



Figure S1 Morphological features of 58 endophytic strains (Red box: SH-1.2-R-15).

Table S1 16S rRNA analysis of 58 endophytic strains.

NO.	Strains	Host plant	Parts	Closest sequences by BlastN	Percent Identity	Genbank accession
1	SH-1.1-R-1	<i>Dendrobium officinale</i> - one year old-1	Root	<i>Bacillus</i> sp. (in: Bacteria) strain 12D6	97.14%	MN784185
2	SH-1.1-R-2		Root	<i>Stenotrophomonas rhizophila</i> strain PgBE58	99.72%	MN784186
3	SH-1.1-R-3		Root	<i>Bacillus</i> sp. BS98	99.90%	MN784187
4	SH-1.1-R-4		Root	<i>Streptomyces</i> sp. strain SHP 1-2	99.80%	MN784188
5	SH-1.1-R-5		Root	<i>Stenotrophomonas</i> sp. strain H9	100.00%	MN784189
6	SH-1.1-R-6		Root	<i>Streptomyces</i> sp. SR3-82 gene	99.85%	MN784190
7	SH-1.1-R-7		Root	<i>Bacillus thuringiensis</i> strain ZLynn1000-39	97.59%	MN784191
8	SH-1.1-R-8		Root	Same as 5	-	-
9	SH-1.1-R-9		Root	<i>Aerococcus viridans</i> strain NBRC 12219	99.78%	MN784192
10	SH-1.1-L-1		Leaf	<i>Bacillus cereus</i> strain BC2	99.90%	MN784193
11	SH-1.1-L-2		Leaf	<i>Bacillus thuringiensis</i> strain GA-A07	99.90%	MN784194
12	SH-1.1-L-3		Leaf	Same as 58	-	-
13	SH-1.1-S-1		Stem	<i>Stenotrophomonas</i> sp. Strain FB14	99.93%	MN784195
14	SH-1.2-R-1	<i>Dendrobium officinale</i> - one year old-2	Root	<i>Streptomyces</i> sp. NK04104	96.58%	MN784196
15	SH-1.2-R-2		Root	<i>Streptomyces</i> sp. CdTB01	97.13%	MN784197
16	SH-1.2-R-3		Root	<i>Pseudomonas</i> sp. BMS12	99.33%	MN784198
17	SH-1.2-R-4		Root	<i>Streptomyces</i> sp. g2b	99.79%	MN784199
18	SH-1.2-R-5		Root	<i>Streptomyces</i> sp. HF-2	96.82%	MN784200
19	SH-1.2-R-6		Root	<i>Pseudomonas</i> sp. Strain IAE244	99.92%	MN784201
20	SH-1.2-R-7		Root	<i>Streptomyces</i> sp. LCB 0297	97.94%	MN784202
21	SH-1.2-R-8		Root	<i>Streptomyces</i> sp. strain QJSt8	97.47%	MN784203
22	SH-1.2-R-9		Root	Same as 7	-	-
23	SH-1.2-R-10		Root	Same as 8	-	-
24	SH-1.2-R-11		Root	Same as 21	-	-
25	SH-1.2-R-12		Root	<i>Bacillus cereus</i> strain ULT15	99.60%	MN784204
26	SH-1.2-R-13		Root	<i>Streptomyces</i> sp. TM-74	97.51%	MN784205
27	SH-1.2-R-14		Root	<i>Streptomyces fulvissimus</i> strain DSM 40593	97.64%	MN784206
28	SH-1.2-R-15		Root	<i>Streptomyces chartreusis</i> strain ISP 5085	99.21%	MN784207
29	SH-1.2-R-16		Root	<i>Streptomyces variabilis</i> strain NRRL B-3984	97.52%	MN784208
30	SH-1.2-R-17		Root	<i>Streptomyces</i> sp. strain TM-A158	99.86%	MN784209
31	SH-1.2-R-18	Root	<i>Bacillus thuringiensis</i> strain GA-A07 chromosome	99.93%	MN784210	
32	SH-1.2-R-19	Root	Same as 58	-	-	
33	SH-1.2-L-1	Leaf	<i>Micromonospora aurantiaca</i> strain IMB16-201	99.92%	MN784211	
34	SH-3.1-R-1	<i>Dendrobium officinale</i> - three years old-1	Root	<i>Bacillus</i> sp. (in: Bacteria) strain 12D6	98.67%	MN784212
35	SH-3.1-R-2		Root	Same as 36	-	-
36	SH-3.1-R-3		Root	<i>Streptomyces</i> sp. GSEUDO-0578	96.80%	MN784213
37	SH-3.1-R-4		Root	Same as 50	-	-
38	SH-3.1-R-5		Root	<i>Streptomyces</i> sp. 13-22	96.92%	MN784214
39	SH-3.1-R-6		Root	<i>Streptomyces</i> sp. MI02-7b	99.58%	MN784215
40	SH-3.1-R-7		Root	<i>Streptomyces anulatus</i> strain 174456	97.06%	MN784216
41	SH-3.1-R-8		Root	Same as 38	-	-
42	SH-3.1-R-9		Root	<i>Streptomyces</i> sp. DSM 40835 clone K12	99.70%	MN784217
43	SH-3.1-R-10		Root	<i>Bacillus thuringiensis</i> strain JW-1	99.81%	MN784218
44	SH-3.1-R-11		Root	<i>Bacillus thuringiensis</i> strain GA-A07	100.00%	MN784219

