Oxadiazole/pyridine-based ligands: a structural tuning for enhancing G-quadruplex binding

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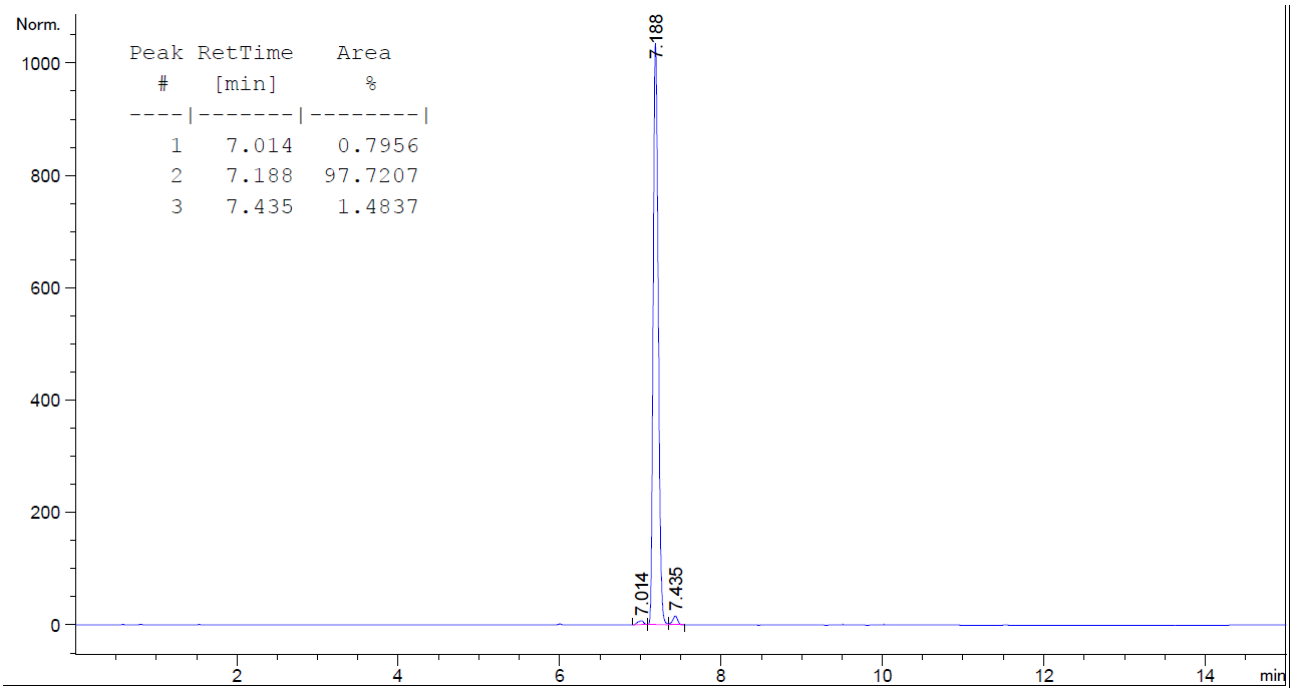
Supplementary Material

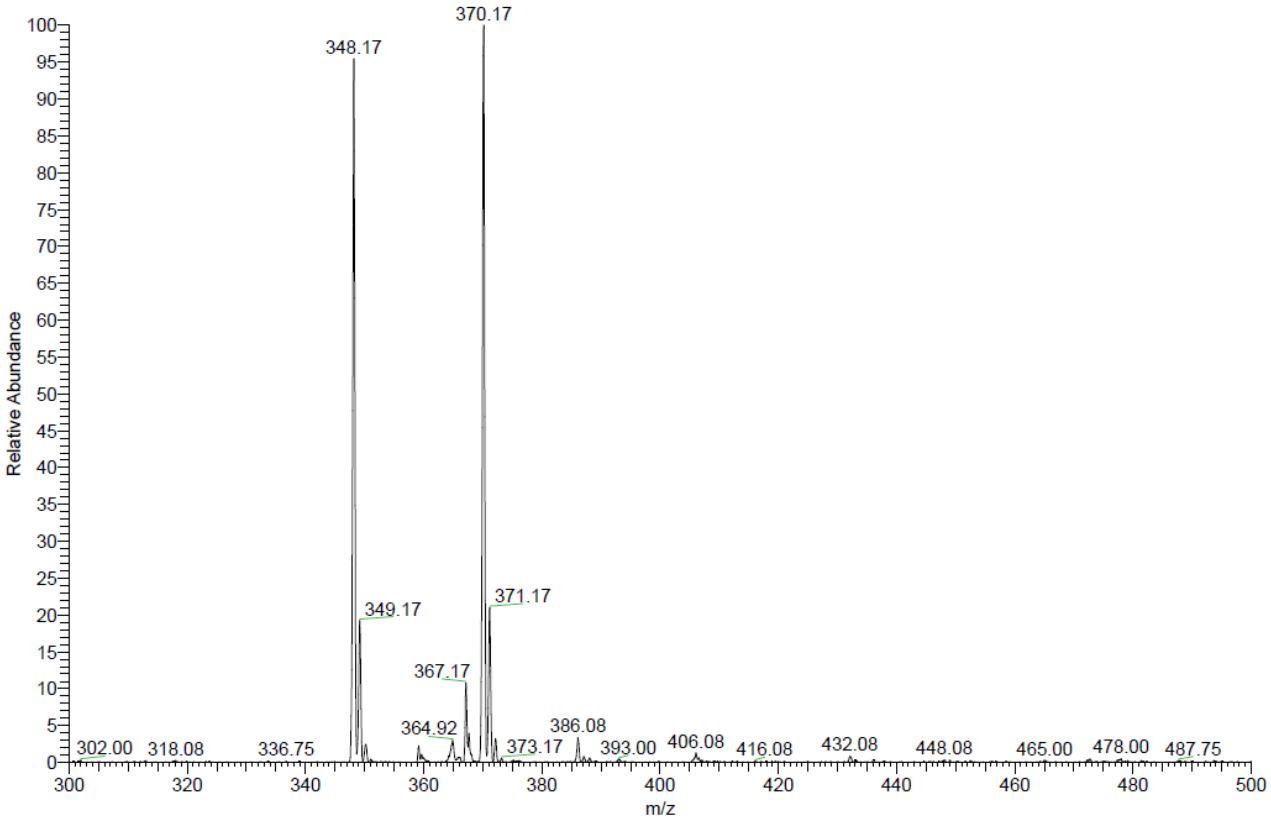
Table of Contents:

LC-MS Analysis

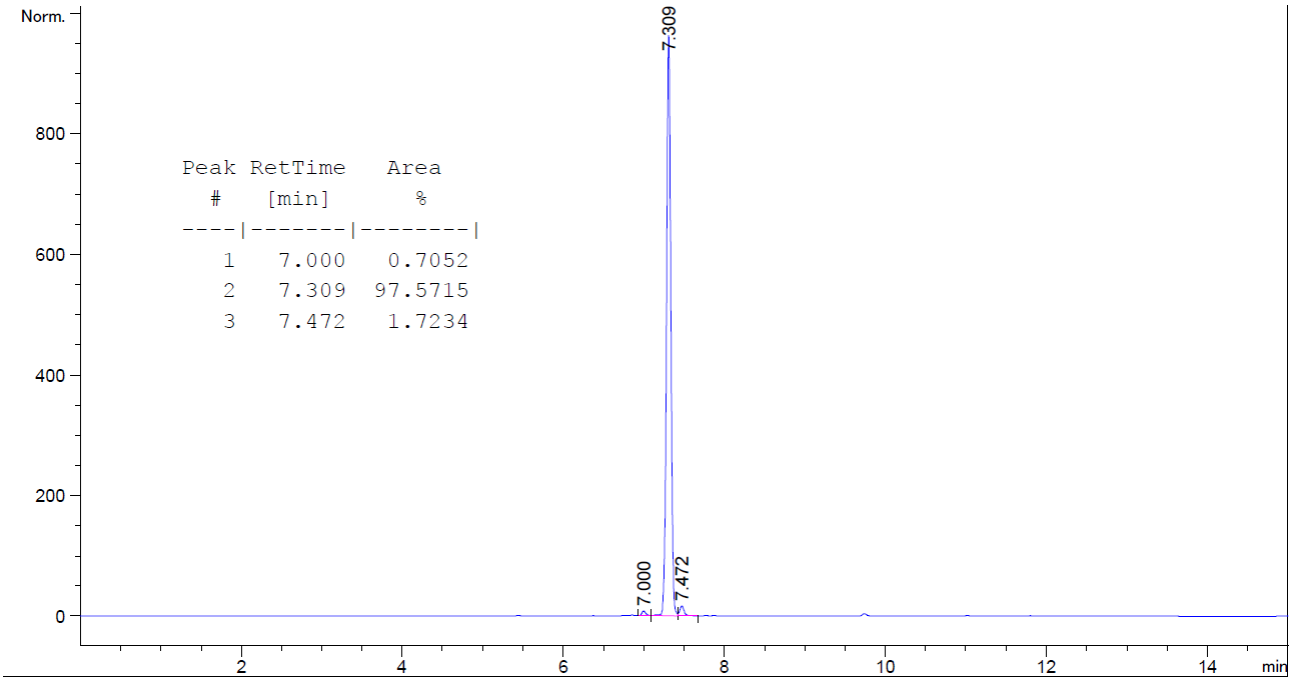
LC-MS analysis was performed using a Jasco UPLC-system combined to a Thermo LTQ-Orbitrap XL. The solvents used for all the LC-MS analyses and purifications were 0.1 % Formic acid in water and acetonitrile. The column was Acquity UPLC BEH C18 (1.7Mm) (50 x 2.1 mm) (Waters). The following analytical method was used, flow: 0.3 mL/min; gradient: 95% aqueous, gradually to 100% aqueous over 11 minutes and then isocratic flow for 4 minutes.

