Supplementary Material

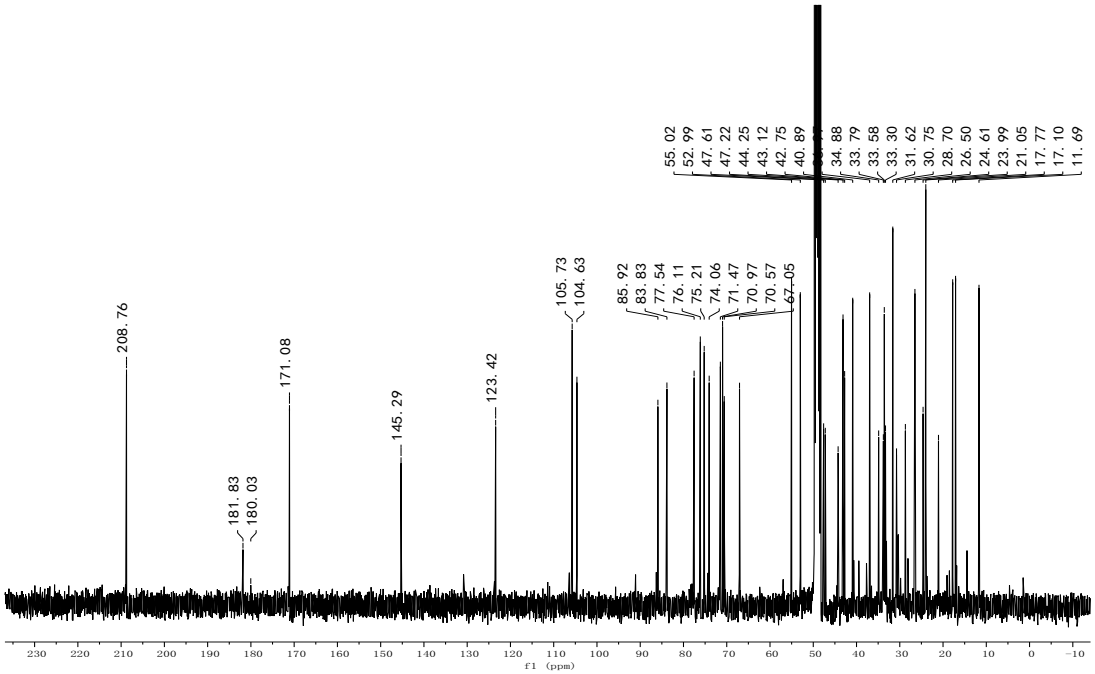

Figure S1 ^{13}C-NMR spectrum of compound 1 is given.

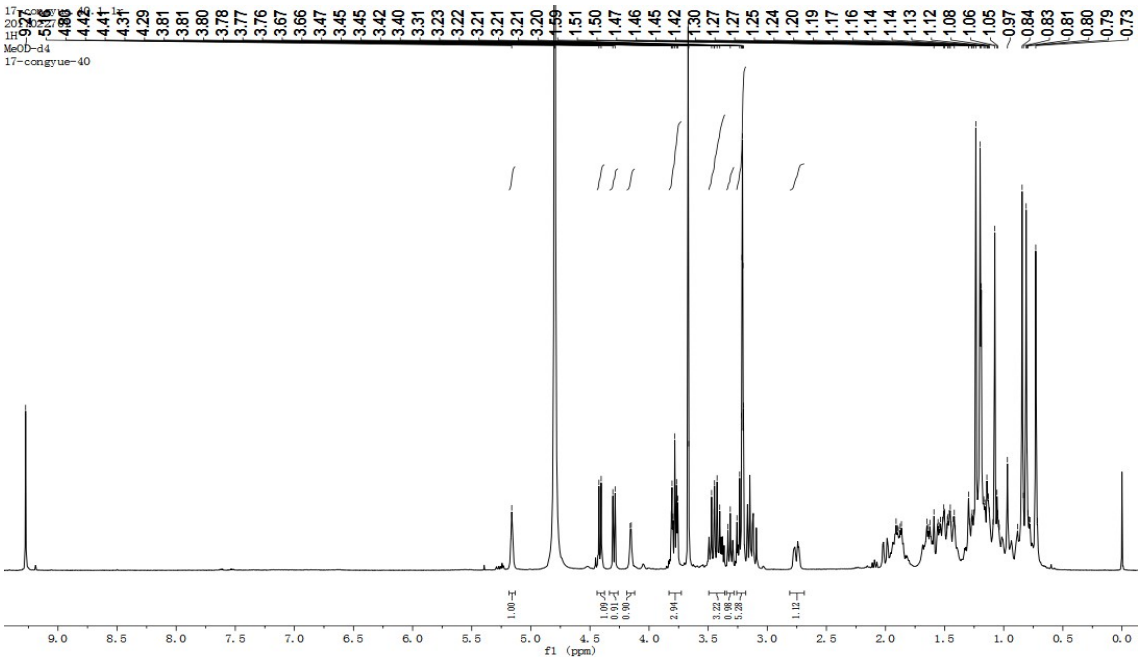

Figure S2 ^{1}H-NMR spectrum of compound 1 is shown.

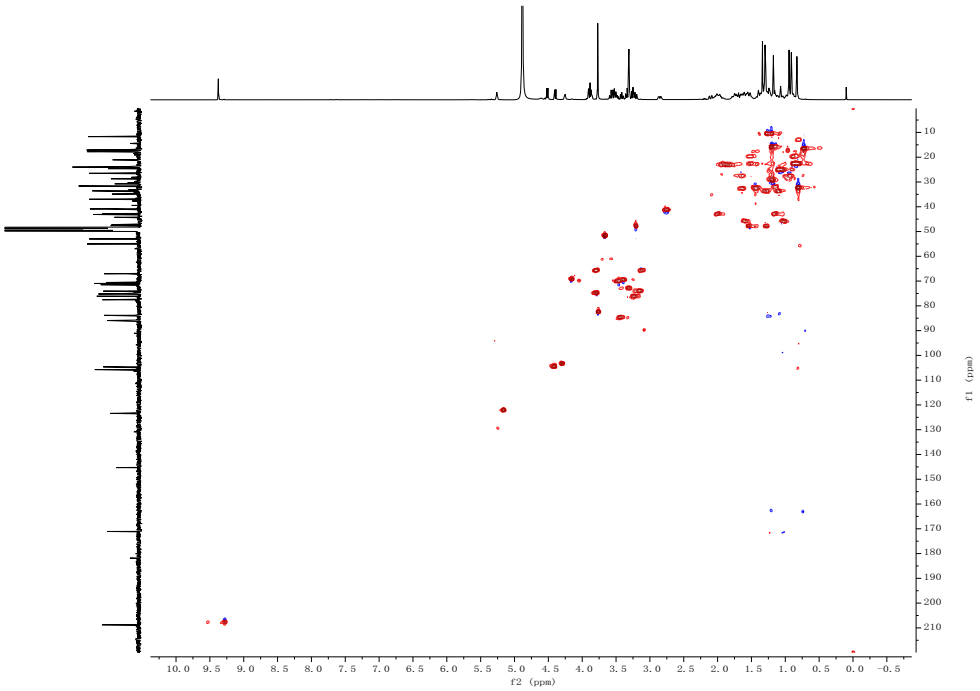

Figure S3 HSQC Spectrum of compound 1 is provided

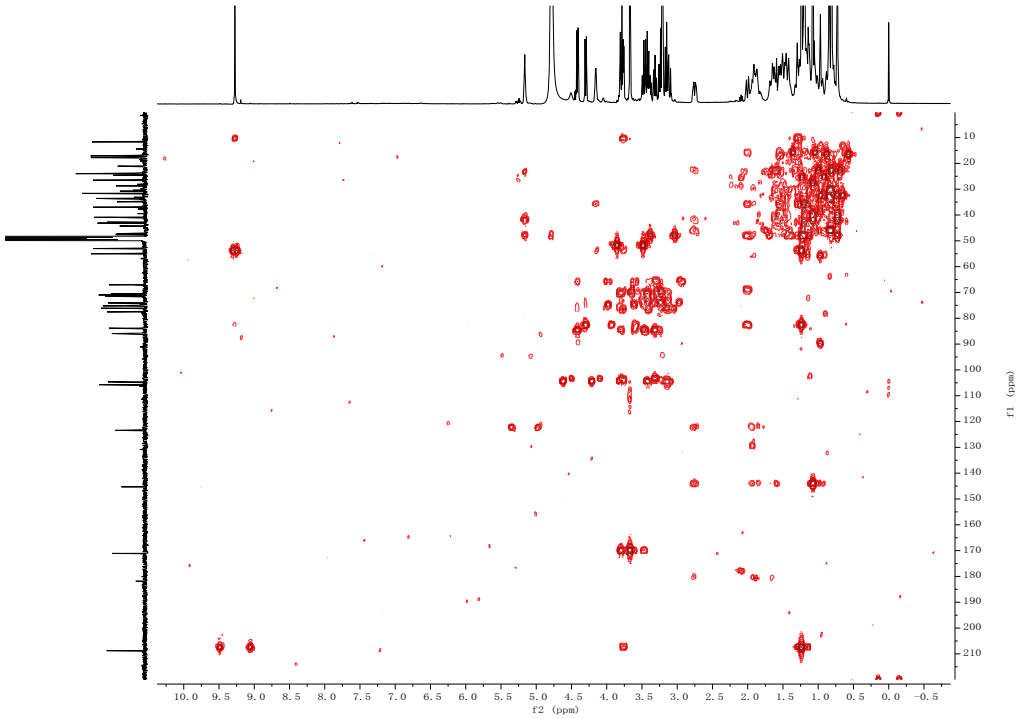

Figure S4 HMBC Spectrum of compound 1 is provided

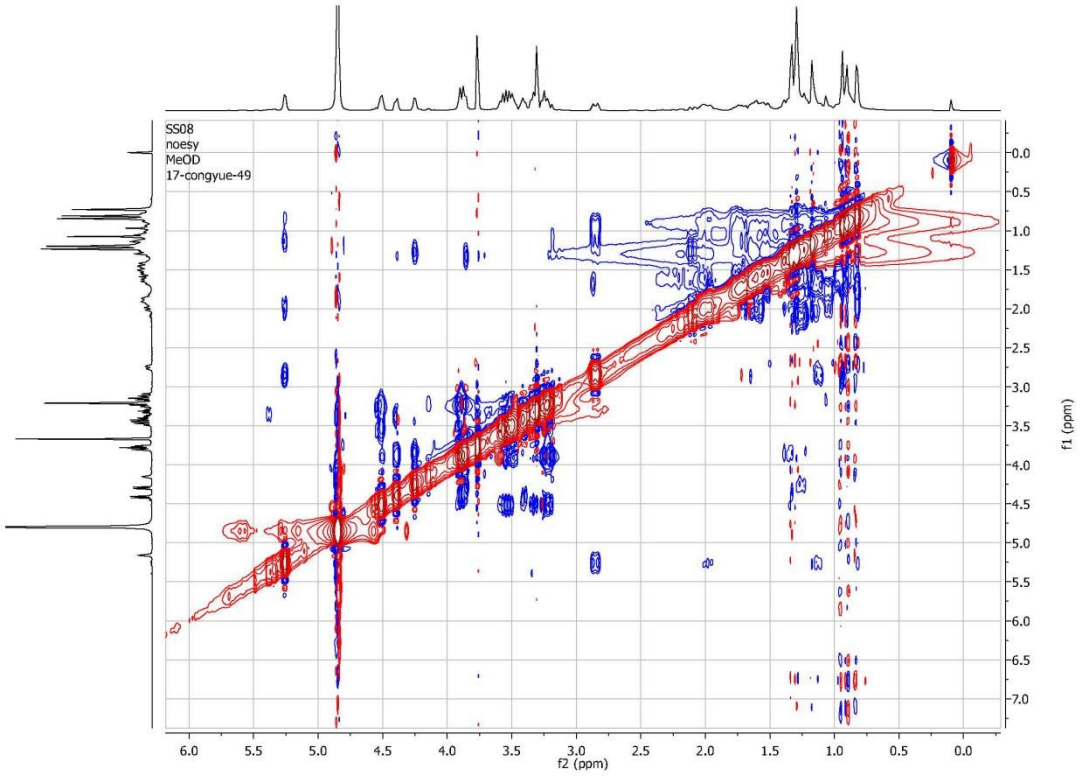

Figure S5 NOESY Spectrum of compound 1 is shown.

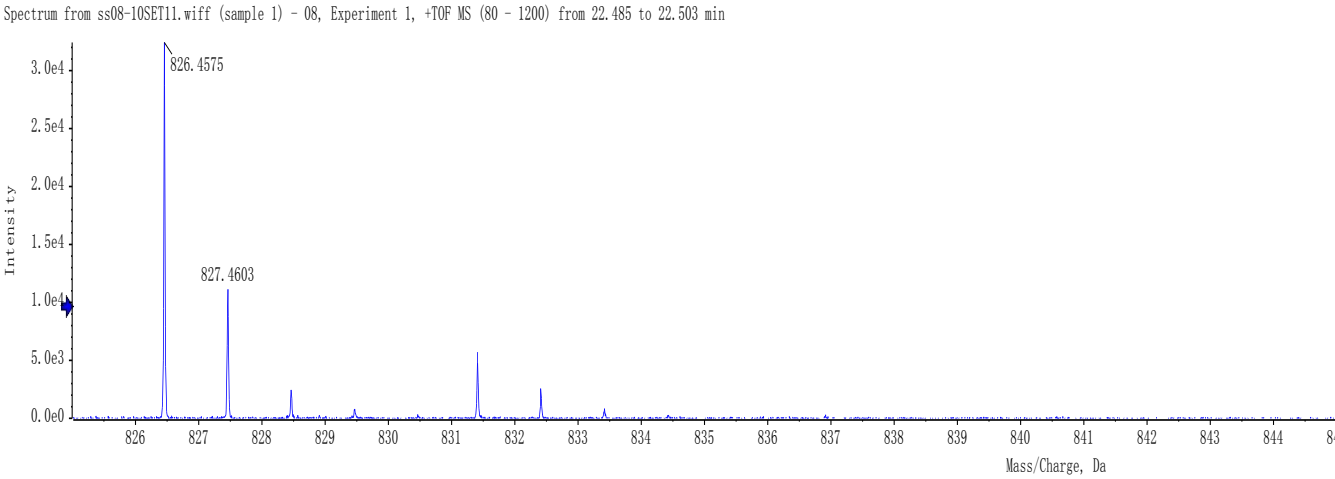

Figure S6 HR-ESI-MS Spectrum of compound 1 is shown.