45	SH-3.1-R-12		Root	Same as 66	-	-	
46	SH-3.1-R-13		Root	<i>Bacillus</i> sp. JAS24-2 chromosome	100.00%	MN784220	
47	SH-3.1-R-14		Root	<i>Streptomyces</i> sp. strain MUSC11	98.46%	MN784221	
48	SH-3.1-R-15		Root	Same as 66	-	-	
49	SH-3.1-R-16		Root	<i>Streptomyces</i> sp. strain BOR09	93.69%	MN784222	
50	SH-3.1-R-17		Root	<i>Viridibacillus</i> sp. strain TM-B117	99.69%	MN784223	
51	SH-3.1-R-19		Root	<i>Streptomyces</i> sp. SR3-82	96.17%	MN784224	
52	SH-3.1-R-20		Root	<i>Bacillus thuringiensis</i> strain GCU1	99.79%	MN784225	
53	SH-3.1-R-21		Root	<i>Streptomyces prunicolor</i> NBRC 13075	99.80%	MN784226	
54	SH-3.1-R-22		Root	<i>Streptomyces</i> sp. strain GDMCC 60254	96.51%	MN784227	
55	SH-3.1-L-1		Leaf	Same as 59	-	-	
56	SH-3.1-L-2		Leaf	Same as 65	-	-	
57	SH-3.1-L-3		Leaf	Same as 60	-	-	
58	SH-3.1-S-1		Stem	<i>Streptomyces</i> sp. strain GDMCC 60254	96.92%	MN784228	
59	SH-3.1-S-2		Stem	<i>Bacillus cereus</i> strain NRRL B-23957	98.73%	MN784229	
60	SH-3.1-S-3		Stem	<i>Streptomyces</i> sp. SM17	99.31%	MN784230	
61	SH-3.1-S-4		Stem	Same as 65	-	-	
62	SH-3.2-R-1		<i>Dendrobium officinale</i> - three years old-2	Root	<i>Bacillus</i> sp. HT-Z74-B2	98.55%	MN784231
63	SH-3.2-R-2			Root	Same as 50	-	-
64	SH-3.2-R-3			Root	Same as 60	-	-
65	SH-3.2-R-4			Root	<i>Bacillus cereus</i> strain GE16	98.78%	MN784232
66	SH-3.2-R-5			Root	<i>Streptomyces</i> sp. GKU 867	100.00%	MN784233
67	SH-3.2-R-6			Root	<i>Bacillus thuringiensis</i> strain QZL38 chromosome	100.00%	MN784234
68	SH-3.2-R-7			Root	<i>Streptomyces rochei</i> 7434AN4 DNA	99.79%	MN784235
69	SH-3.2-R-8			Root	<i>Streptomyces</i> sp. Endophyte N2 chromosome	100.00%	MN784236
70	SH-3.2-R-9			Root	<i>Bacillus cereus</i> strain Sneb2000	100.00%	MN784237
71	SH-3.2-R-10			Root	<i>Brevundimonas</i> sp. strain 7002-176	100.00%	MN784238
72	SH-3.2-R-11			Root	<i>Corynebacterium</i> sp. strain ABYHD3-2	99.85%	MN784239
73	SH-3.2-R-12			Root	<i>Streptomyces</i> sp. TJ-27	97.98%	MN784240
74	SH-3.2-R-13			Root	<i>Bacillus</i> sp. AR4-2 chromosome	100.00%	MN784241
75	SH-3.2-L-1			Leaf	<i>Bacillus thuringiensis</i> strain GA-A07	100.00%	MN784242

