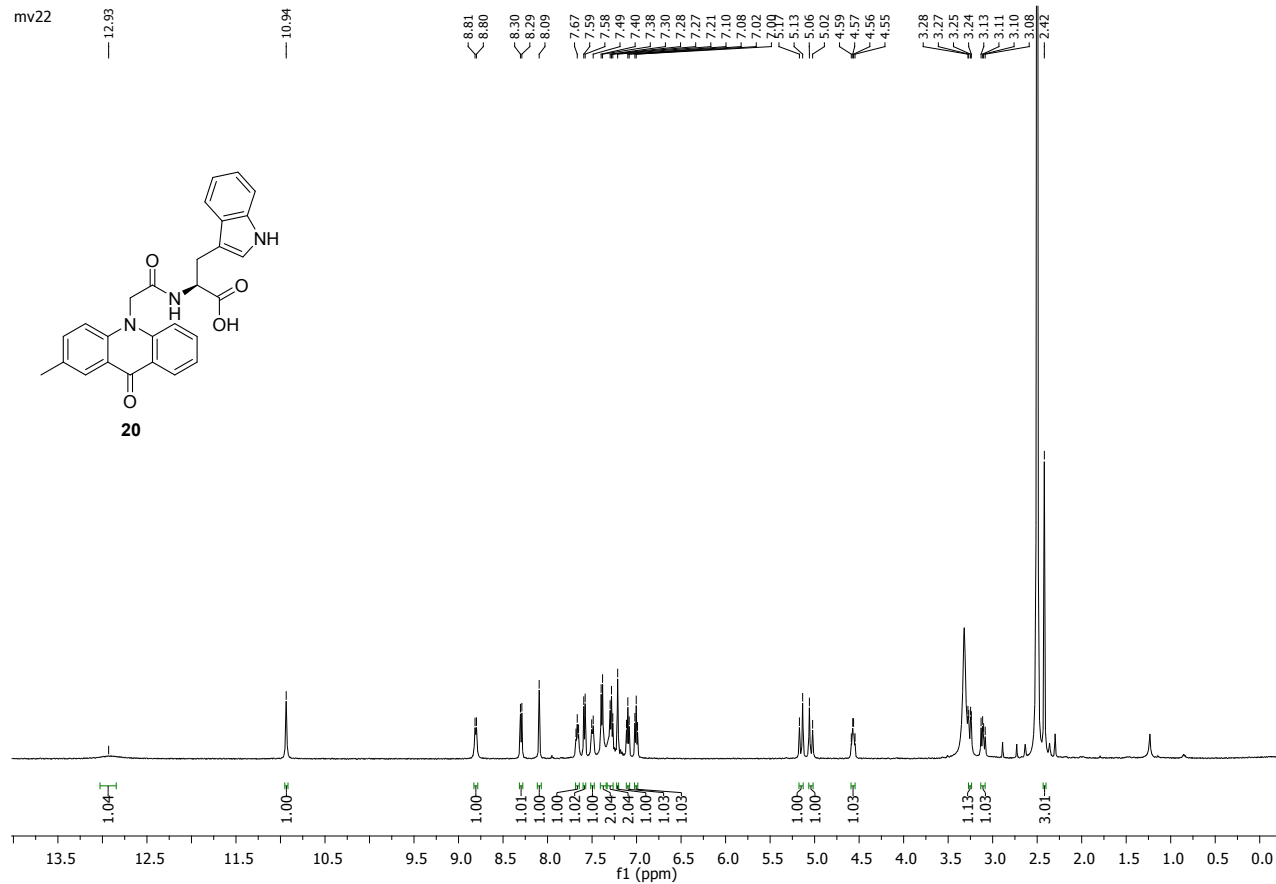
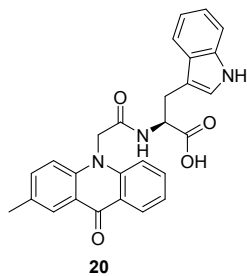
mv21 carbon



mv22

12.93

10.94

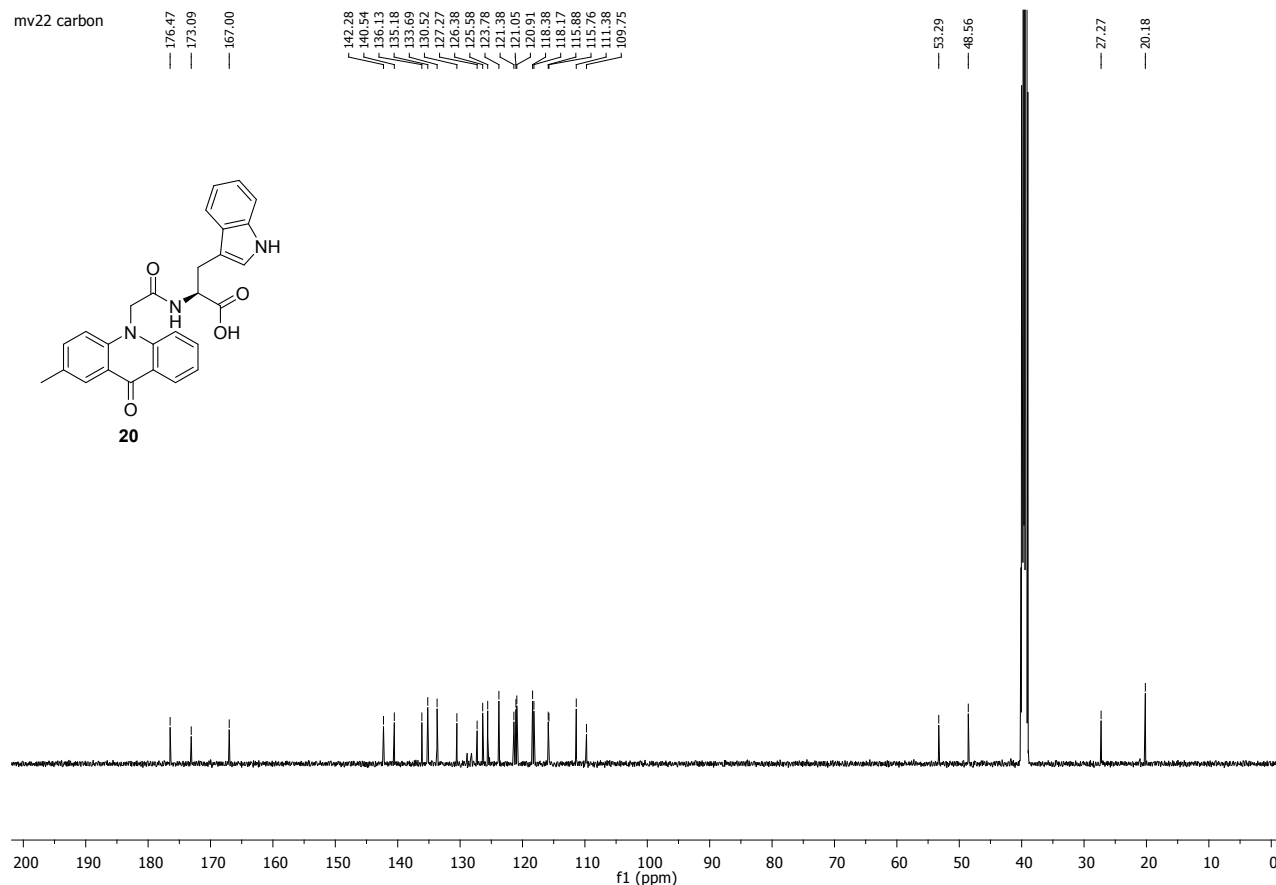
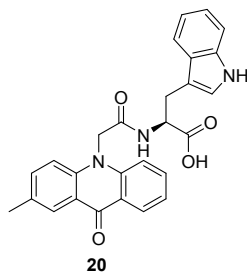