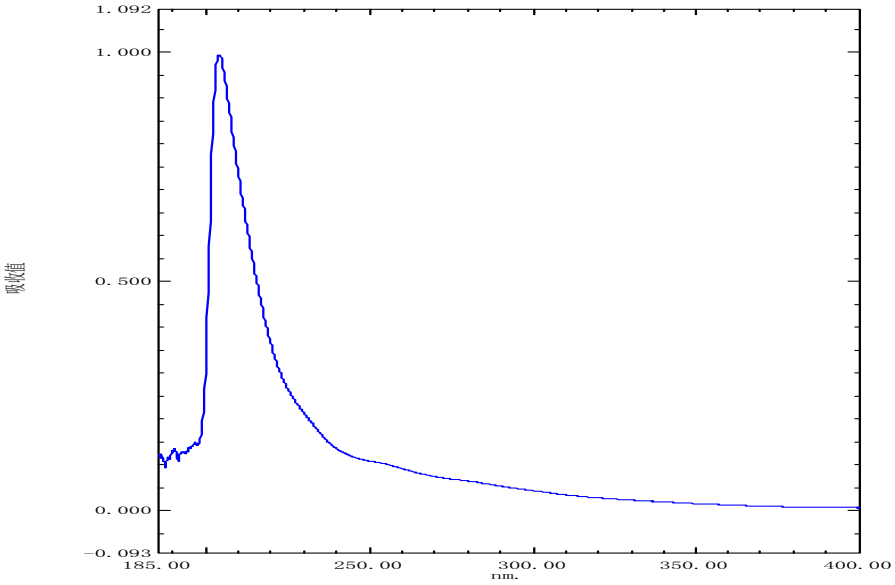

Figure S7 UV Spectrum of compound 1 is given.

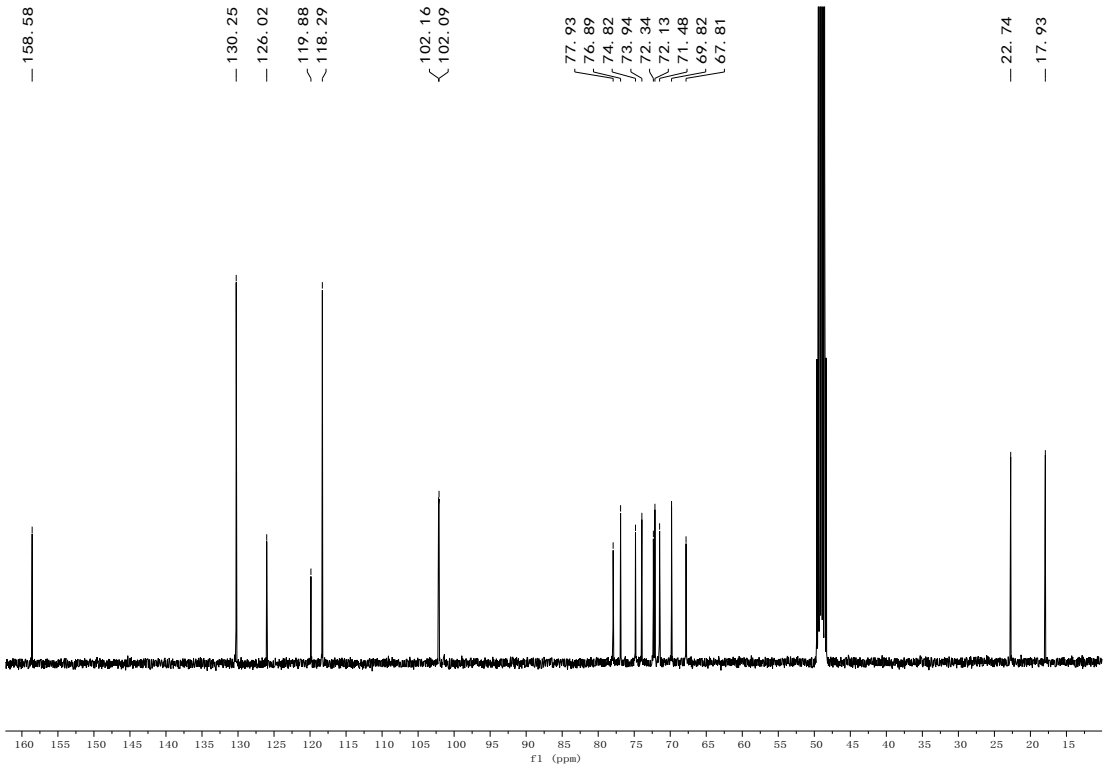

Figure S8 ^{13}C-NMR Spectrum of compound 2 is given.

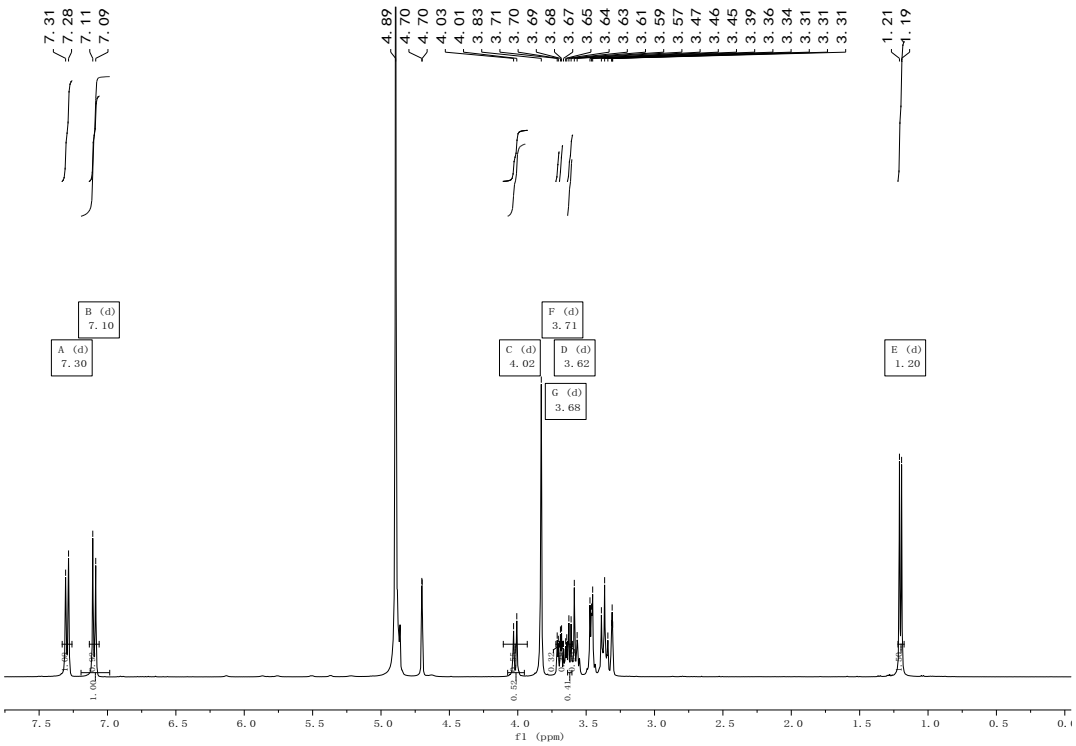

Figure S9 ^{1}H-NMR Spectrum of compound 2 is shown.

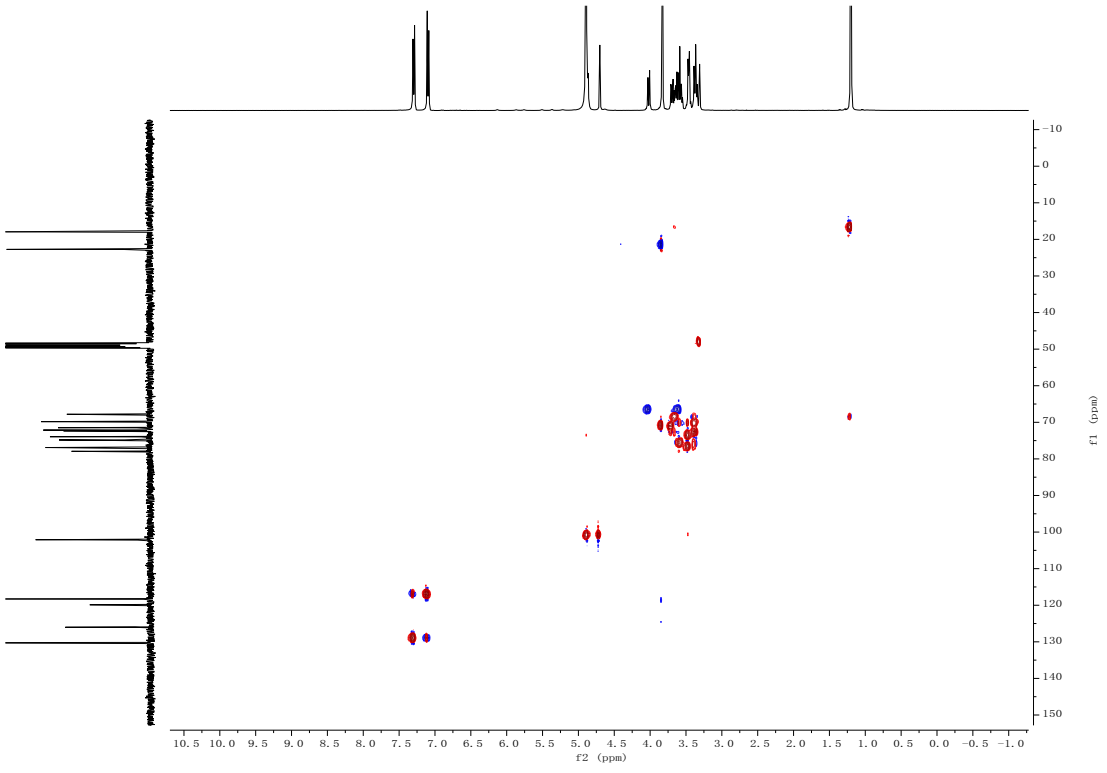

Figure S10 HSQC Spectrum of compound 2 is provided.

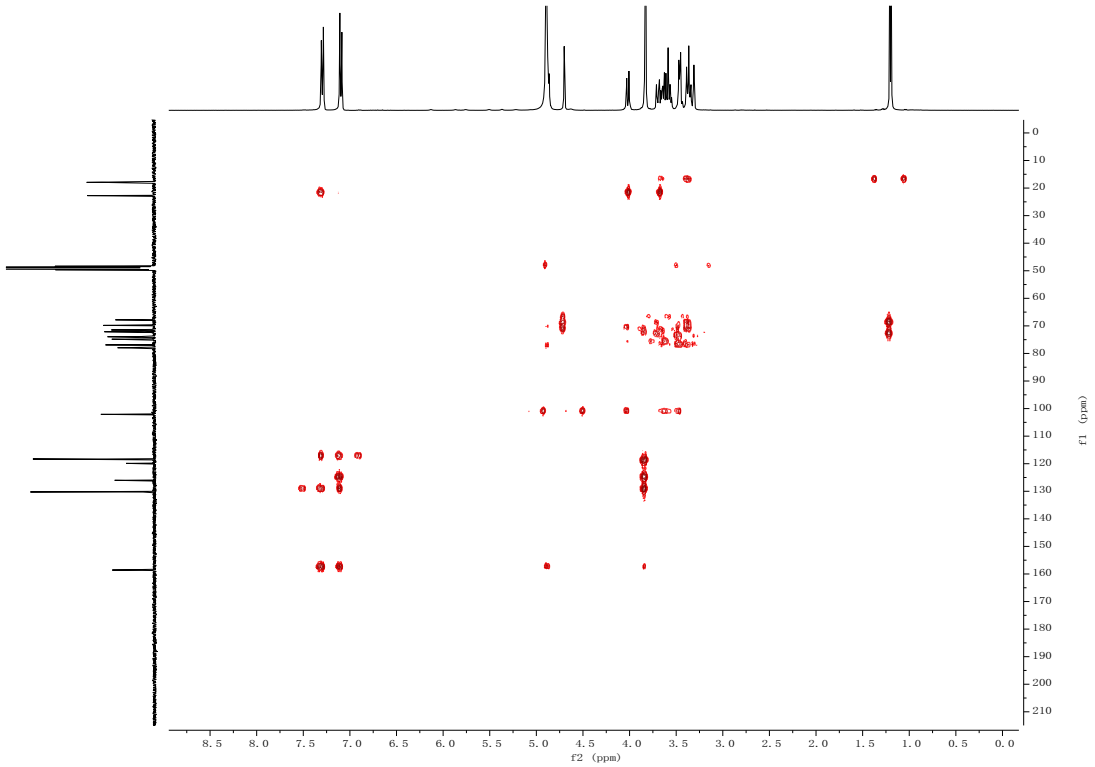

Figure S11 HMBC Spectrum of compound 2 is provided.