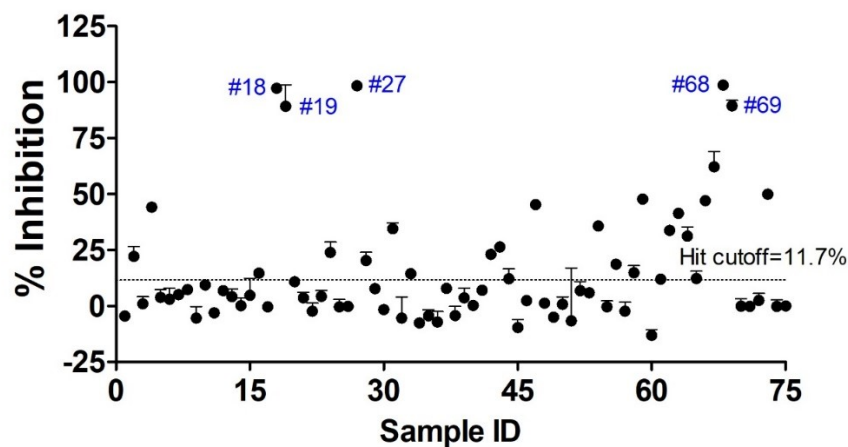


Figure S2 Scatterplot of 75 cultured endophytic strains screened in triplicate at 25 or 50 $\mu\text{g}/\text{mL}$ in Hep3B2.1-7 cell viability assay. Data are shown normalized to percent max response of the high control (Medium only group). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 11.7%.

Table S2. Strains showed inhibition against Hep3B2.1-7 cell more than the hit cutoff ($>11.7\%$).

No.	Endophytic strains	%Inhibition	No.	Endophytic strains	%Inhibition
2	SH-1.1-R-2	22.14 \pm 4.46	54	SH-3.1-R-22	35.74 \pm 2.31
4	SH-1.1-R-4	44.24 \pm 1.39	56	SH-3.1-L-2	18.64 \pm 1.16
16	SH-1.2-R-3	14.67 \pm 1.99	58	SH-3.1-S-1	14.87 \pm 3.17
18	SH-1.2-R-5	97.24 \pm 0.38	59	SH-3.1-S-2	47.80 \pm 0.99
19	SH-1.2-R-6	89.27 \pm 9.58	61	SH-3.1-S-4	12.00 \pm 1.38
24	SH-1.2-R-11	23.97 \pm 4.63	62	SH-3.2-R-1	33.77 \pm 2.22
27	SH-1.2-R-14	98.44 \pm 0.36	63	SH-3.2-R-2	41.40 \pm 1.71
28	SH-1.2-R-15	20.30 \pm 3.76	64	SH-3.2-R-3	31.27 \pm 4.01
31	SH-1.2-R-18	34.47 \pm 2.74	65	SH-3.2-R-4	12.30 \pm 3.31
33	SH-1.2-L-1	14.47 \pm 1.28	66	SH-3.2-R-5	47.07 \pm 1.86
42	SH-3.1-R-9	23.14 \pm 1.77	67	SH-3.2-R-6	62.20 \pm 6.76
43	SH-3.1-R-10	26.37 \pm 2.21	68	SH-3.2-R-7	98.67 \pm 0.62
44	SH-3.1-R-11	12.17 \pm 4.47	69	SH-3.2-R-8	89.50 \pm 2.46
47	SH-3.1-R-14	45.34 \pm 1.71	73	SH-3.2-R-12	49.97 \pm 1.41