Compound **1**

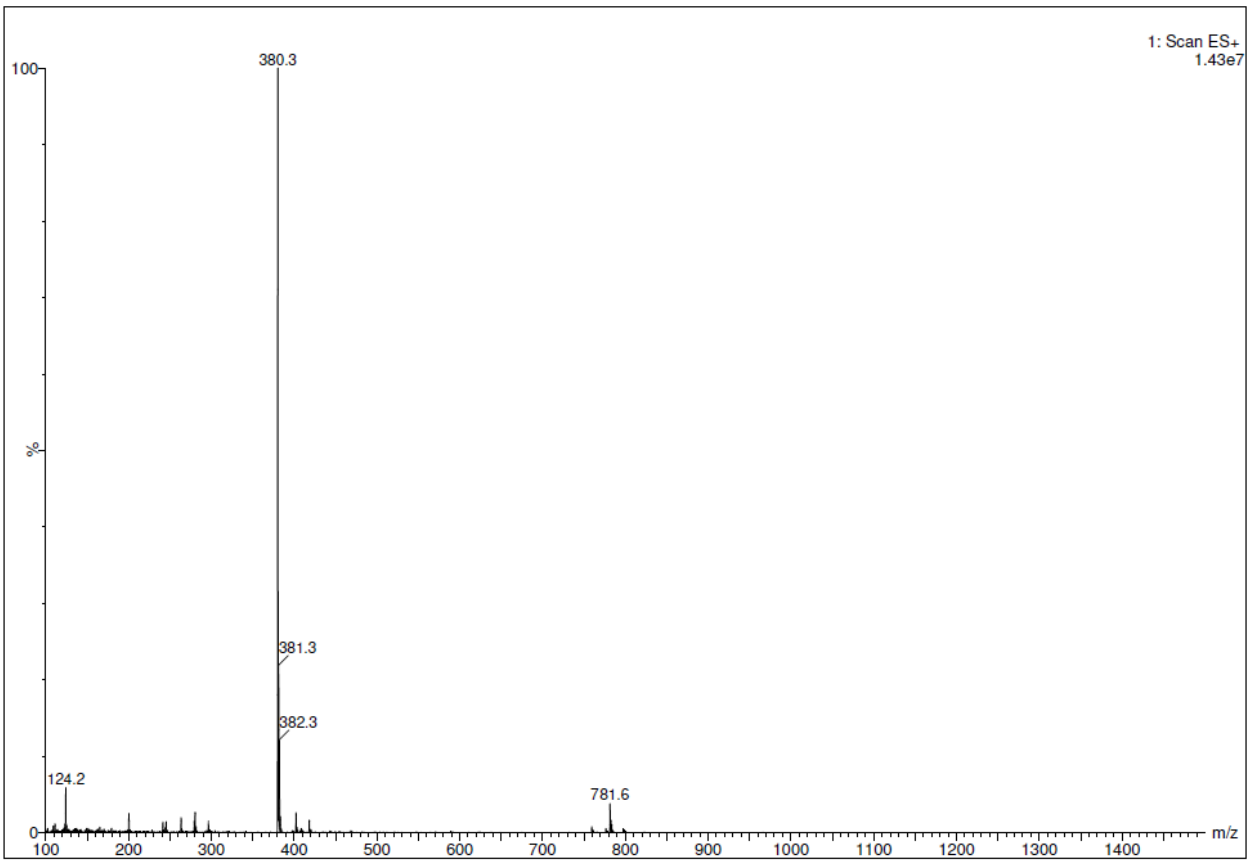




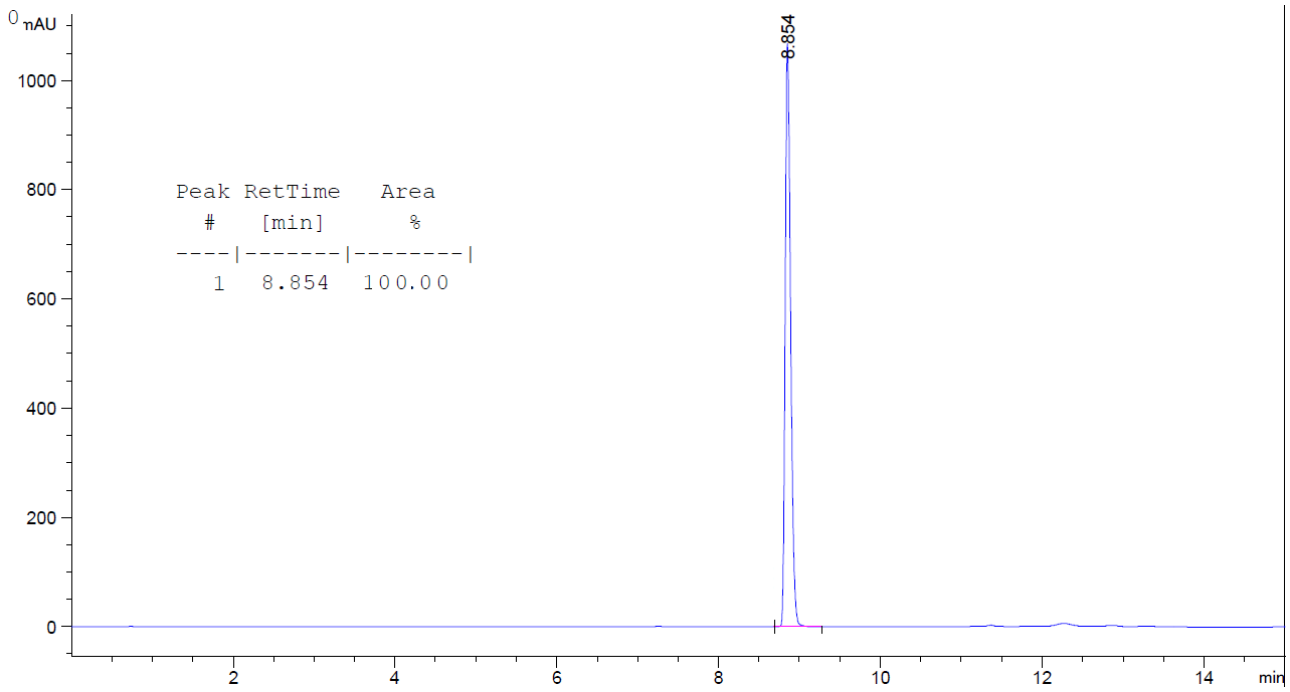
Compound **2**

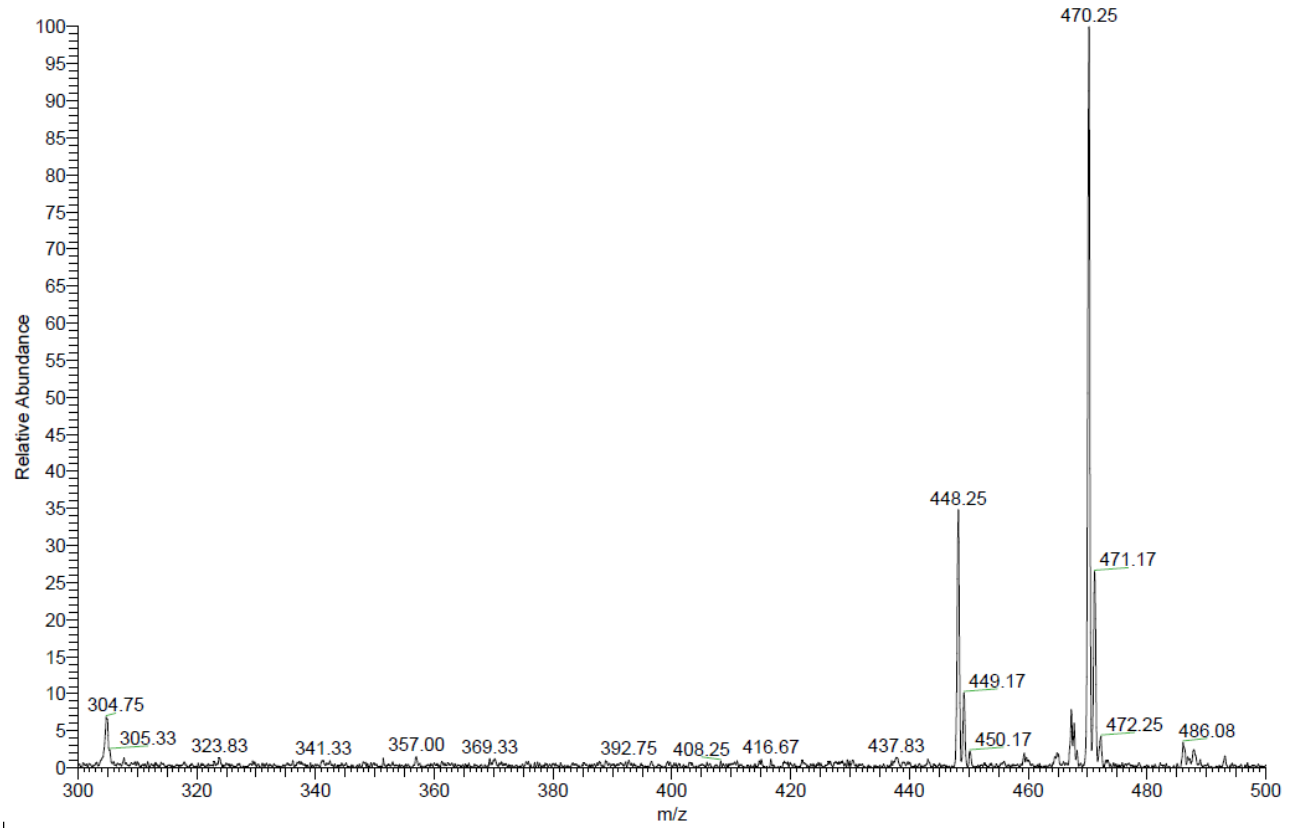


Peak #	RetTime [min]	Area %
1	7.000	0.7052
2	7.309	97.5715
3	7.472	1.7234

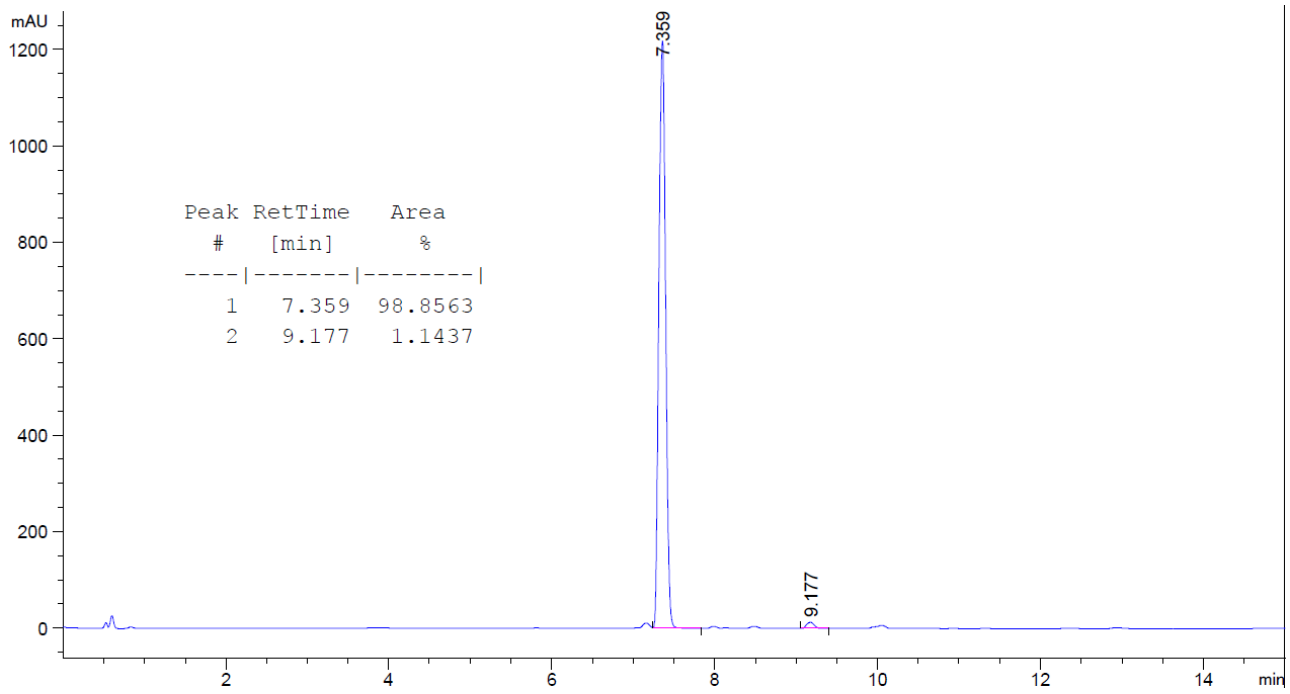


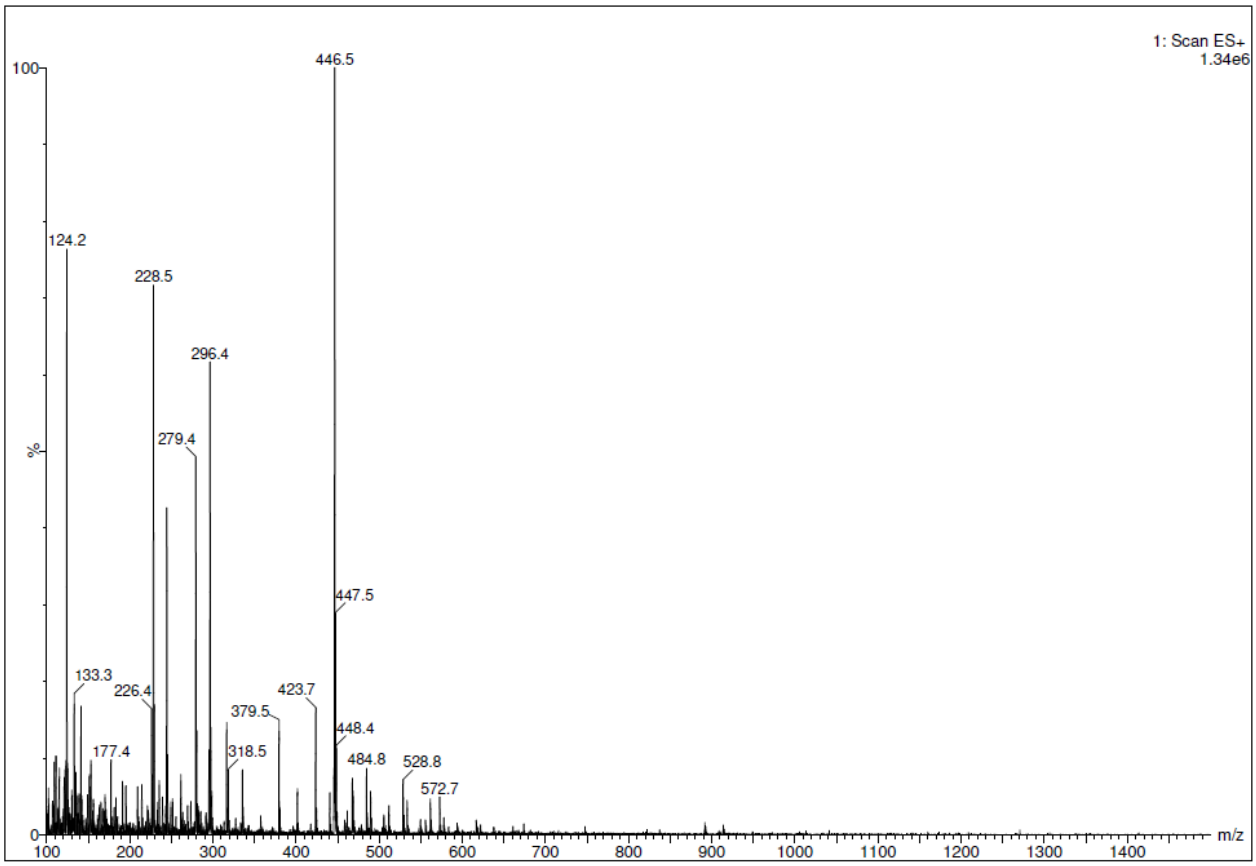
Compound **3**


mAU
1000
800
600
400
200
0
8.854
Peak RetTime Area
[min] %
1 8.854 100.00
2
4
6
8
10
12
14
min

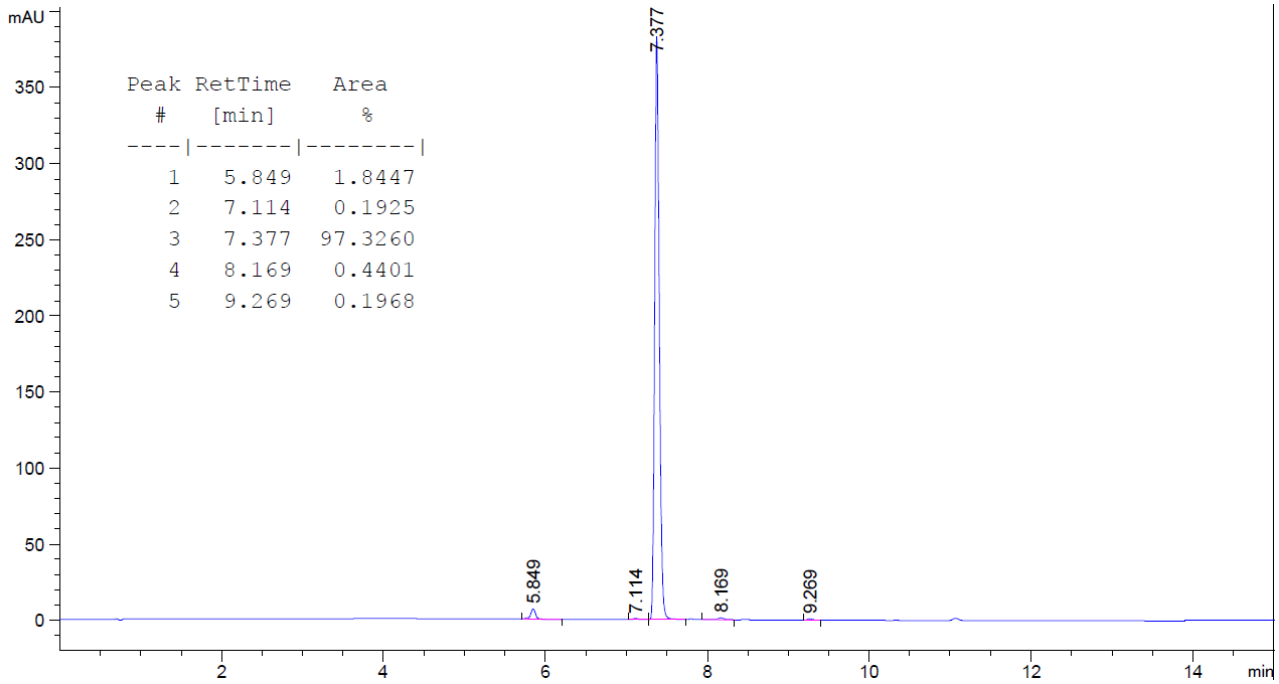

Relative Abundance
m/z
470.25
448.25
471.17
449.17
450.17
472.25
486.08
304.75
305.33
323.83
341.33
357.00
369.33
392.75
408.25
416.67
437.83