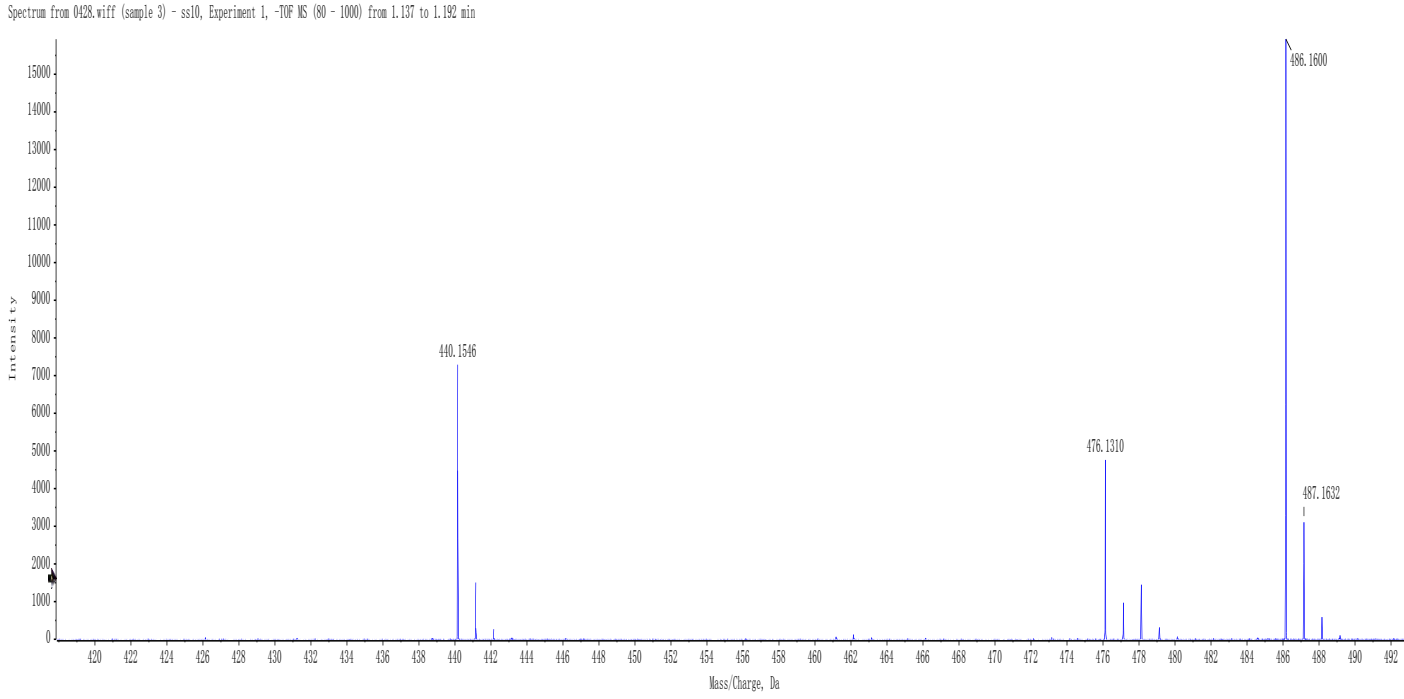

Figure S12 HR-ESI-MS Spectrum of compound 2 is shown.

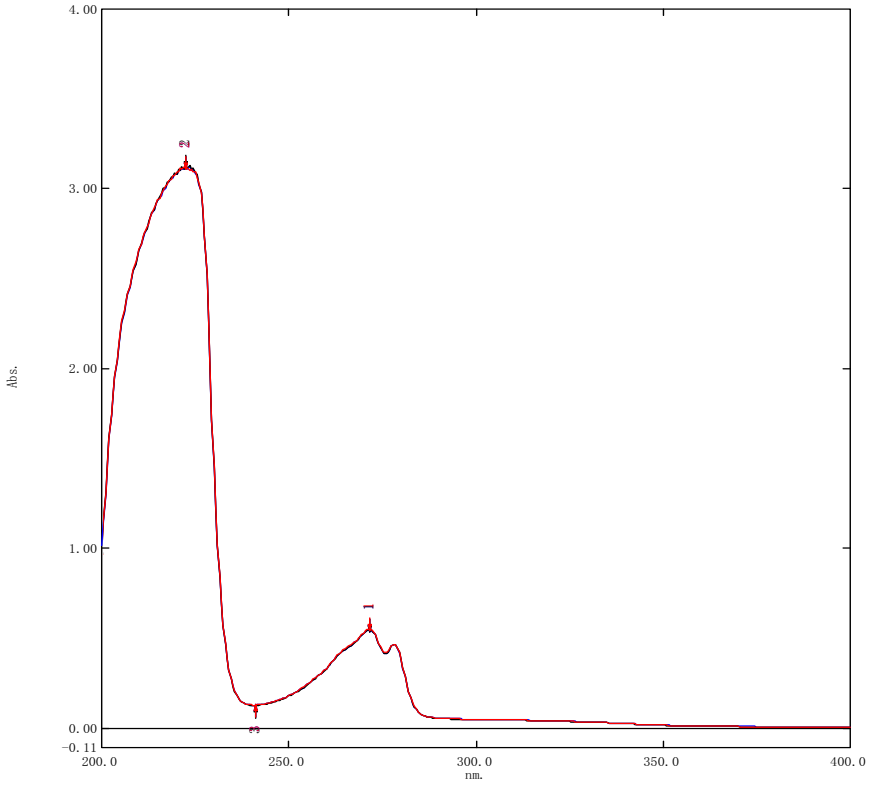

Figure S13 UV spectrum of compound **2** is shown.

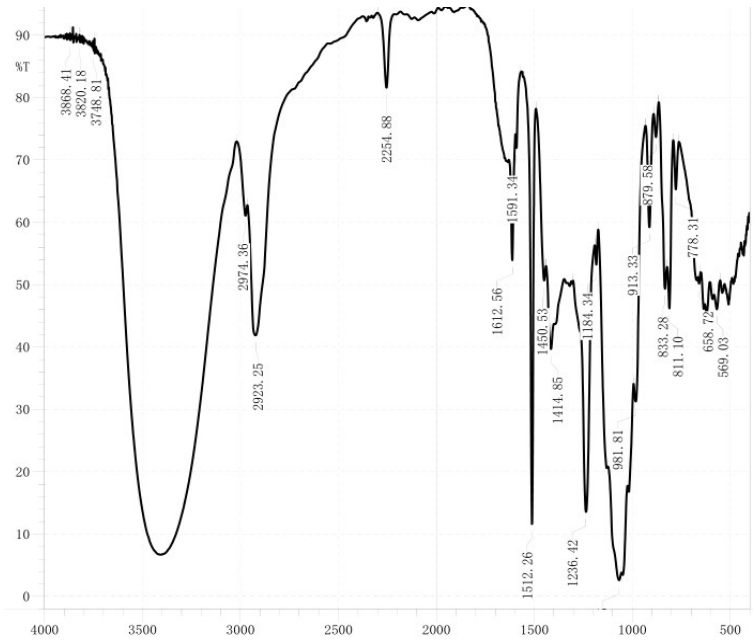

Figure S14 IR spectrum of compound 2 is given.

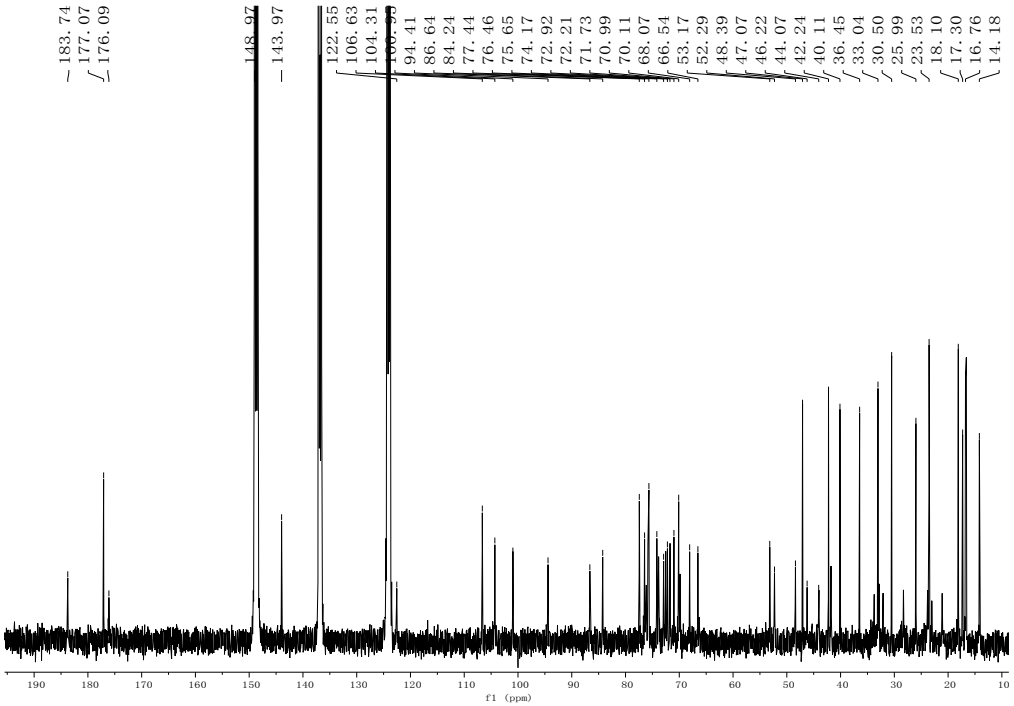

Figure S15 ^{13}C-NMR Spectrum of compound 3 is shown.

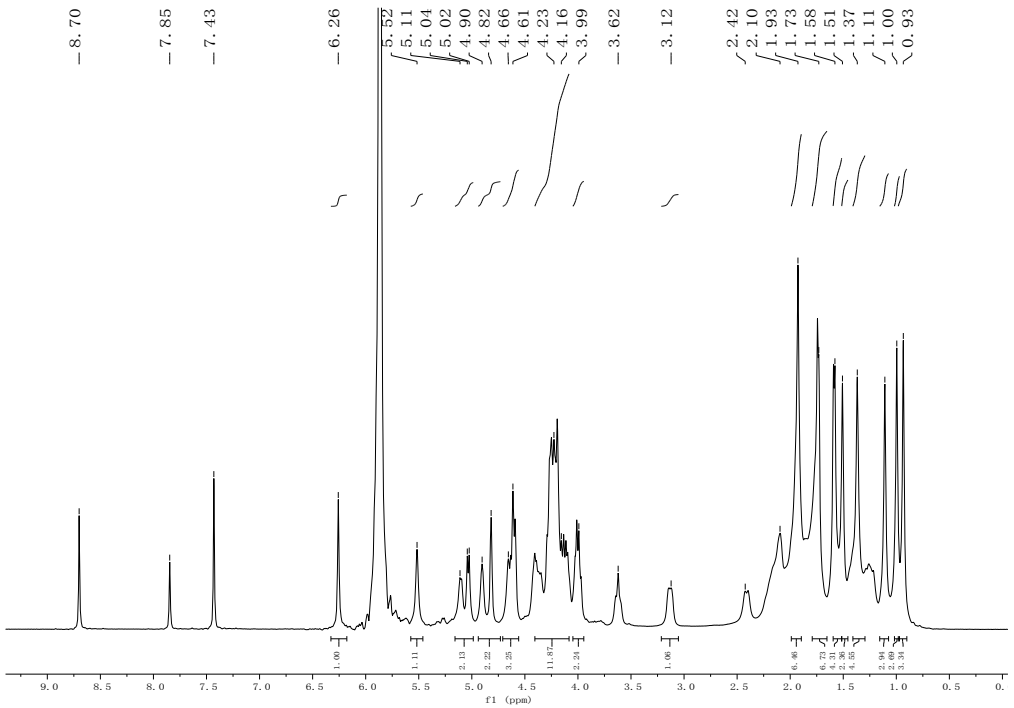

Figure S16 ^{1}H-NMR Spectrum of compound 3 is given.

Figure S17 ESI-MS Spectrum of compound 3

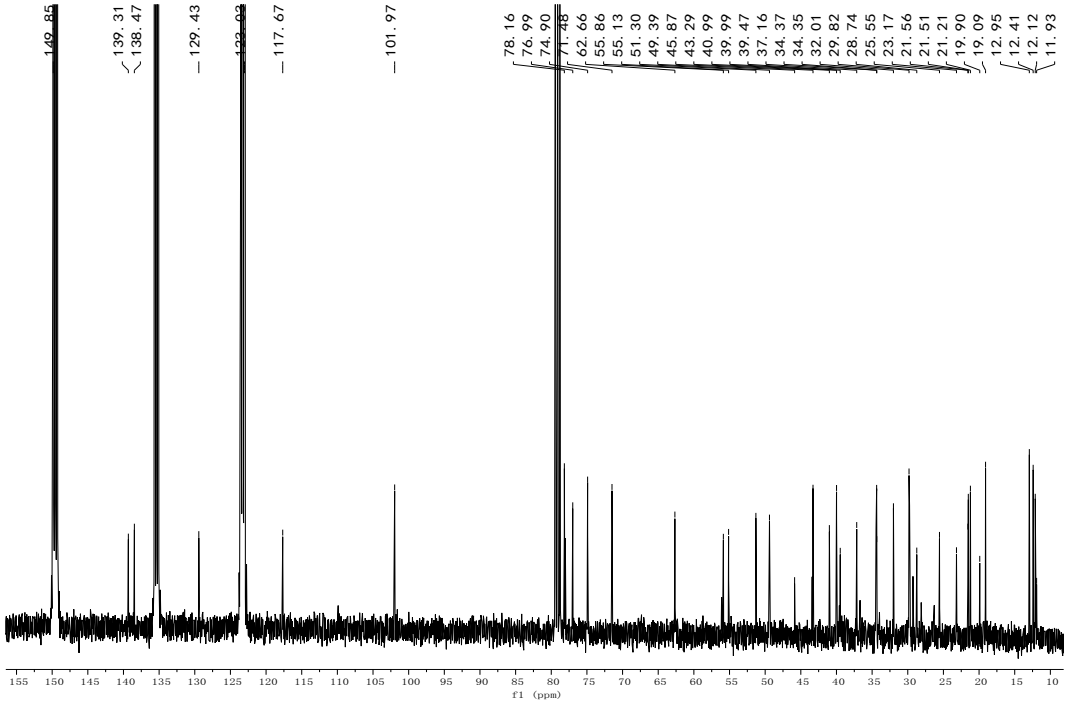

Figure S18 ^{13}C-NMR Spectrum of compound 4 is provided.