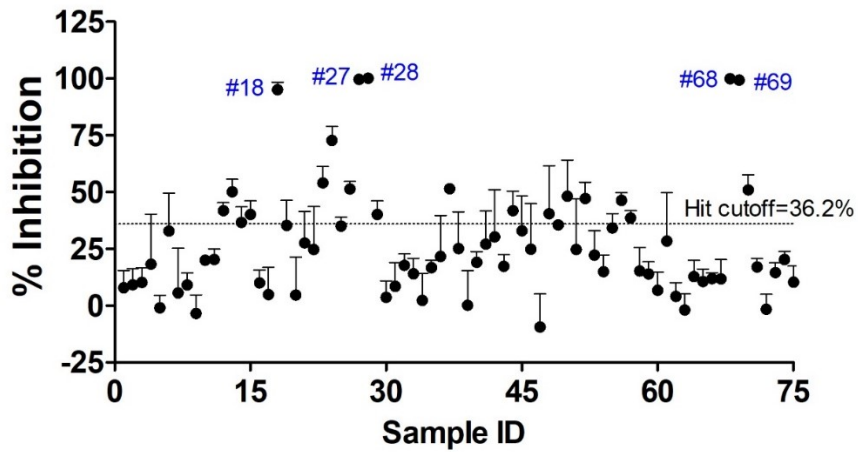


Figure S3 Scatterplot of 75 cultured endophytic strains screened in triplicate at 25 or 50 $\mu\text{g}/\text{mL}$ in *S. aureus* inhibitory assay. Data are shown normalized to percent max response of the high control (Bacterial treated with 100 $\mu\text{g}/\text{mL}$ Ampicillin). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 36.2%.

Table S3 Strains showed inhibition against *S. aureus* more than the hit cutoff (>36.2%).

No.	Endophytic strains	%Inhibition	No.	Endophytic strains	%Inhibition
12	SH-1.1-L-3	41.86 \pm 3.50	37	SH-3.1-R-4	51.50 \pm 1.96
13	SH-1.1-S-1	50.13 \pm 5.59	44	SH-3.1-R-11	41.81 \pm 8.64
14	SH-1.2-R-1	36.70 \pm 6.74	48	SH-3.1-R-15	40.45 \pm 21.15
15	SH-1.2-R-2	40.17 \pm 5.94	50	SH-3.1-R-17	48.24 \pm 15.86
18	SH-1.2-R-5	95.12 \pm 3.34	52	SH-3.1-R-20	47.21 \pm 7.18
23	SH-1.2-R-10	54.04 \pm 7.21	56	SH-3.1-L-2	46.37 \pm 3.41
24	SH-1.2-R-11	72.75 \pm 6.14	57	SH-3.1-L-3	38.59 \pm 3.27
26	SH-1.2-R-13	51.38 \pm 3.27	68	SH-3.2-R-7	100.00 \pm 0.24
27	SH-1.2-R-14	99.66 \pm 0.58	69	SH-3.2-R-8	99.32 \pm 0.53
28	SH-1.2-R-15	100.12 \pm 0.09	70	SH-3.2-R-9	51.01 \pm 6.67
29	SH-1.2-R-16	40.21 \pm 5.97			