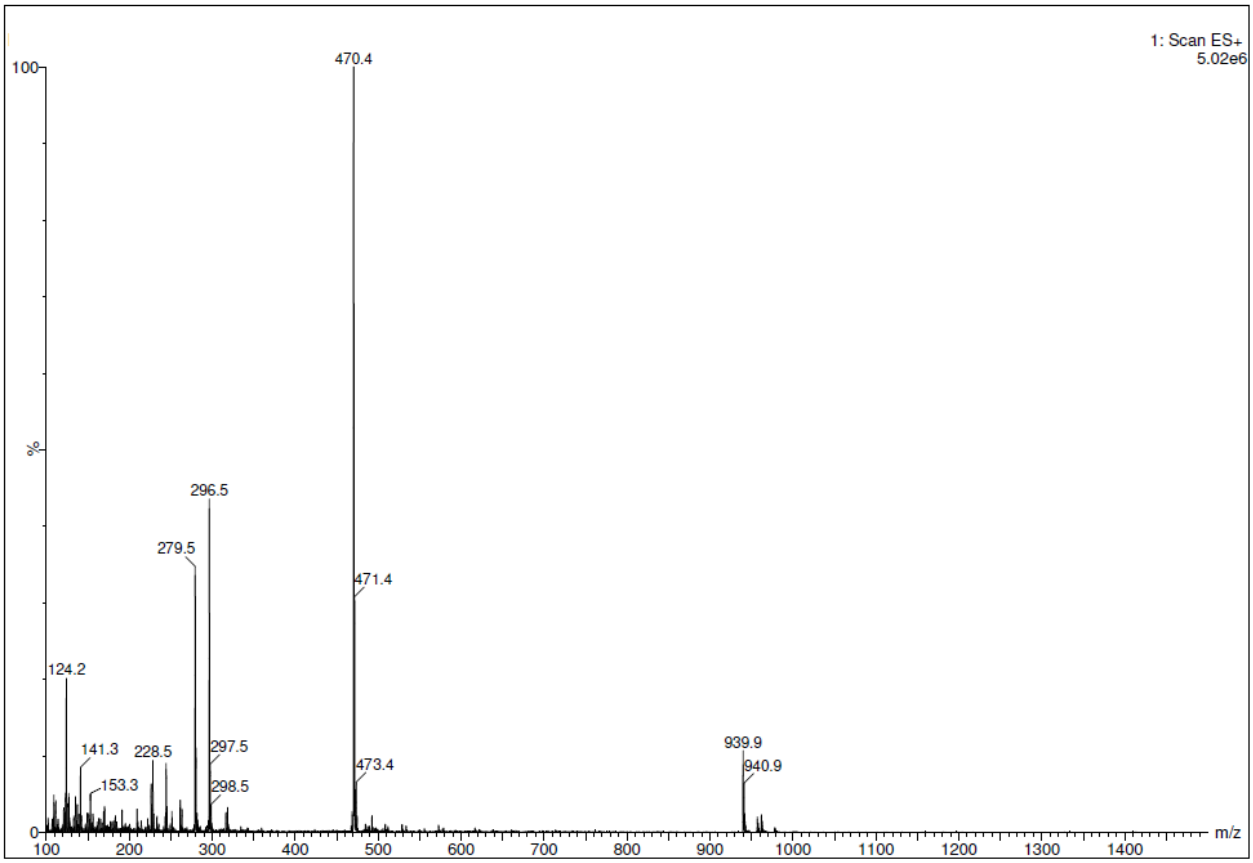
Compound **4**


mAU
1200
1000
800
600
400
200
0
7.359
9.177
Peak RetTime Area
[min] %
1 7.359 98.8563
2 9.177 1.1437
2
4
6
8
10
12
14
min

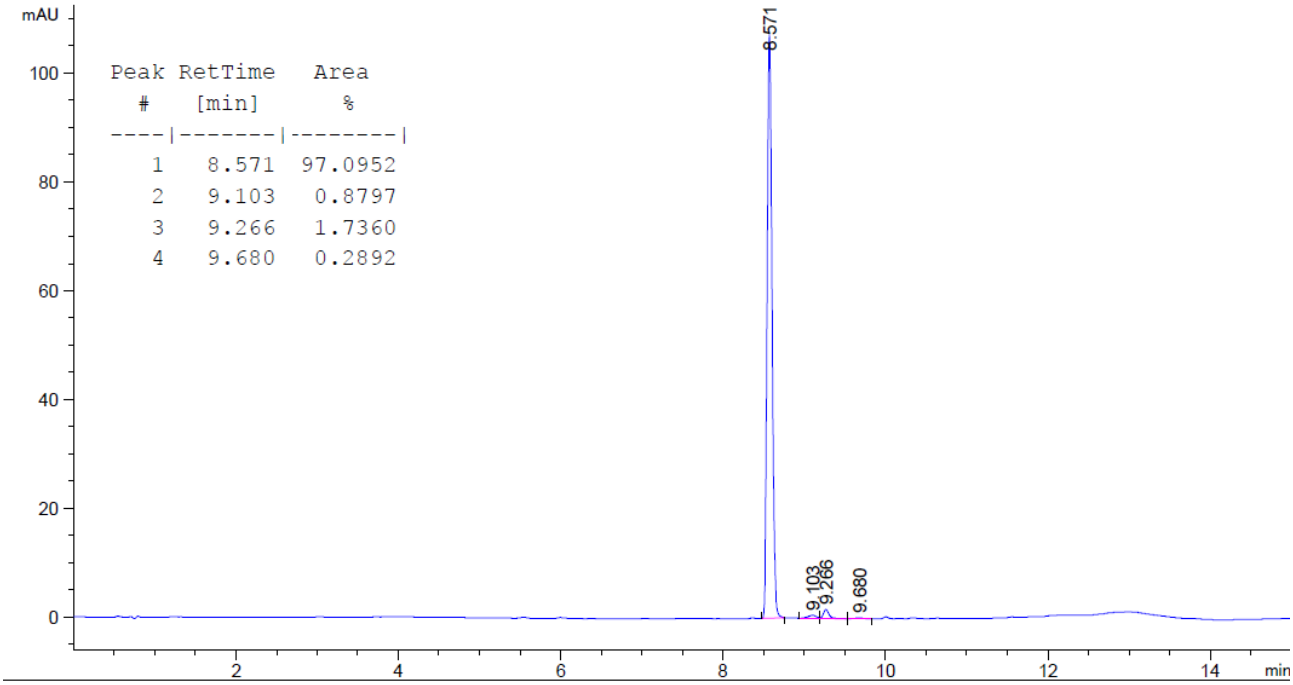

1: Scan ES+
1.34e6
100
%
0
446.5
124.2
228.5
296.4
279.4
447.5
133.3
226.4
423.7
379.5
448.4
177.4
318.5
484.8
528.8
572.7
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
1400
m/z

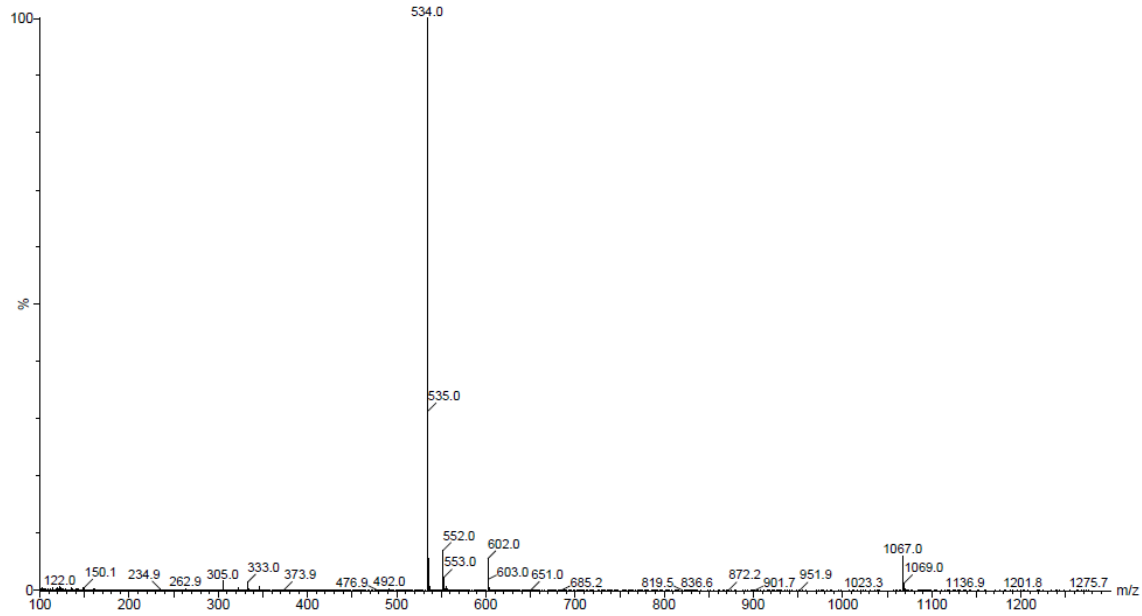
Compound **5**


mAU
Peak RetTime Area
[min] %
1 5.849 1.8447
2 7.114 0.1925
3 7.377 97.3260
4 8.169 0.4401
5 9.269 0.1968
7.377
5.849
7.114
8.169
9.269
min

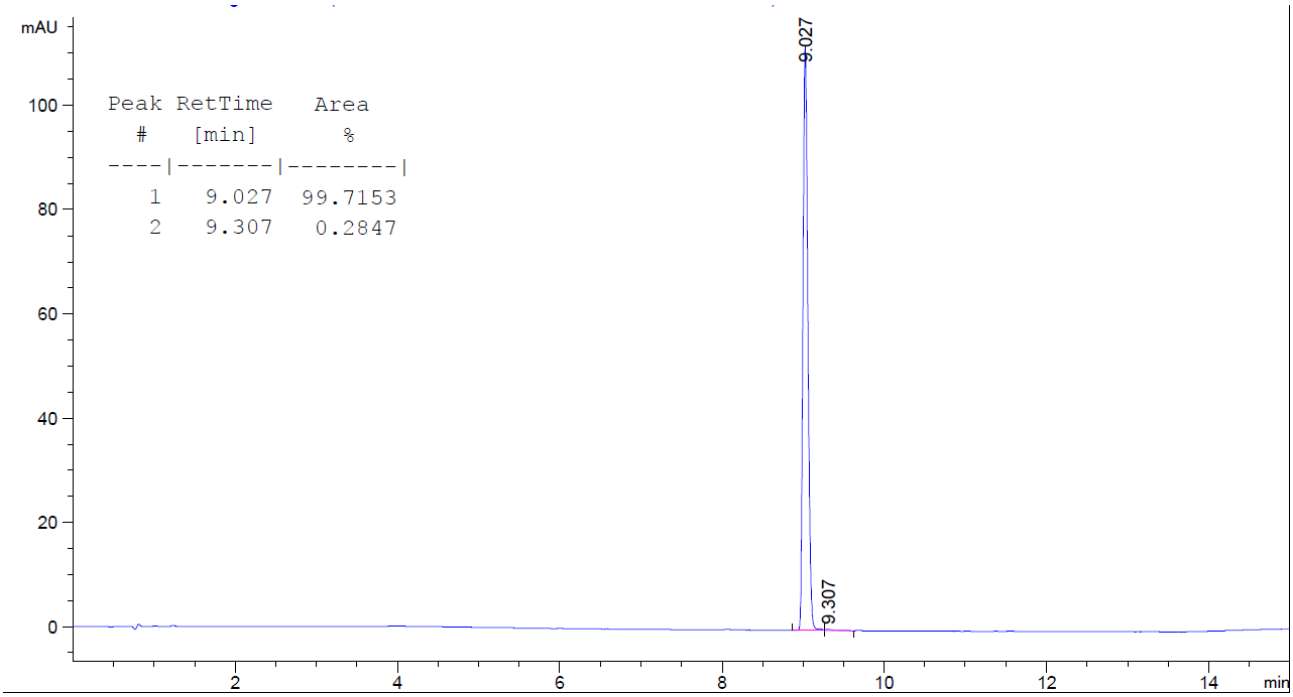

1: Scan ES+
5.02e6
470.4
296.5
279.5
471.4
124.2
141.3
228.5
297.5
153.3
298.5
473.4
939.9
940.9
%
m/z

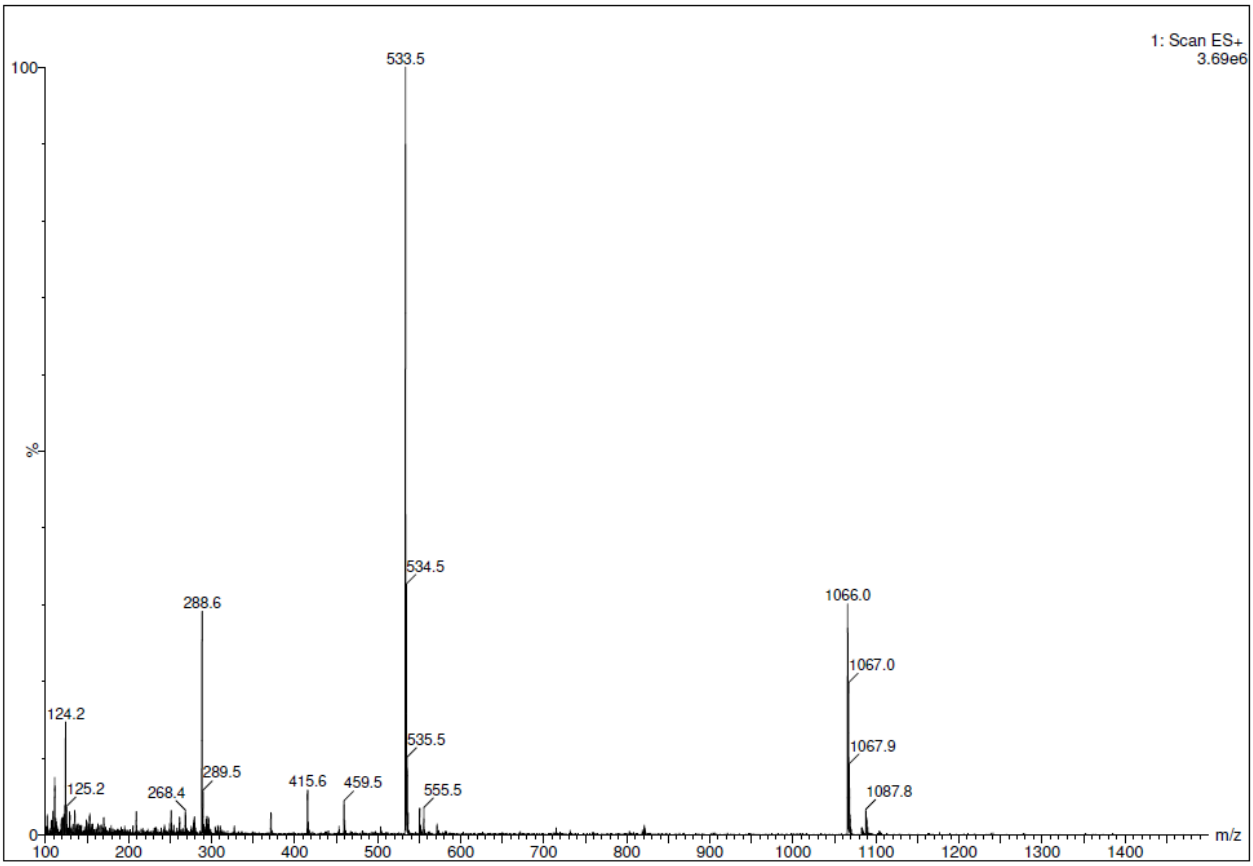
Compound **6**


mAU
Peak RetTime Area
[min] %
1 8.571 97.0952
2 9.103 0.8797
3 9.266 1.7360
4 9.680 0.2892
8.571
9.103
9.266
9.680
min