mv22 carbon

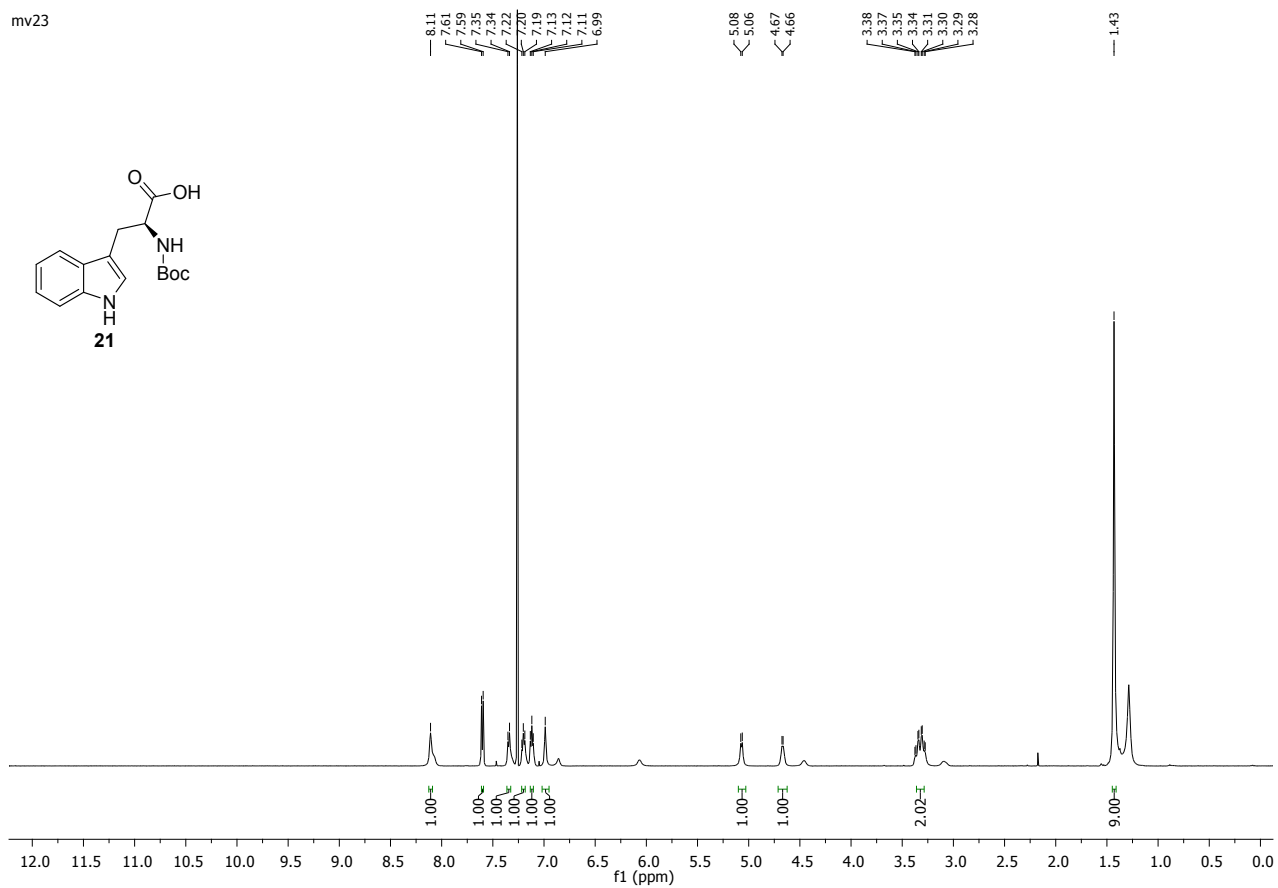
176.47

173.09

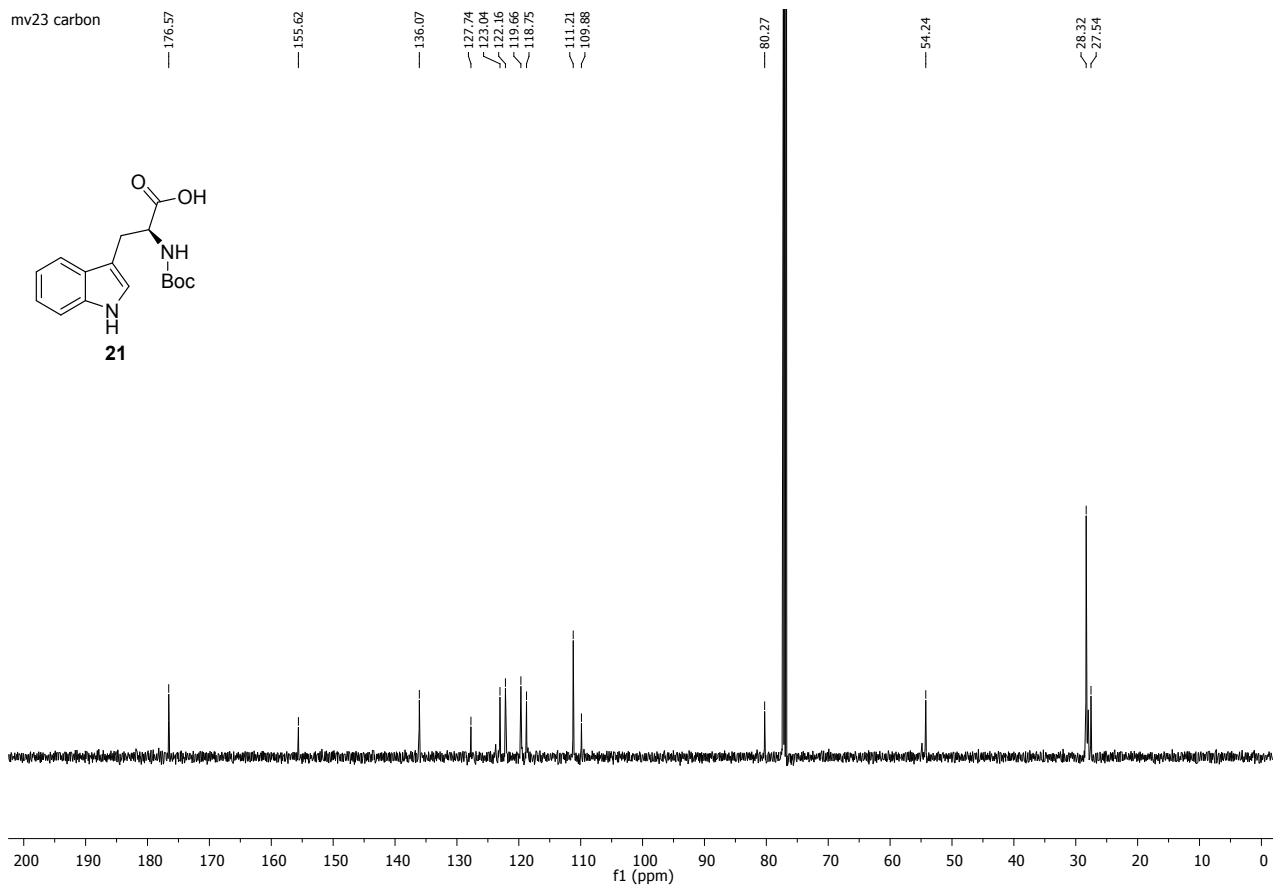
167.00



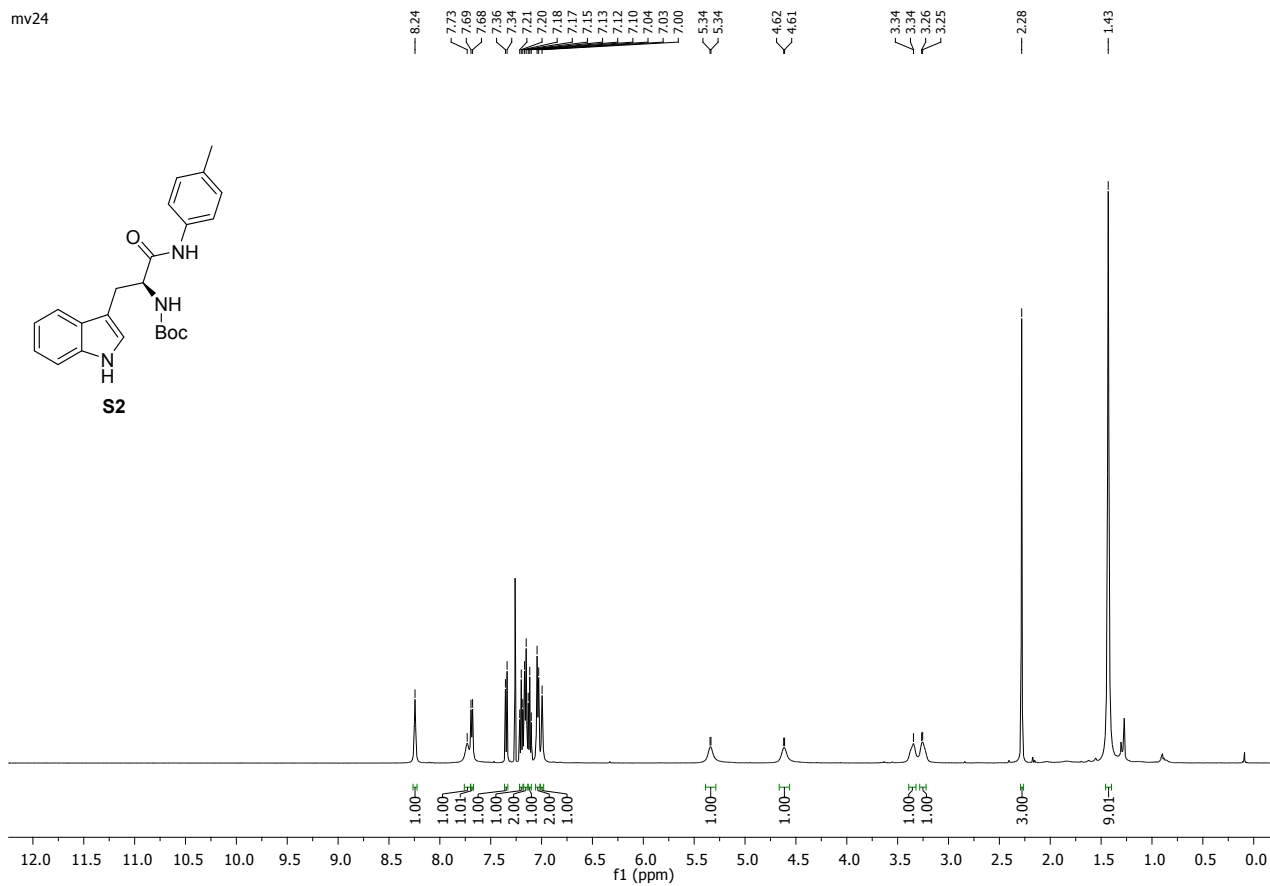
mv23



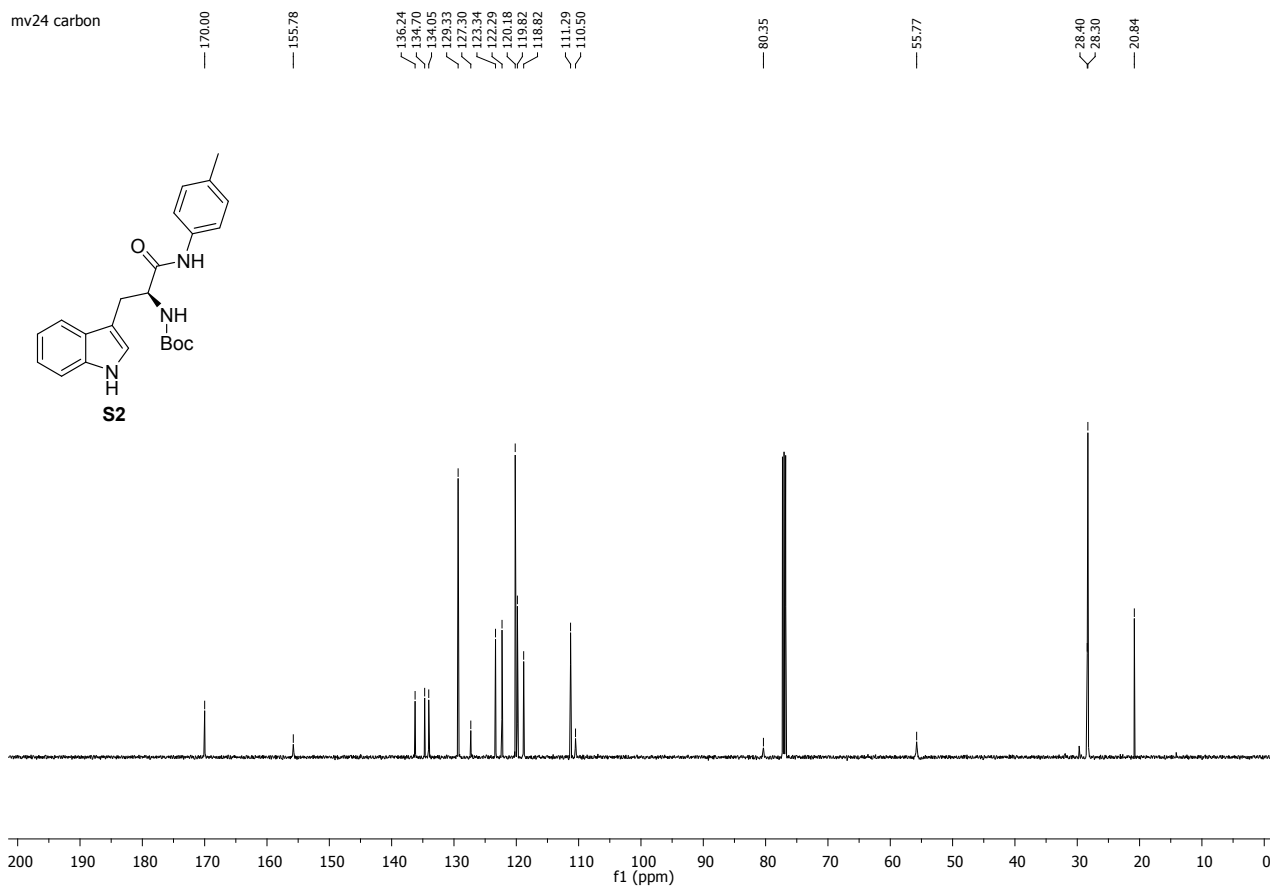
mv23 carbon



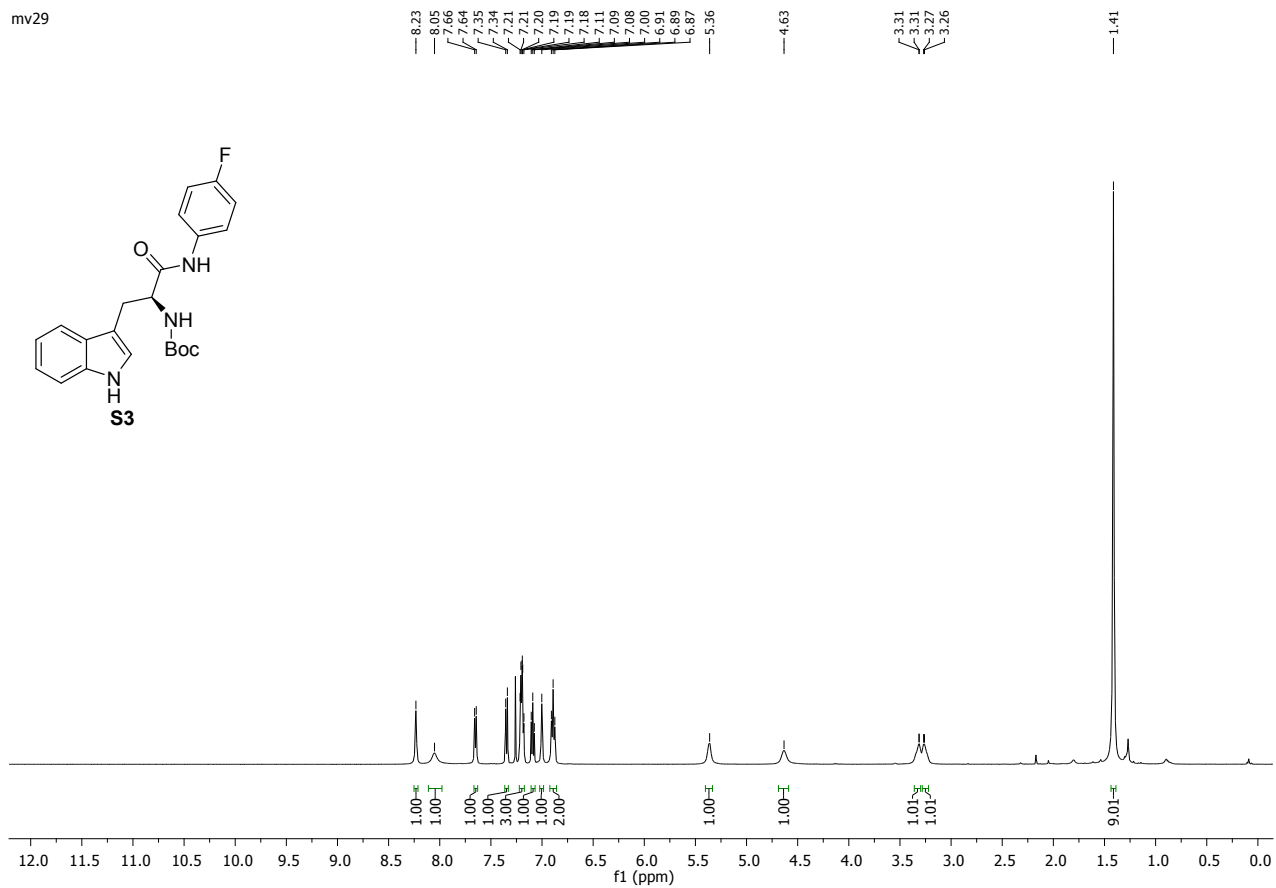
mv24



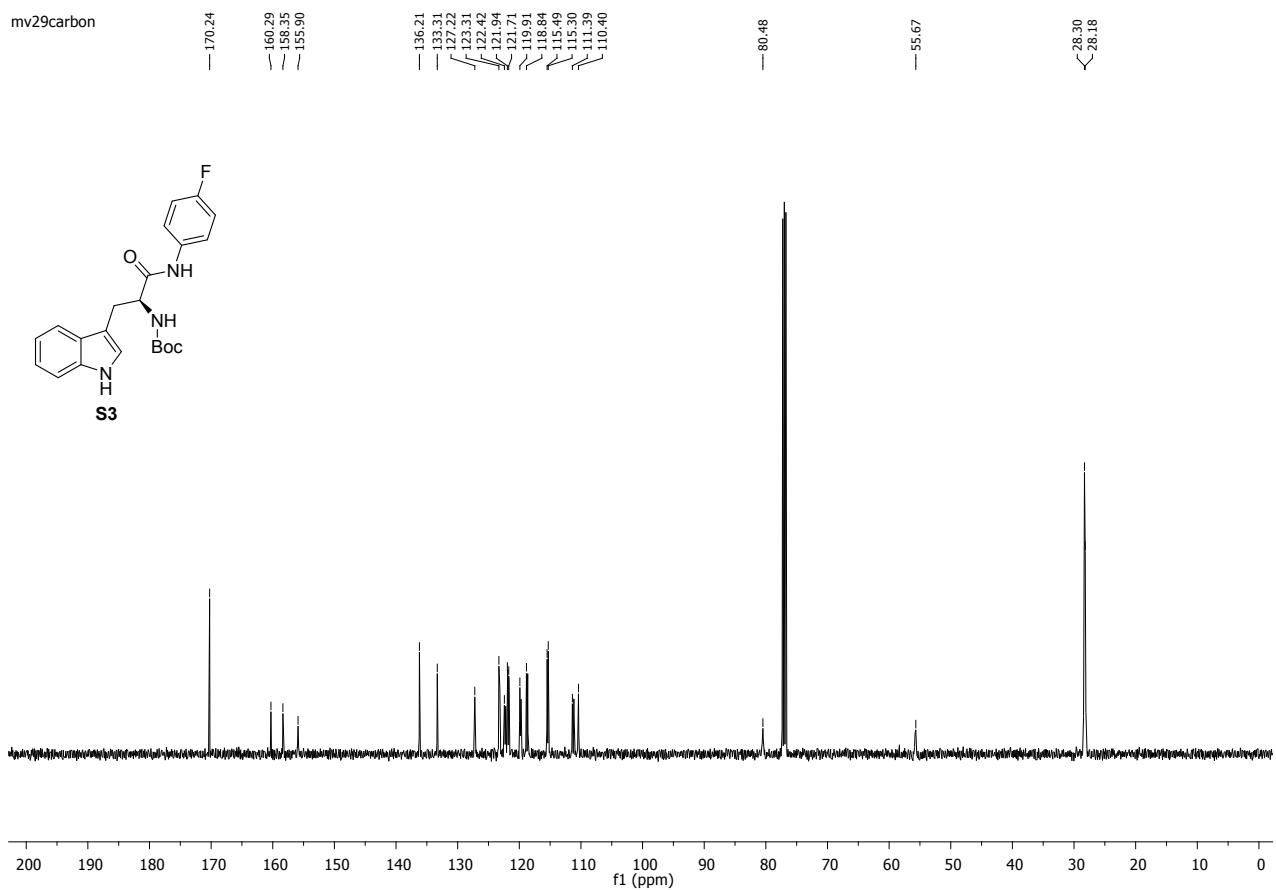
mv24 carbon



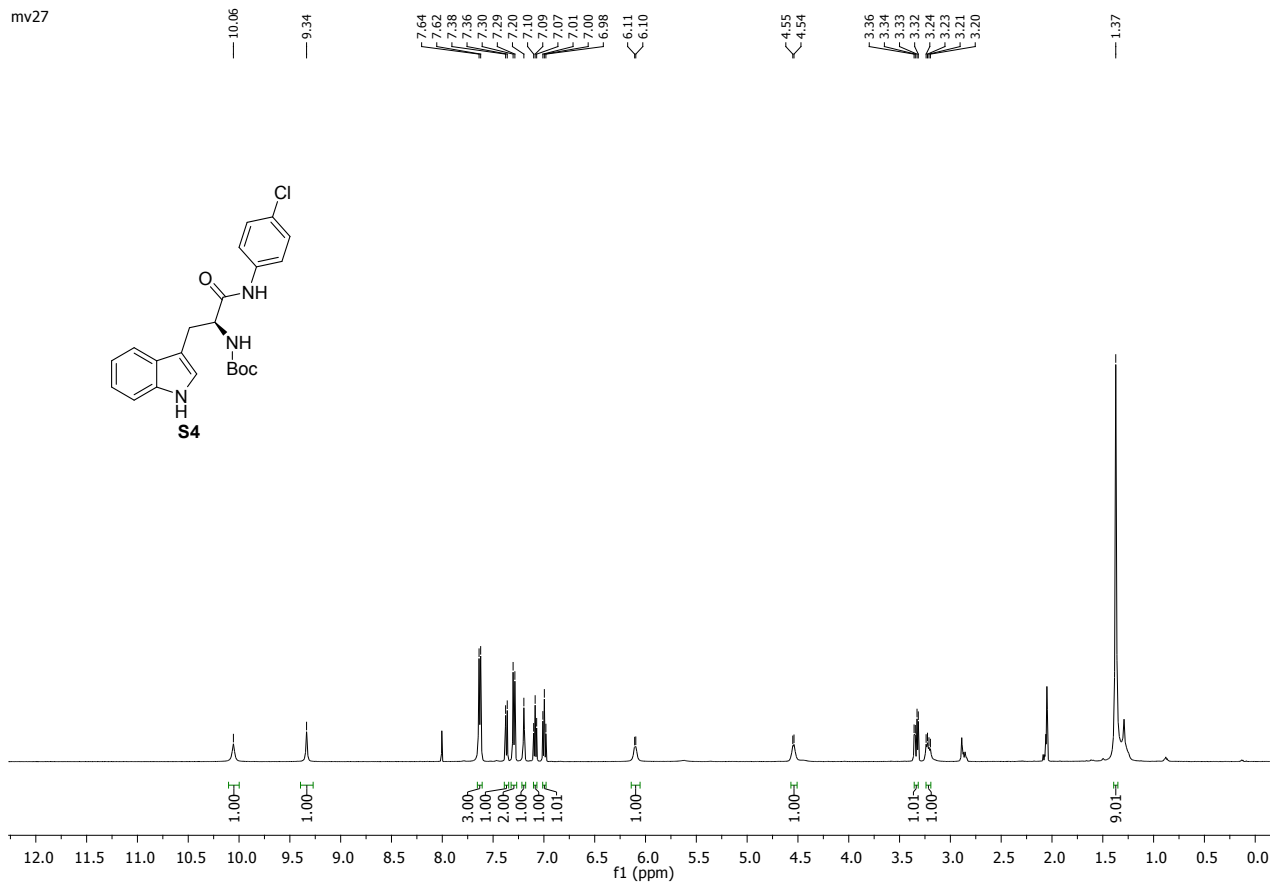
mv29



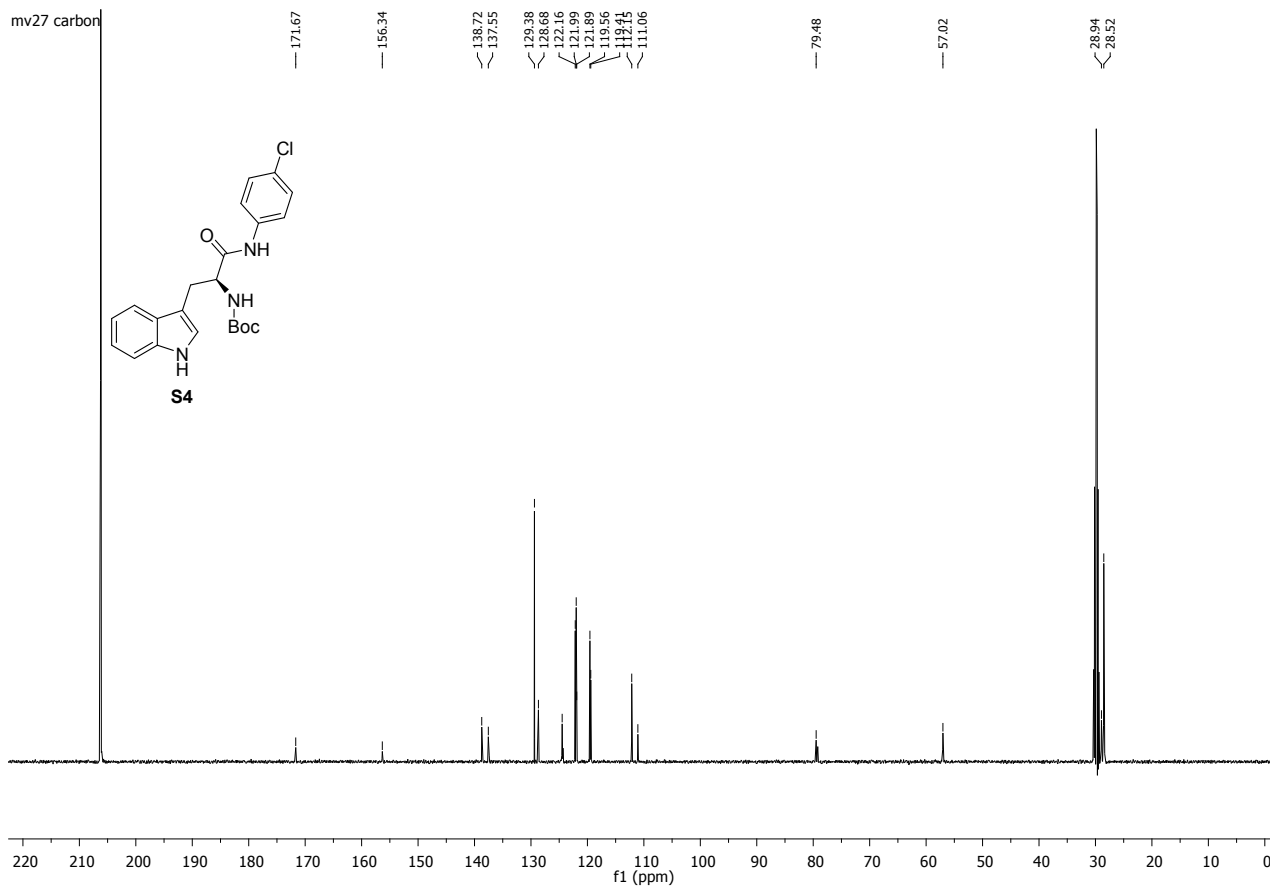
mv29carbon



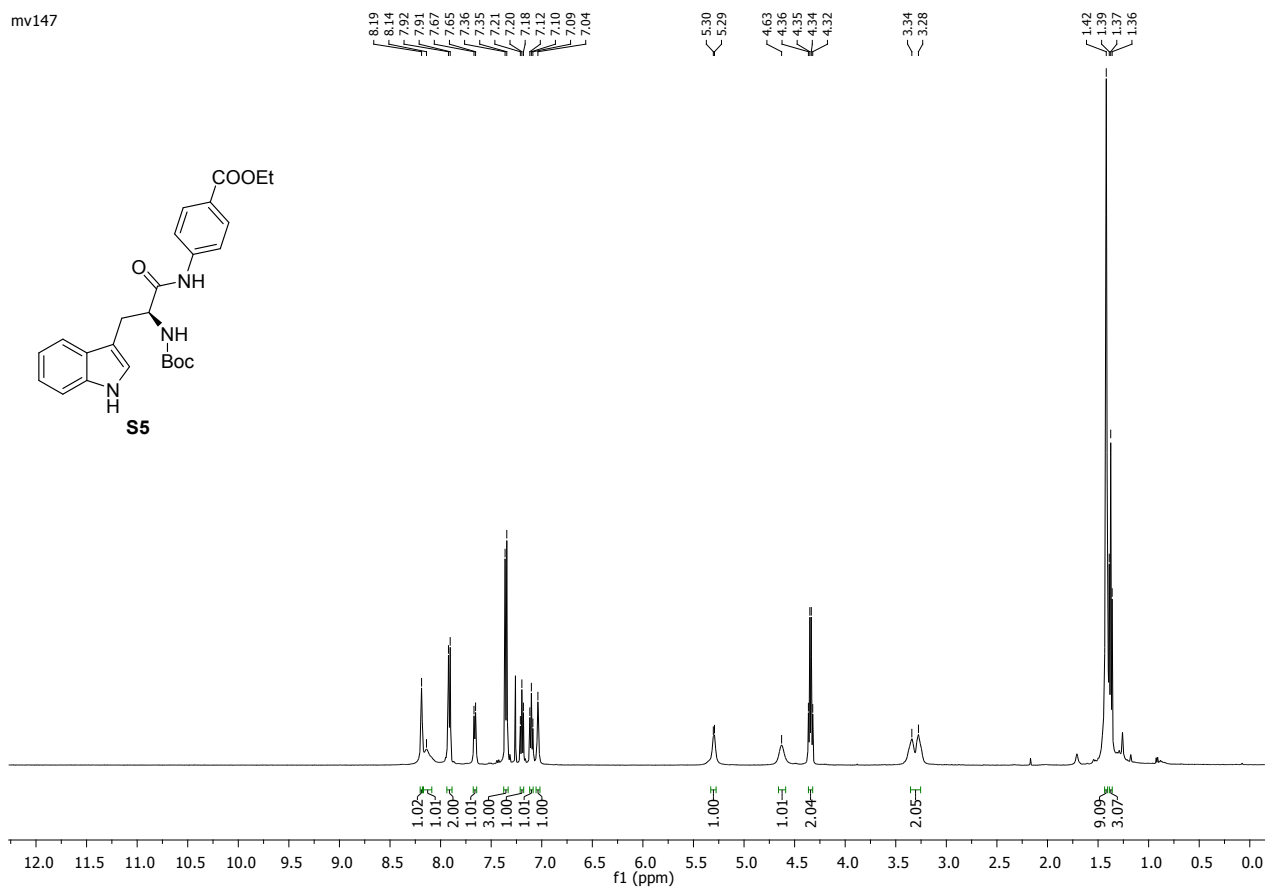
mv27



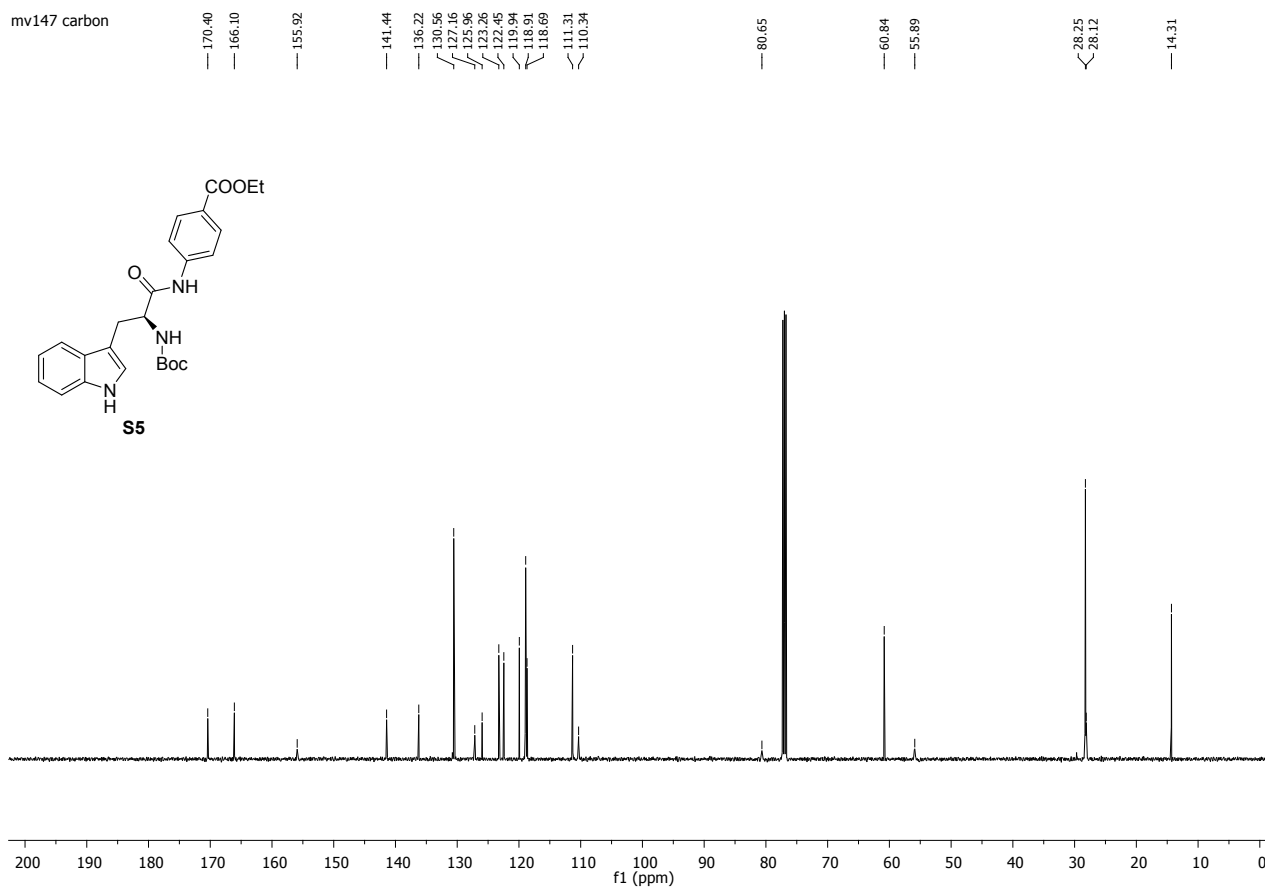
mv27 carbon



mv147



mv147 carbon



mv30 HCl salt

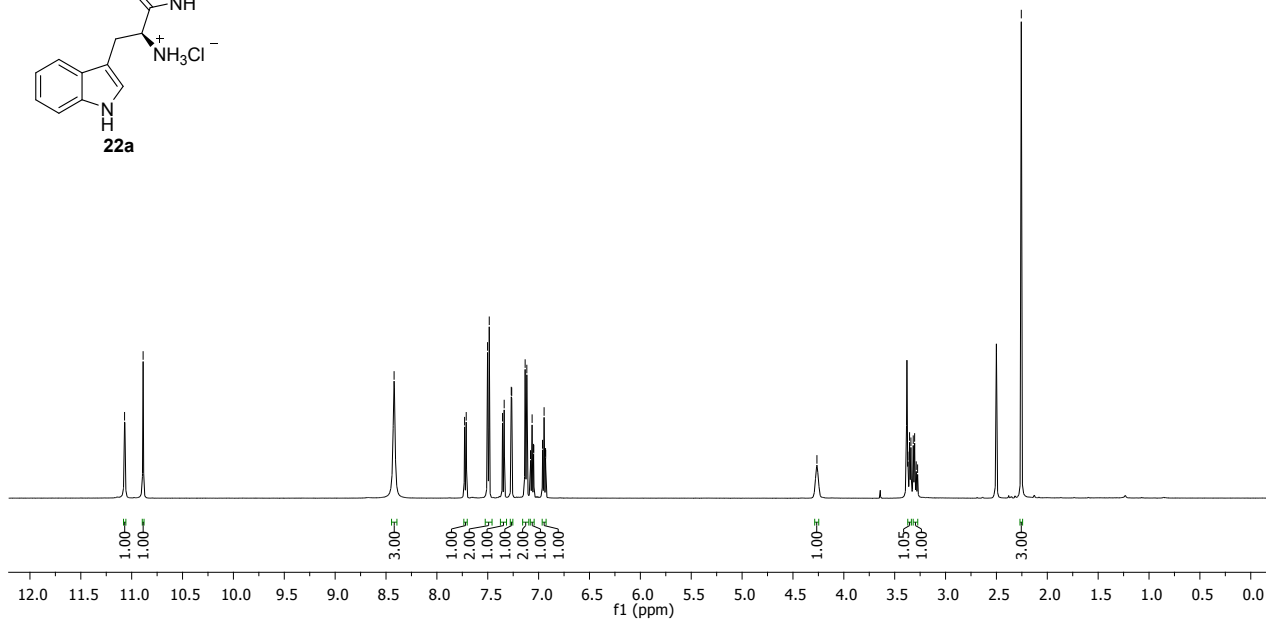
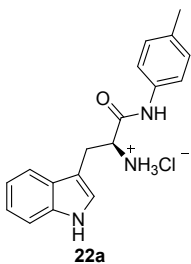
11.07
10.89

8.42
7.73
7.71
7.50
7.49
7.35
7.34
7.27
7.26
7.13
7.08
7.06
7.05
7.05
6.96
6.95
6.93