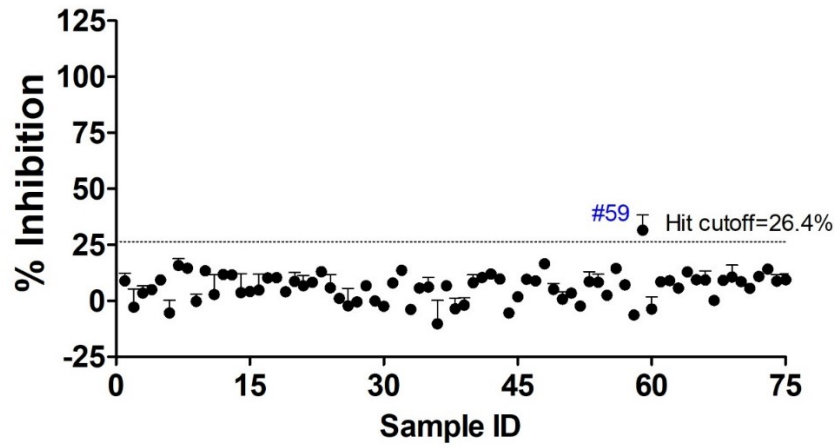
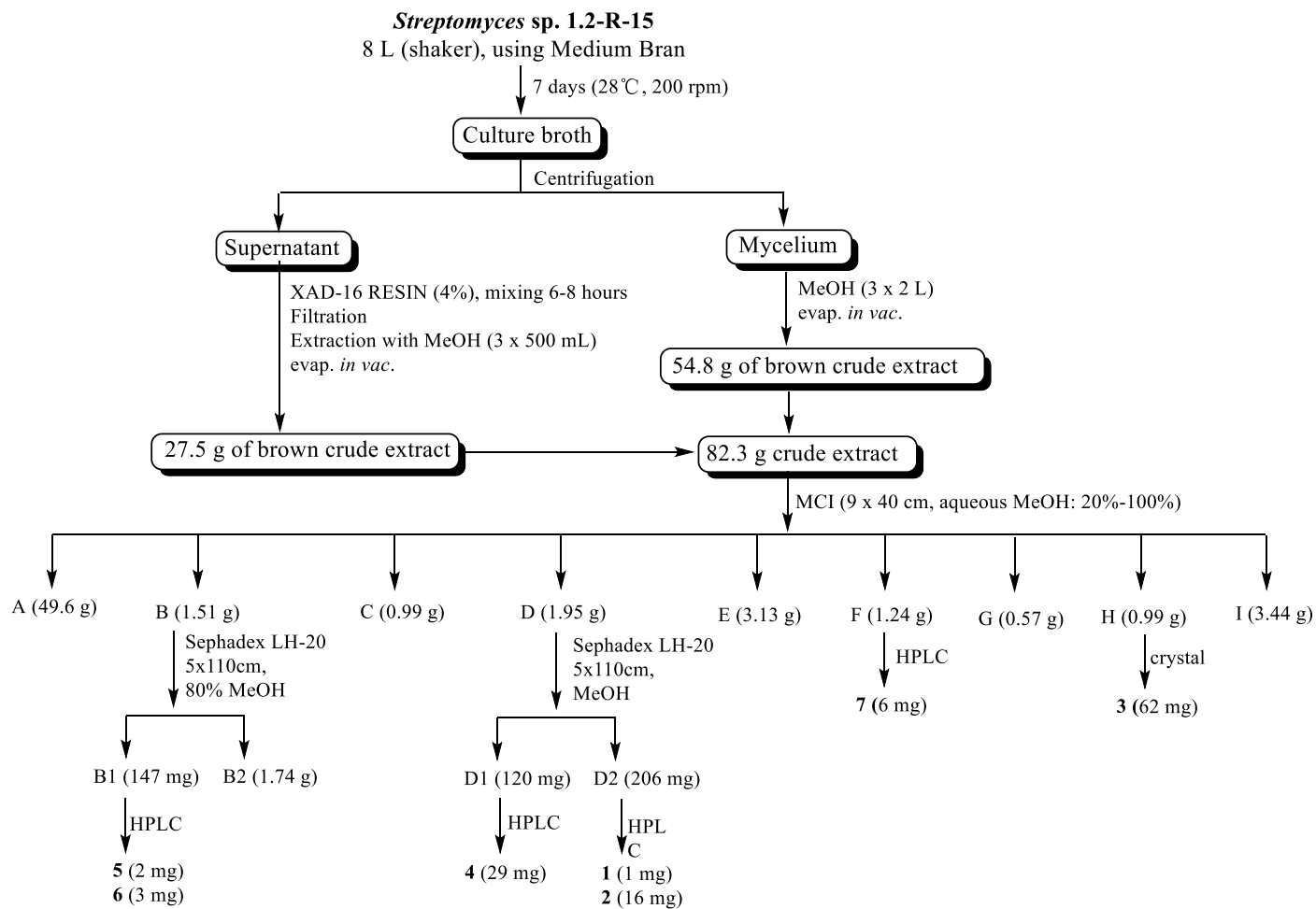