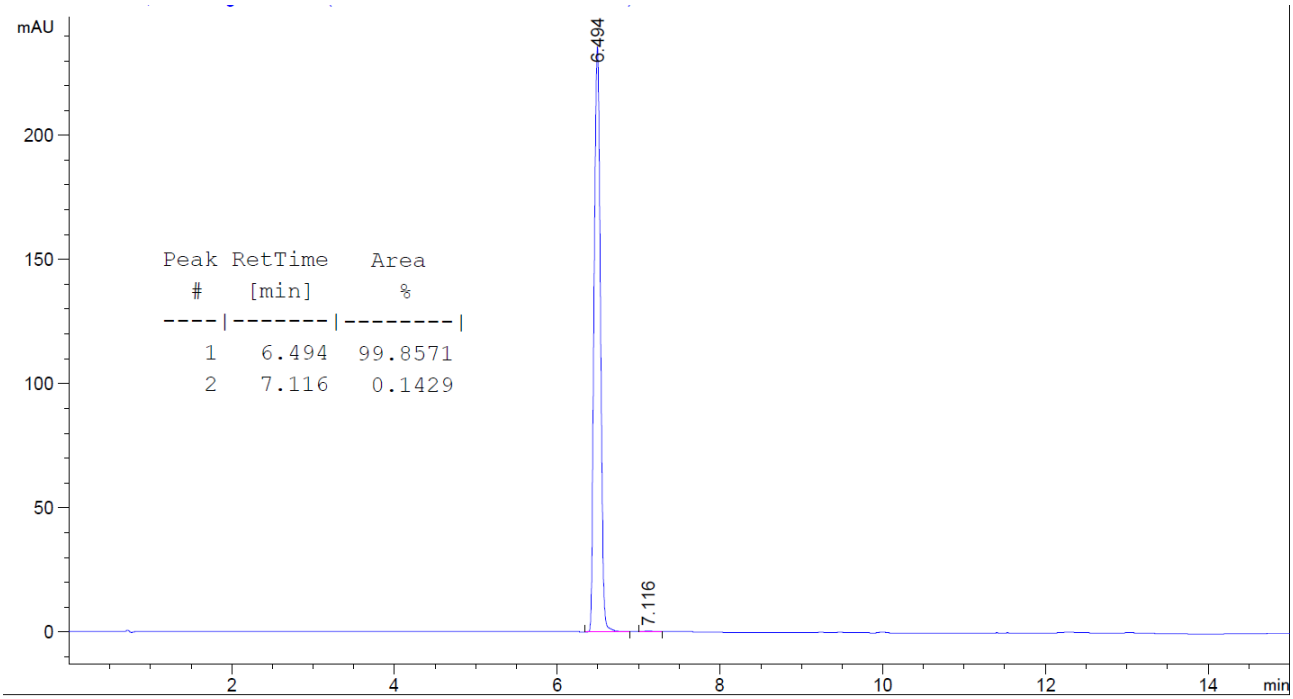

534.0
535.0
552.0
553.0
602.0
603.0
651.0
1067.0
1069.0
%
m/z

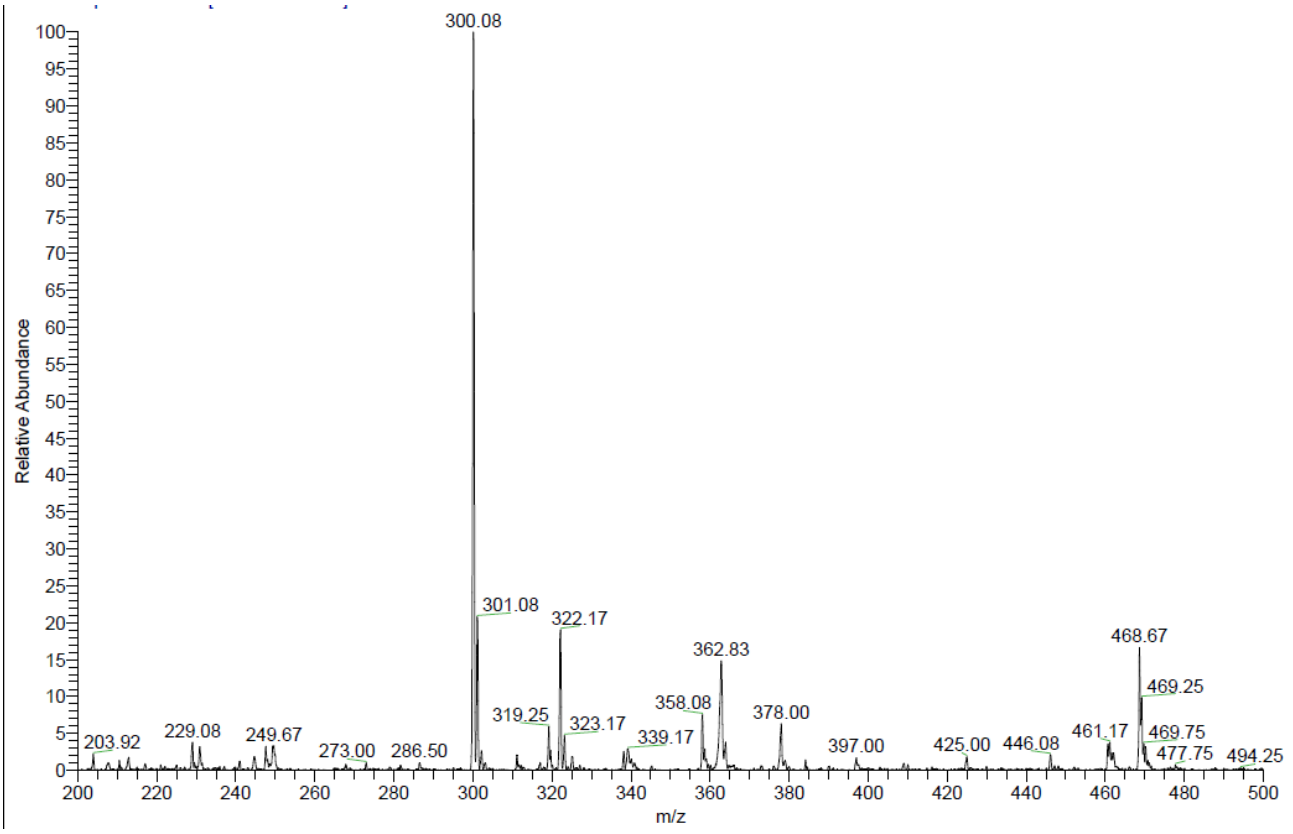
Compound **7**


mAU
Peak RetTime Area
[min] %
1 9.027 99.7153
2 9.307 0.2847
9.027
9.307
min

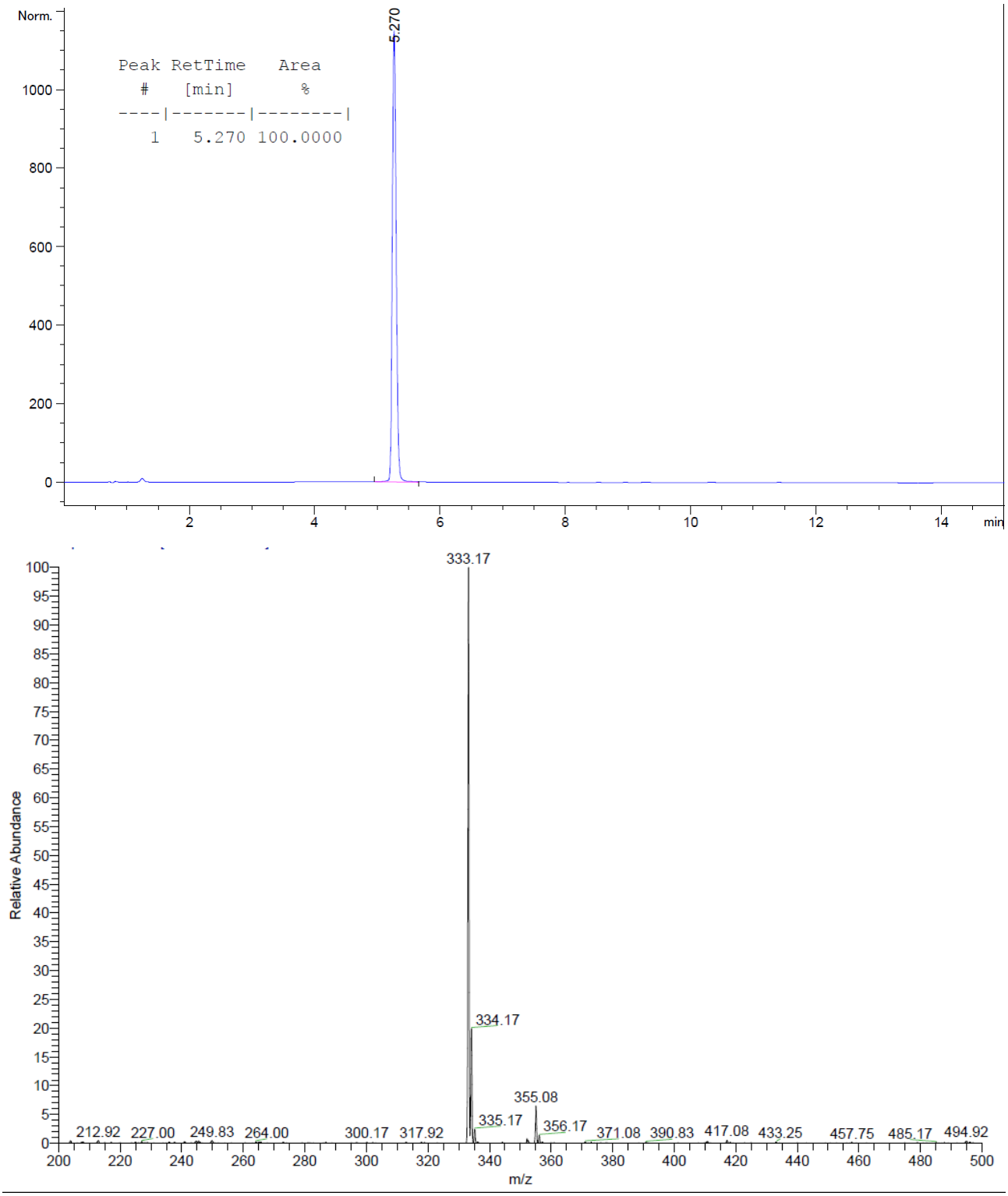

1: Scan ES+
3.69e6
%
533.5
534.5
288.6
1066.0
1067.0
124.2
535.5
1067.9
289.5
125.2
268.4
415.6
459.5
555.5
1087.8
m/z

Compound **15**


mAU
200
150
100
50
0
6.494
7.116
Peak RetTime Area
[min] %
1 6.494 99.8571
2 7.116 0.1429
2
4
6
8
10
12
14
min

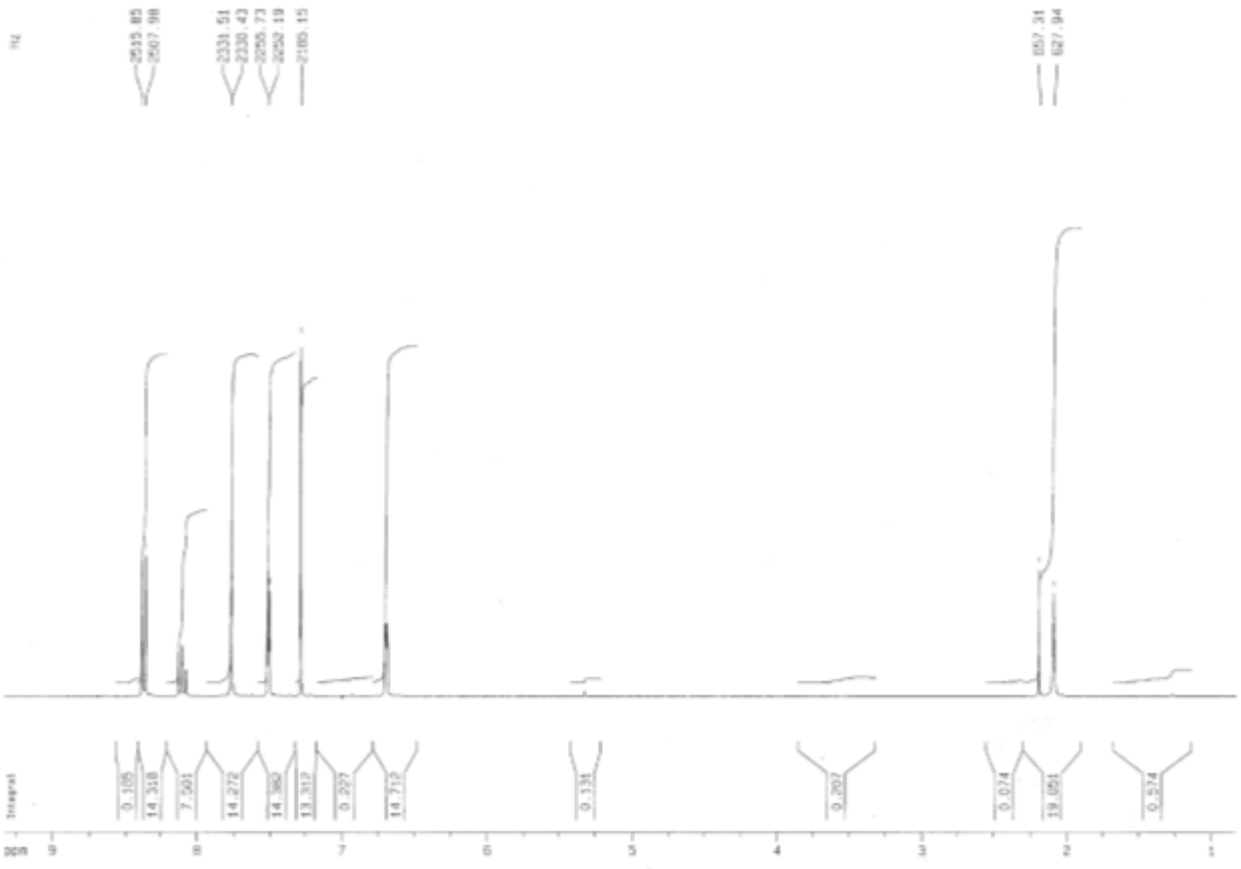

Relative Abundance
m/z
300.08
301.08
322.17
362.83
468.67
469.25
319.25
323.17
358.08
339.17
378.00
203.92
229.08
249.67
273.00
286.50
397.00
425.00
446.08
461.17
469.75
477.75
494.25