4.26

3.37
3.35
3.34
3.30
3.29
3.27

2.26



mv30 HCl salt carbon

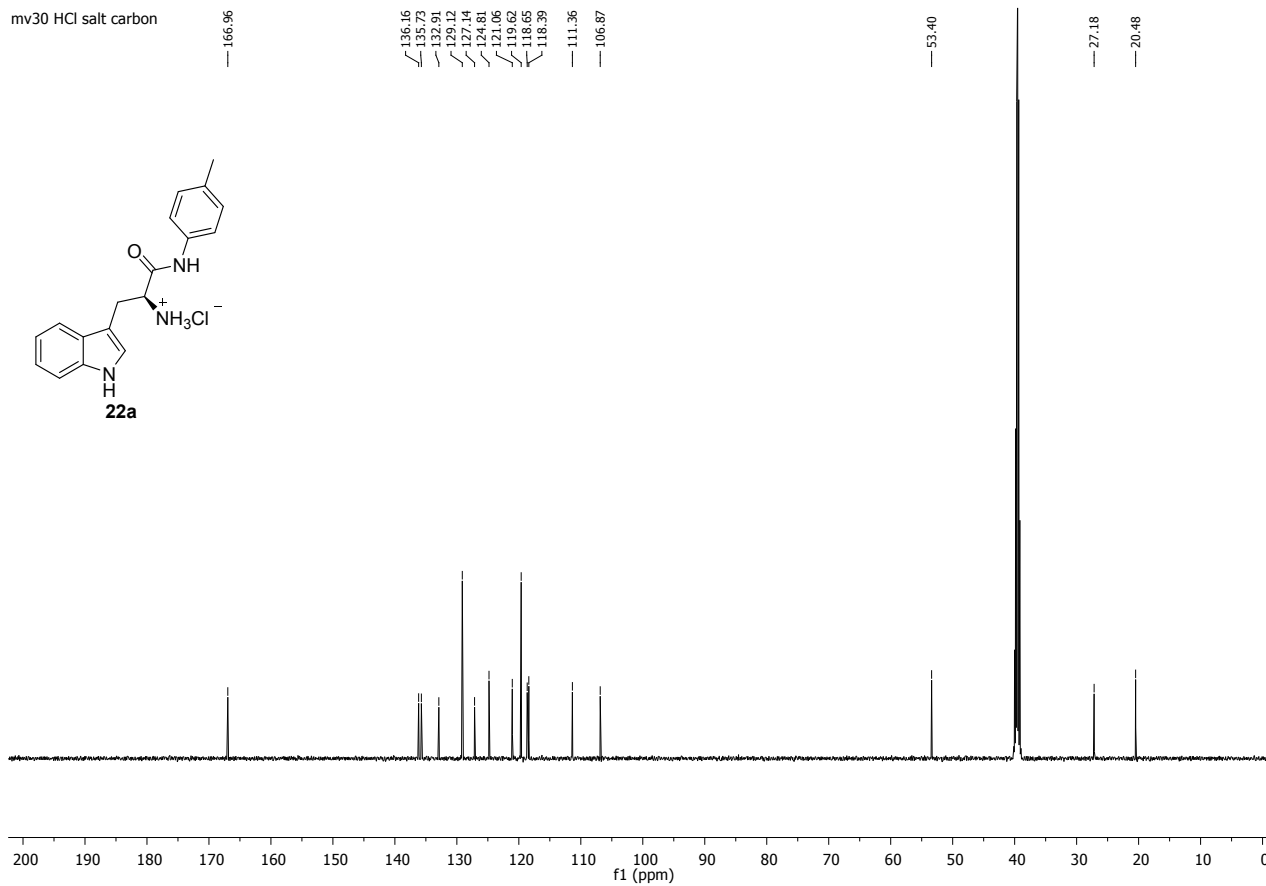
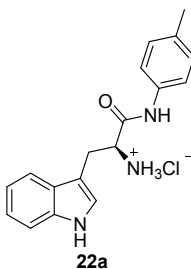
166.96

136.16
135.73
132.91
129.12
127.44
127.06
121.96
119.62
118.65
118.39
111.36
106.87

53.40

27.18

20.48



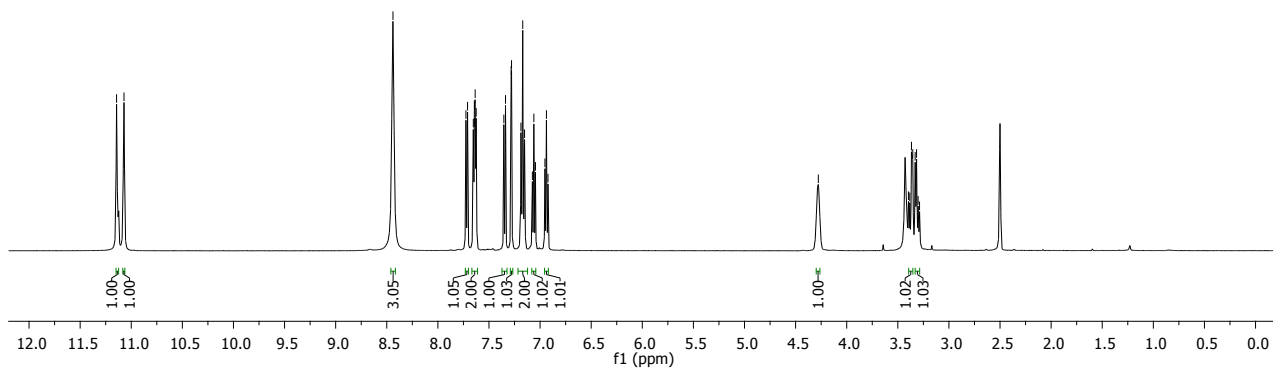
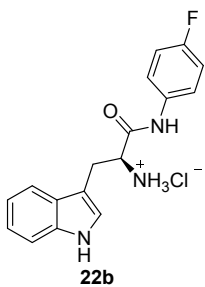
mv35 HCl salt⁺

11.14
11.07

8.44
7.73
7.71
7.65
7.64
7.64
7.63
7.53
7.52
7.38
7.28
7.19
7.17
7.15
7.08
7.06
7.05
6.95
6.94
6.92

4.28

3.40
3.38
3.37
3.35
3.33
3.32
3.30
3.29



mv35 HCl salt carbon

167.15

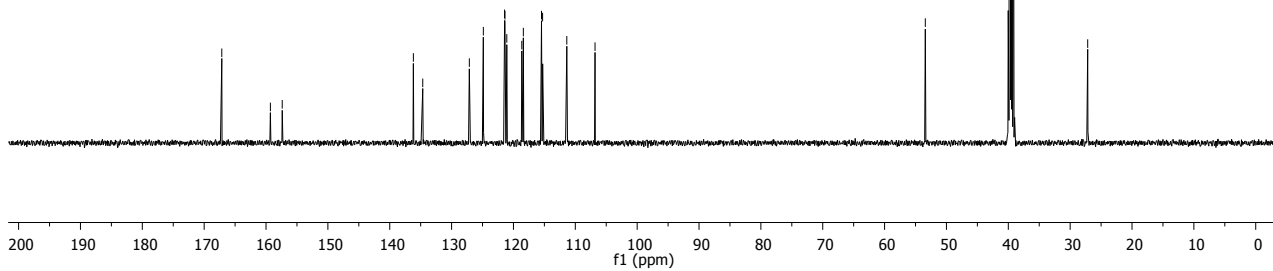
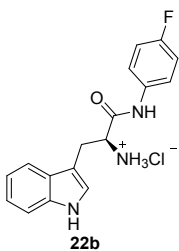
159.29
157.38

136.18
134.66

127.13
124.87
121.43
121.37
121.07
118.65
118.40
115.97
115.29
113.27
106.81

53.42

27.16

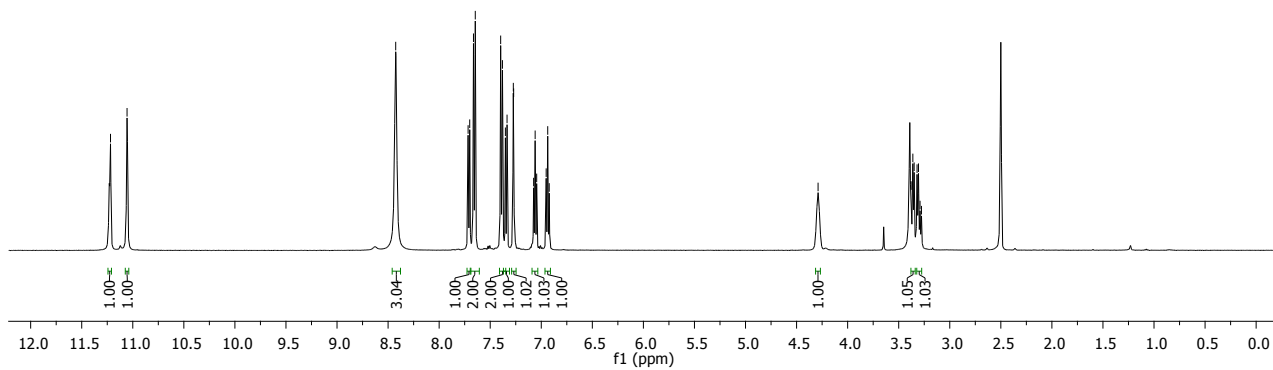
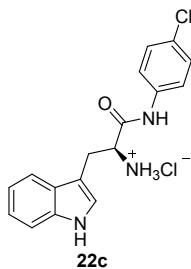


mv33 HCl salt
11.72
11.06

8.43
7.72
7.70
7.66
7.65
7.40
7.38
7.35
7.34
7.27
7.27
7.07
7.04
6.95
6.94
6.92

4.29

3.38
3.36
3.35
3.32
3.31
3.29
3.28



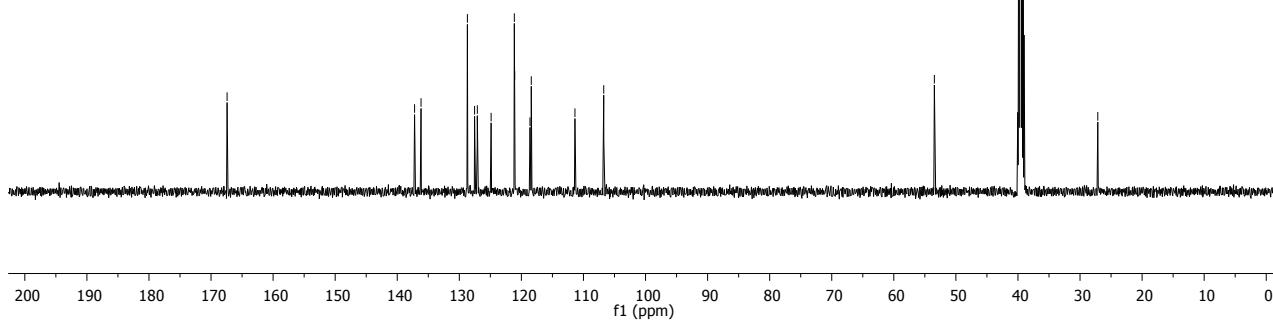
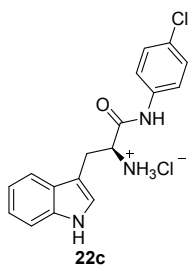
mv33 HCl salt carbon

167.41

137.21
136.17
128.70
127.54
127.10
124.88
121.14
121.08
118.62
118.41
111.37
106.73

53.47

27.14

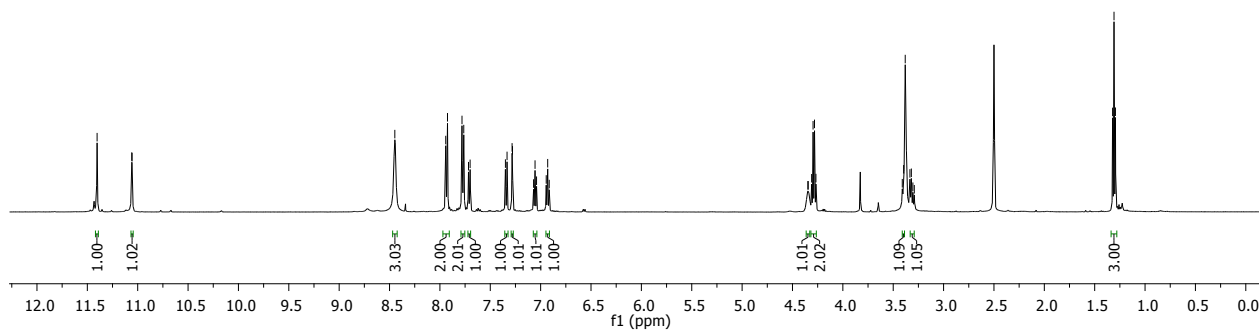
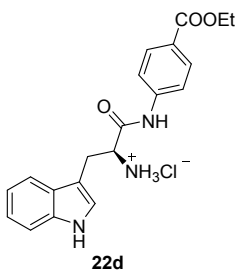


mv150 HCl
11.91
11.06
11.06

8.45
7.94
7.92
7.78
7.76
7.70
7.35
7.33
7.28
7.28
7.07
7.06
7.04
6.94
6.93
6.91

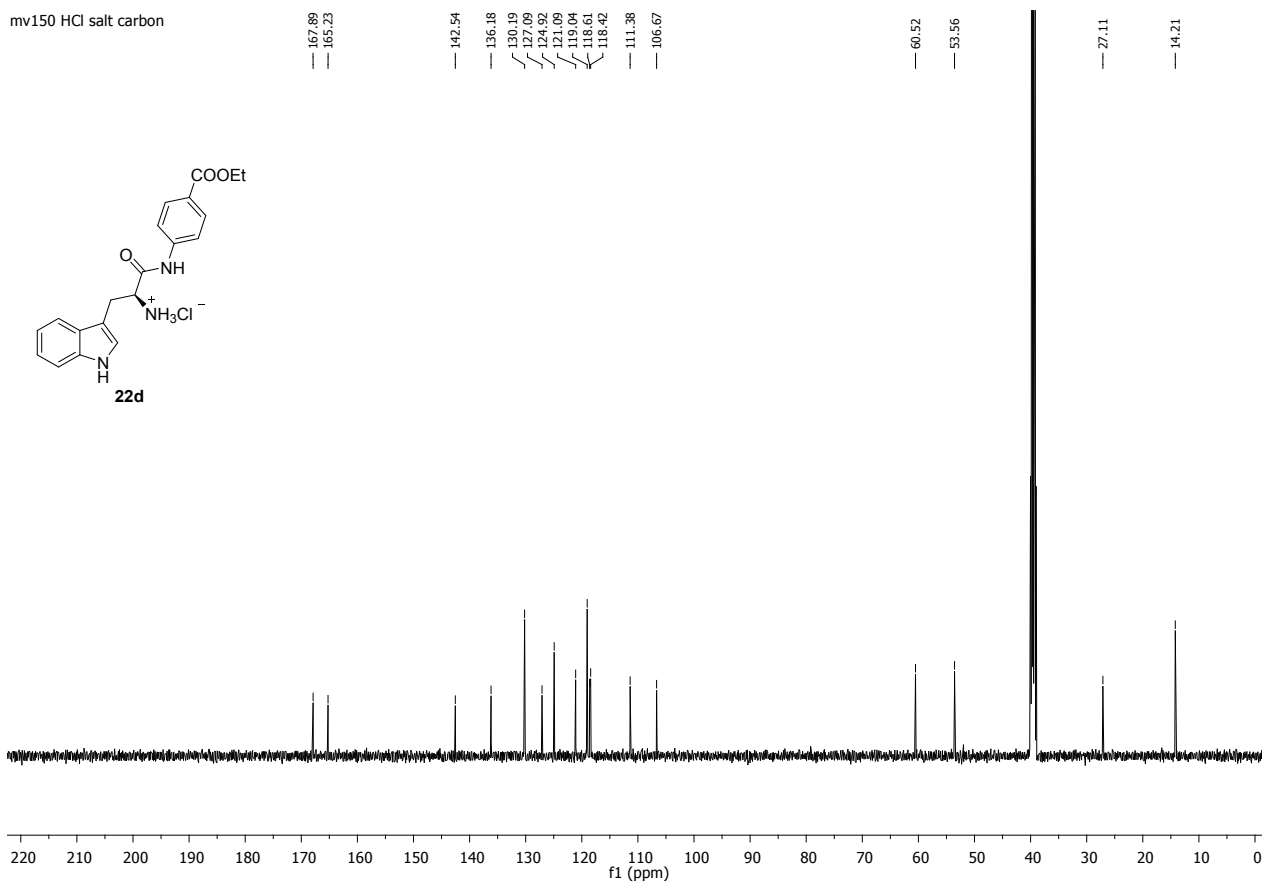
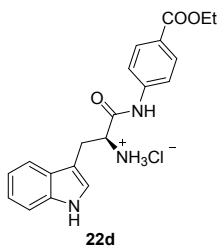
4.35
4.34
4.31
4.30
4.28
4.27
3.41
3.40
3.38
3.35
3.32
3.30
3.29

1.32
1.31
1.29

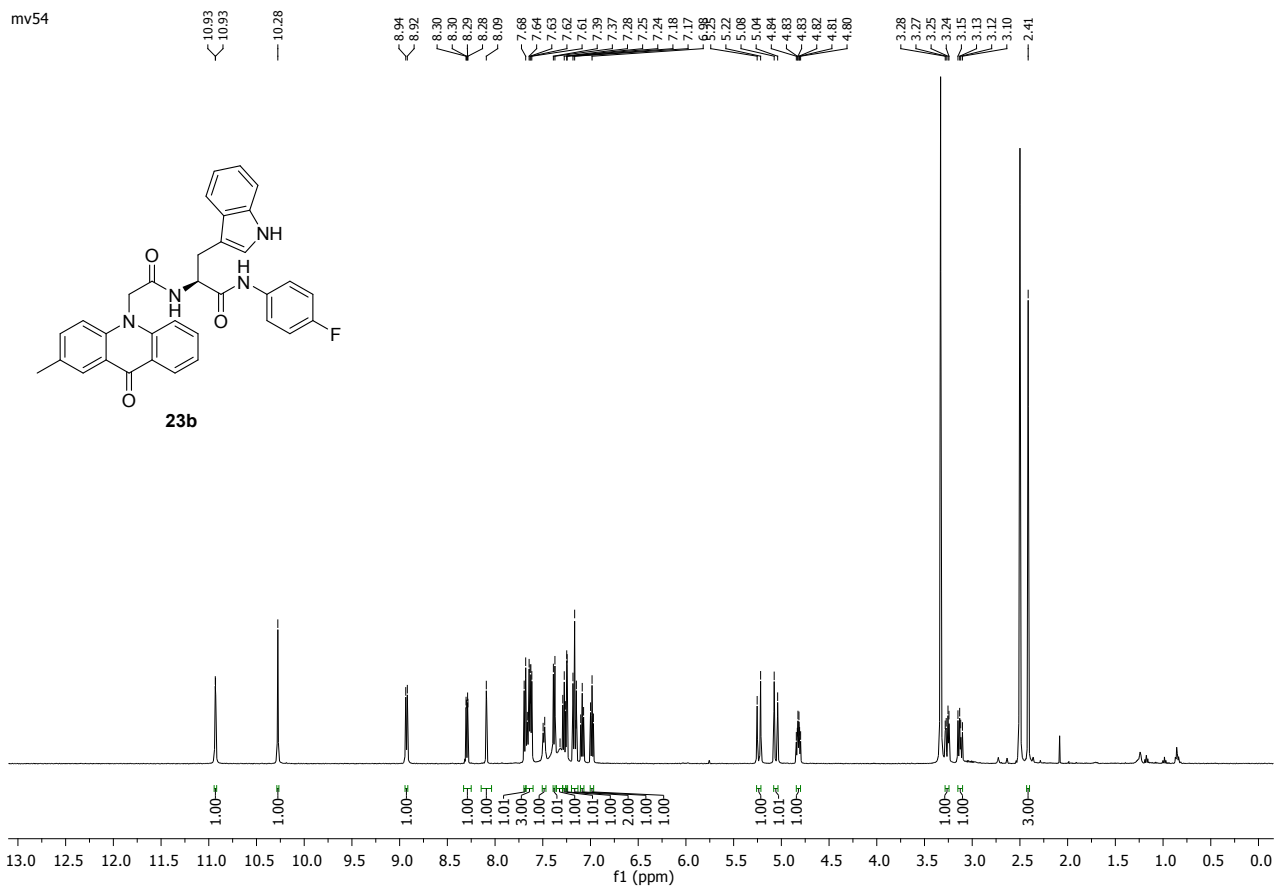


mv150 HCl salt carbon

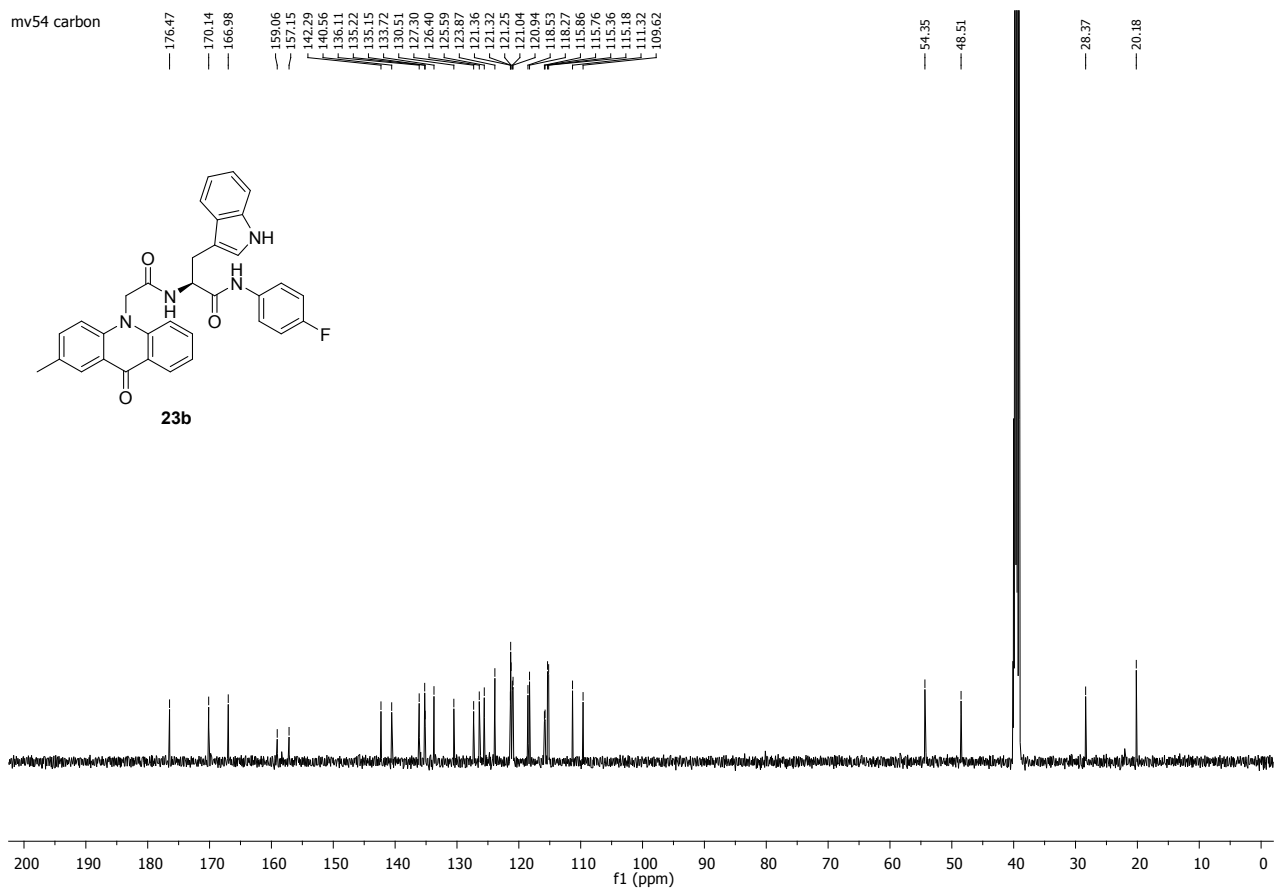
167.89
165.23
142.54
136.18
130.19
127.09
124.92
121.09
119.04
118.61
118.42
111.38
106.67
60.52
53.56
27.11
14.21