Figure S4 Scatterplot of 75 samples screened in triplicate at 25 or 50 $\mu\text{g/mL}$ in *E. coli* inhibitory assay. Data are shown normalized to percent max response of the high control (Bacterial treated with 100 $\mu\text{g/mL}$ Ampicillin). Each data point represents the mean and standard deviation of three replicates in 96 wells. The hit cutoff calculated as the average percent inhibition plus three times the standard deviation of the low control wells, is shown as the black line at 26.4%.

Table S4 Strains showed inhibition against *E. coli* more than the hit cutoff (>26.4%).

No.	Endophytic strains	%Inhibition
59	SH-3.1-S-2	31.49 \pm 6.86



Scheme S1 Work-up scheme for the *Streptomyces* sp. SH-1.2-R-15.

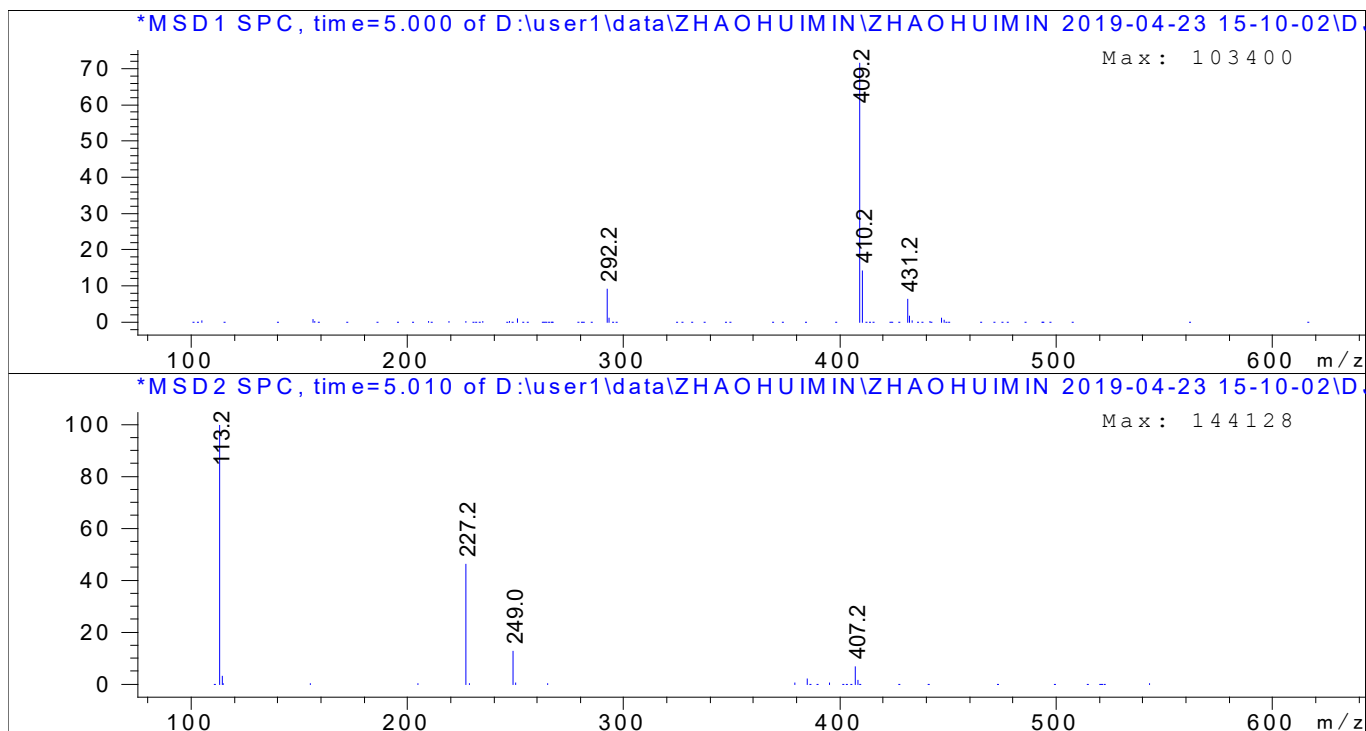


Figure S5. (+) and (-)-ESI-MS of compound **1**.

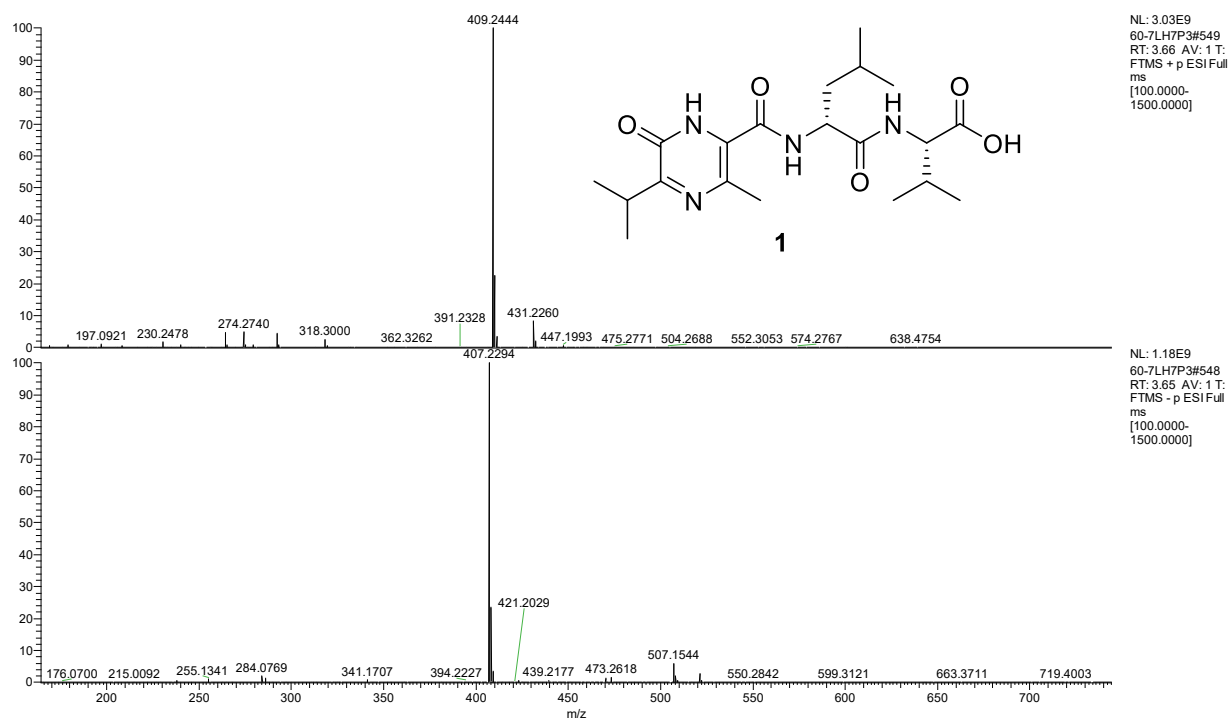


Figure S6. HRMS spectrum of compound **1**.