Compound **16**

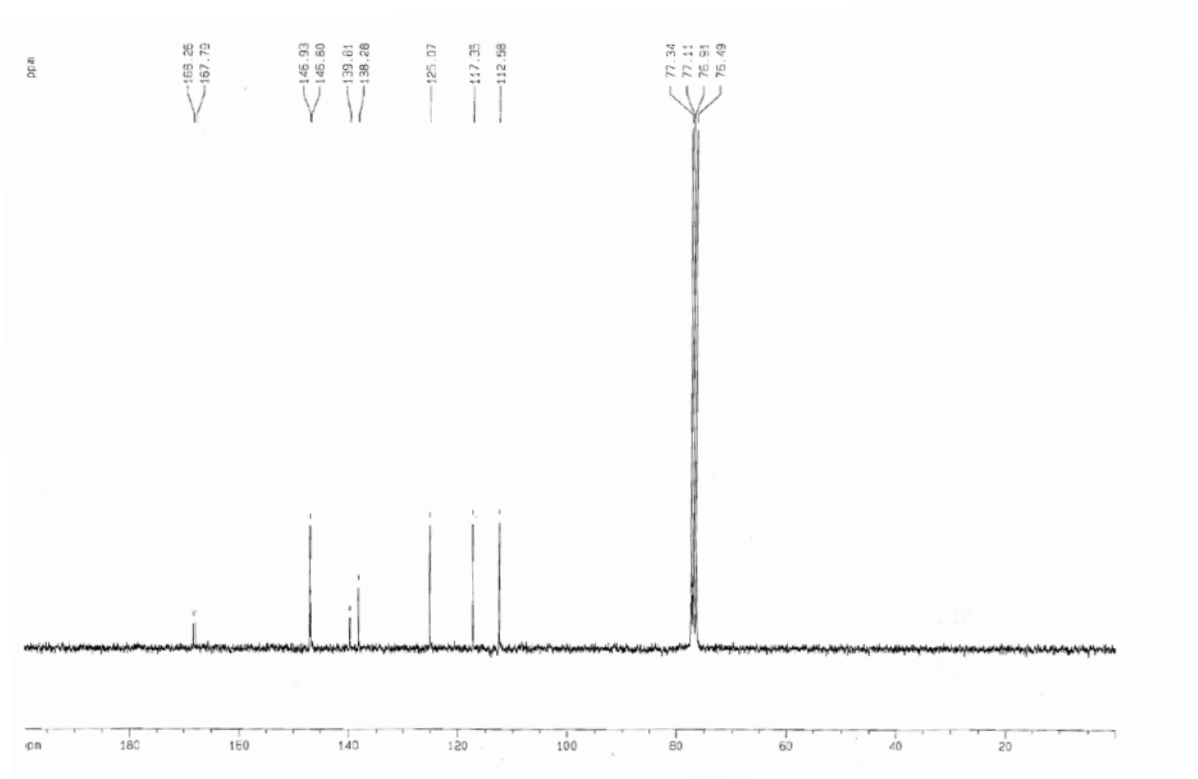

Norm.
Peak RetTime Area
[min] %
1 5.270 100.0000
5.270
min
Relative Abundance
m/z
333.17
334.17
355.08
335.17
356.17
212.92
227.00
249.83
264.00
300.17
317.92
371.08
390.83
417.08
433.25
457.75
485.17
494.92

NMR characterization:

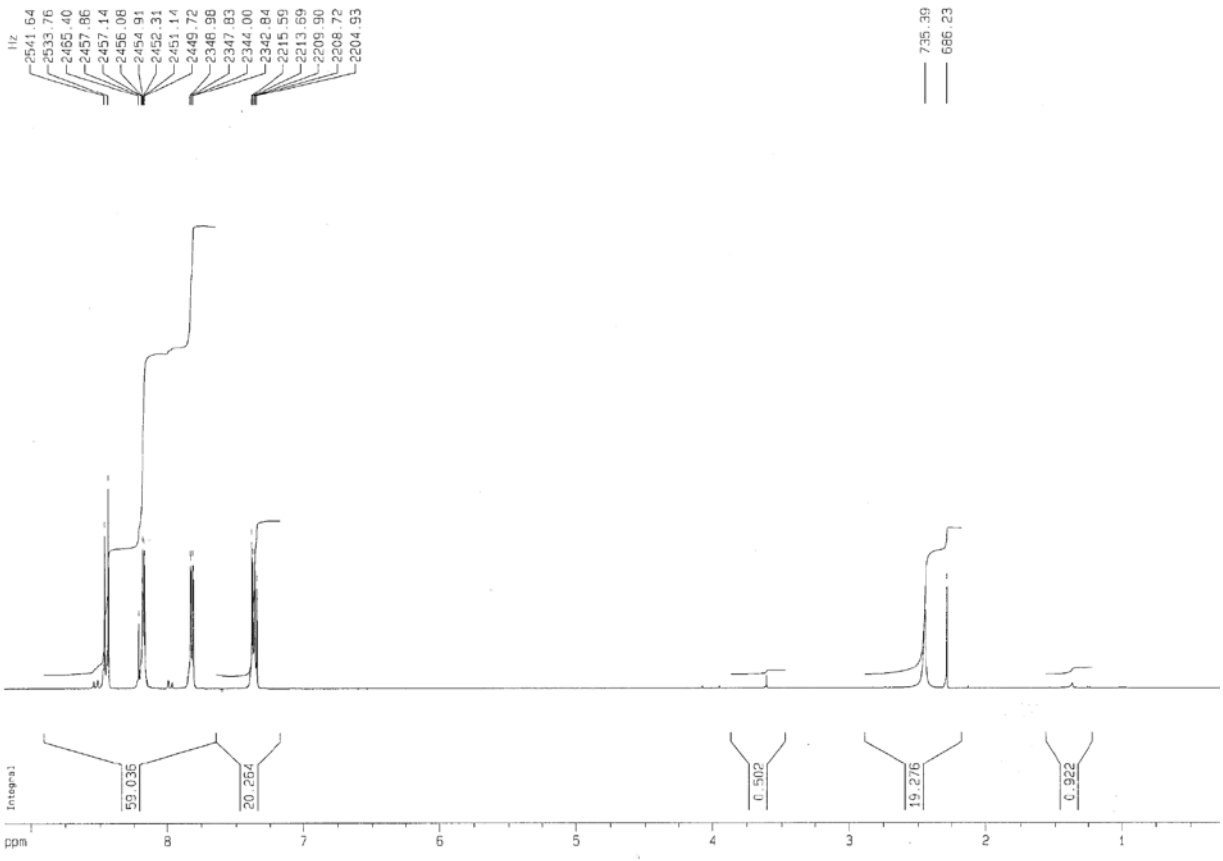
^{1}H-NMR – $CDCl_3$: **1**



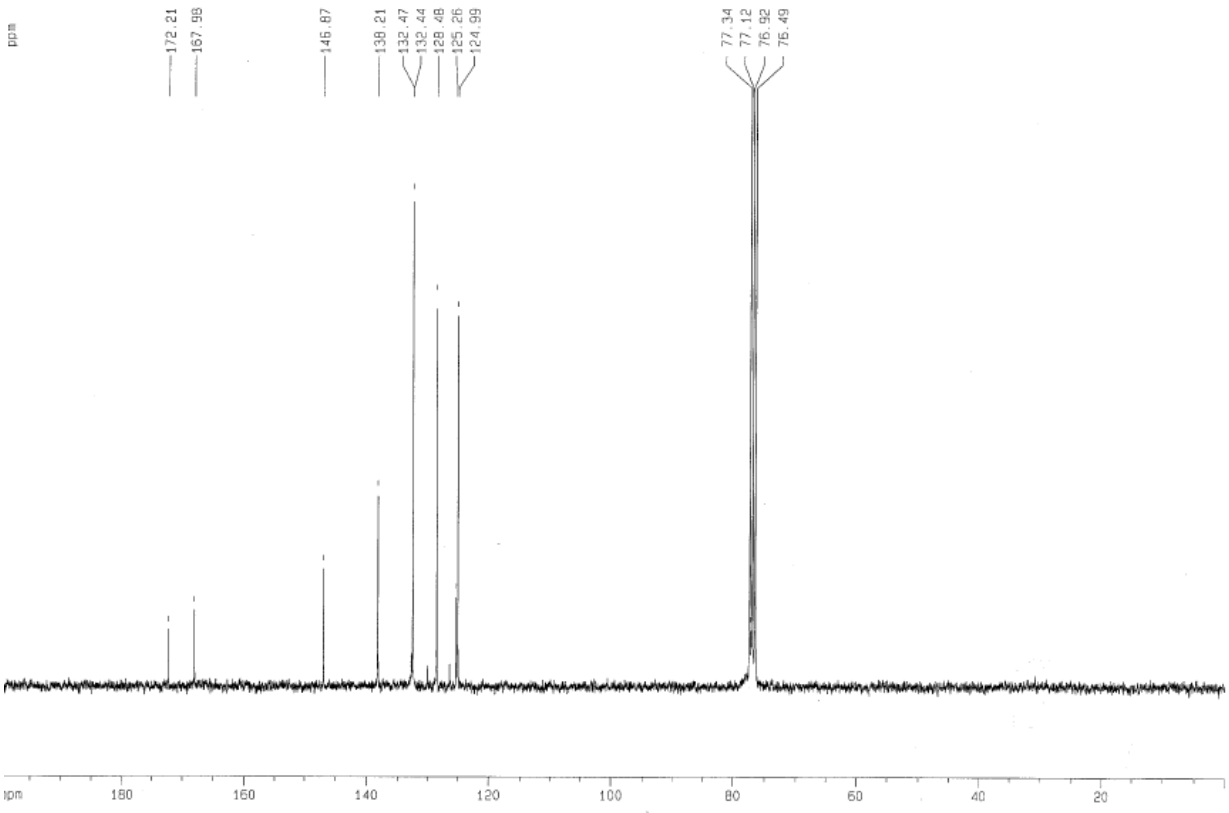
^{13}C-NMR – $CDCl_3$: **1**



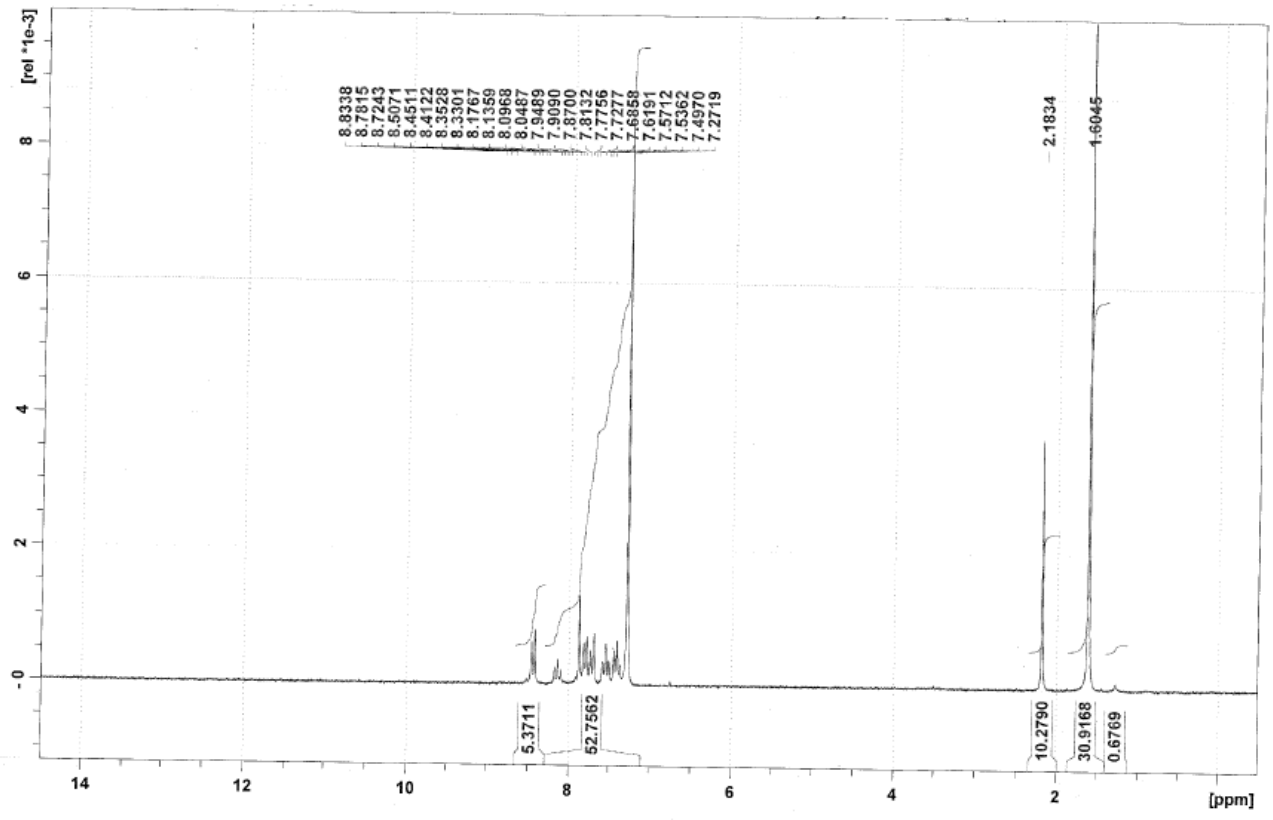
^{1}H-NMR – $CDCl_3$: **2**



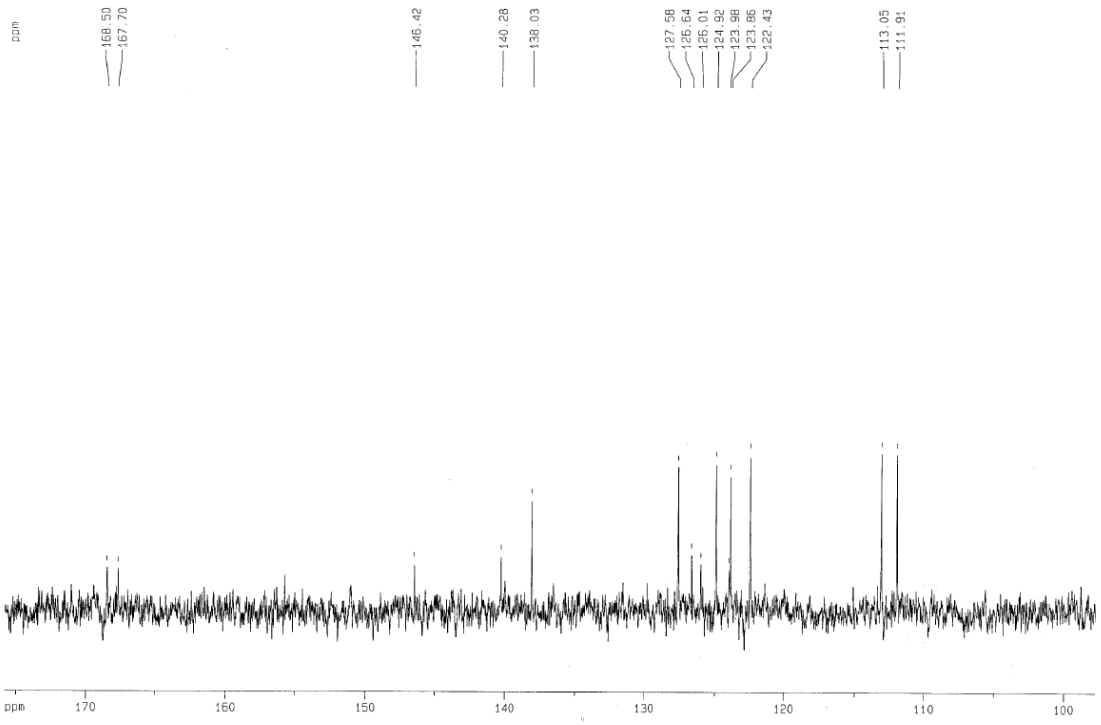
^{13}C-NMR – DMSO d6: **2**



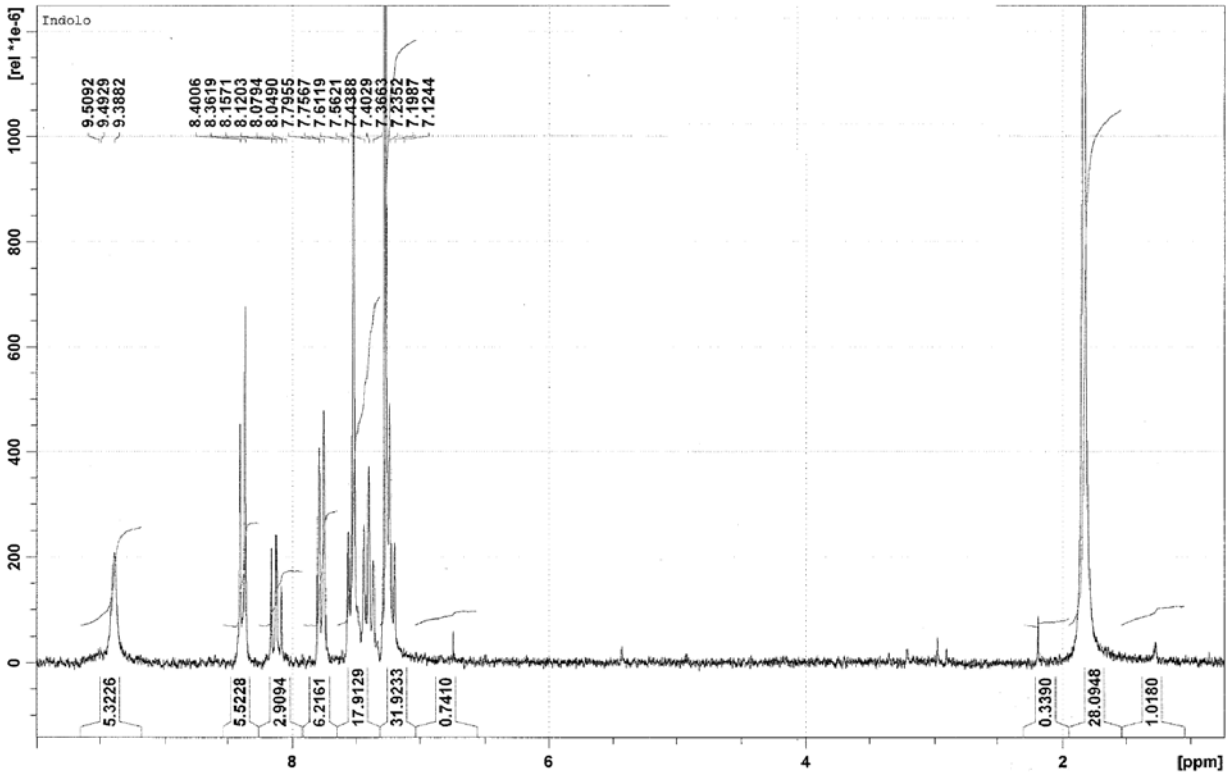
^{1}H-NMR – $CDCl_3$: **3**



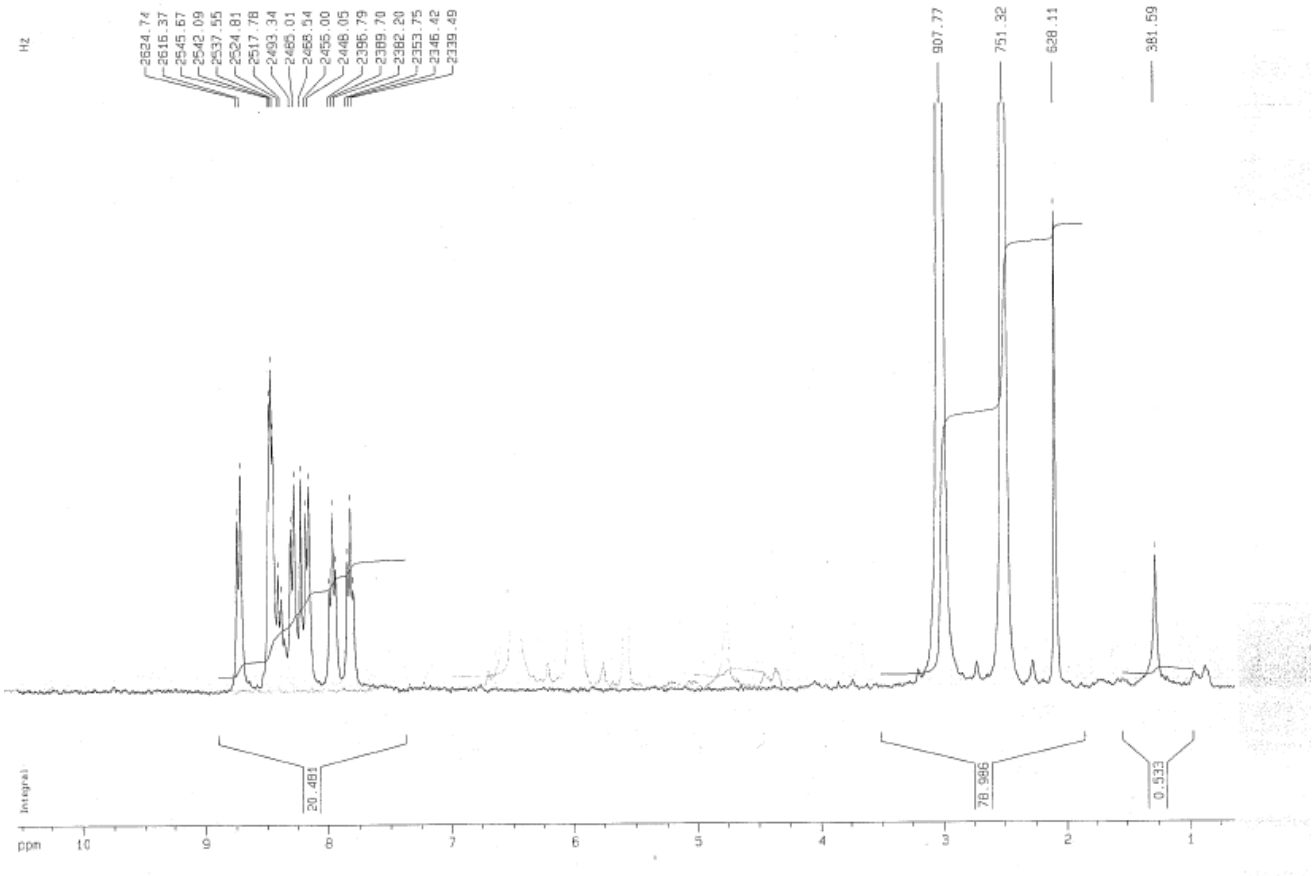
^{13}C-NMR – $CDCl_3$: **3**



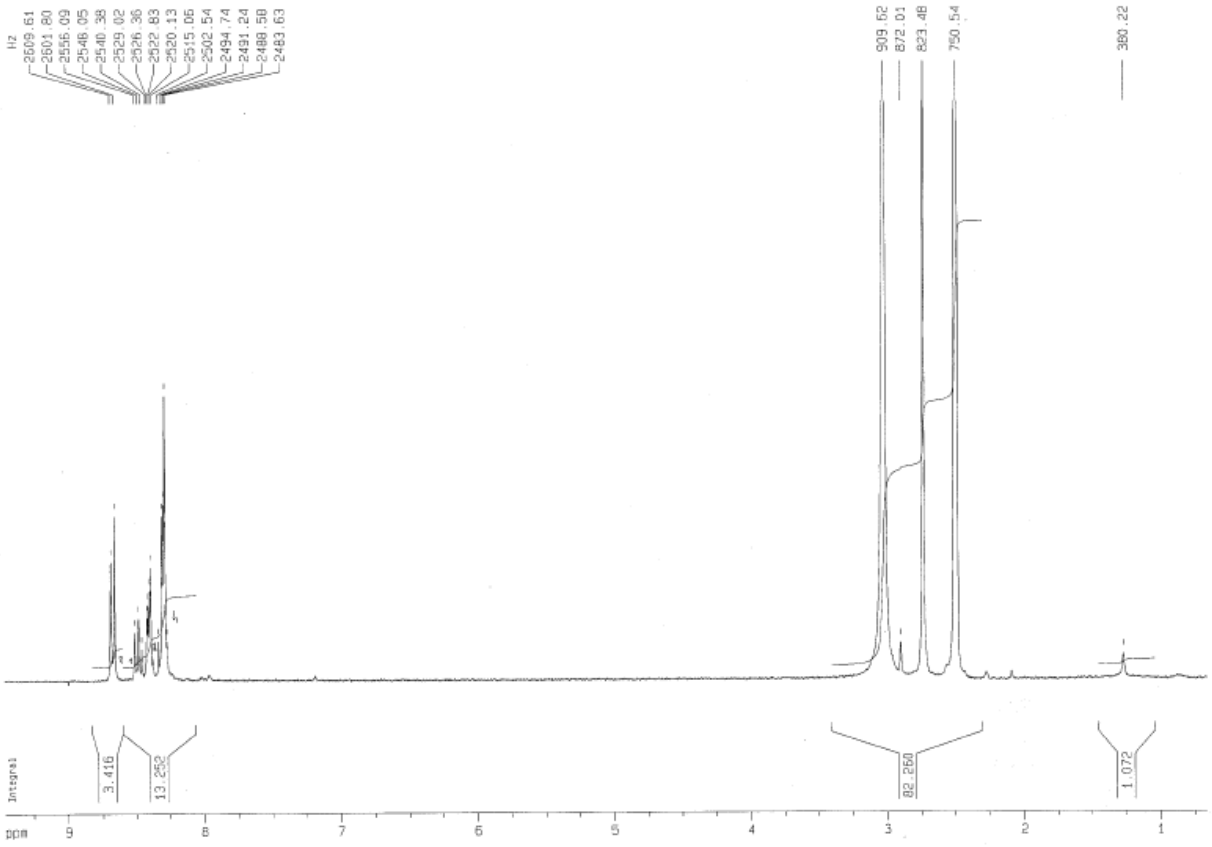
^{1}H-NMR – DMSO d6: **4**



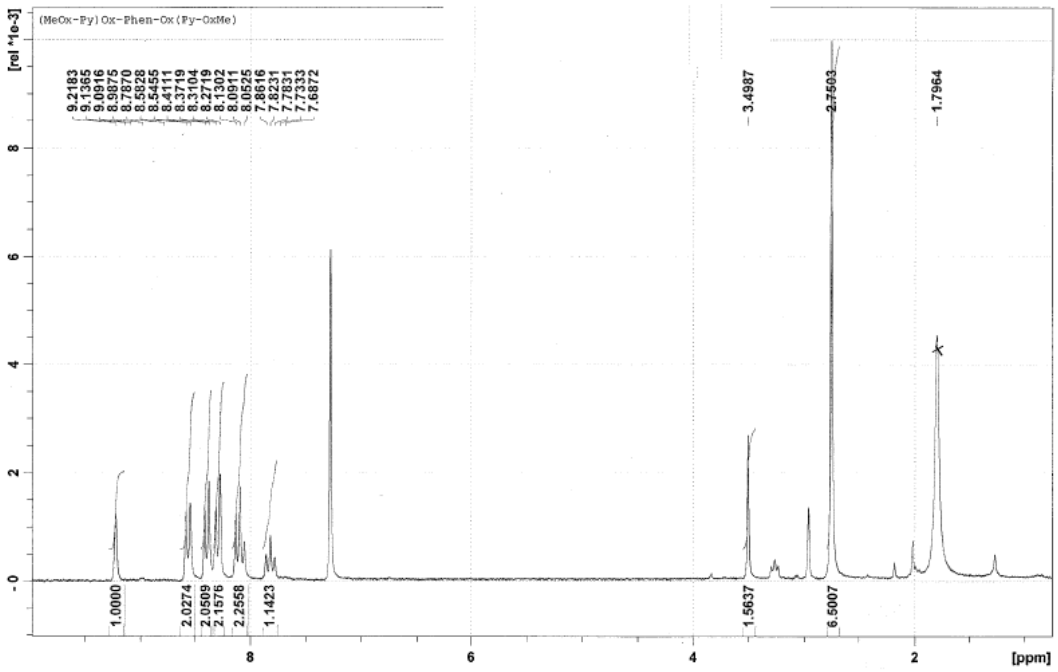
^{1}H-NMR – DMSO d6: Fragment **5**



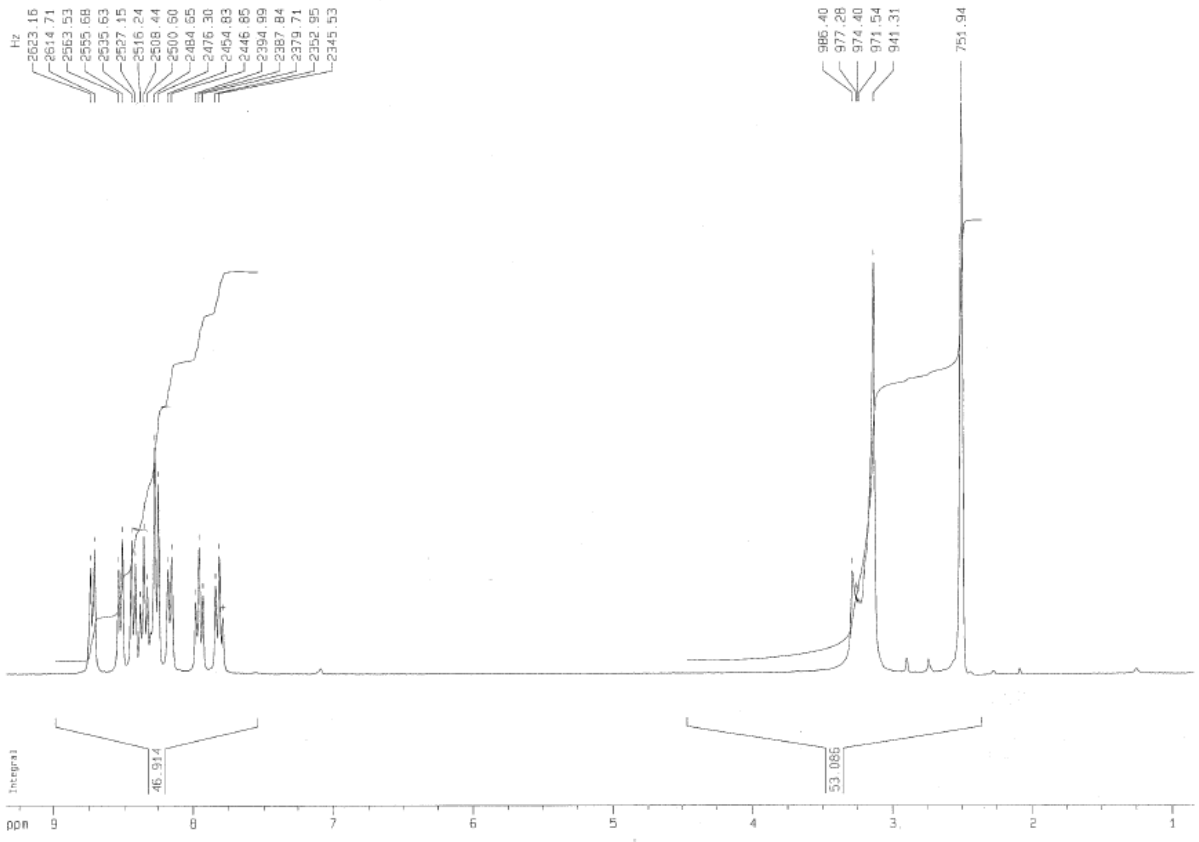