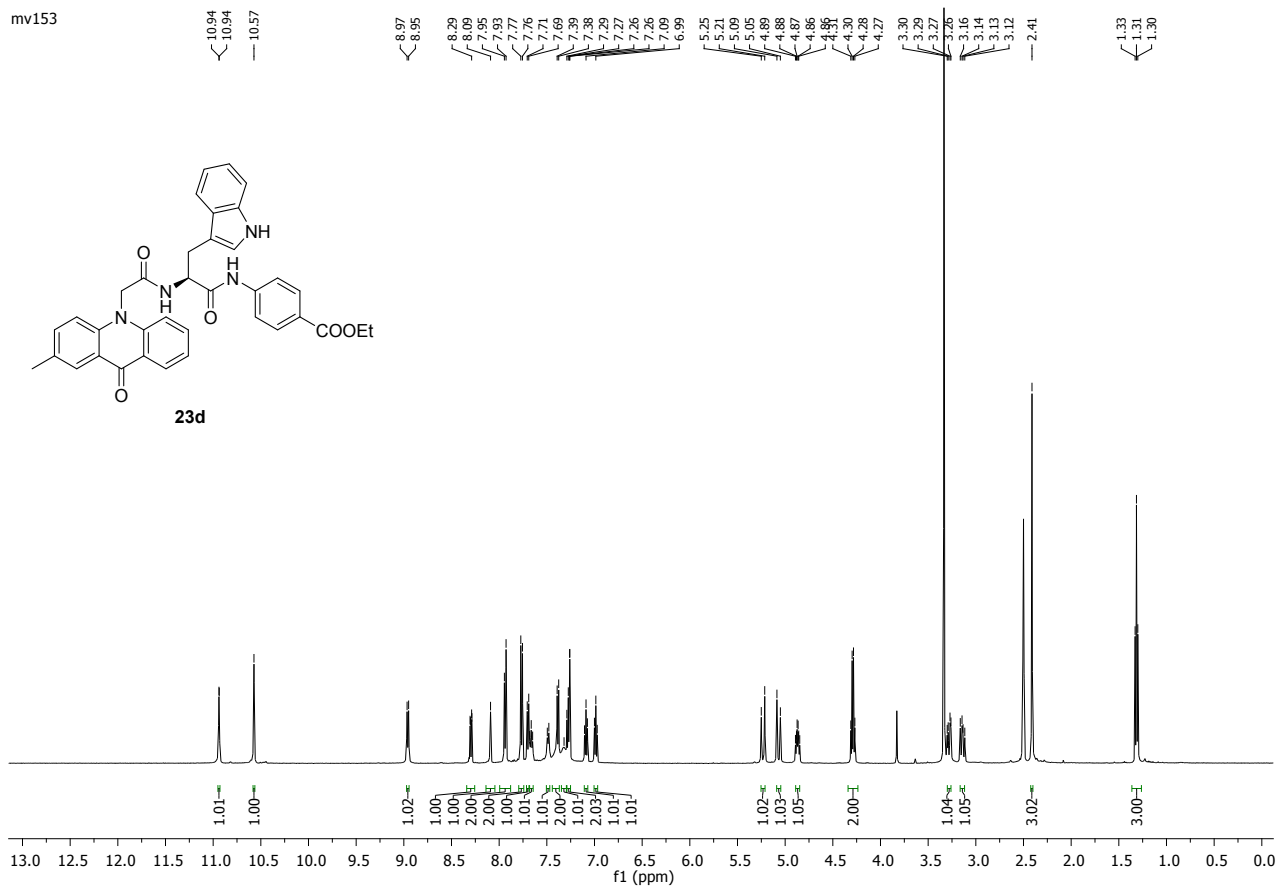
mv54



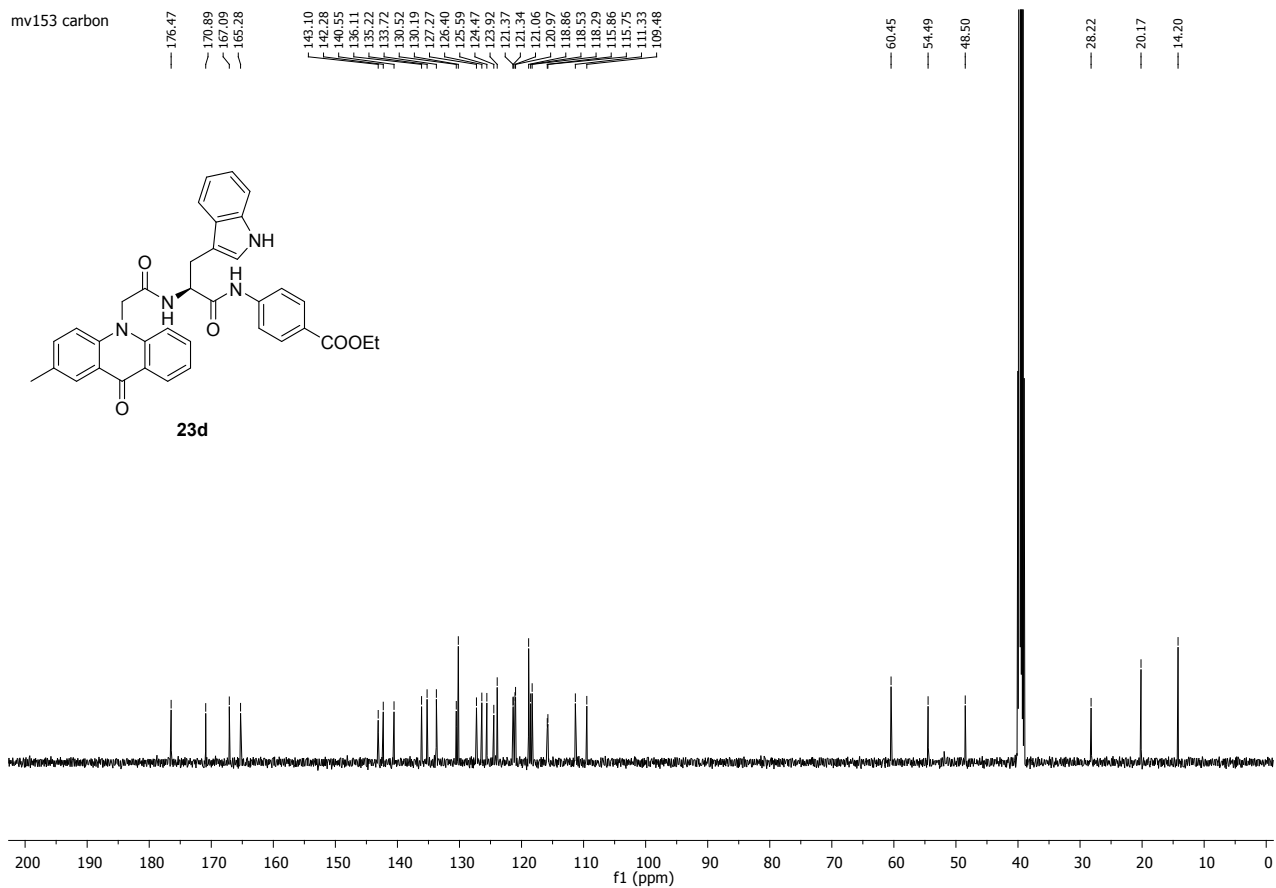
mv54 carbon



mv153



mv153 carbon



Analytical method for compounds **9a-i** and **10**:

LC-MS/HPLC: LC-20AD Shimadzu connected to Shimadzu LCMS-2010EV

Mobile Phase A: 0.1% FA in water

Mobile Phase B: methanol

HPLC column: Poroshell 120 EC-C18, 4.6 x 100 mm, 2.7 μ m

Flow rate: 0.4 mL/min

Run time: 20 min

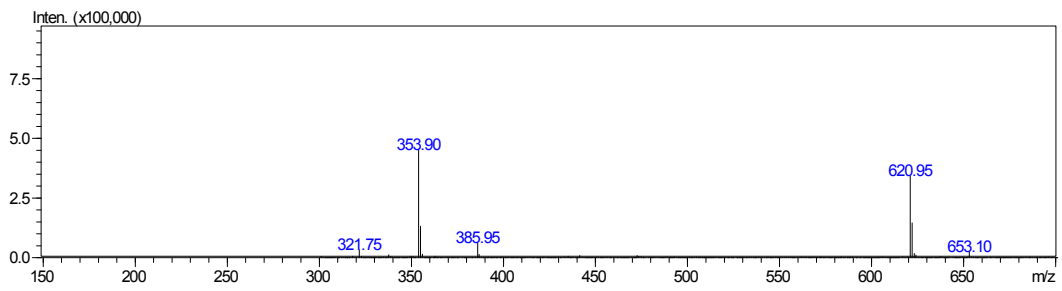
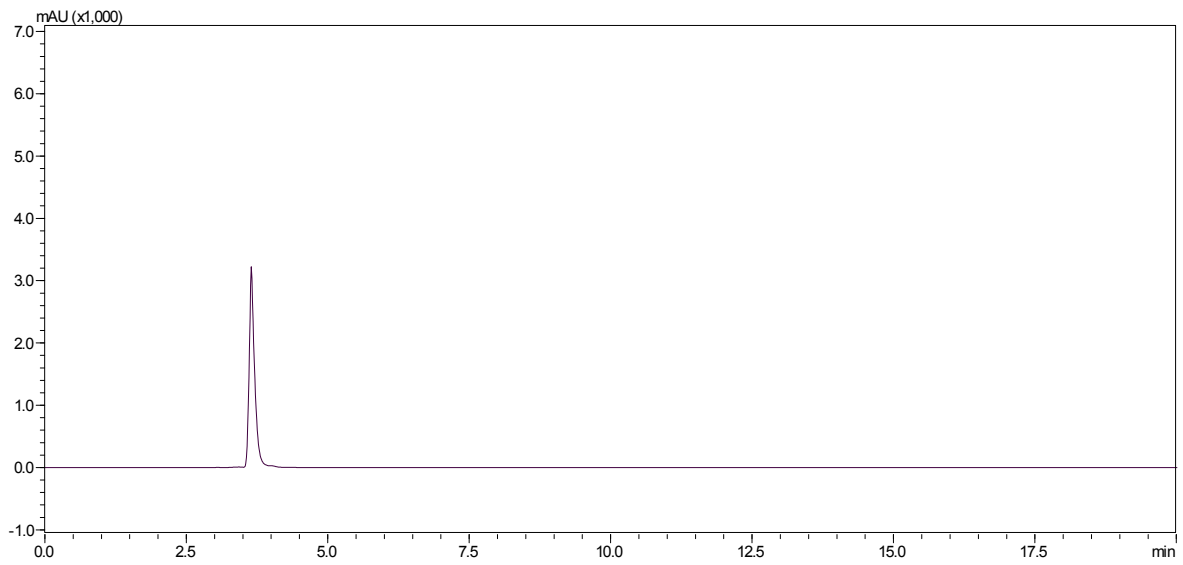
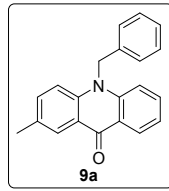
Column temperature: 26°C

UV detector: 254 nm

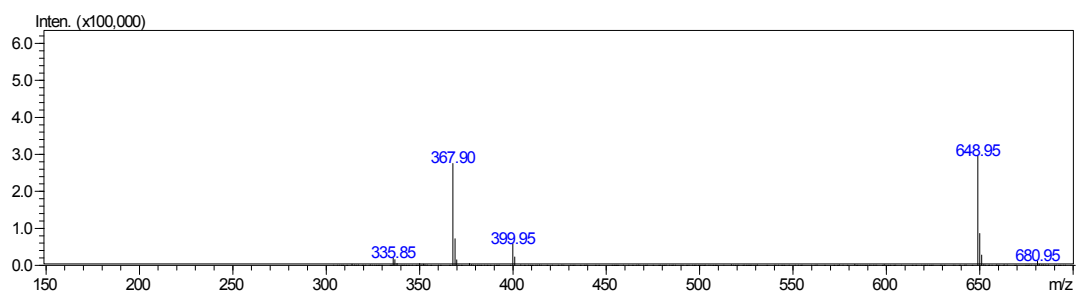
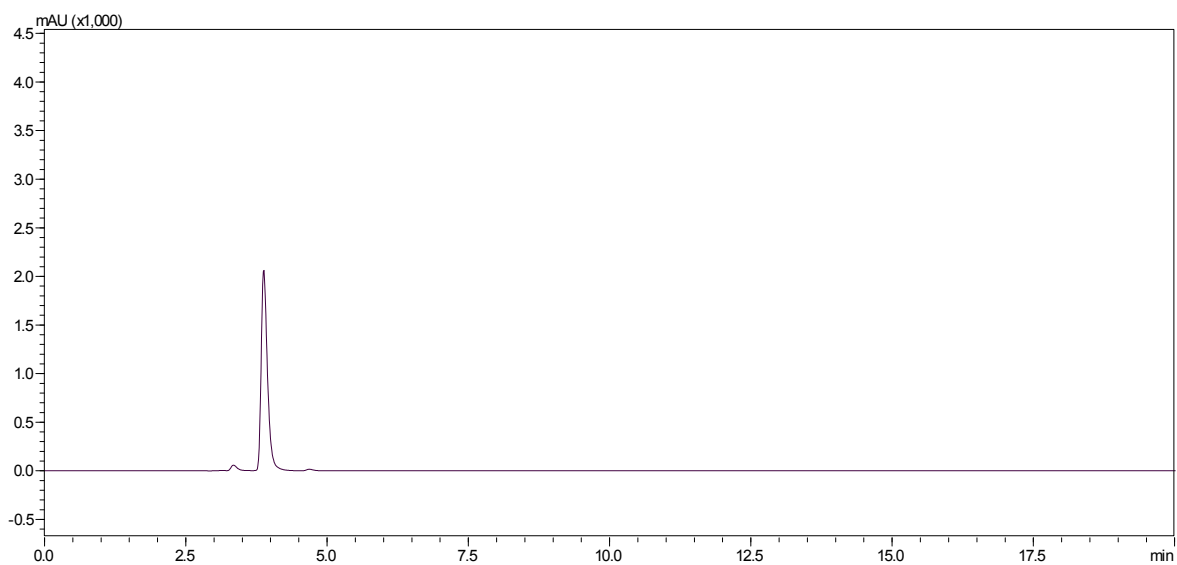
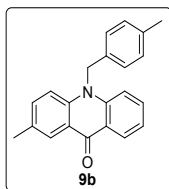
MS detector: 1.65 kV

LC isocratic:

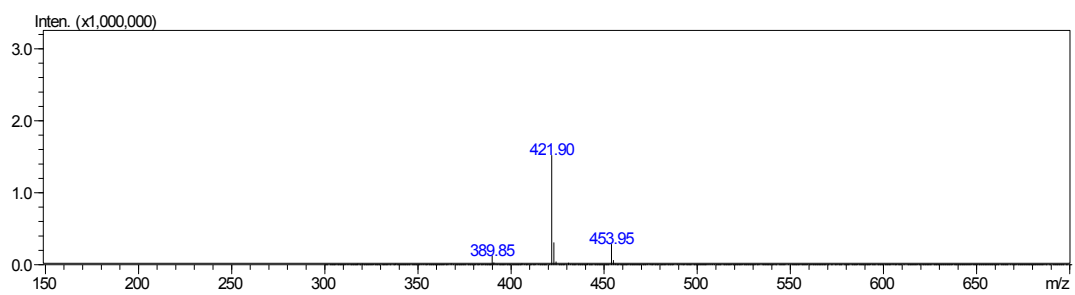
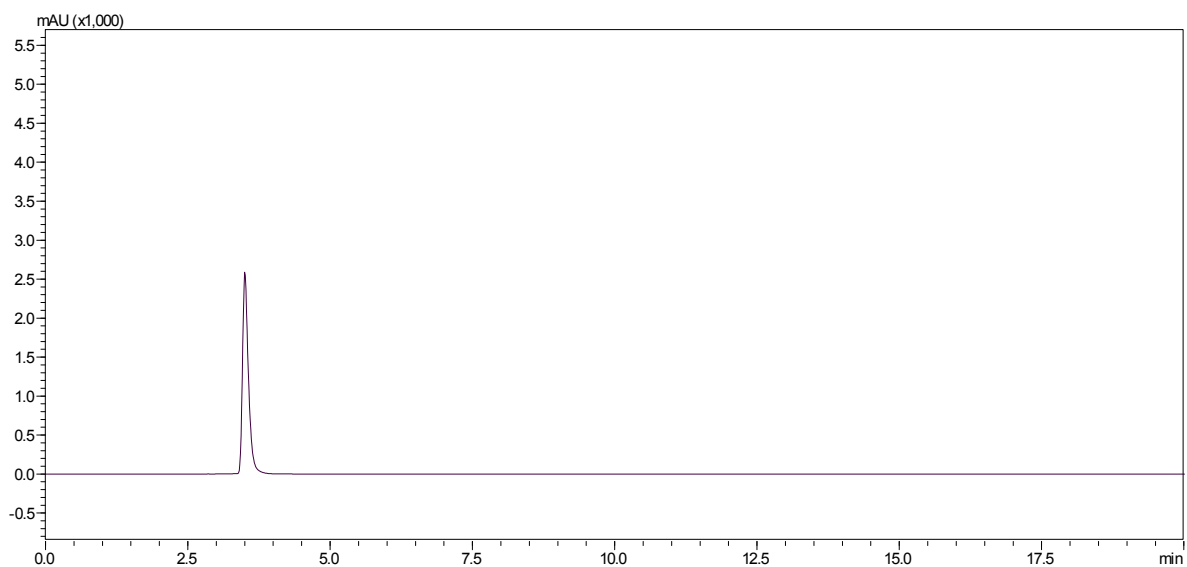
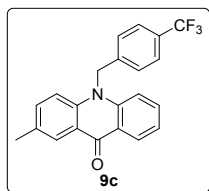
Time (min)	Mobile Phase A (%)	Mobile Phase B (%)
0	0	100
20	0	100



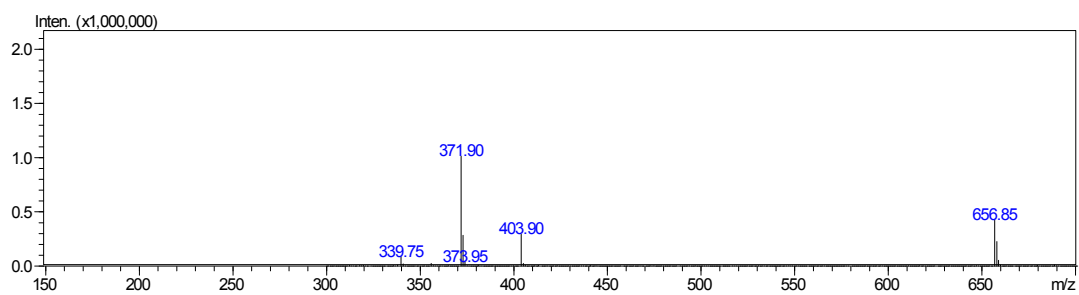
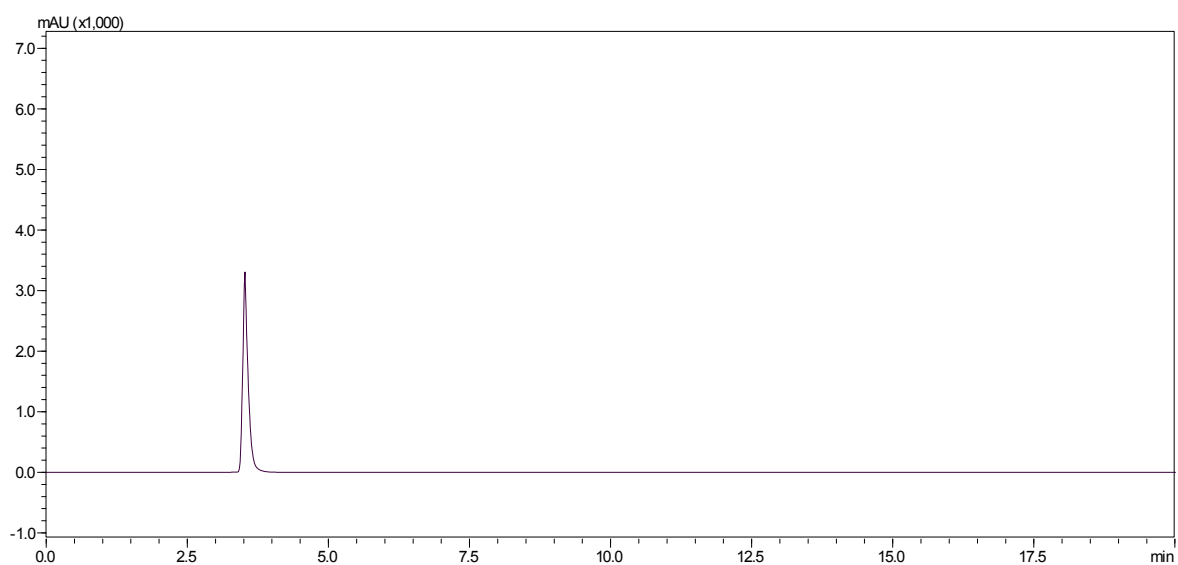
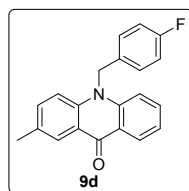
ESI-MS, positive mode: m/z calcd mass for $C_{22}H_{21}NO_2Na$ $[M + MeOH + Na]^+ = 454.15$; found 353.90.



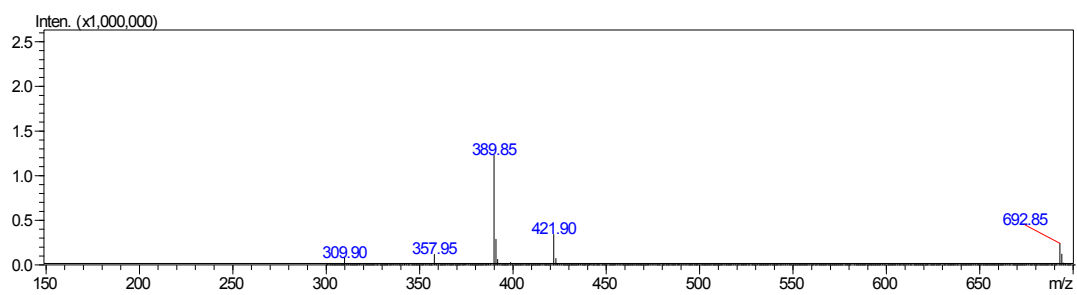
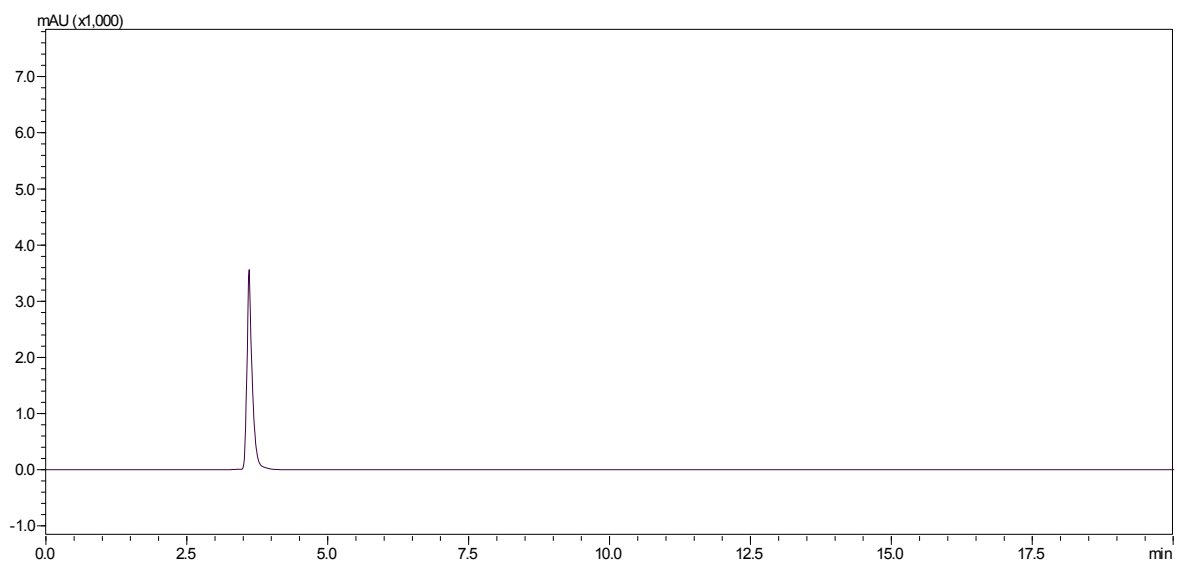
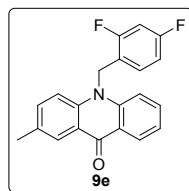
ESI-MS, positive mode: m/z calcd mass for $C_{23}H_{23}NO_2Na$ $[M + MeOH + Na]^+ = 368.16$; found 367.90.