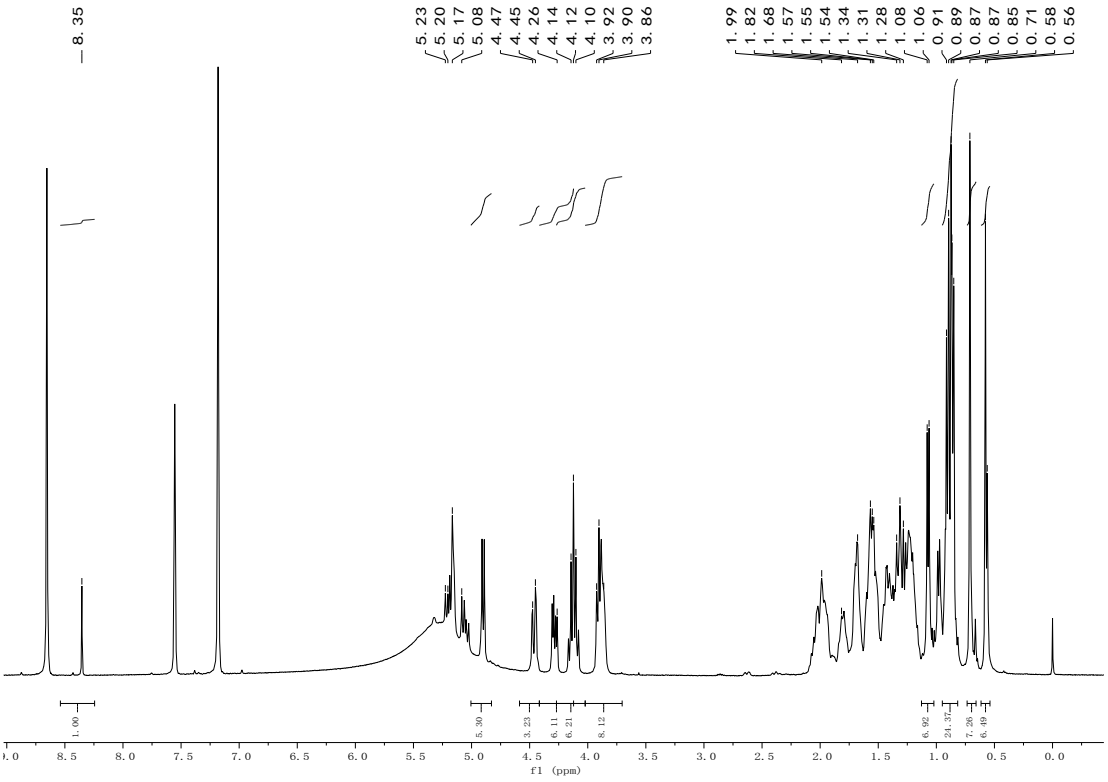

Figure S19 ^{1}H-NMR Spectrum of compound 4 is shown.

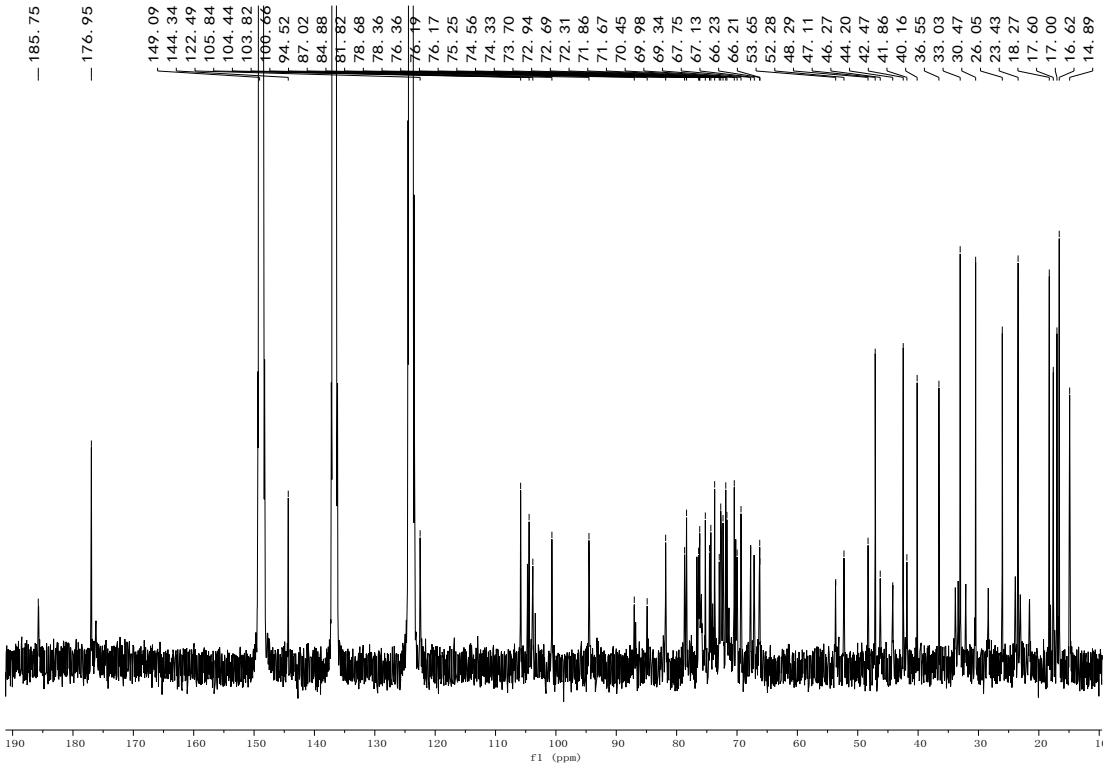

Figure S20 ^{13}C-NMR Spectrum of compound 5 is given.

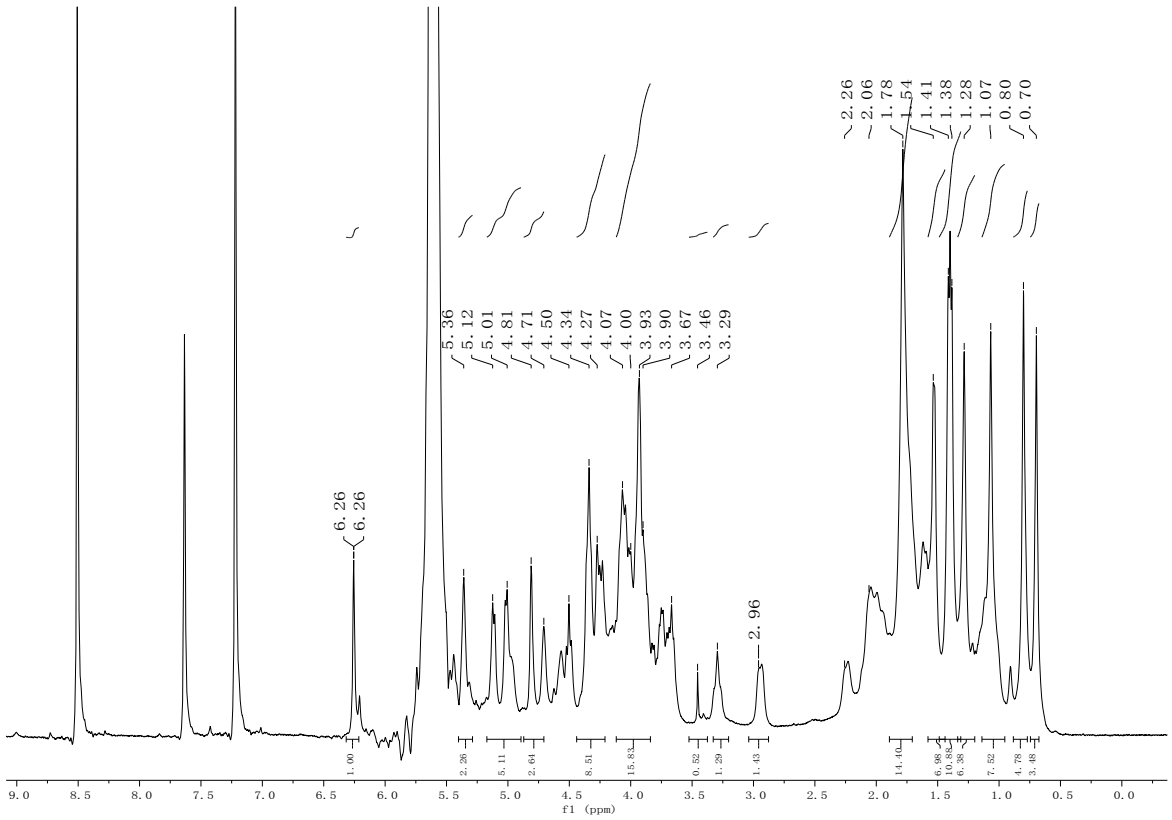

Figure S21 ^{1}H-NMR Spectrum of compound **5** is shown.

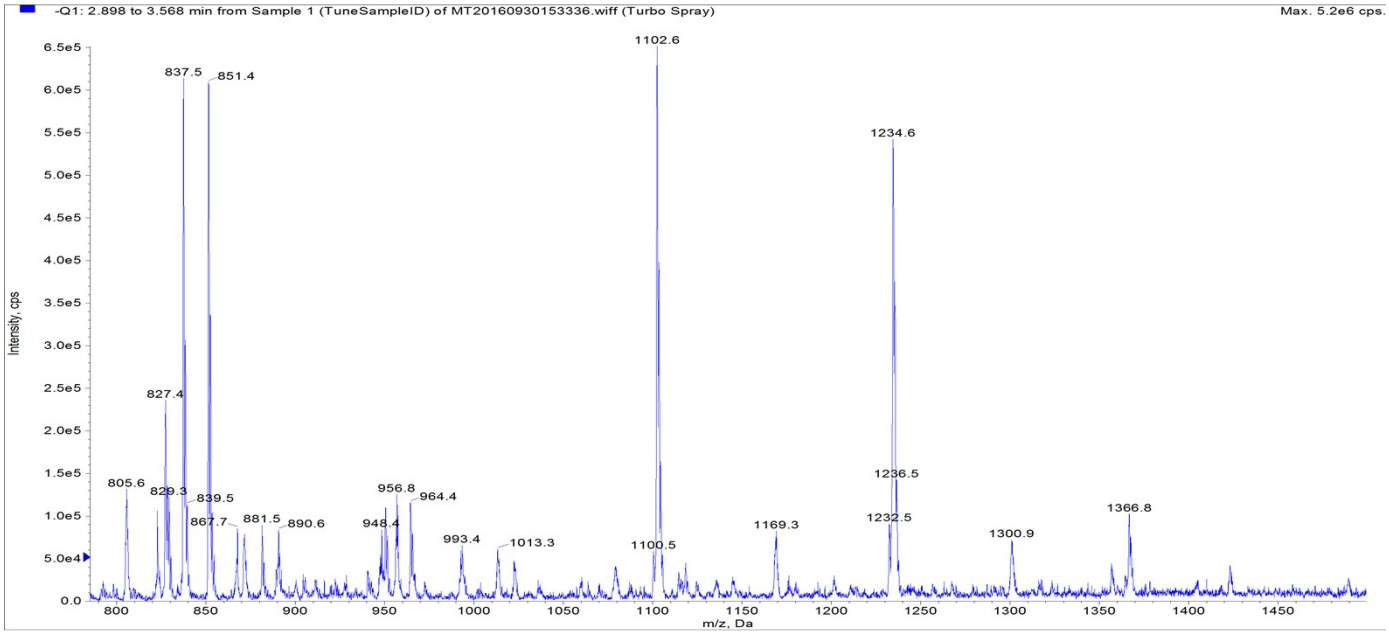

Figure S22 ESI-MS Spectrum of compound 5 is shown.

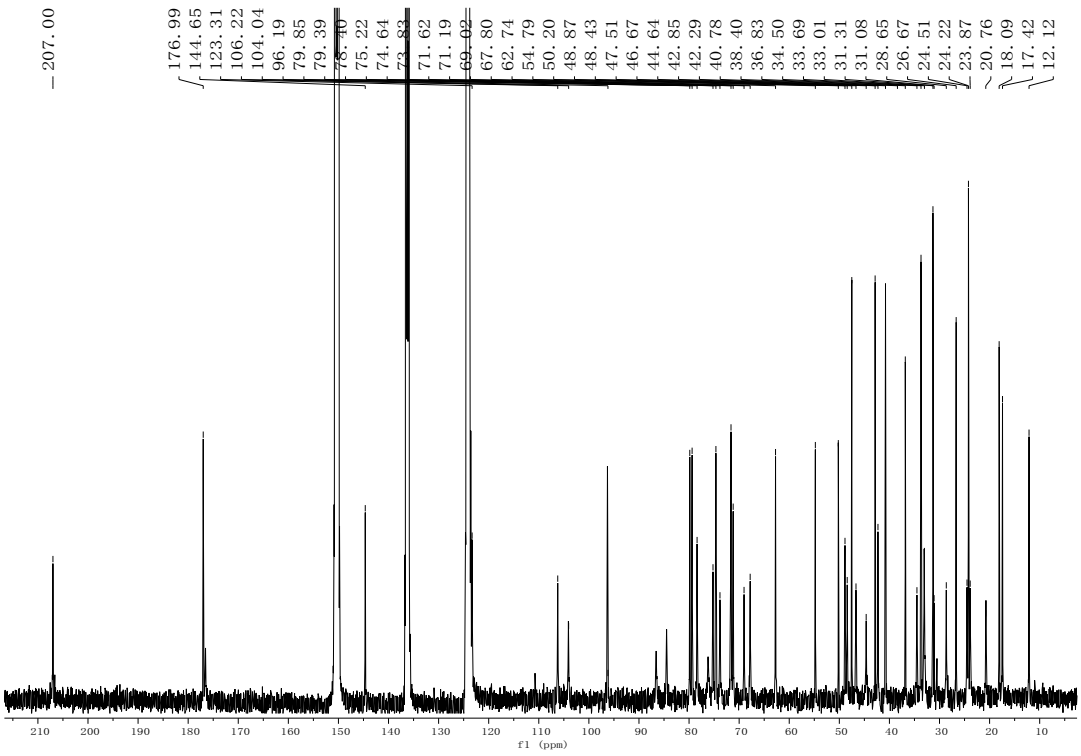

Figure S23 ^{13}C-NMR Spectrum of compound 6 is provided.