^{1}H-NMR – DMSO d6: Fragment **6**



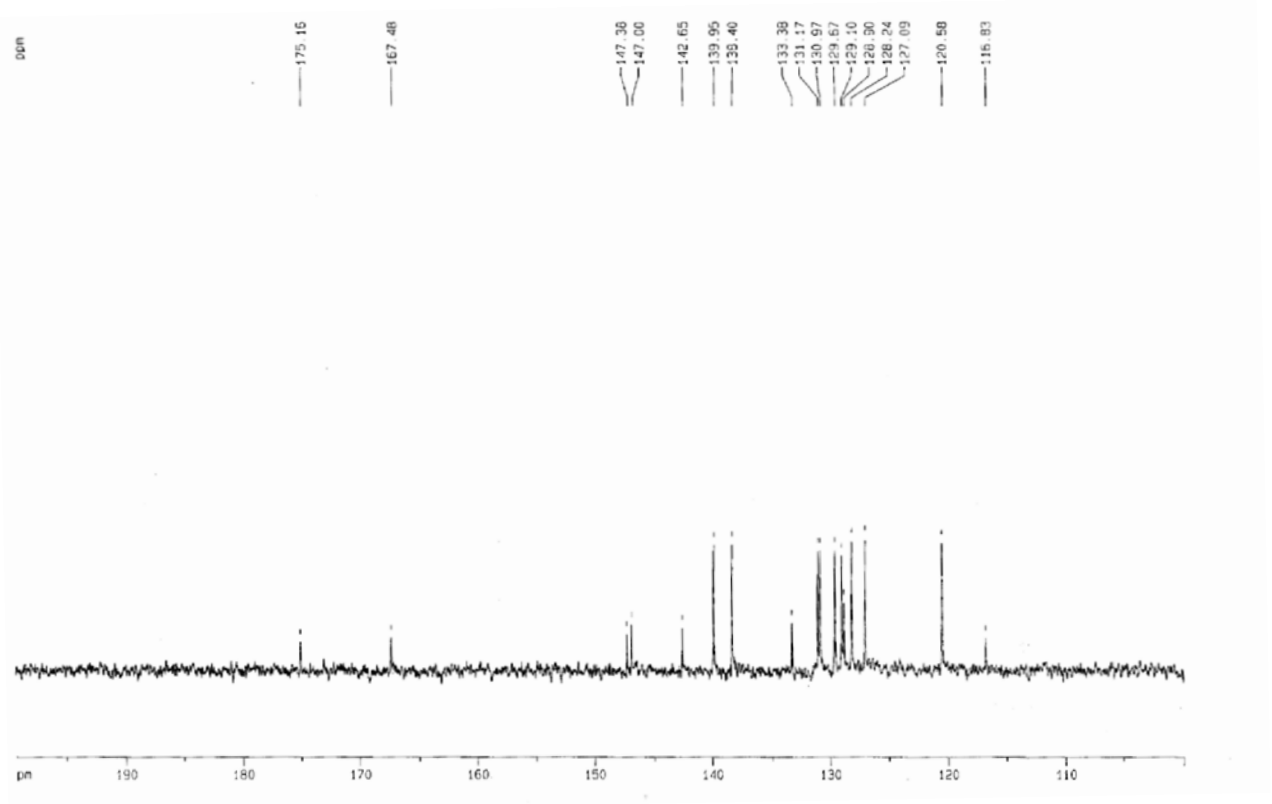
^{1}H-NMR – $CDCl_3$: Fragment **7**



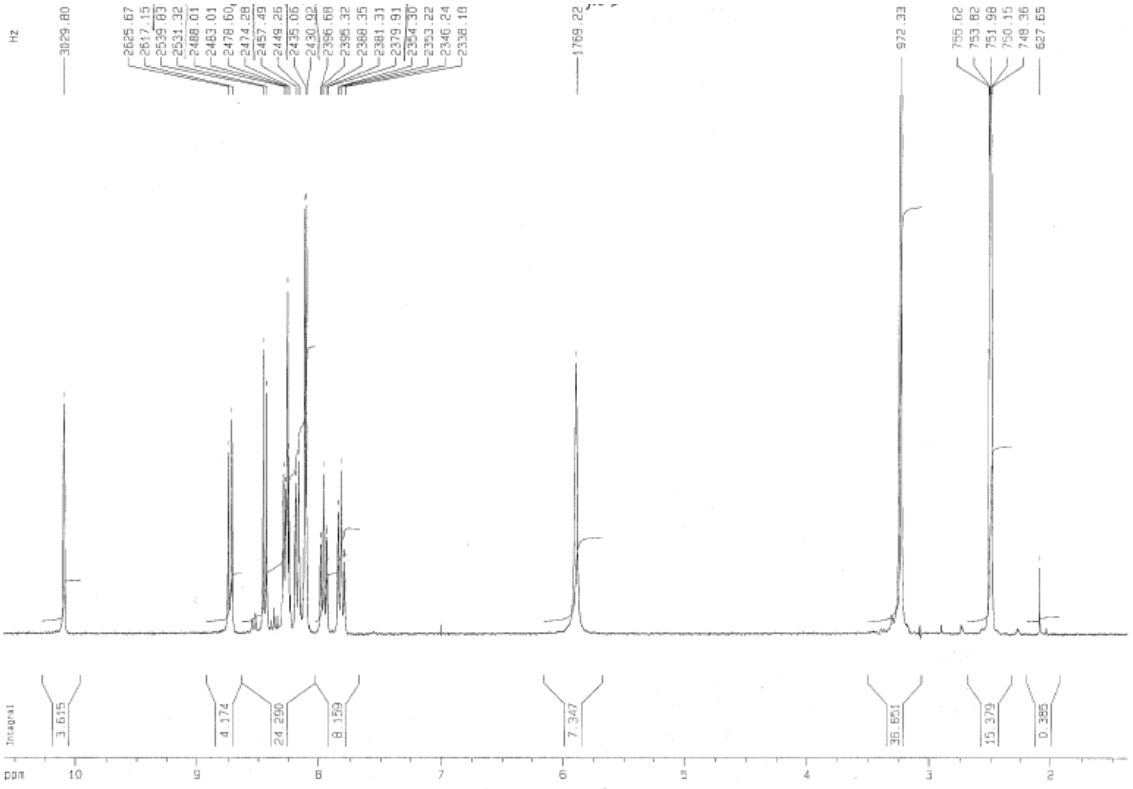
^{1}H-NMR – DMSO d6: **15**



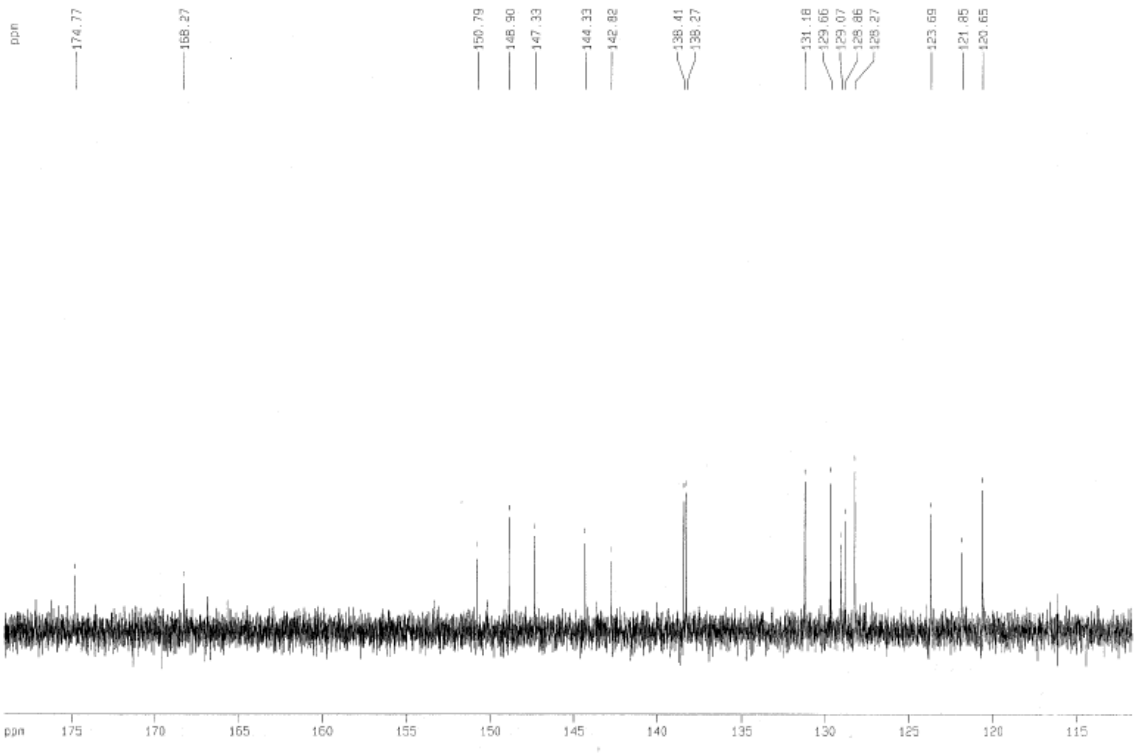
^{13}C-NMR – DMSO d6: **15**



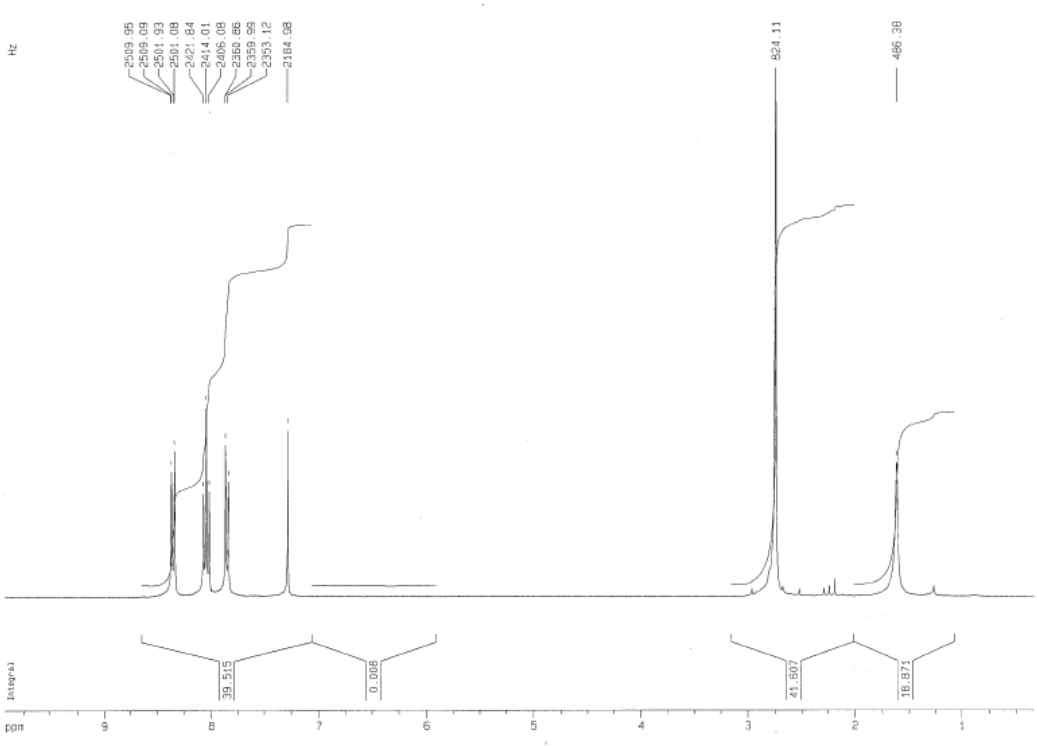
^{1}H-NMR – DMSO d6: **16**



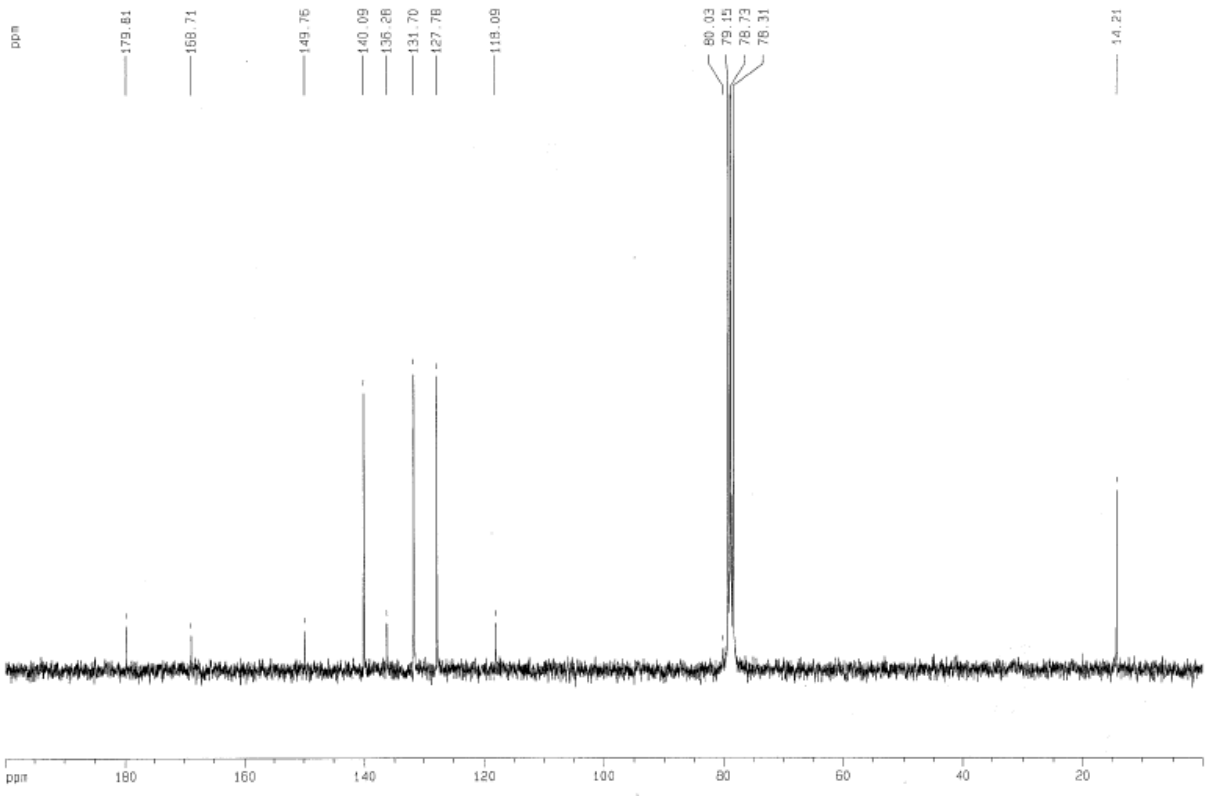
^{13}C-NMR – DMSO d6: **16**



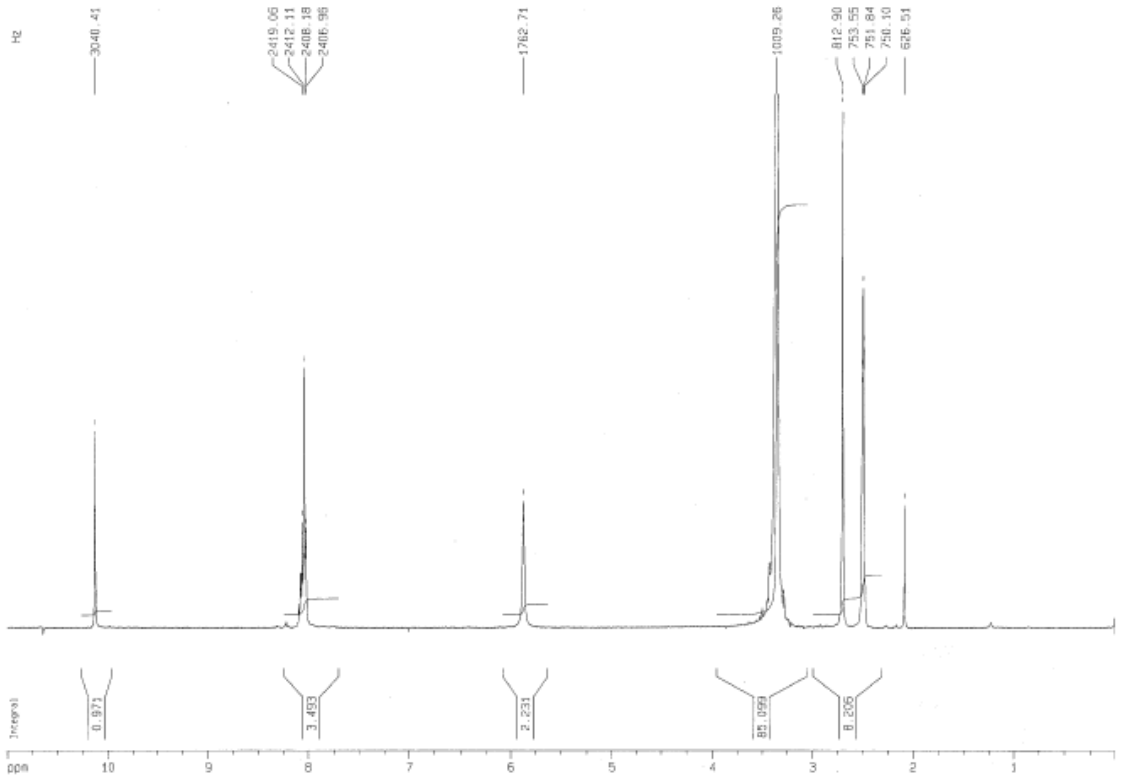
^{1}H-NMR – $CDCl_3$: **17**



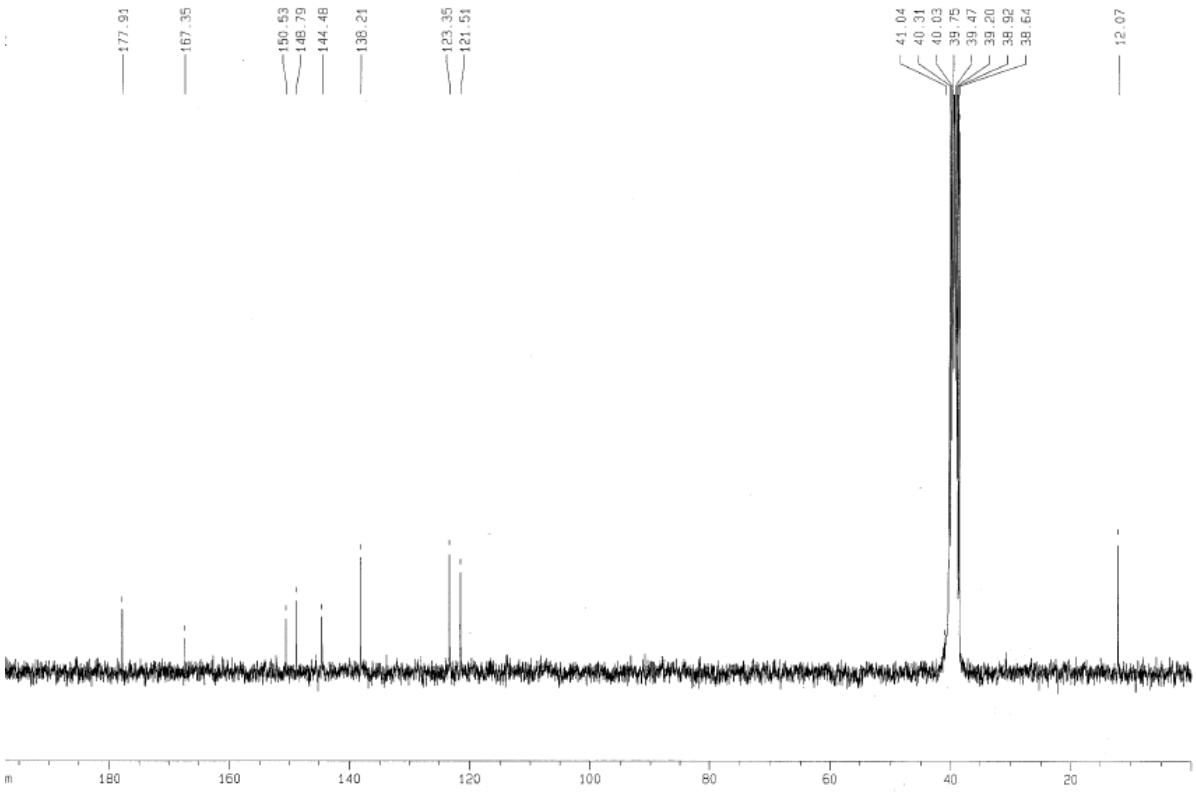
^{13}C-NMR – $CDCl_3$ d6: **17**



^{1}H-NMR – DMSO d6: **18**