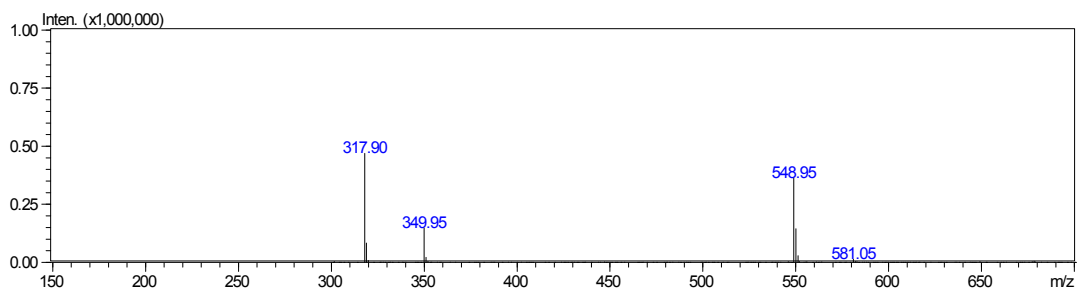
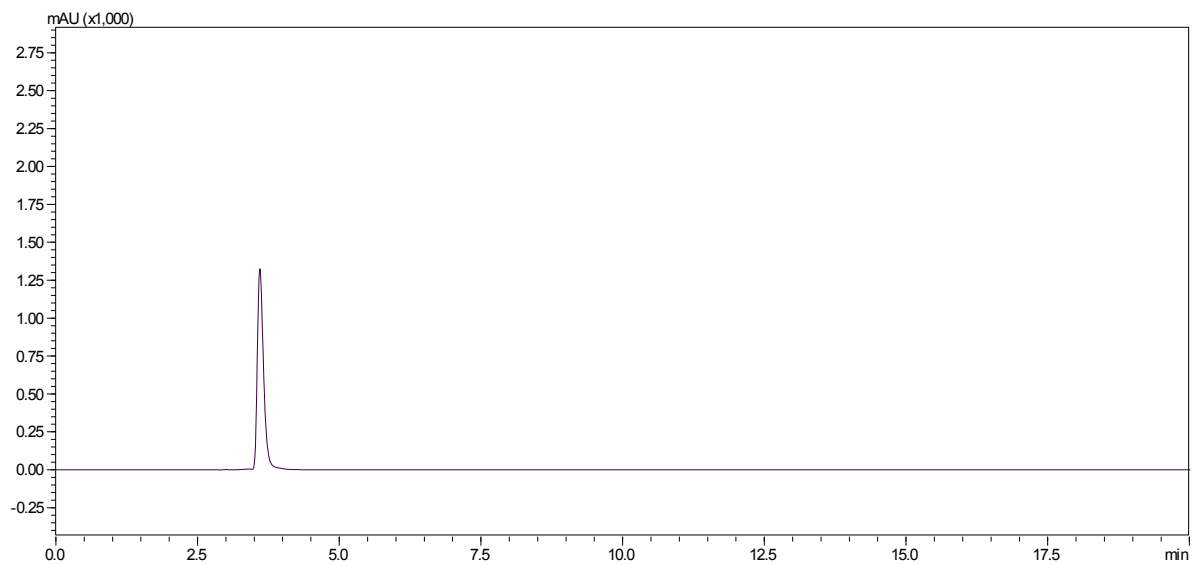
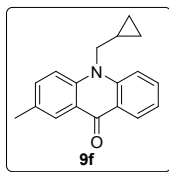
ESI-MS, positive mode: m/z calcd mass for $C_{23}H_{20}F_3NO_2Na$ $[M + MeOH + Na]^+$ = 422.13; found 421.90.



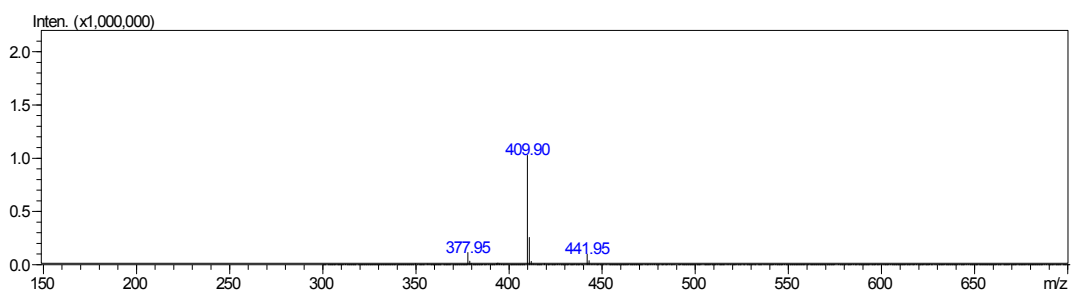
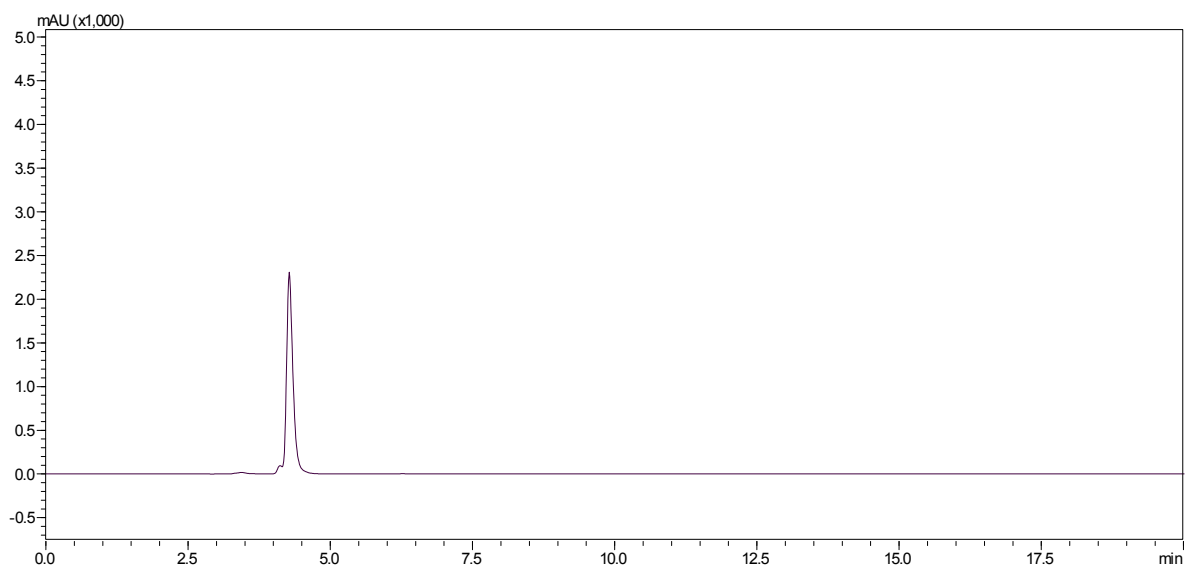
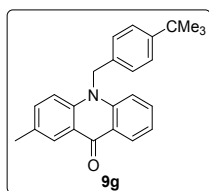
ESI-MS, positive mode: m/z calcd mass for $C_{22}H_{20}FNO_2Na$ $[M + MeOH + Na]^+ = 372.14$; found 371.90.



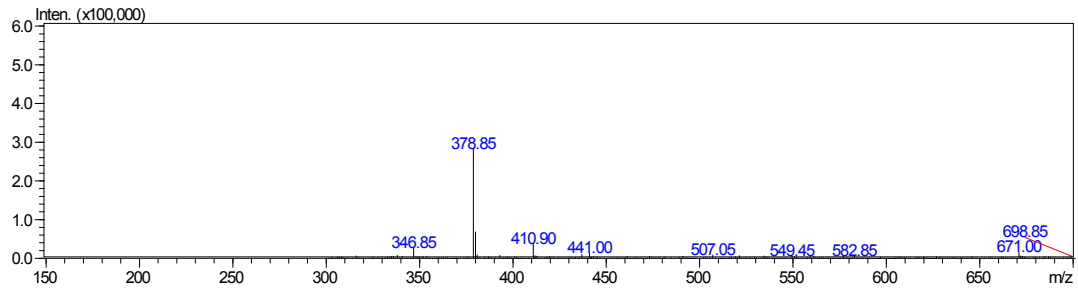
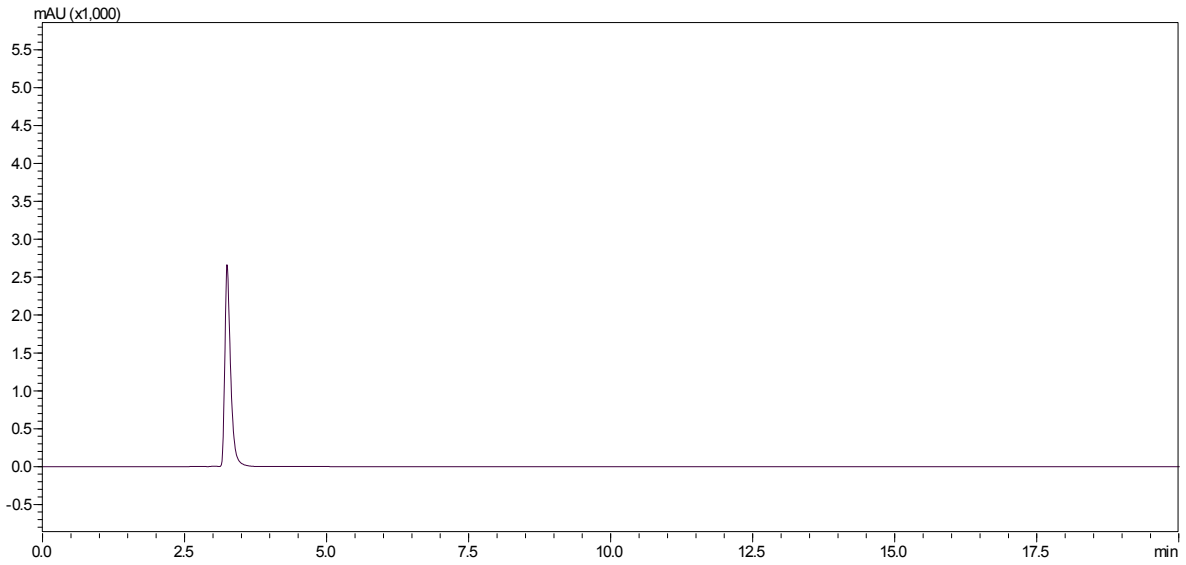
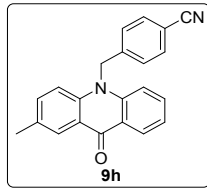
ESI-MS, positive mode: m/z calcd mass for $C_{22}H_{19}F_2NO_2Na$ $[M + MeOH + Na]^+ = 390.13$; found 389.85.



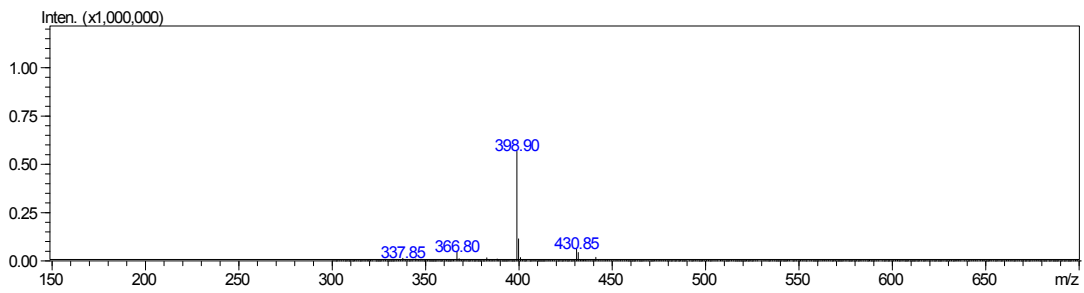
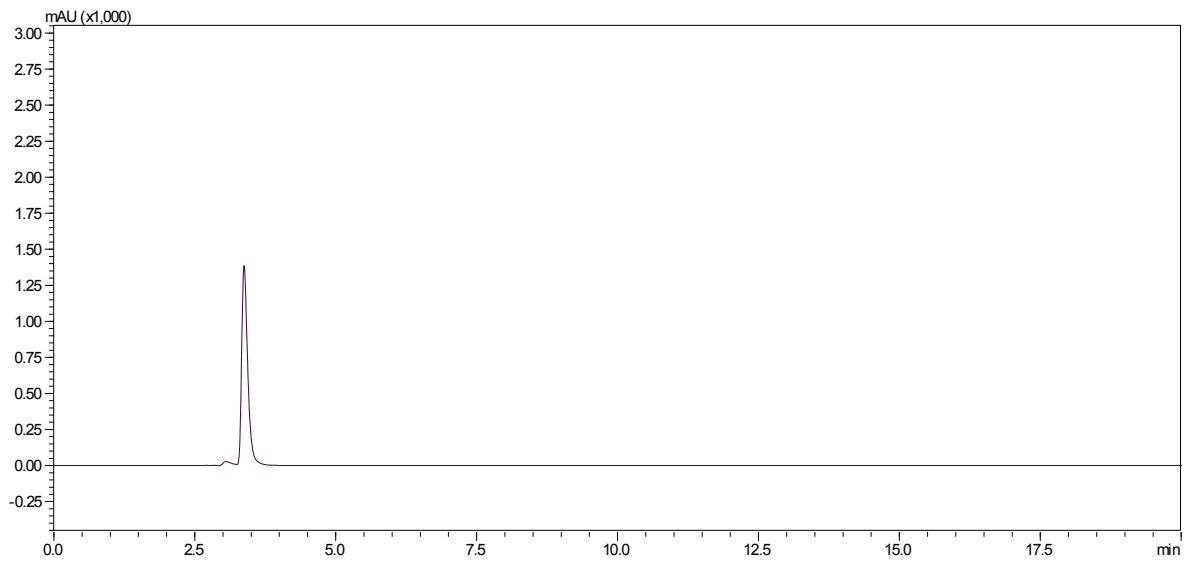
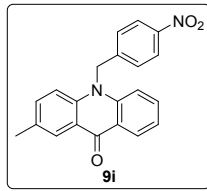
ESI-MS, positive mode: m/z calcd mass for $C_{19}H_{21}NO_2Na$ $[M + MeOH + Na]^+$ = 318.15; found 317.90.



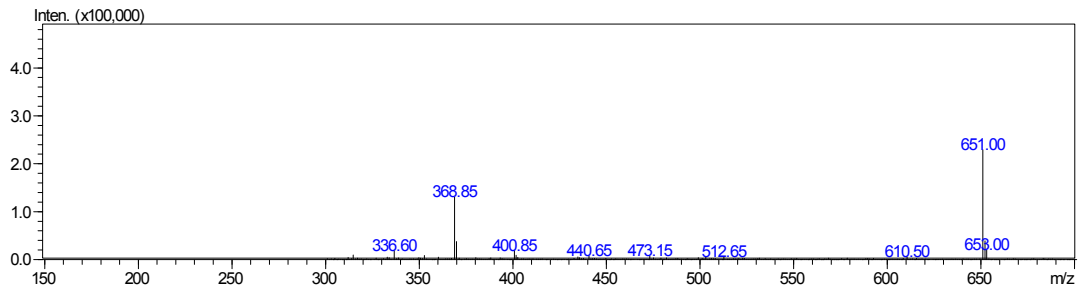
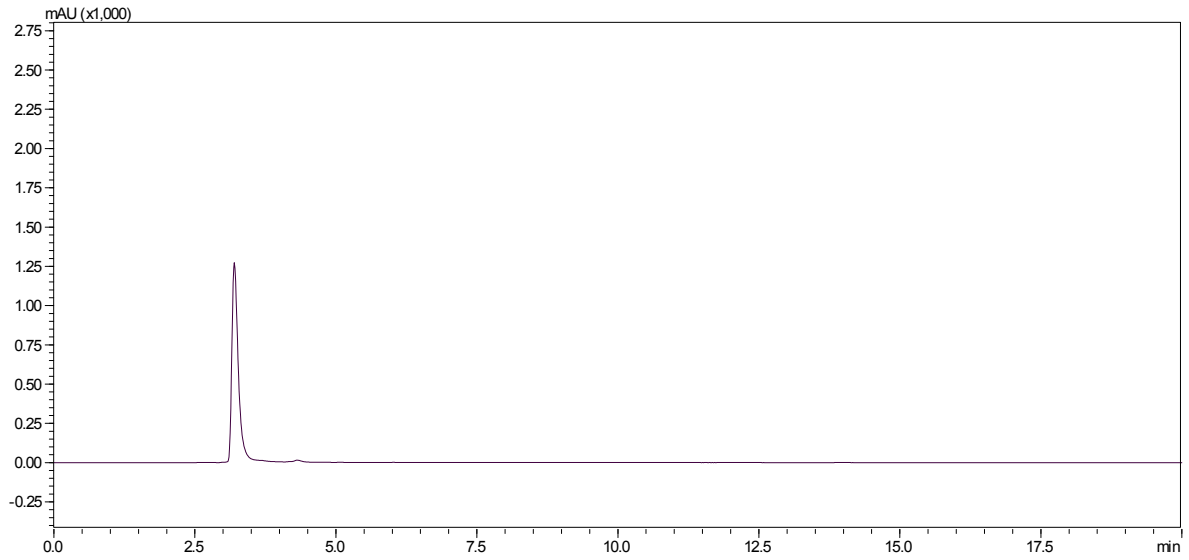
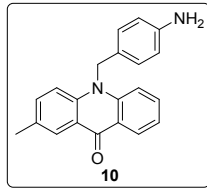
ESI-MS, positive mode: m/z calcd mass for $C_{26}H_{29}NO_2Na$ $[M + MeOH + Na]^+ = 410.21$; found 409.90.



ESI-MS, positive mode: m/z calcd mass for $C_{23}H_{20}N_2O_2Na$ $[M + MeOH + Na]^+$ = 379.14; found 378.85.



ESI-MS, positive mode: m/z calcd mass for $C_{22}H_{20}N_2O_4Na$ $[M + MeOH + Na]^+ = 399.13$; found 398.90.



ESI-MS, positive mode: m/z calcd mass for $C_{22}H_{22}N_2O_2Na$ $[M + MeOH + Na]^+ = 369.16$; found 368.85.

Analytical method for compounds **S1**, **15a-d** and **16a-h**:

LC-MS/HPLC: LC-20AD Shimadzu connected to Shimadzu LCMS-2010EV

Mobile Phase A: 0.1% FA in water

Mobile Phase B: methanol

HPLC column: SUPELCO Discovery C18 25 cm x 4.6 mm, 5 μ m

Flow rate: 0.4 mL/min

Run time: 20 min

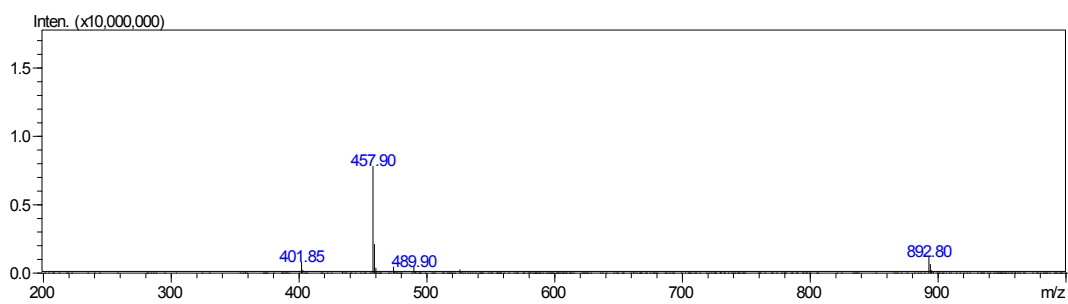
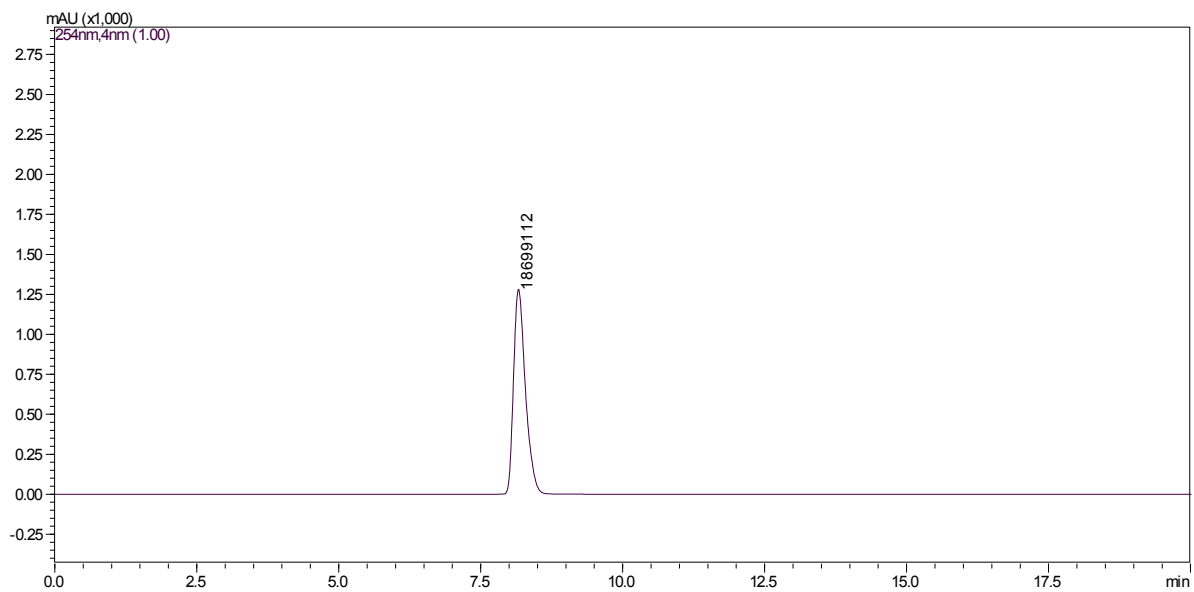
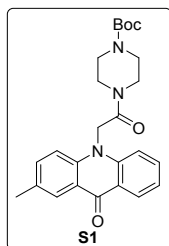
Column temperature: 26°C

UV detector: 254 nm

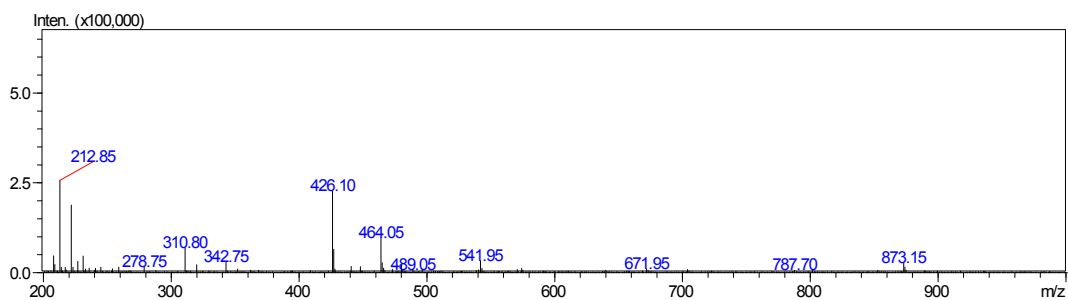
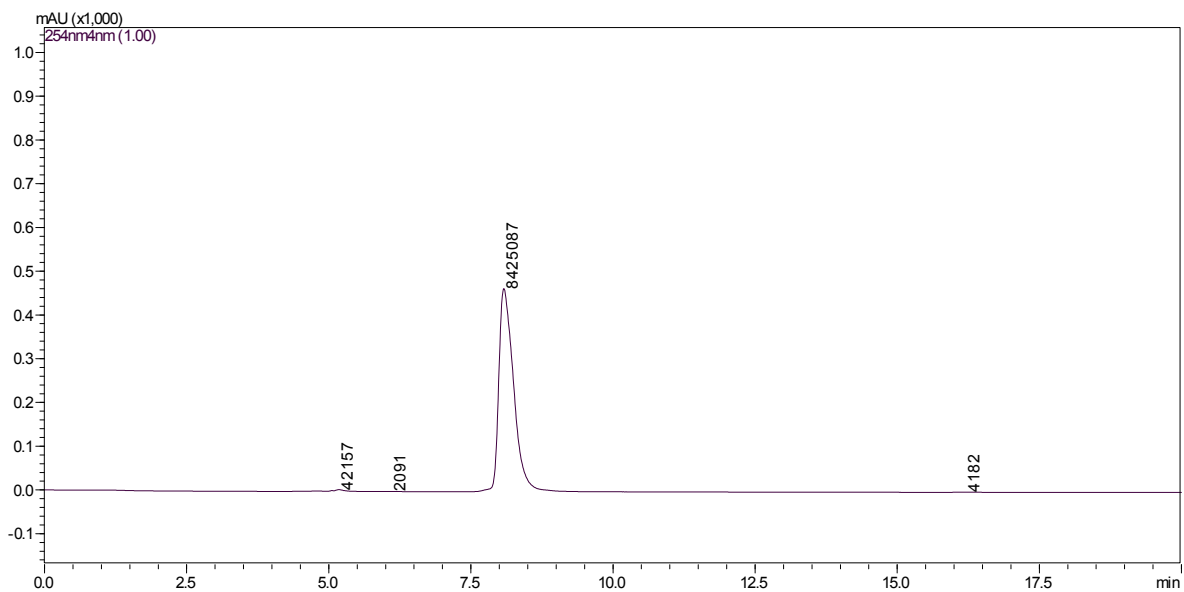
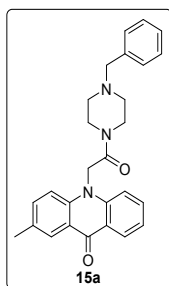
MS detector: 1.65 kV