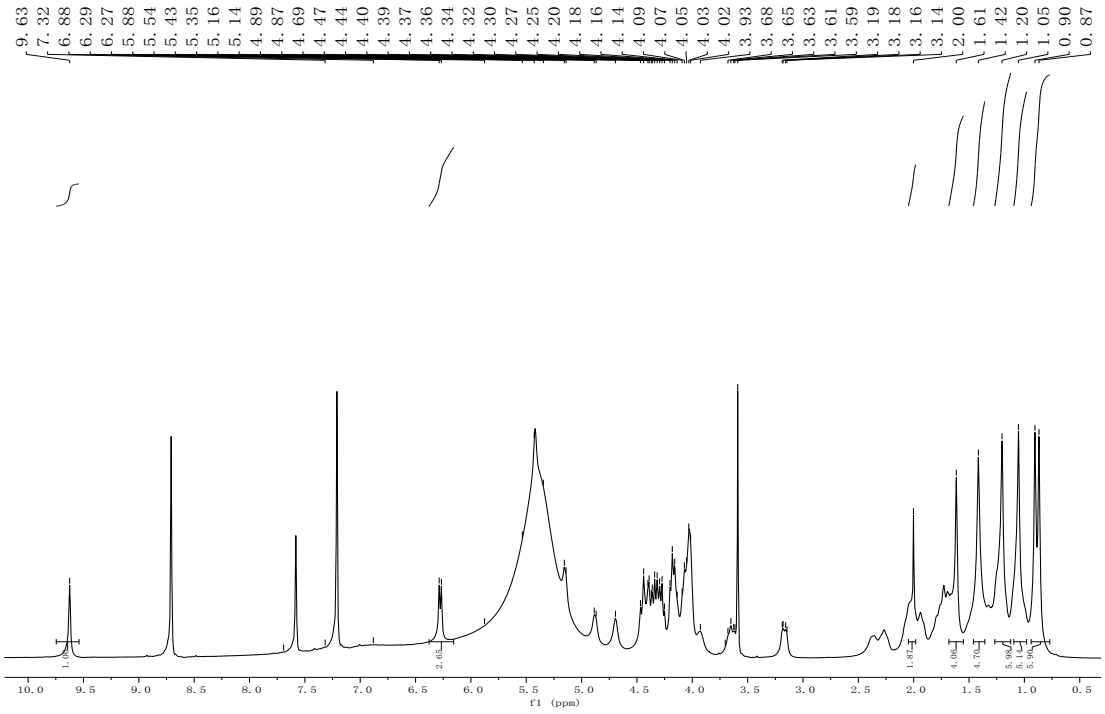

Figure S24 ^{1}H-NMR Spectrum of compound 6 is provided.

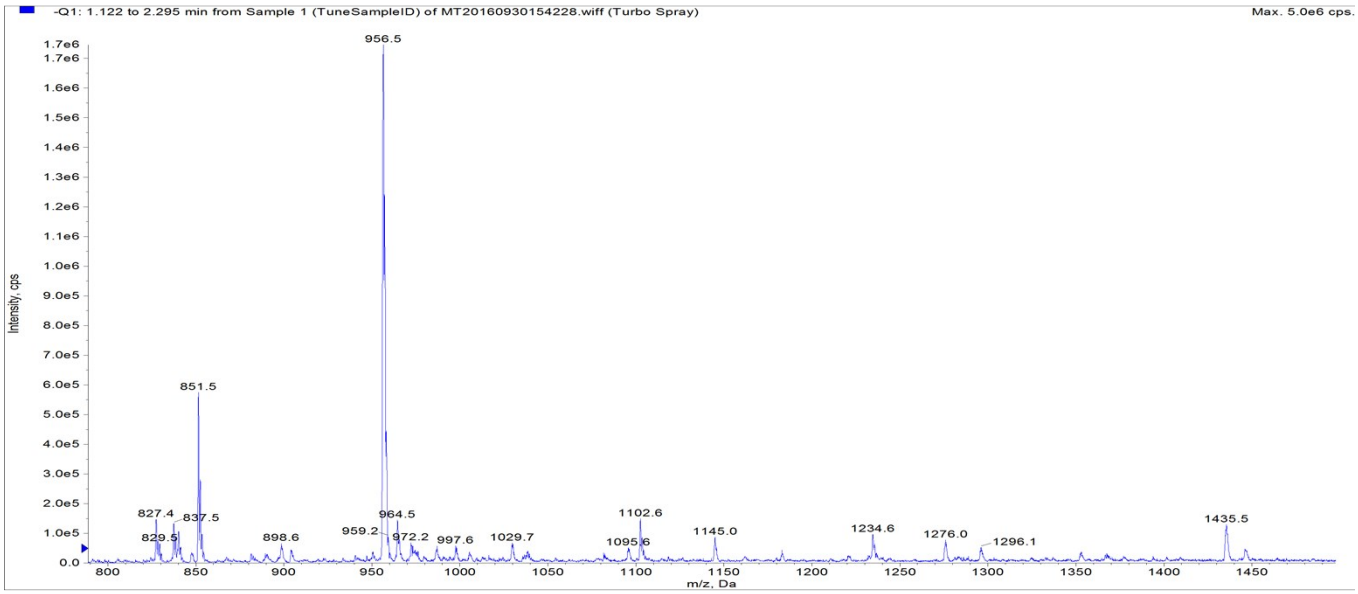

Figure S25 ESI-MS Spectrum of compound 6 is shown.

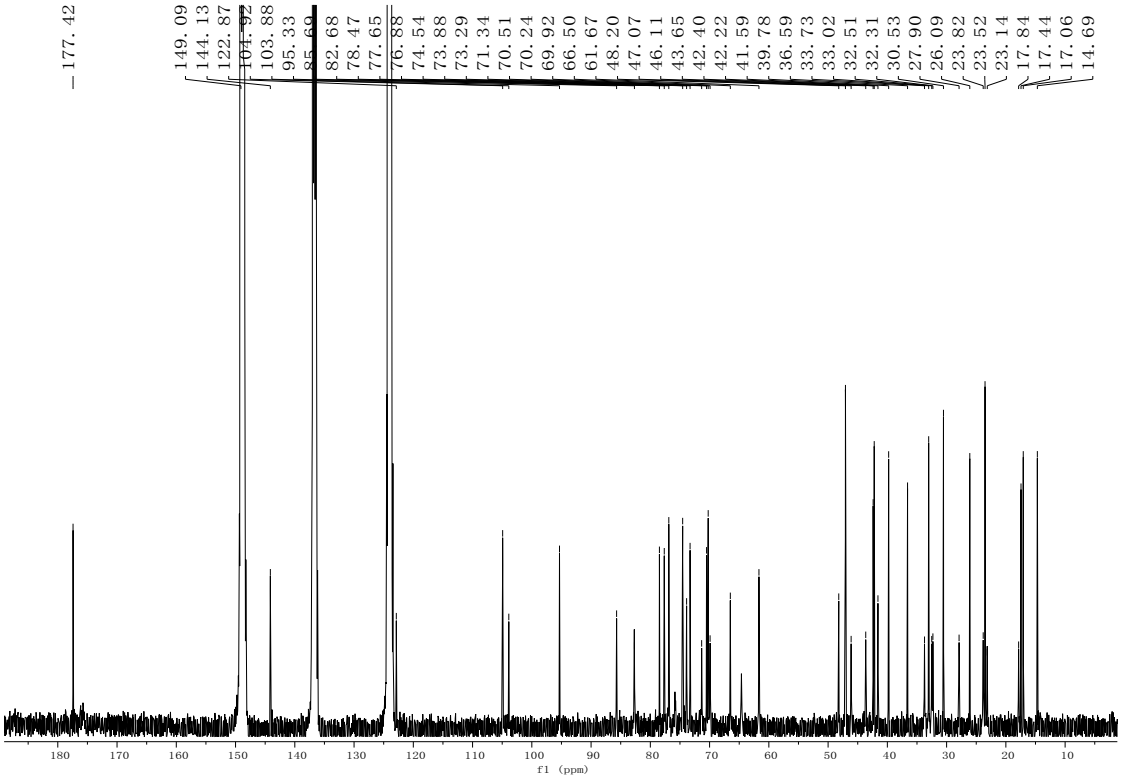

Figure S26 ^{13}C-NMR Spectrum of compound **7** is given.

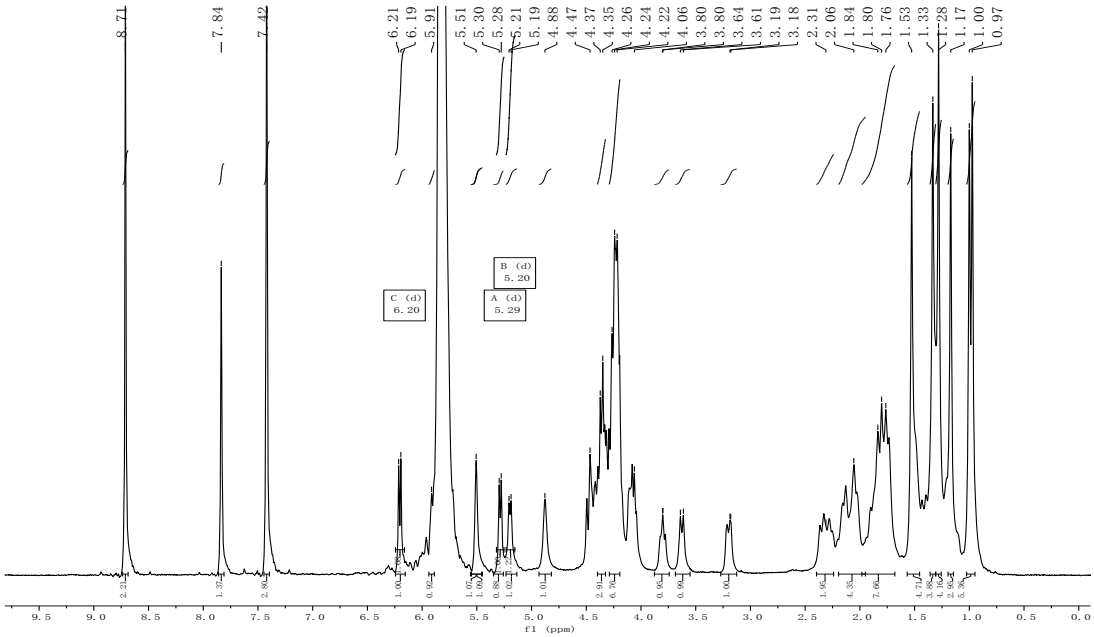

Figure S27 ^{1}H-NMR Spectrum of compound 7 is shown.

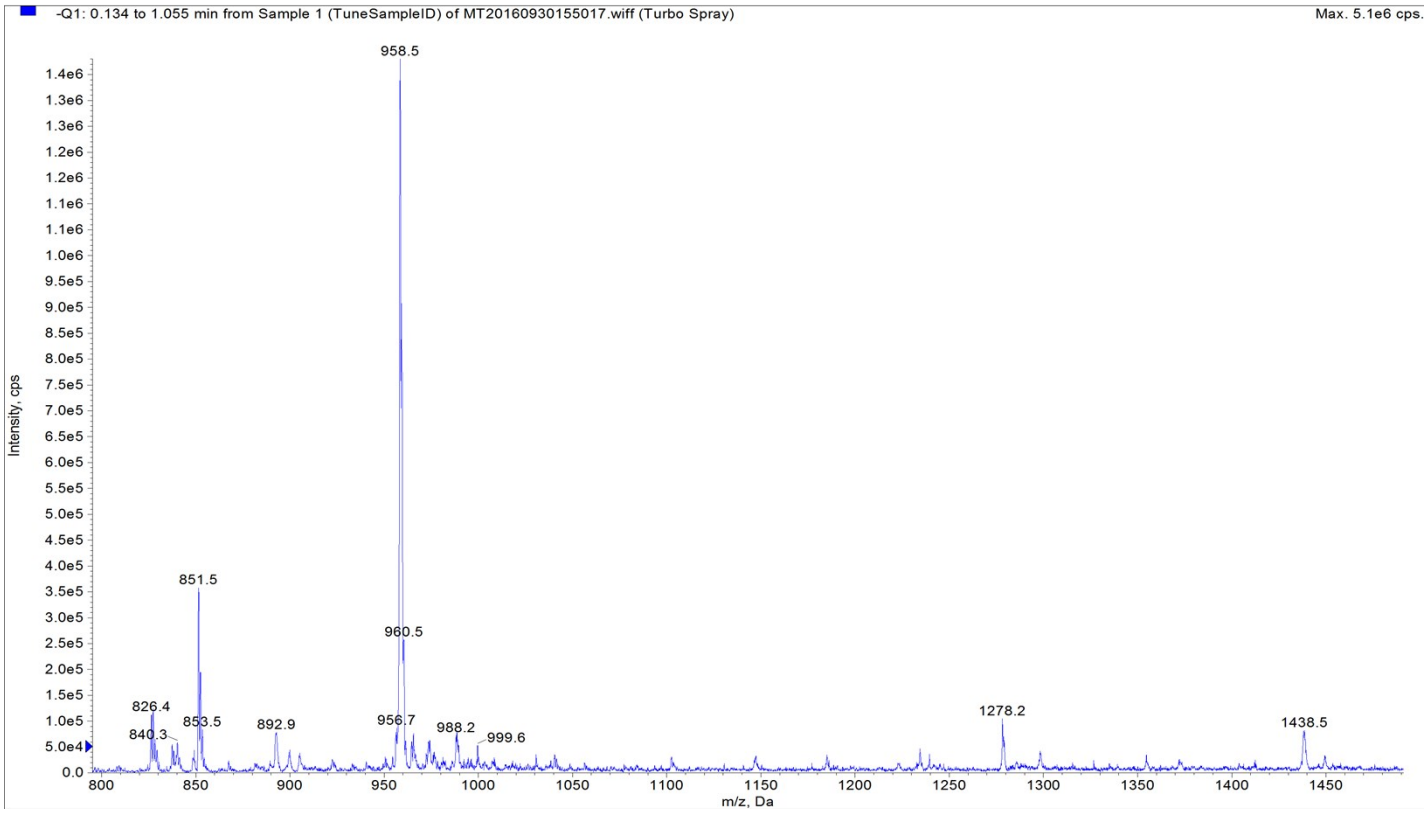

Figure S28 ESI-MS Spectrum of compound 7 is given.