^{13}C-NMR – DMSO d6: **18**



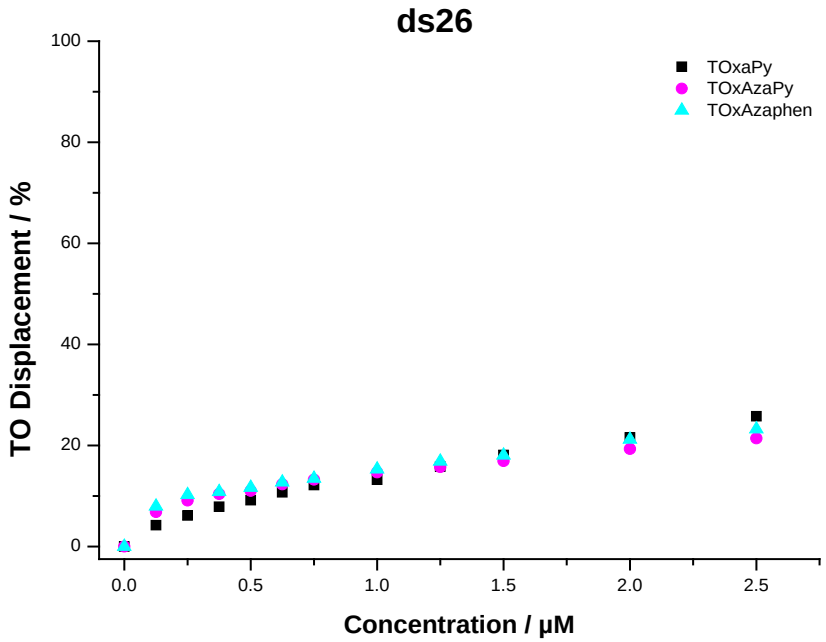


Figure S1: G4-FID plots of TOxAzaPy and TOxAzaPhen in the presence of ds26 (ds DNA). TOxaPy is used as a reference compound.

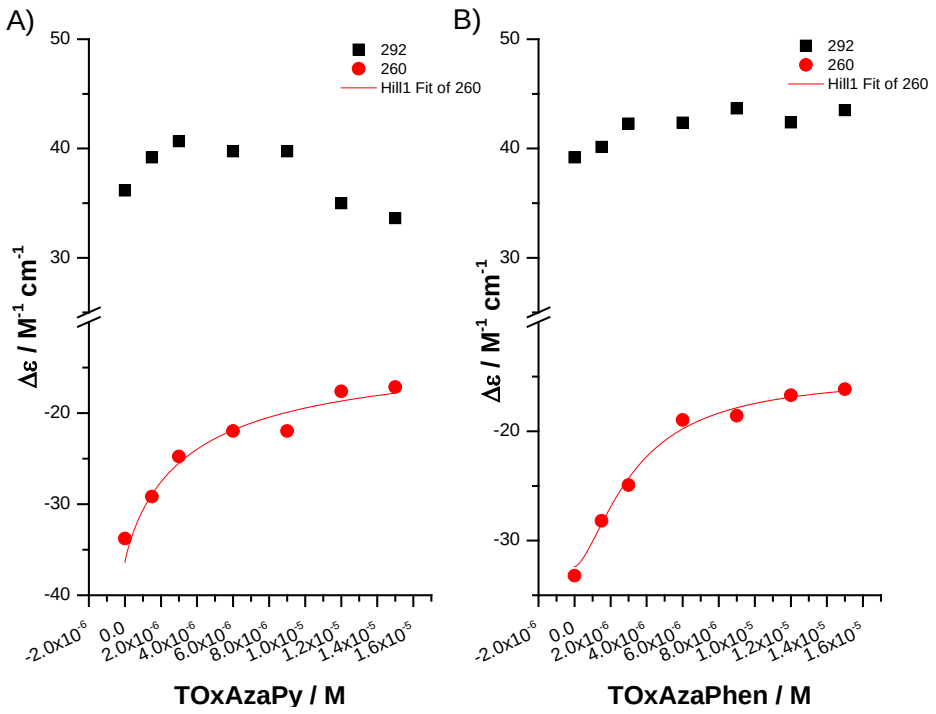


Figure S2: Titration plots representing the change in ellipticity of 22AG in Na^+-rich buffer at 292 nm (black squares) and 260 nm (red dots), with the addition of TOxAzaPy A) and TOxAzaPhen B). Variation of the ellipticity as a function of concentration of ligand A) TOxAzaPyand B) TOxAzaPhen. Lines in A) and B) correspond to the non-linear regressions performed as fitting at 260 nm.