LC isocratic:

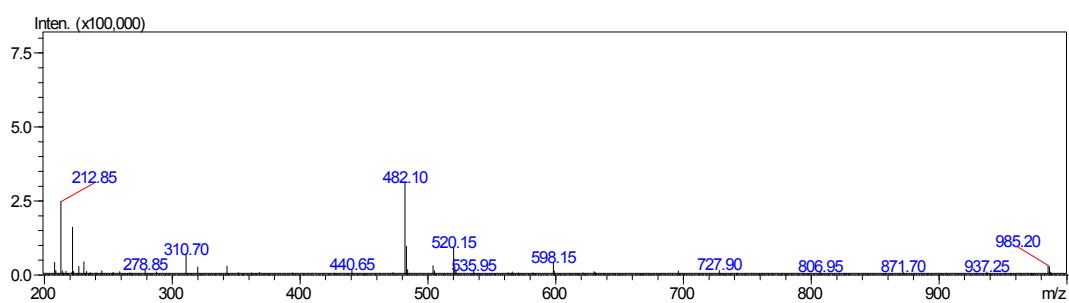
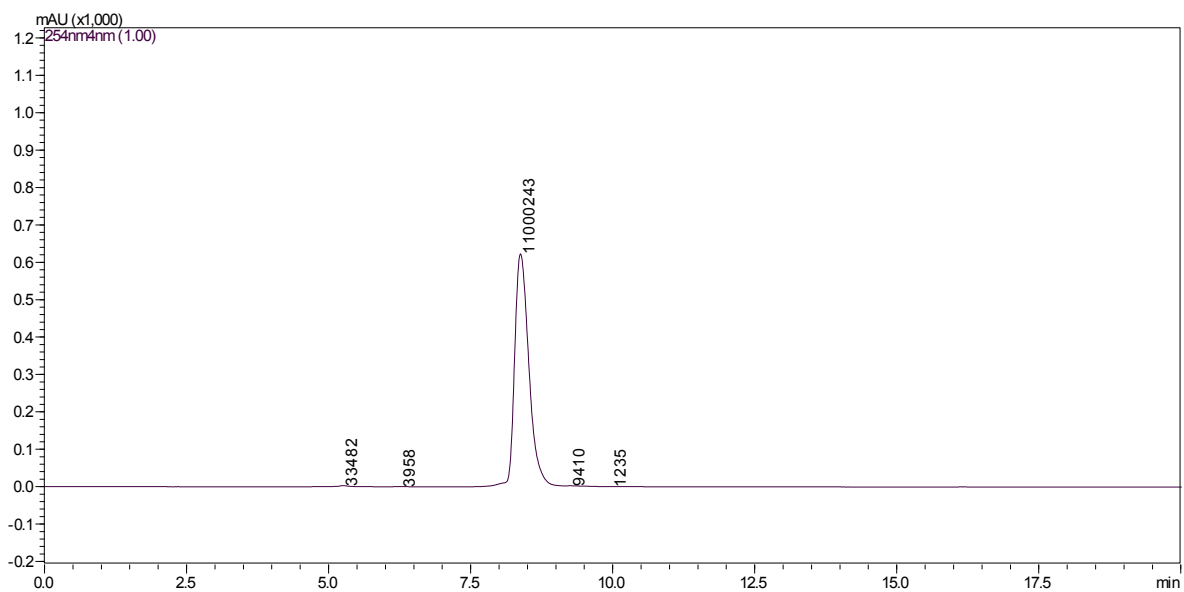
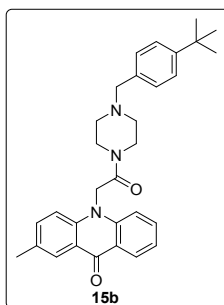
Time (min)	Mobile Phase A (%)	Mobile Phase B (%)
0	0	100
20	0	100



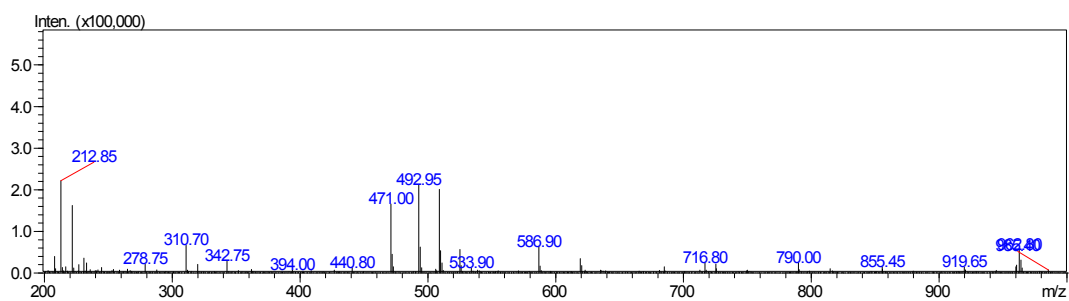
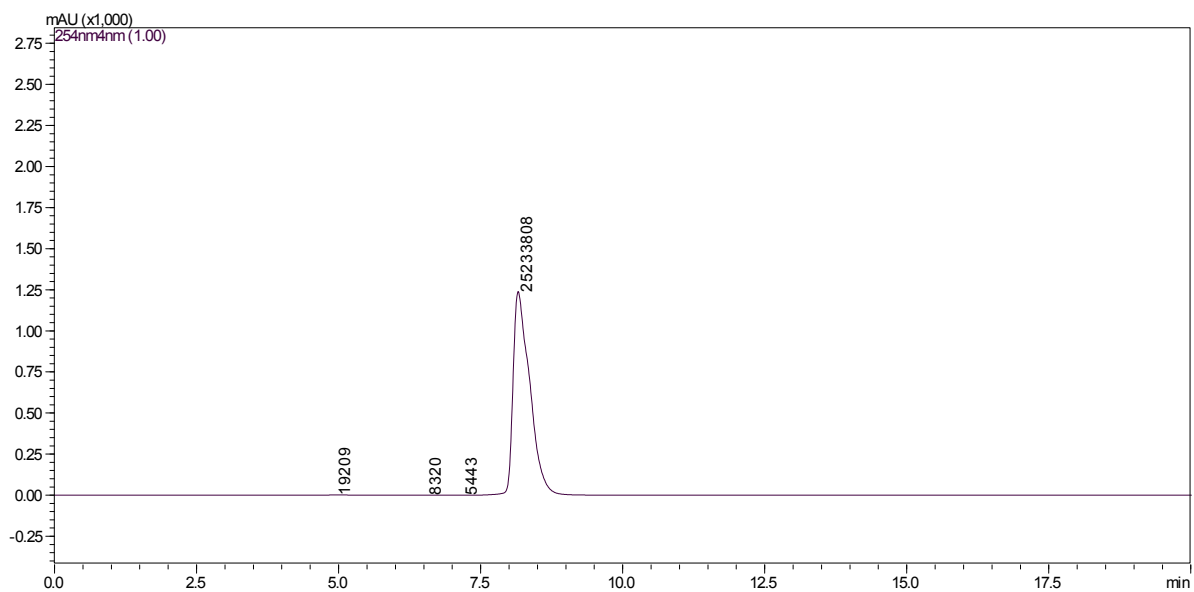
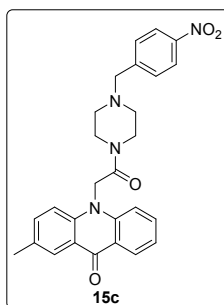
ESI-MS, positive mode: m/z calcd mass for $C_{25}H_{29}N_3O_4Na$ $[M + Na]^+ = 458.20$; found 457.90.



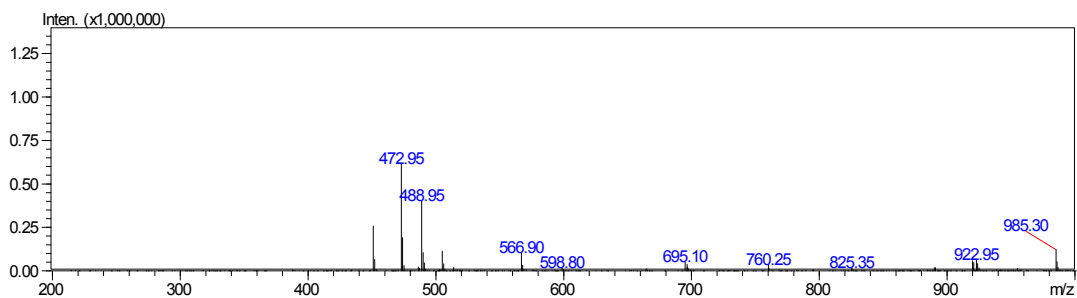
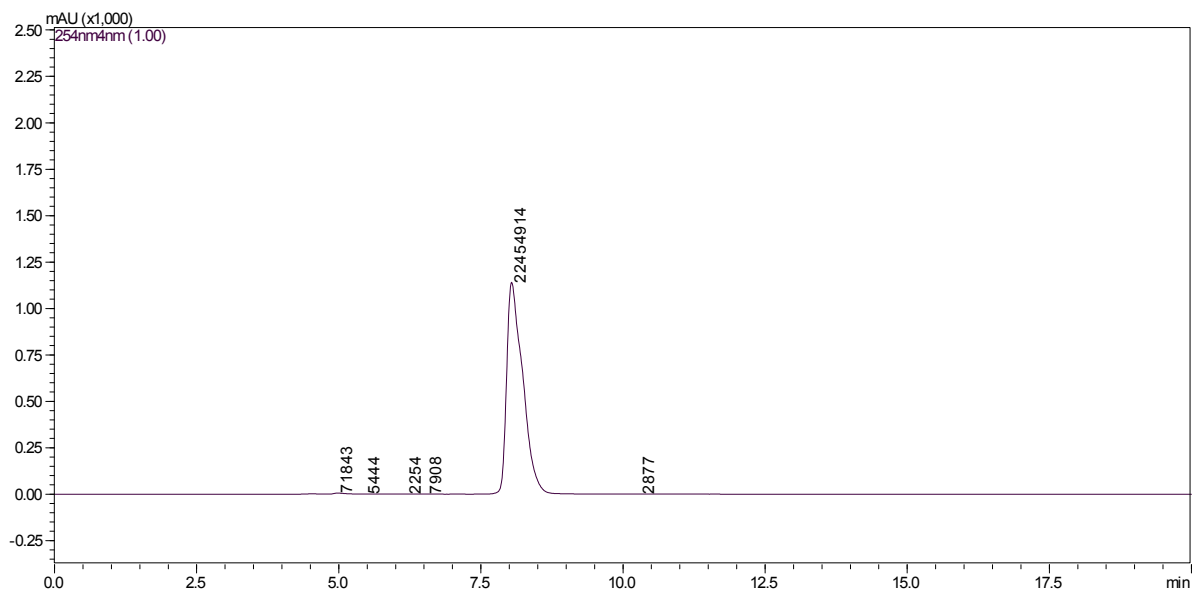
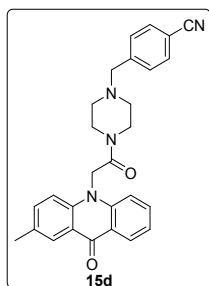
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{28}N_3O_2$ $[M + H]^+$ = 426.22; found 426.10.



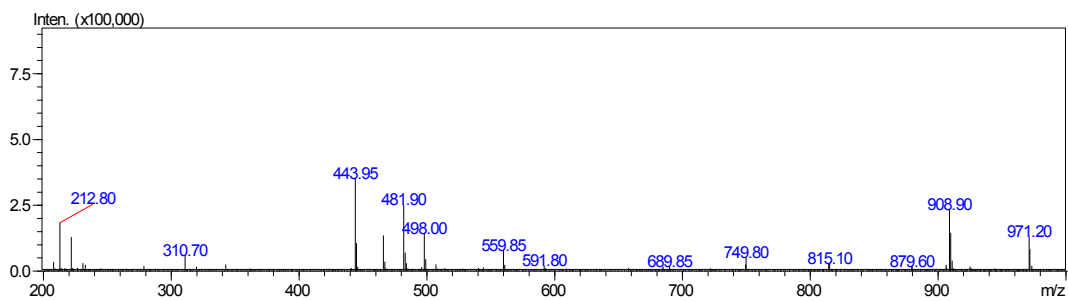
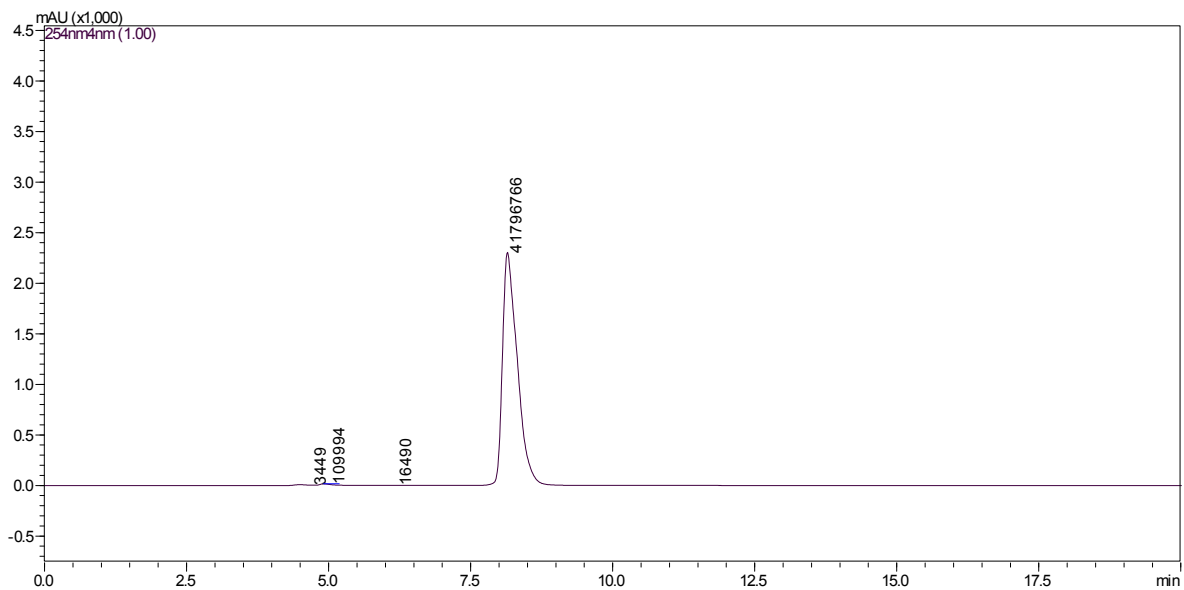
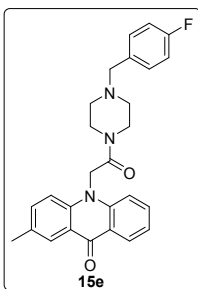
ESI-MS, positive mode: m/z calcd mass for $C_{31}H_{36}N_3O_2$ $[M + H]^+$ = 482.28; found 482.10.



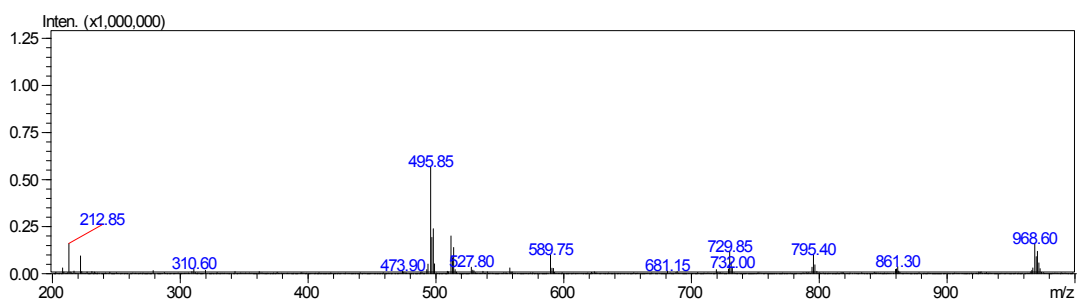
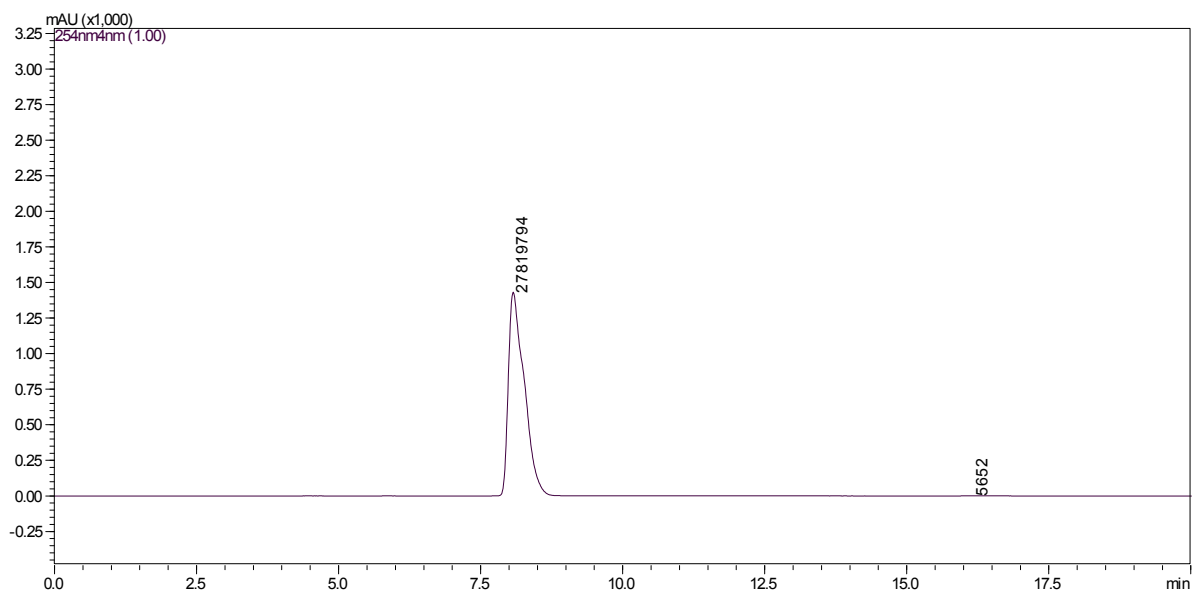
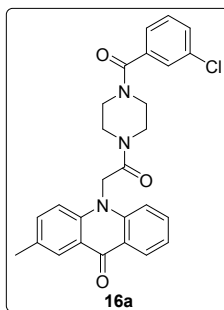
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{27}N_4O_4$ $[M + H]^+$ = 471.20; found 471.00.



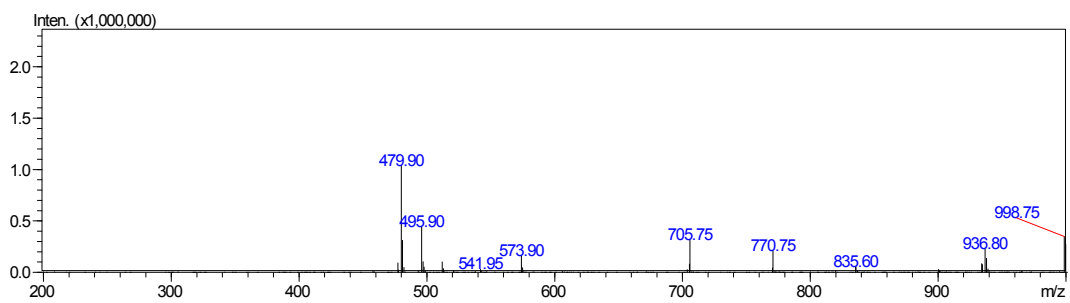
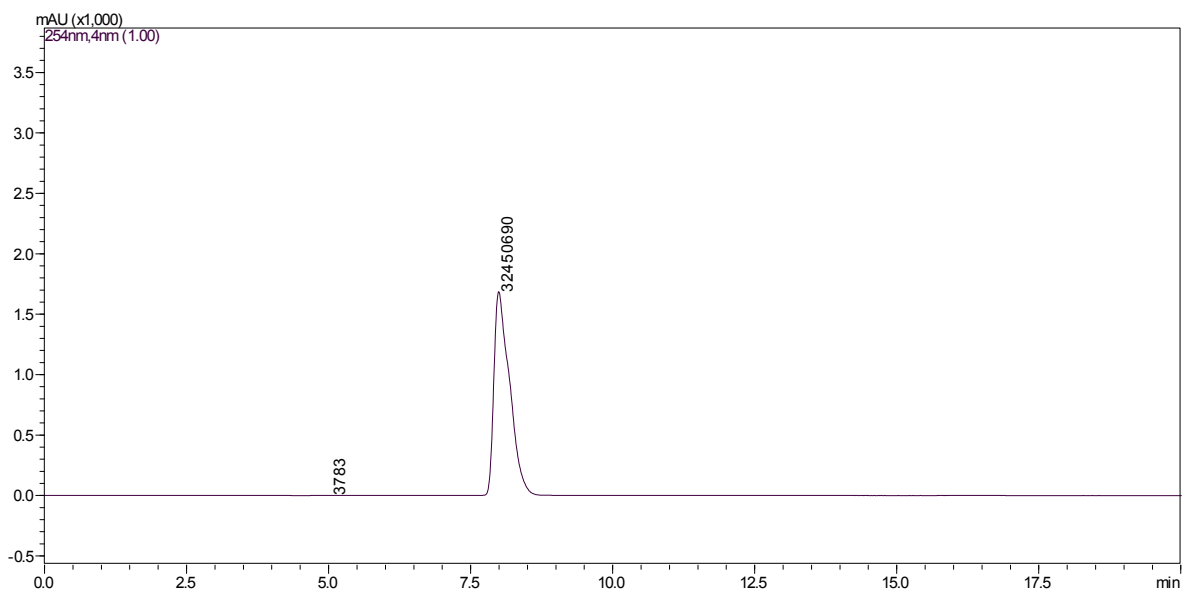
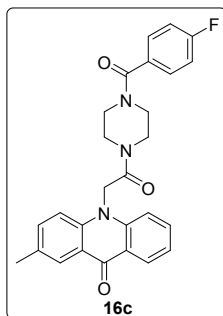
ESI-MS, positive mode: m/z calcd mass for $C_{28}H_{26}N_4O_2Na$ $[M + Na]^+ = 473.19$; found 472.95.