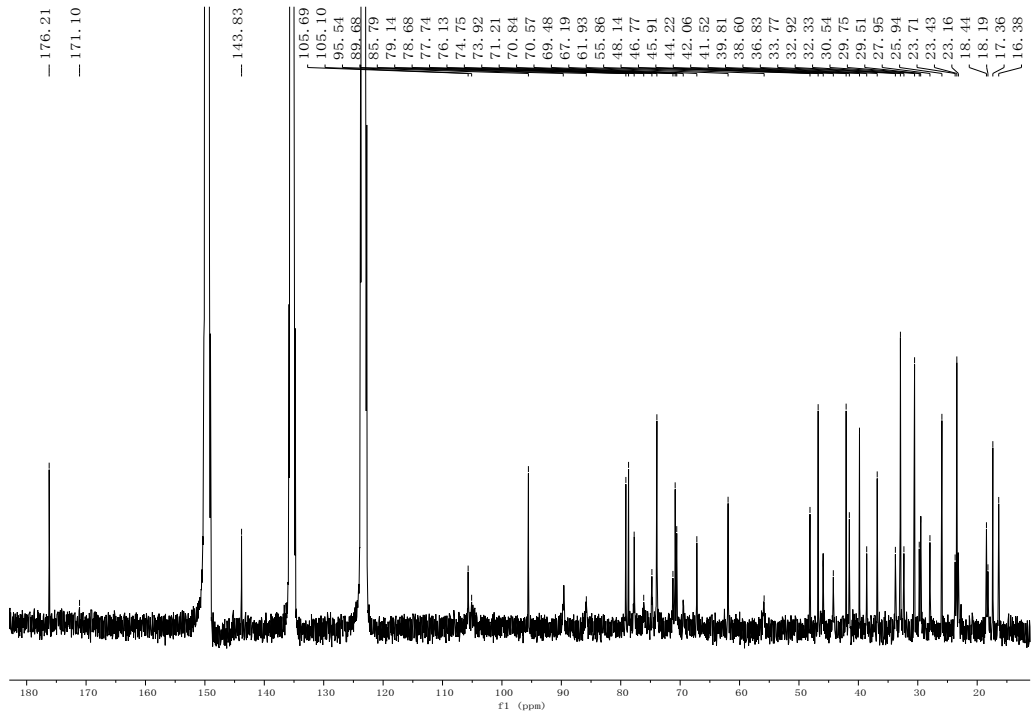

Figure S29 ^{13}C-NMR Spectrum of compound 8 is provided.

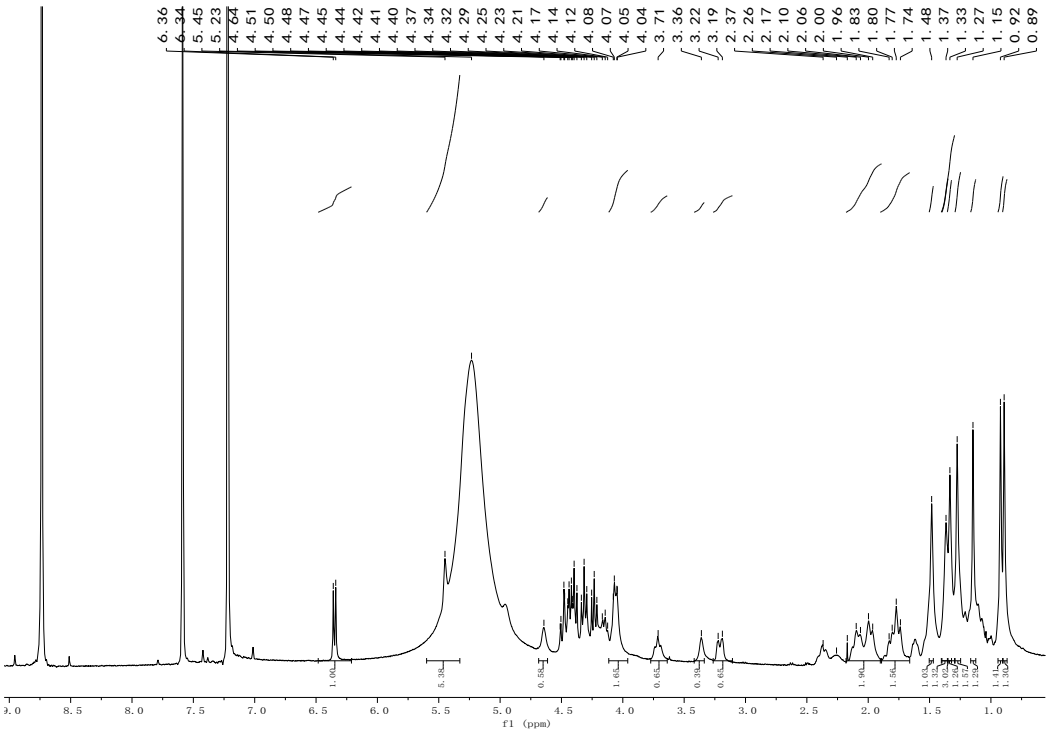

Figure S30 ^{1}H-NMR Spectrum of compound 6 is shown.

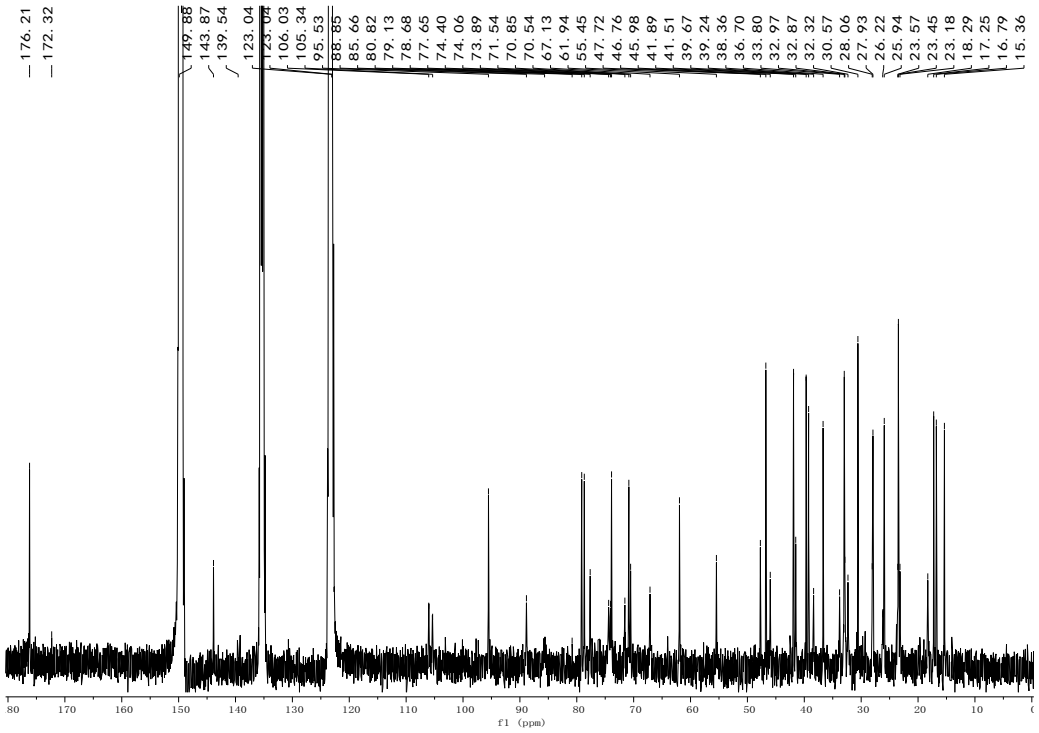

Figure S31 ^{13}C-NMR Spectrum of compound 9 is provided.

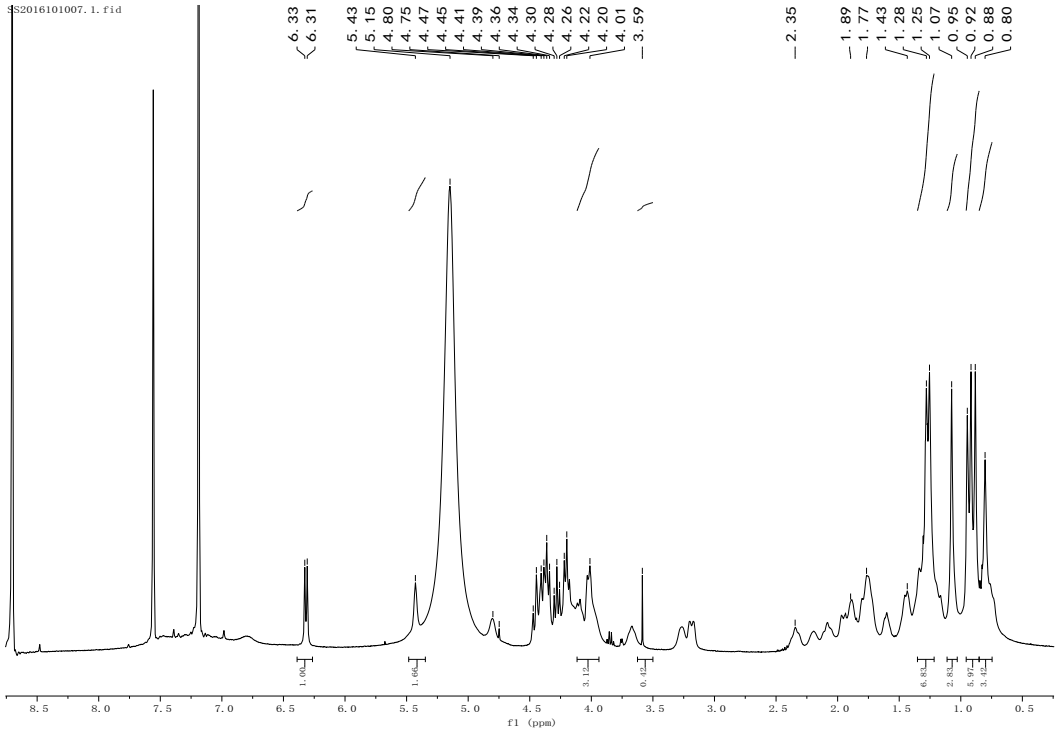

Figure S32 ^{1}H-NMR Spectrum of compound **9** is shown.

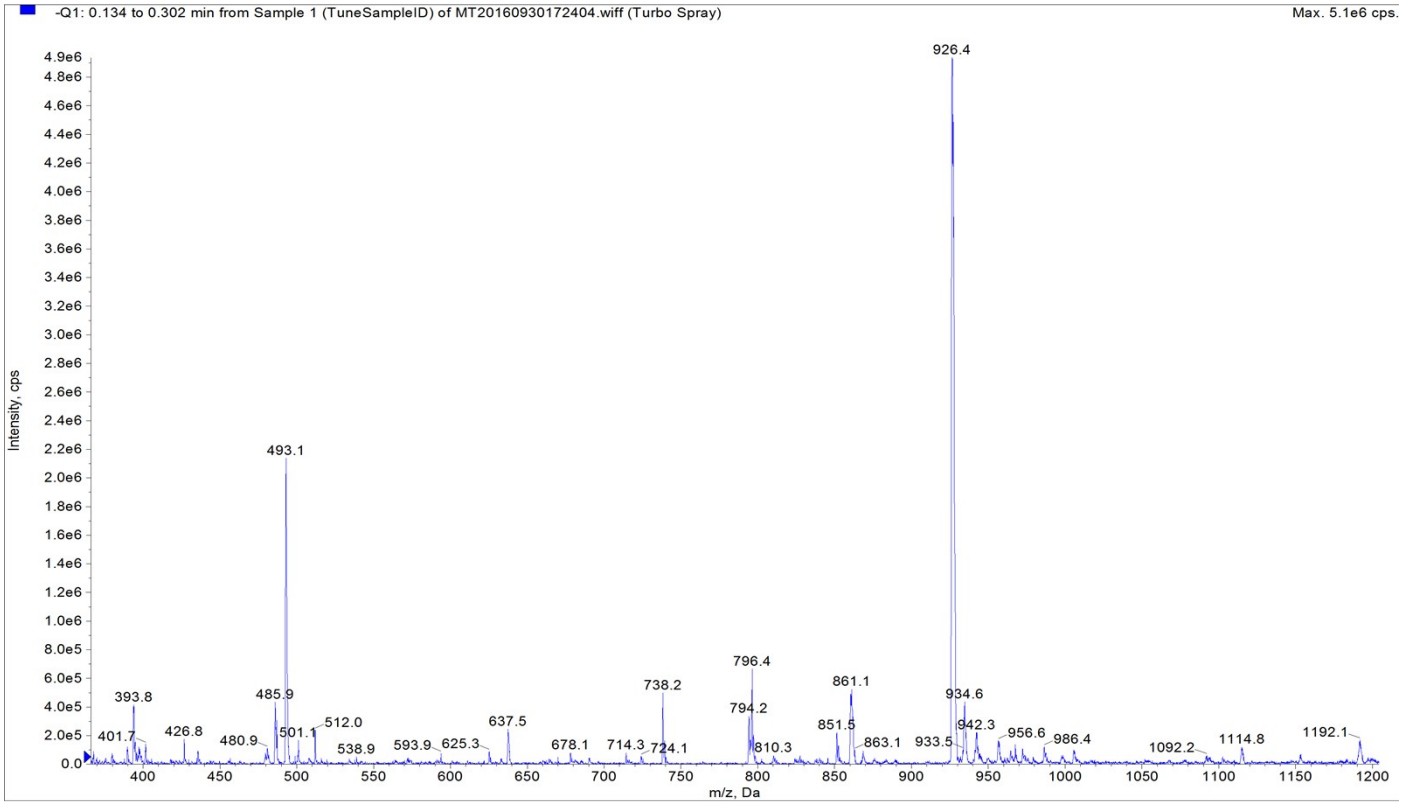

Figure S33 ESI-MS Spectrum of compound 9 is given.