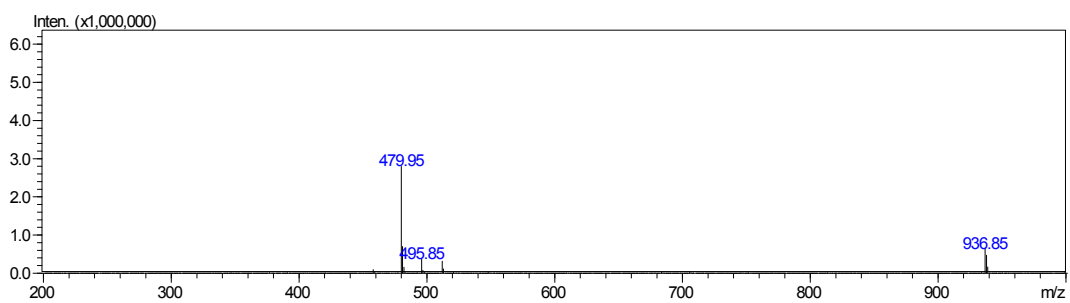
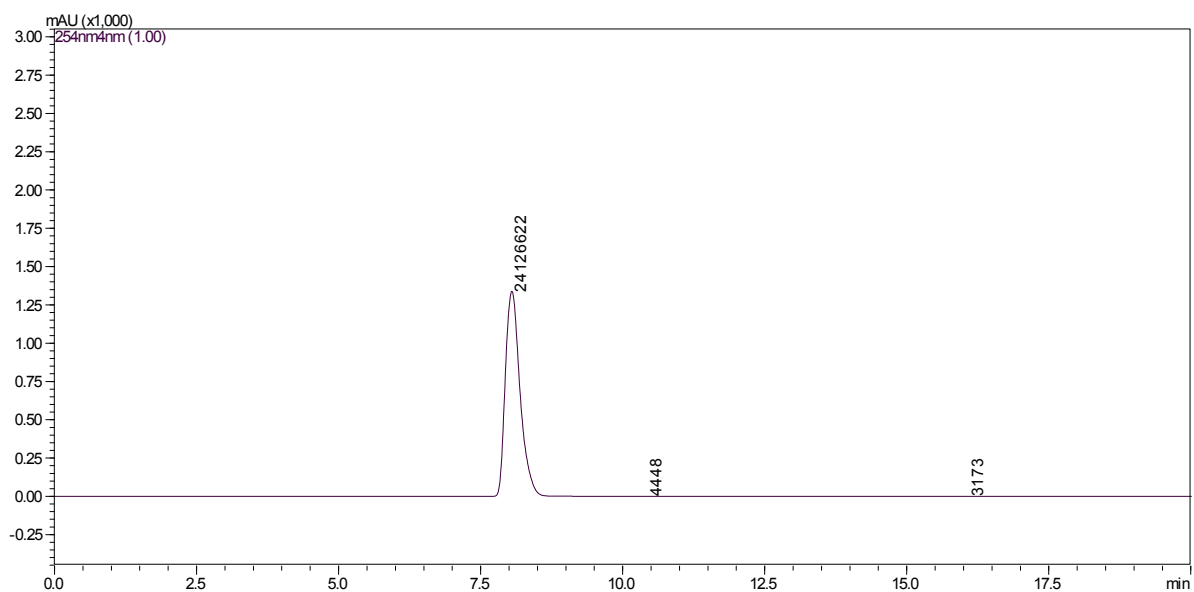
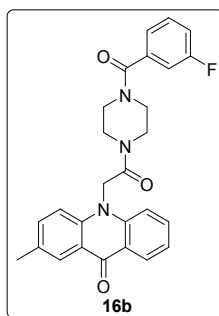
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{27}FN_3O_2$ $[M + H]^+ = 444.21$; found 441.95.



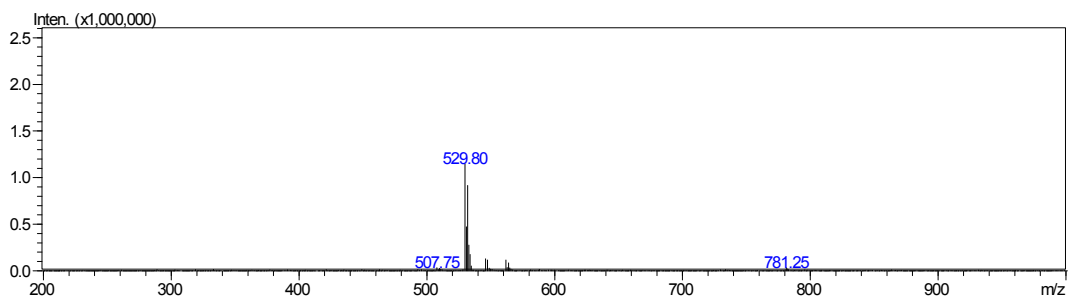
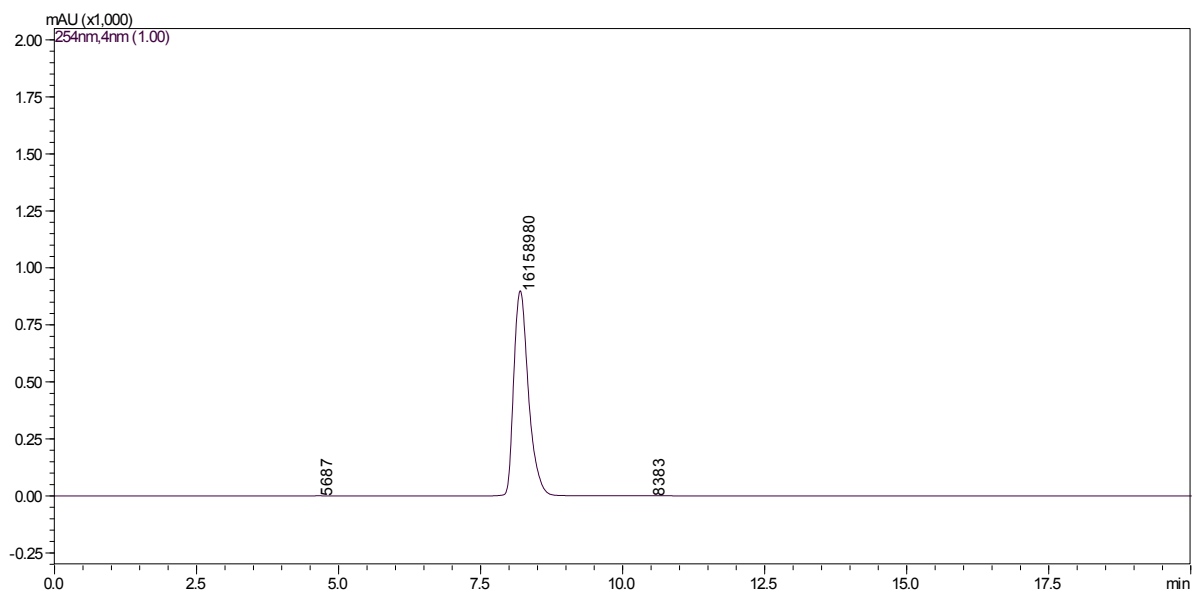
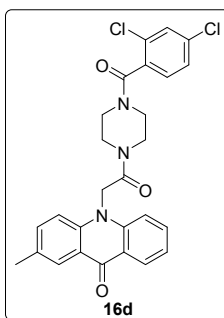
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{24}ClN_3O_3Na$ $[M + Na]^+ = 496.14$; found 495.85.



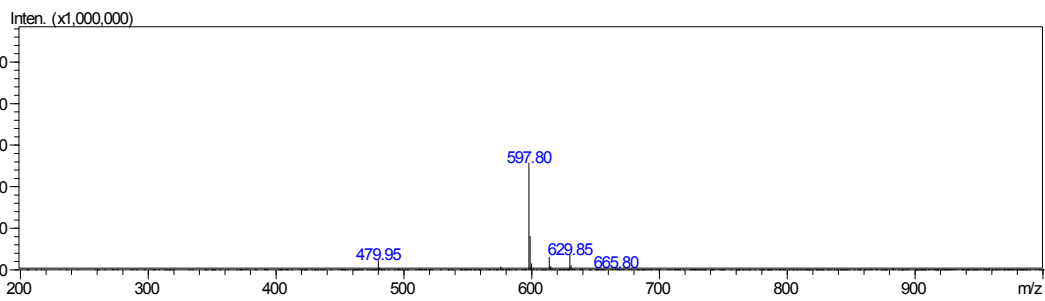
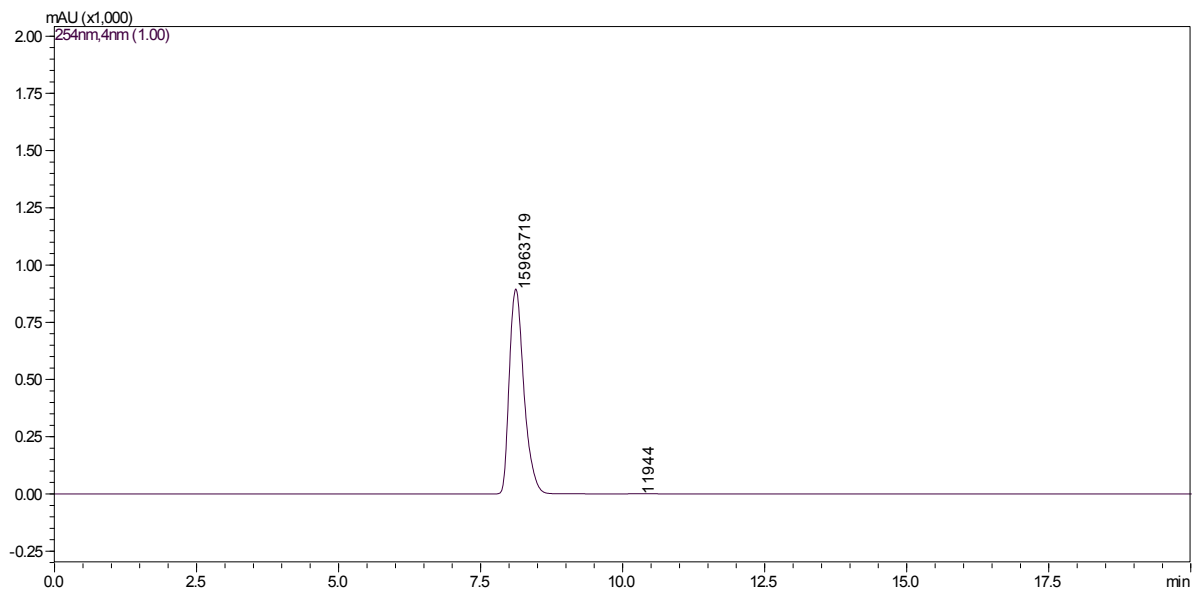
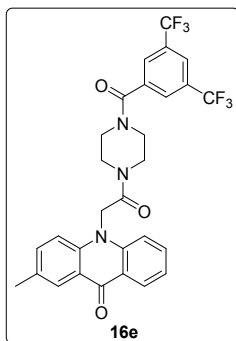
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{24}FN_3O_3Na$ $[M + Na]^+$ = 480.17; found 479.90.



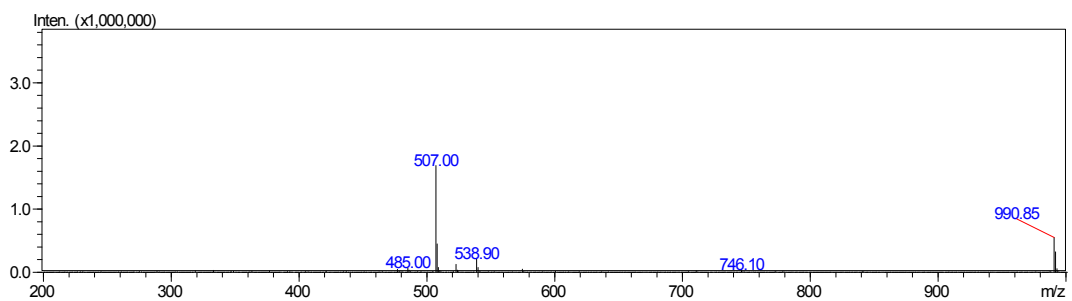
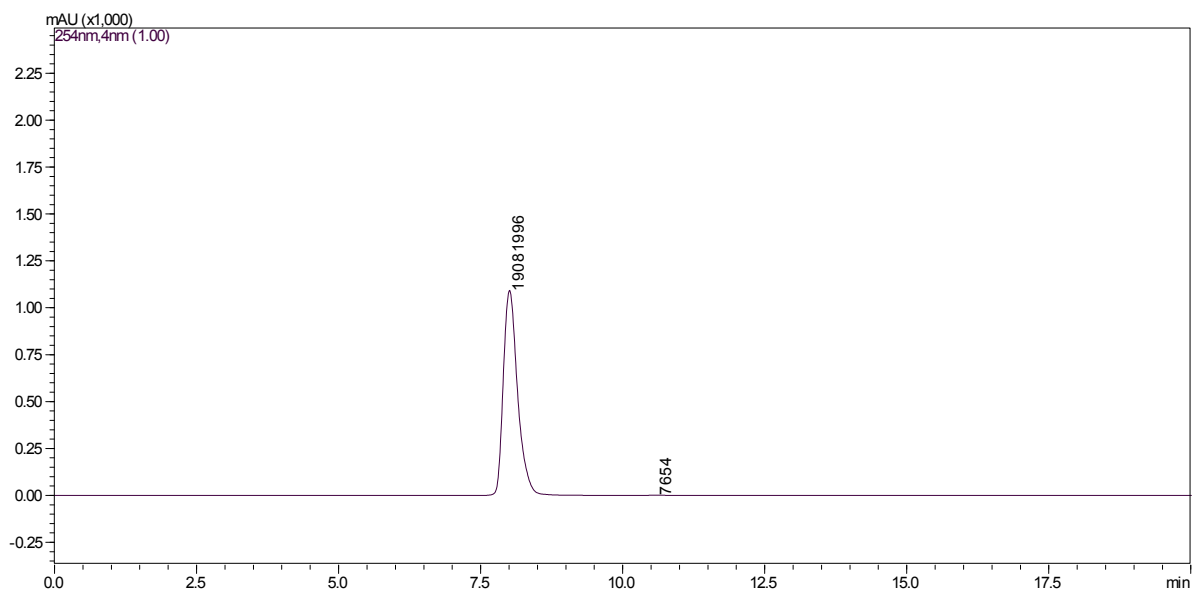
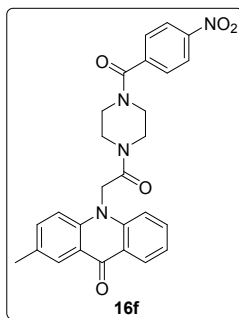
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{24}FN_3O_3Na$ $[M + Na]^+$ = 480.17; found 479.95.



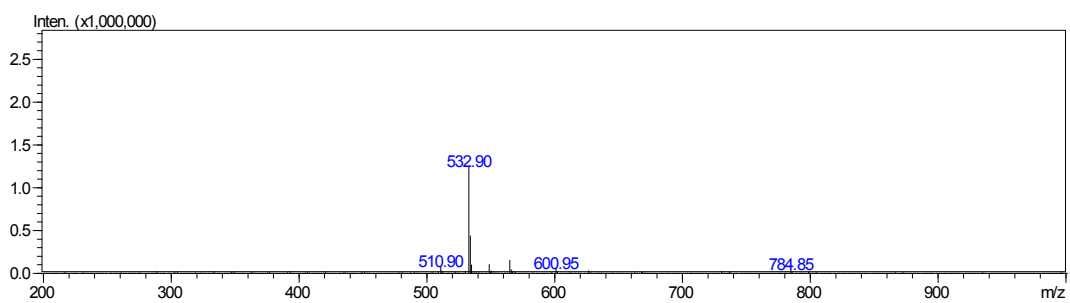
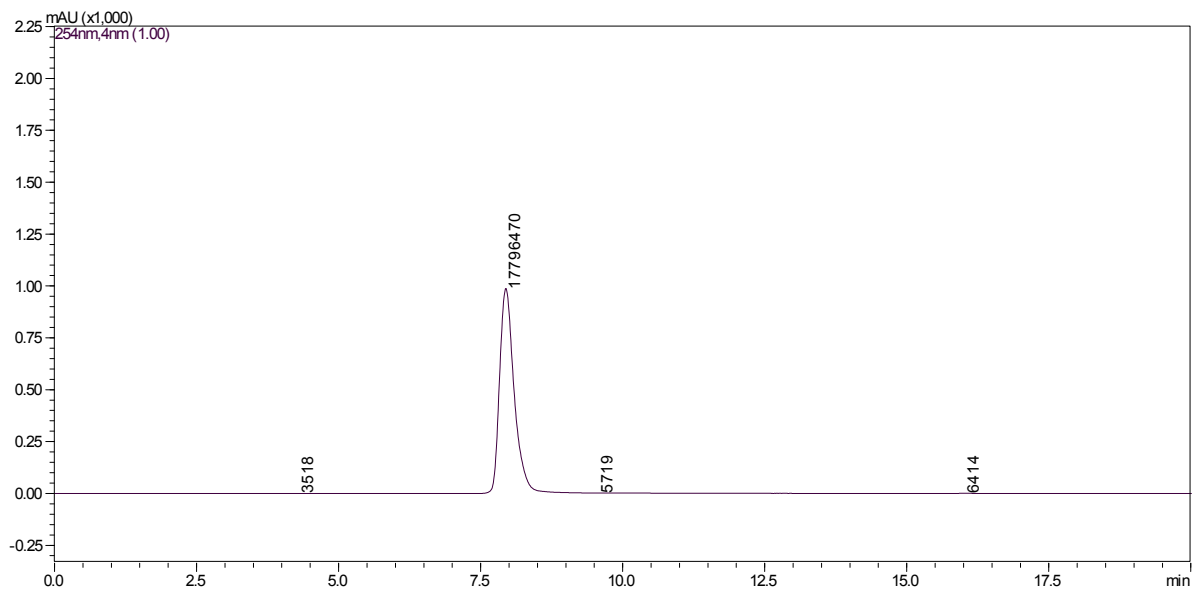
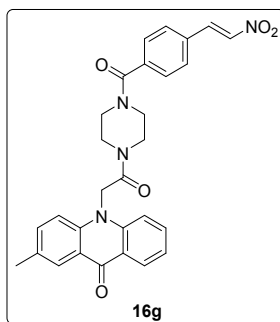
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{23}Cl_2N_3O_3Na$ $[M + Na]^+ = 530.10$; found 529.80.



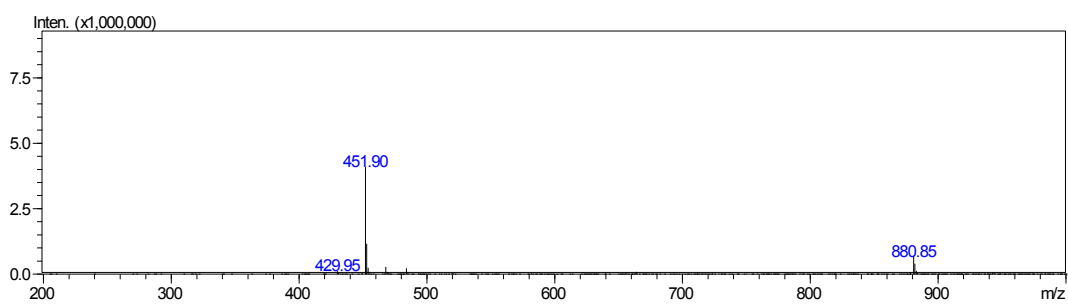
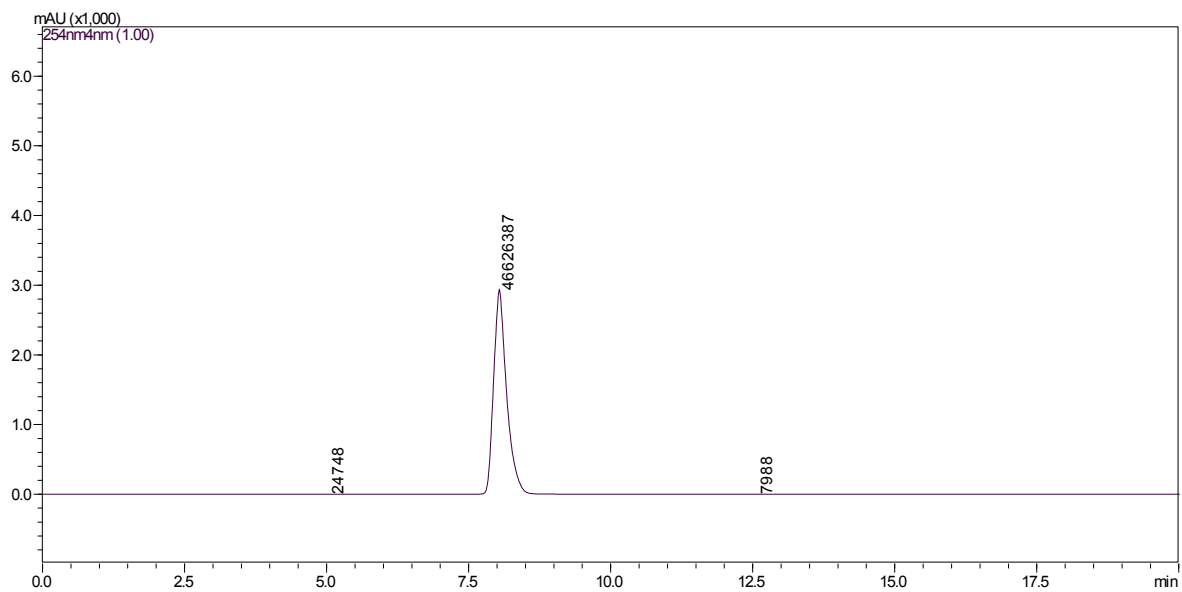
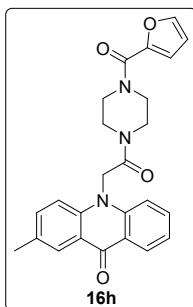
ESI-MS, positive mode: m/z calcd mass for $C_{29}H_{23}F_6N_3O_3Na$ $[M + Na]^+ = 598.15$; found 597.80.



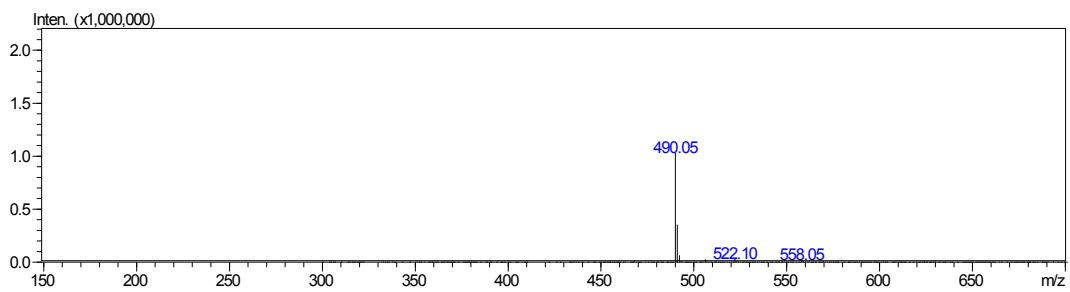
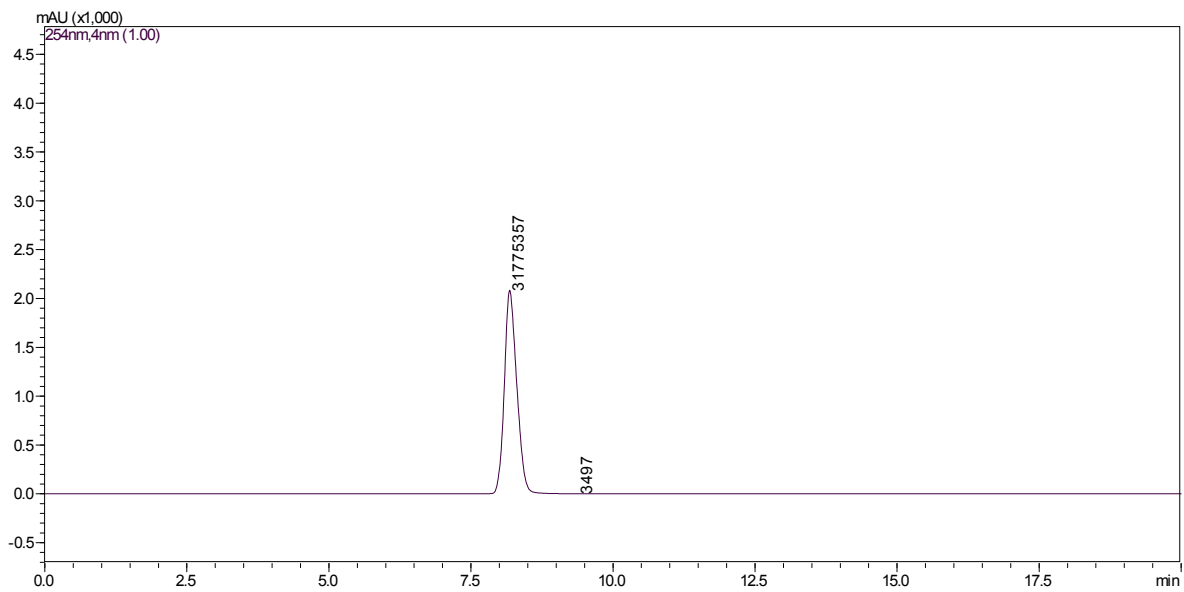
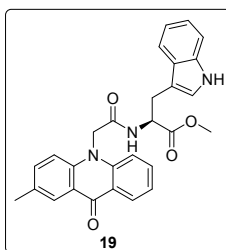
ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{24}N_4O_5Na$ $[M + Na]^+ = 507.16$; found 507.00.