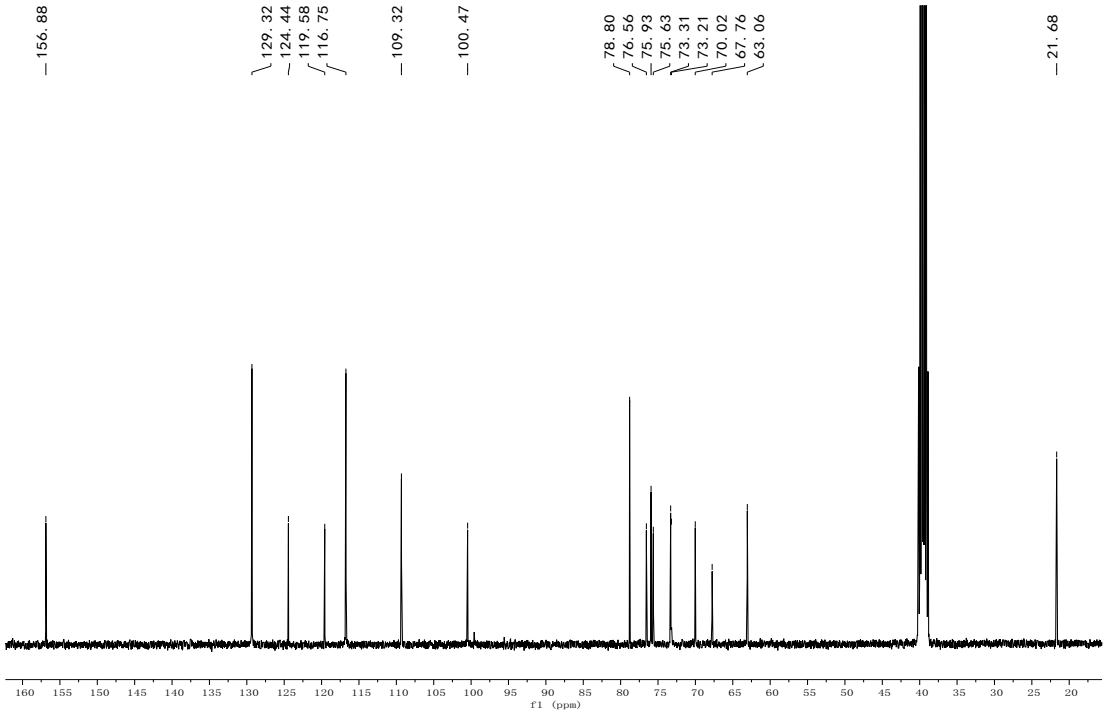

Figure S34 ^{13}C-NMR spectrum of compound 10 is provided.

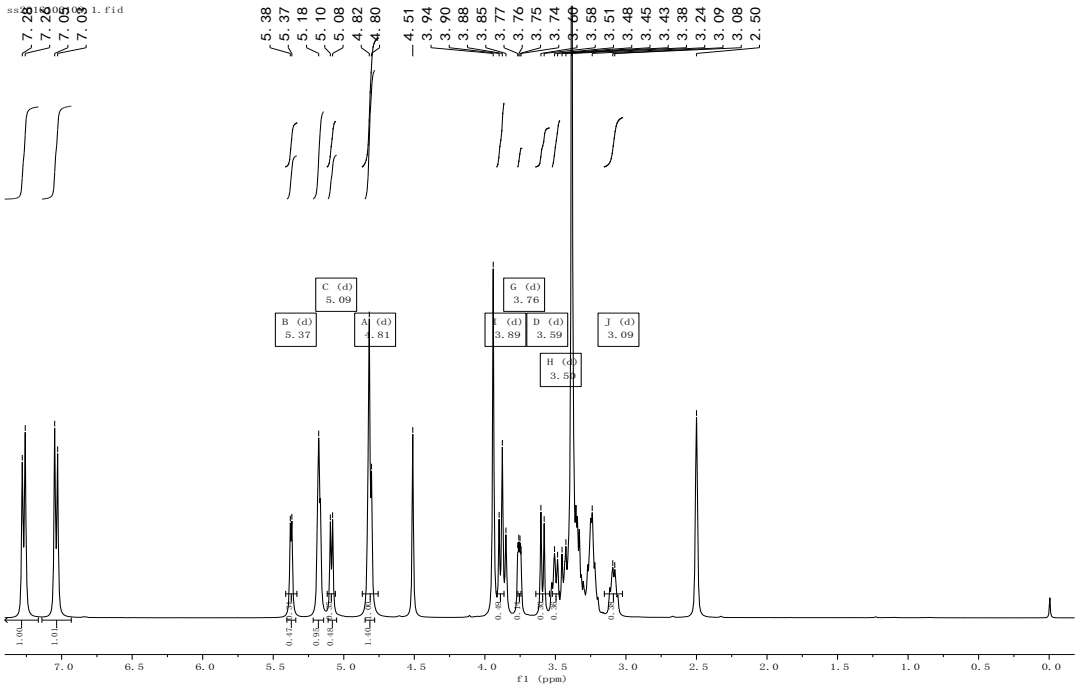

Figure S35 ^{1}H-NMR spectrum of compound 10 is shown.

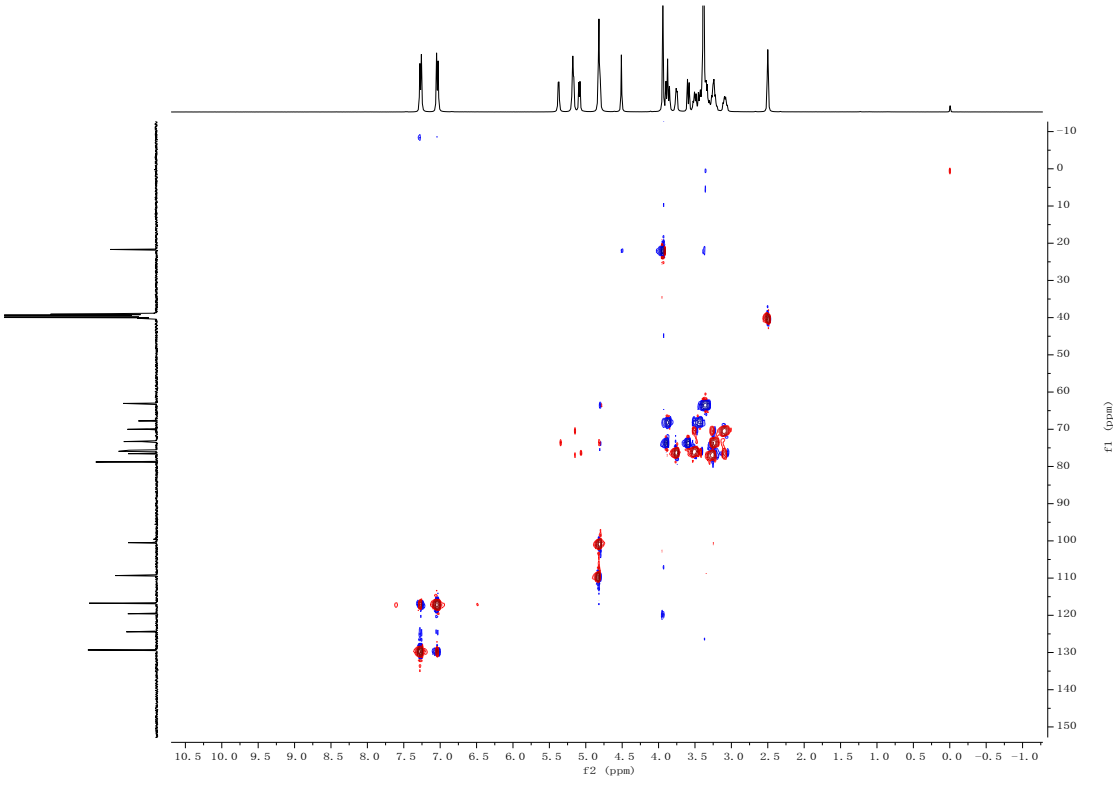

Figure S36 HSQC spectrum of compound 10 is given.

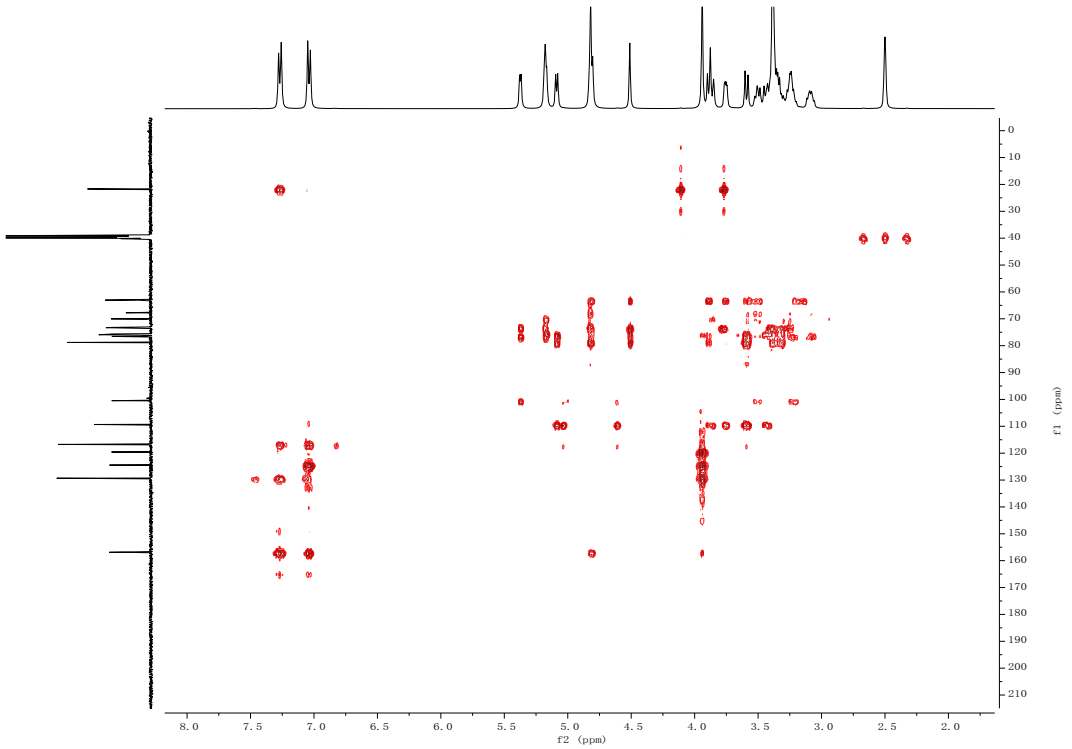

Figure S37 HMBC spectrum of compound **10** is provided.

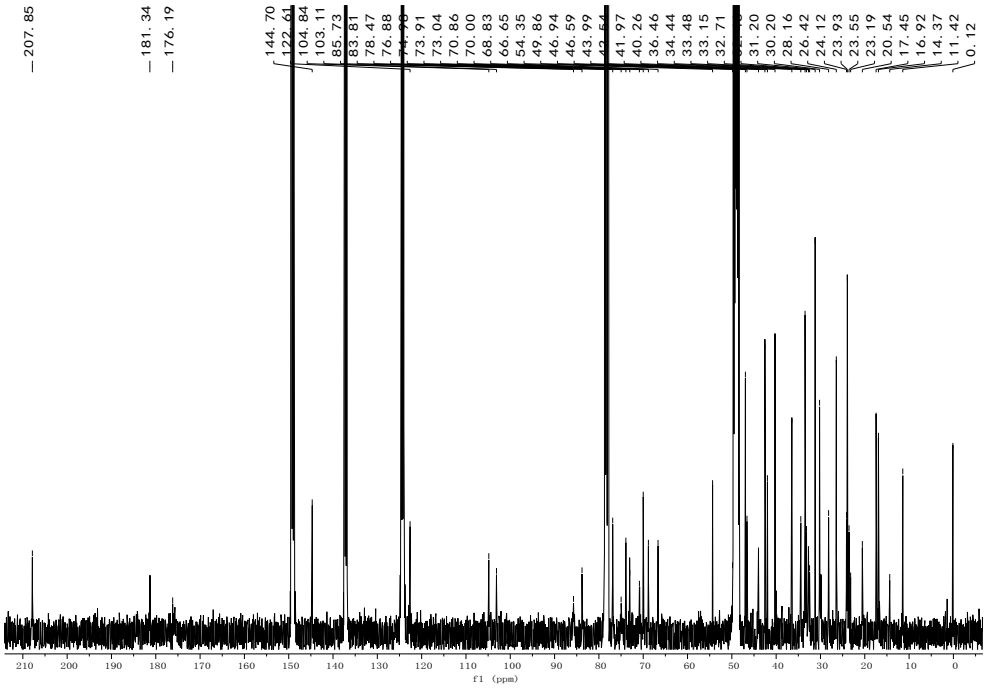

Figure S38 ^{13}C-NMR spectrum of compound **11** is shown.

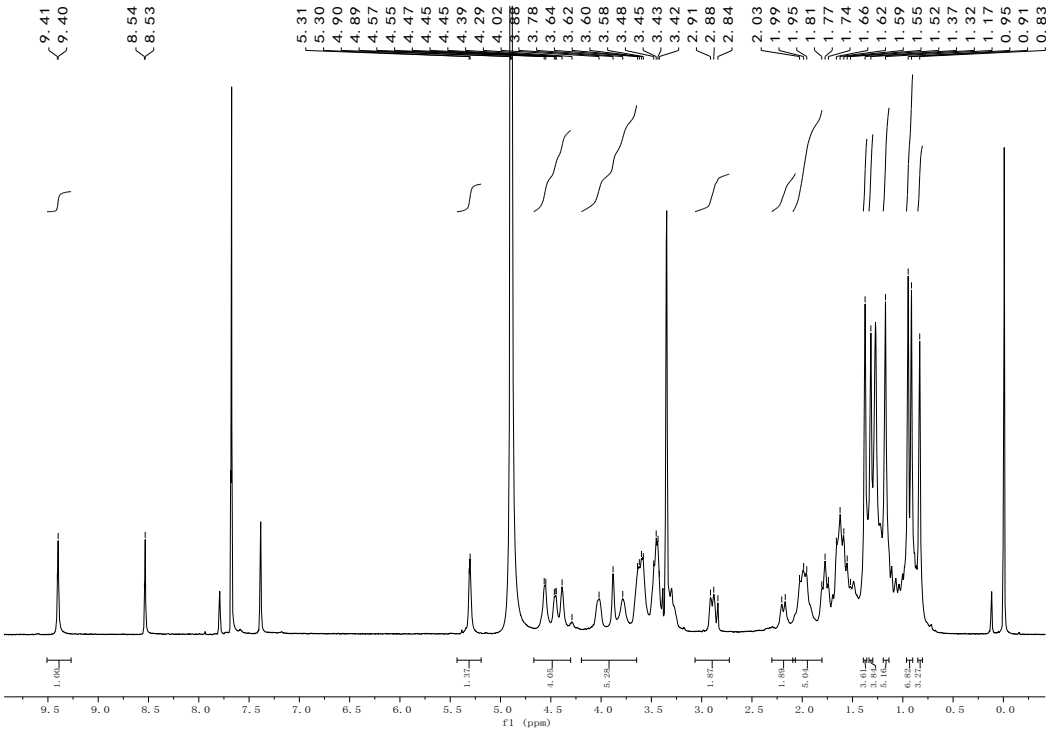

Figure S39 [1]H-NMR spectrum of compound **11** is given.

Table S1 Calibration curves and linear range of five analytes (n=3)

Num.	Analytes	Calibration curve	Correlation coefficient	Linear range（μg）
3	Celosin I	y=229390x-12331	0.9999	1.4 ~ 19.6
5	Celosin J	y=147428x+25956	0.9992	0.4 ~ 12.18
6	Celosin H	y=329896x+13094	0.9996	0.3 ~ 13.5
8	Celosin K	y=276693x-17644	0.9992	0.4 ~ 2.0
9	Chikusetsusaponin Ⅳ	y=254256x-7243.8	0.9995	0.4 ~ 1.8

Table S2 Precision, repeatability and stability of the five analytes (n=6)

Num.	Analytes	RSD（%）		
		Precision	Repeatability	Stability
3	Celosin I	1.79	0.63	0.84
5	Celosin J	1.16	1.56	1.63
6	Celosin H	0.92	2.53	0.97
8	Celosin K	1.69	0.39	0.95
9	Chikusetsusaponin Ⅳ	1.15	1.03	0.86

Table S3 Results from a recovery test of the five analytes (n=6)

Num.	Original (mg)	Added (mg)	Found (mg)	Recovery (%)	Average (%)	RSD (%)
3	0.712	0.700	1.427	102.1	101.5	2.11
	0.712		1.429	102.4		
	0.714		1.435	103.0		
	0.717		1.414	99.6		
	0.715		1.441	103.8		
	0.720		1.408	98.2		
5	0.417	0.400	0.808	97.8	100.3	2.91
	0.417		0.826	102.2		
	0.418		0.807	97.1		
	0.420		0.828	102.1		
	0.418		0.812	98.5		

	0.422		0.839	104.3		
6	0.412	0.400	0.827	103.6	102.8	1.41
	0.412		0.831	104.8		
	0.414		0.822	101.9		
	0.415		0.829	103.5		
	0.414		0.824	102.6		
	0.417		0.820	100.6		
8	0.058	0.060	0.117	98.1	97.5	1.45
	0.058		0.117	98.6		
	0.058		0.115	95.7		
	0.058		0.118	99.2		
	0.058		0.116	97.1		
	0.058		0.116	96.0		
9	0.081	0.080	0.161	100.5	99.9	1.32
	0.081		0.160	99.4		
	0.081		0.162	100.6		
	0.081		0.163	101.8		
	0.081		0.160	99.0		
	0.082		0.160	98.2		

Recovery (%) = (Found – Original) / Added×100%

Table S4 Calibration curves and linear range of two analytes (n=3)

Num.	Analytes	Calibration curve	Correlation coefficient	Linear range（μg）
2	4-hydroxyl-phenylacetonitrile4-*O*-*α*-L-rhamnopyranosyl-(1→6)-*β*-D-glucopyranoside	y=1E+06x-9516	0.9999	0.13 ~ 4.02

10	4-hydroxyl-phenylacetonitrile 4-*O*-*β*-D-apiofu ranosyl-(1→6)-*β*-D-glucopyranoside	y=1E+06x-11338	0.9999	0.13 ~ 4.02

Table S5 Precision, repeatability and stability of the five analytes (n=6)

Num.	Analytes	RSD（%）		
		Precision	Repeatability	Stability
2	4-hydroxyl-phenylacetonitrile4-*O*-*α*-L-rhamnopyranosyl-(1→6)-*β*-D- glucopyranoside	0.15	0.41	0.63
10	4-hydroxyl-phenylacetonitrile 4-*O*-*β*-D-apiofu ranosyl-(1→6)-*β*-D-glucopyranoside	0.08	1.27	0.66

Table S6 Results from a recovery test of the two analytes (n=6)

Num.	Original (mg)	Added (mg)	Found (mg)	Recovery (%)	Average (%)	RSD (%)
2	0.049	0.045	0.093	97.9	99.1	2.39
	0.049		0.093	98.2		
	0.049		0.092	96.3		
	0.049		0.093	98.4		
	0.049		0.094	100.6		
	0.049		0.096	103.0		
10	0.046	0.044	0.089	99.5	100.6	1.23
	0.046		0.090	100.9		
	0.046		0.090	101.2		
	0.046		0.089	100.2		
	0.046		0.091	102.5		
	0.046		0.089	99.1		

Molecular docking analysis

According to the interaction energy, the best docking pose was selected and listed in Table S7 and Figure S41. The lowest negative of interaction energy indicates that the interaction between ligand and protein is the strongest, and vice versa. Consequently, compound **7-2** was predicted to be the most likely inhibitor of Keap1 with interaction of e -47.78 kcal/mol. The 3D and corresponding surface scheme for active site of complex of Keap1 and compound **7-2** is shown in Figure S42.

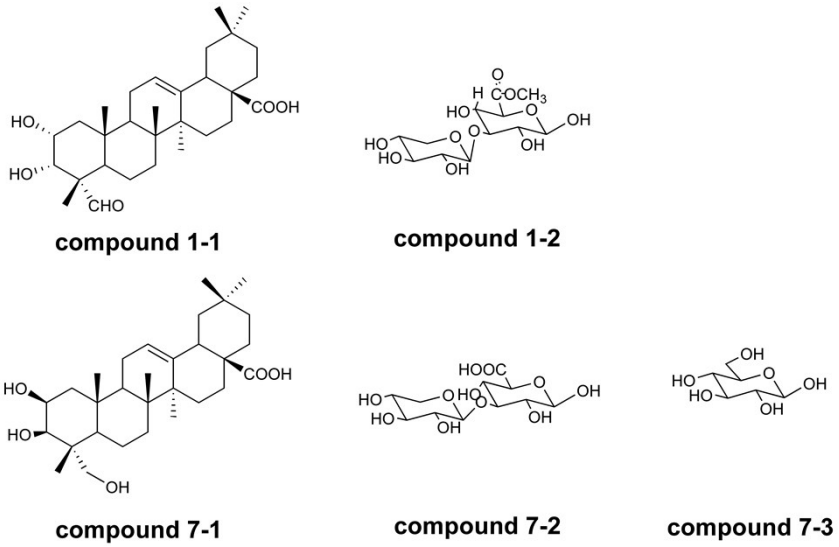

Figure S40 The aglycone and sugar moiety of compounds **1** and **7.**

Table S7 The interaction energy obtained by CD DOCK for compounds **1** and **7** as well as their aglycone and sugar moiety

Compound	CDocker interaction energy(kcal/mol)
compound **1**	Failed
compound **1-1**	-41.62
compound **1-2**	-44.68
compound **7**	Failed
compound **7-1**	-40.68
compound **7-2**	-47.78
compound **7-3**	-26.35

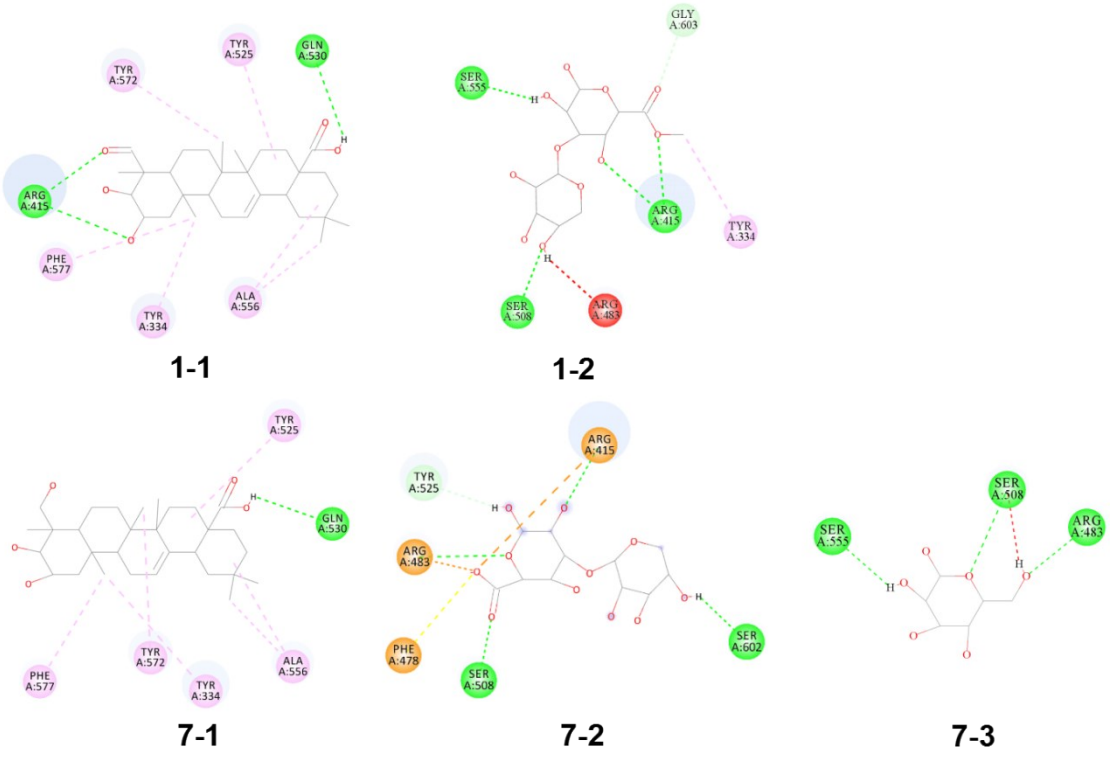

Figure S41 Interaction mode of ligands with Keap1 binding site. Dark green: hydrogen bond; light green: van der Waals; red: electron donor-donor interaction; pink-violet: hydrophobic interaction; brown: π-cation interaction.

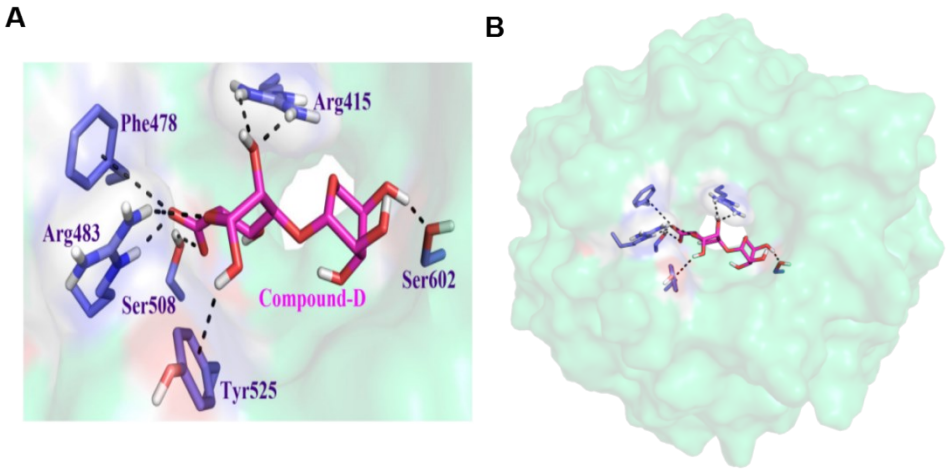

Figure S42 (A) Predicted binding mode of compound **7-2** (compound-D) and Keap1. Compound **7-2** is shown in hotpink, and the key residues of Keap1 is shown in

purple; (B) The panorama of interaction between compound **7-2** and Keap1. The dashed lines (black) represent hydrogen-bonding interactions, and the KEAP1 is shown as surface mode.