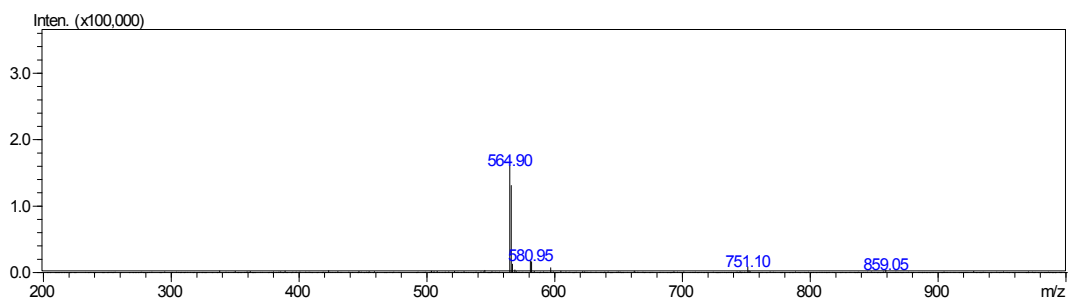
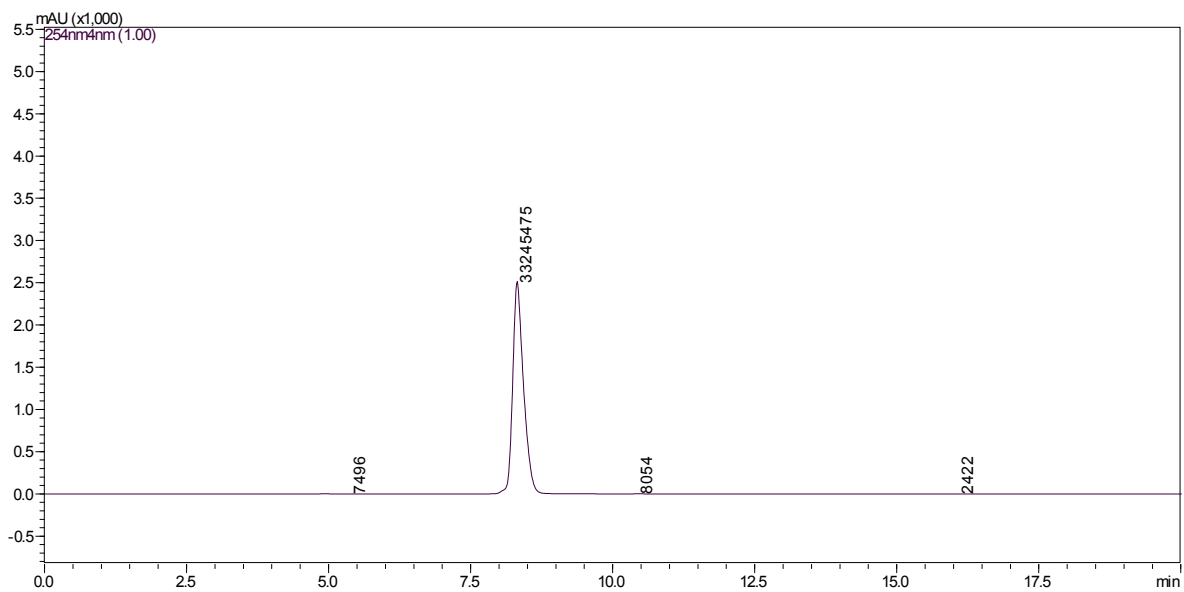
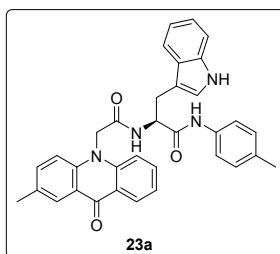
ESI-MS, positive mode: m/z calcd mass for $C_{29}H_{26}N_4O_5Na$ $[M + Na]^+ = 533.18$; found 532.90.



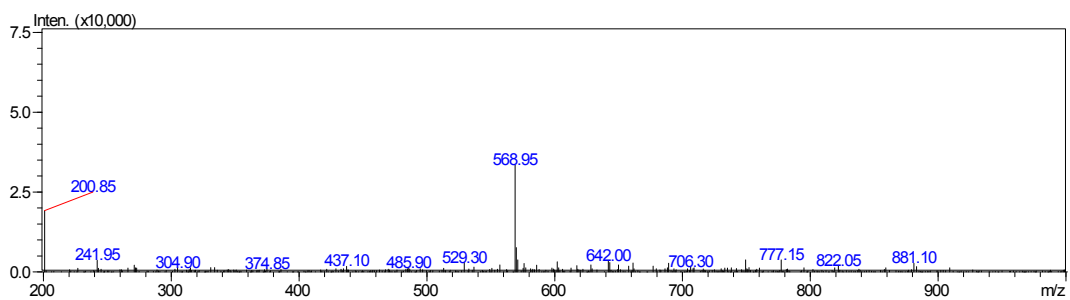
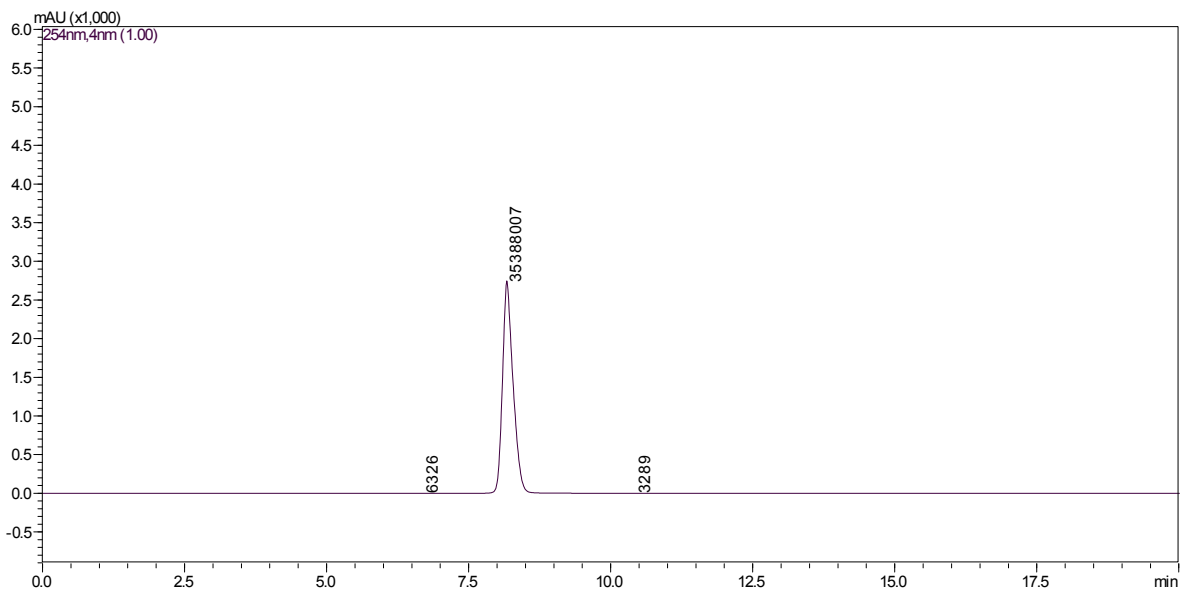
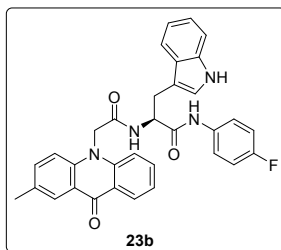
ESI-MS, positive mode: m/z calcd mass for $C_{25}H_{23}N_3O_4Na$ $[M + Na]^+ = 452.16$; found 451.90.



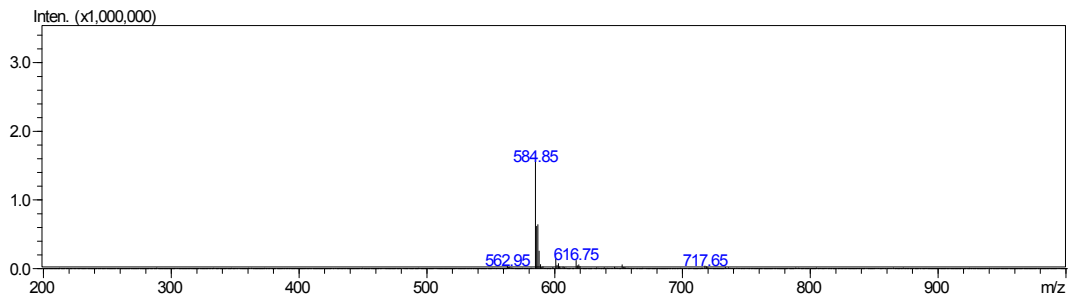
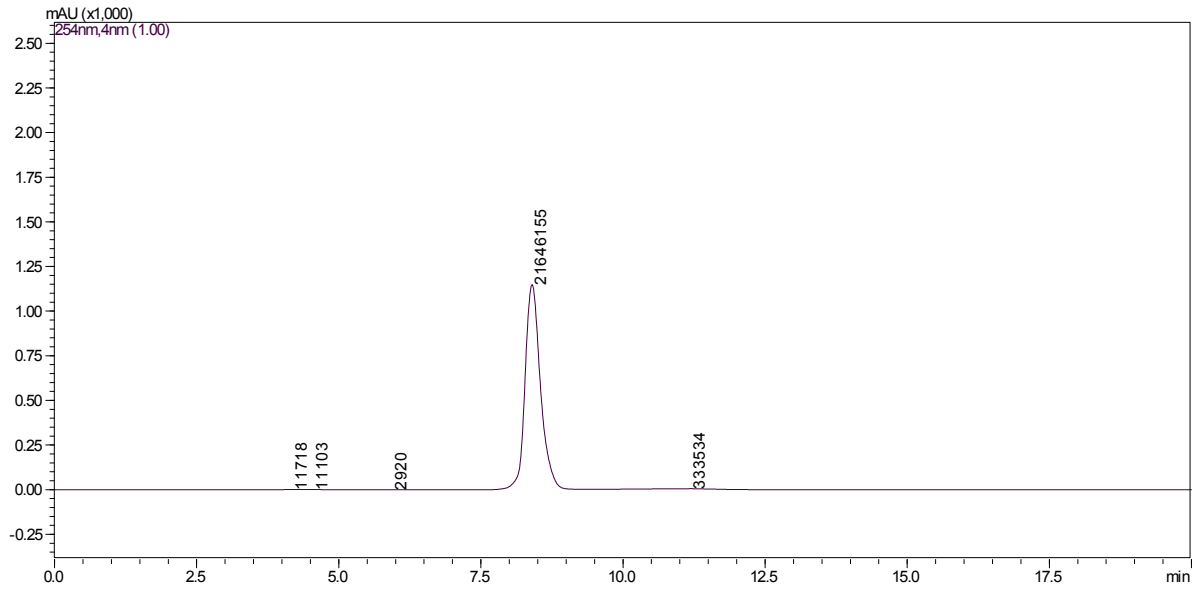
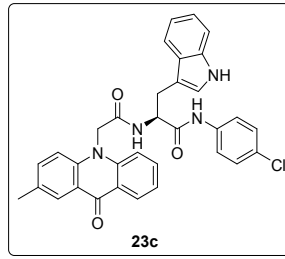
ESI-MS, positive mode: m/z calcd mass for $C_{28}H_{25}N_3O_4Na$ $[M + Na]^+ = 490.17$; found 490.05.



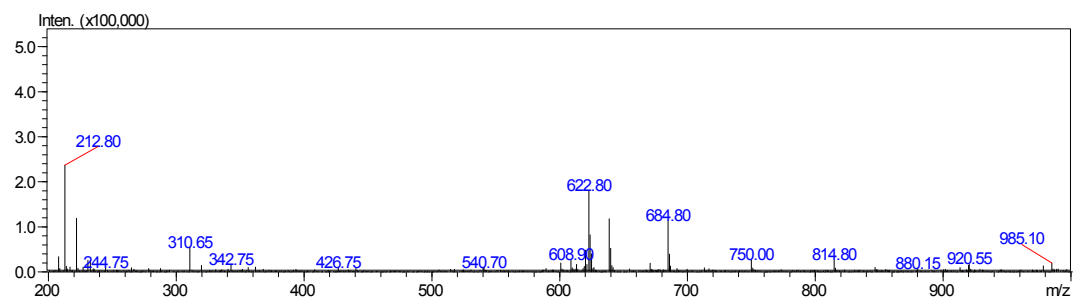
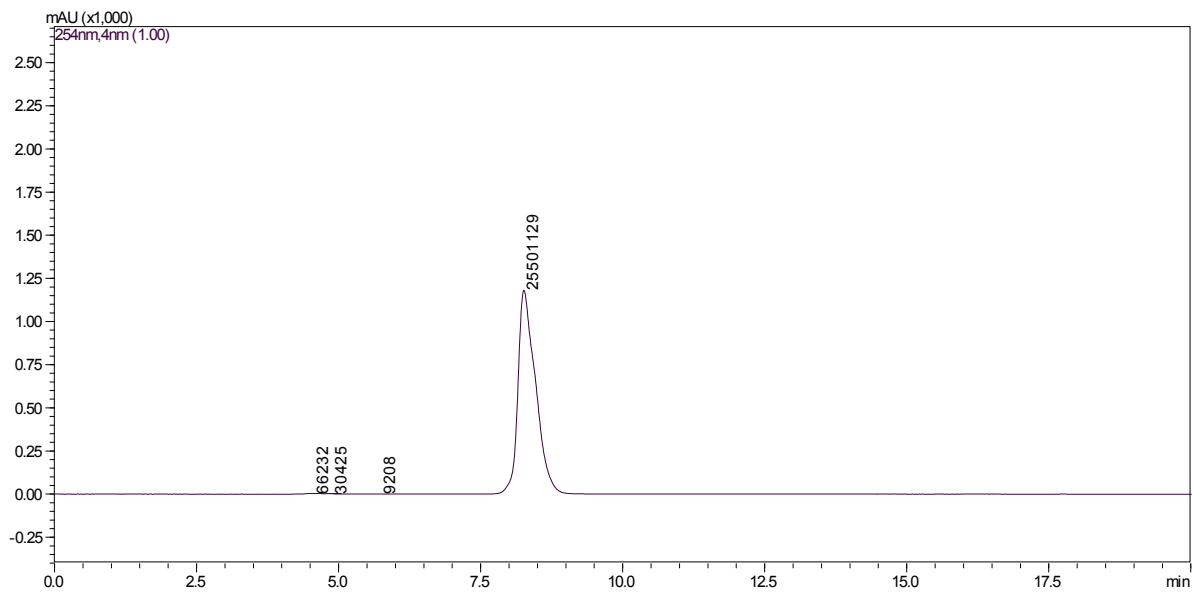
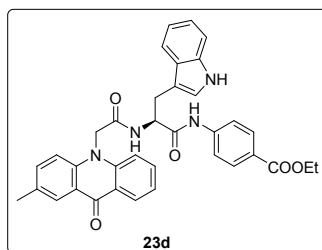
ESI-MS, positive mode: m/z calcd mass for $C_{34}H_{30}N_4O_3Na$ $[M + Na]^+ = 565.22$; found 564.90.



ESI-MS, positive mode: m/z calcd mass for $C_{33}H_{27}FN_4O_3Na$ $[M + Na]^+$ = 569.20; found 568.95.



ESI-MS, positive mode: m/z calcd mass for $C_{33}H_{27}ClN_4O_3Na$ $[M + Na]^+$ = 585.17; found 584.85.



ESI-MS, positive mode: m/z calcd mass for $C_{36}H_{32}N_4O_5Na$ $[M + Na]^+ = 623.22$; found 622.80.

Analytical method for compounds **14** and **20**:

LC-MS/HPLC: LC-20AD Shimadzu connected to Shimadzu LCMS-2010EV

Mobile Phase A: 0.1% FA in water

Mobile Phase B: 0.1% FA in acetonitrile

HPLC column: Poroshell 120 EC-C18, 4.6 x 100 mm, 2.7 μ m

Flow rate: 0.4 mL/min

Run time: 40 min

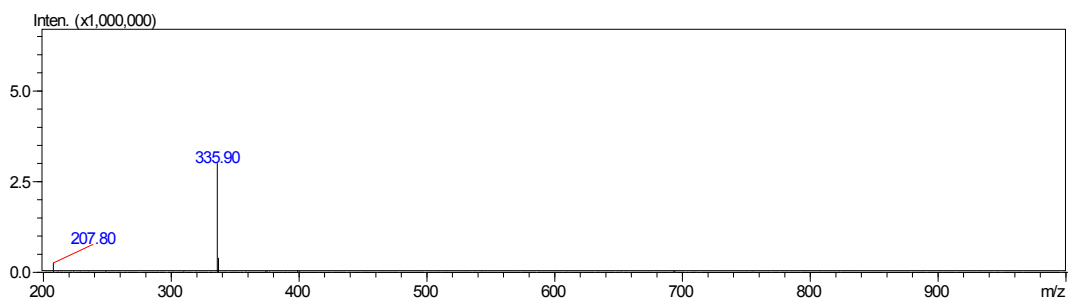
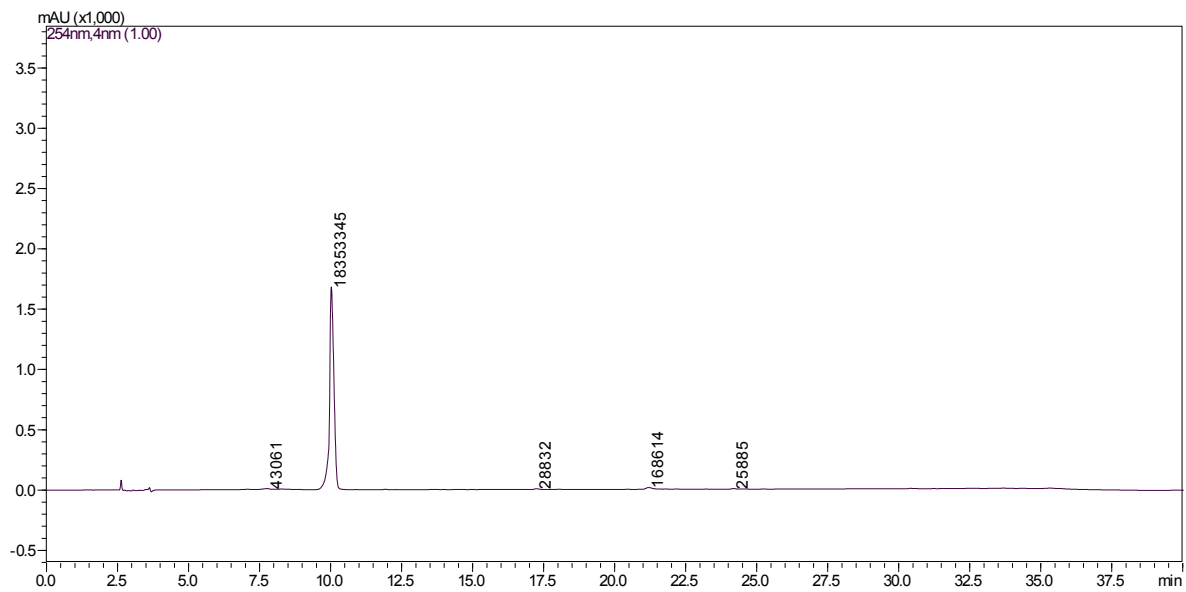
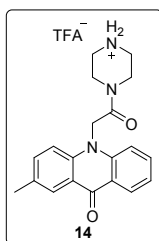
Column temperature: 26°C

UV detector: 254 nm

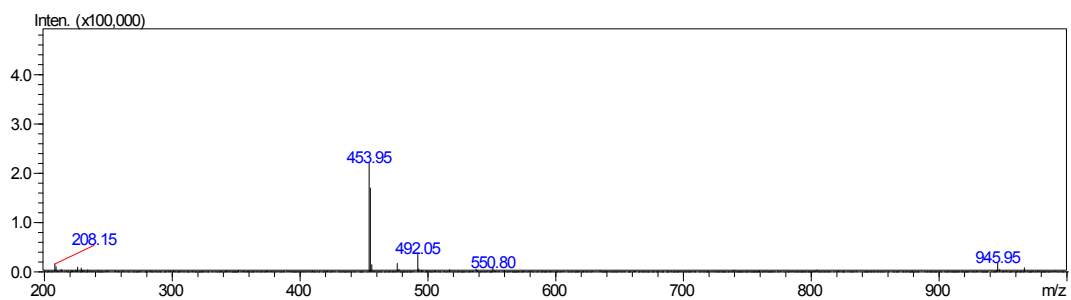
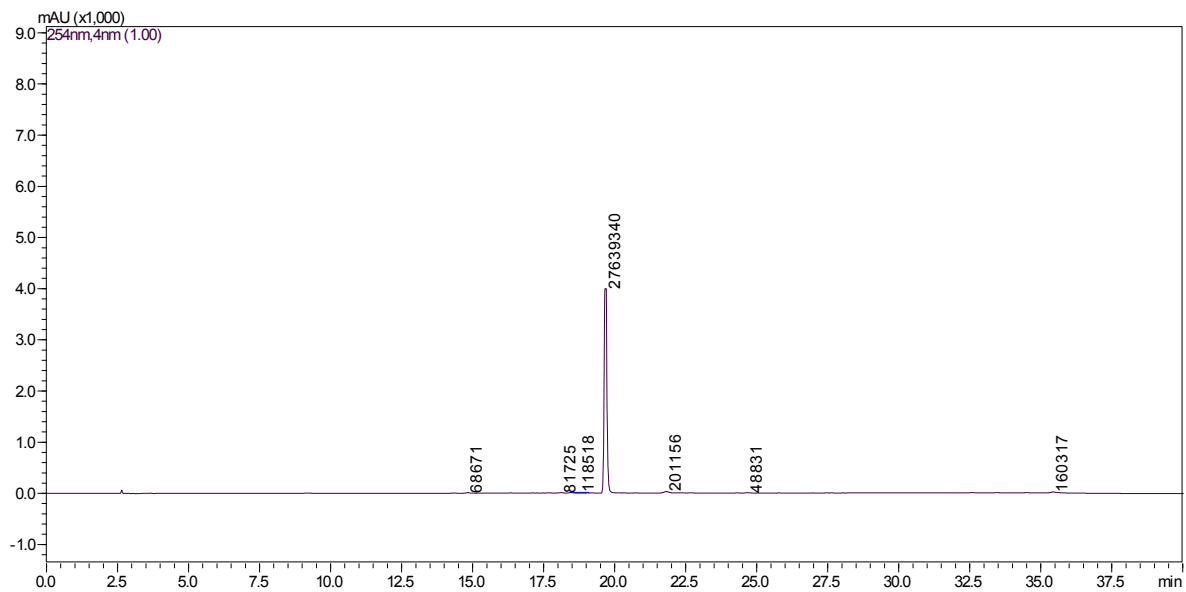
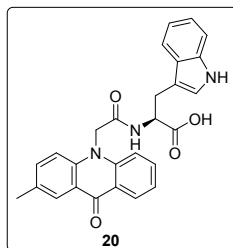
MS detector: 1.65 kV

LC isocratic:

Time (min)	Mobile Phase A (%)	Mobile Phase B (%)
0	90	10
30	10	90
32	10	90
35	10	90
40	90	10



ESI-MS, positive mode: m/z calcd mass for C₂₀H₂₂N₃O₂ [M + H]⁺ = 336.17; found 335.90.



ESI-MS, positive mode: m/z calcd mass for $C_{27}H_{24}N_3O_4$ $[M + H]^+ = 454.17$; found 453.95.