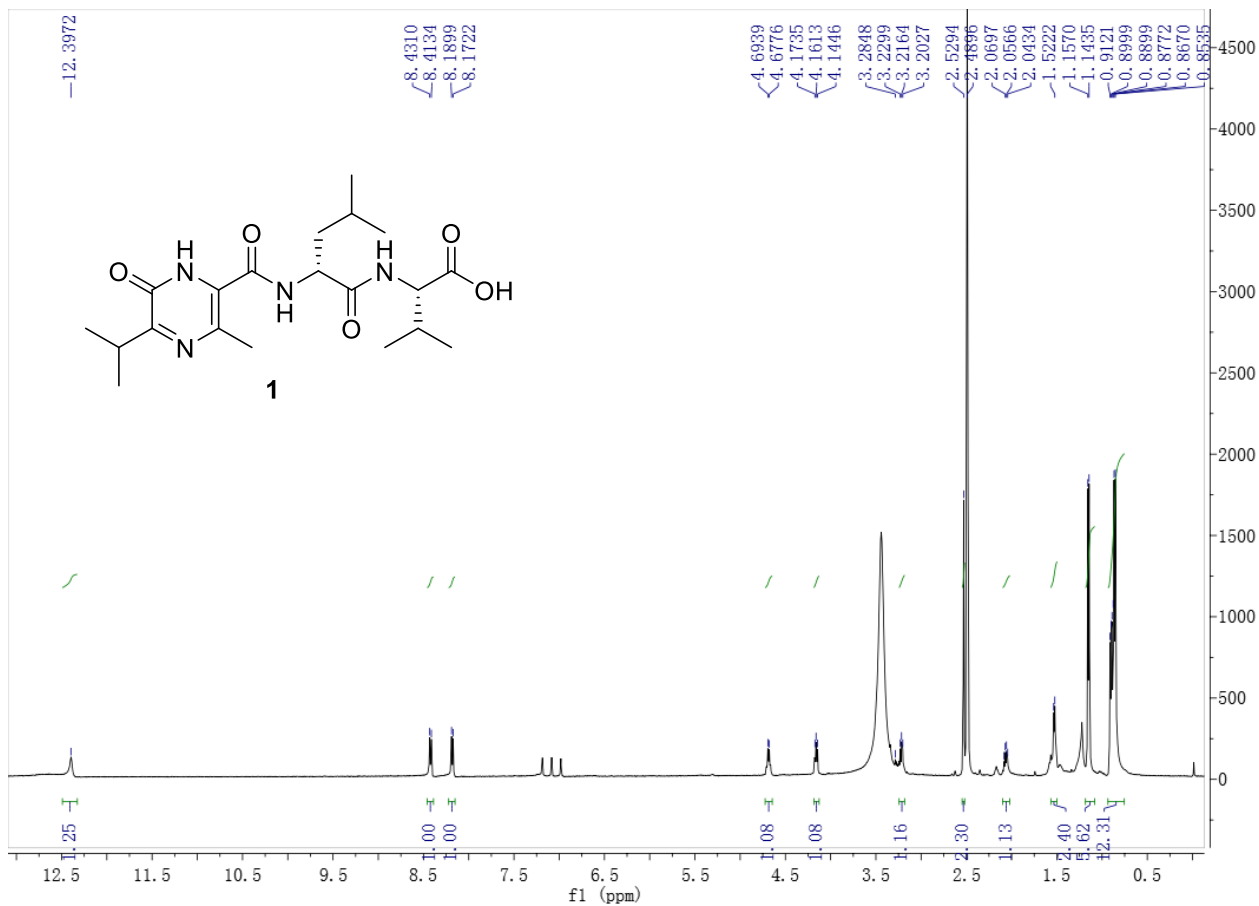


Figure S7. ^1H NMR (500 MHz, $\text{DMSO}-d_6$) spectrum of compound **1**.

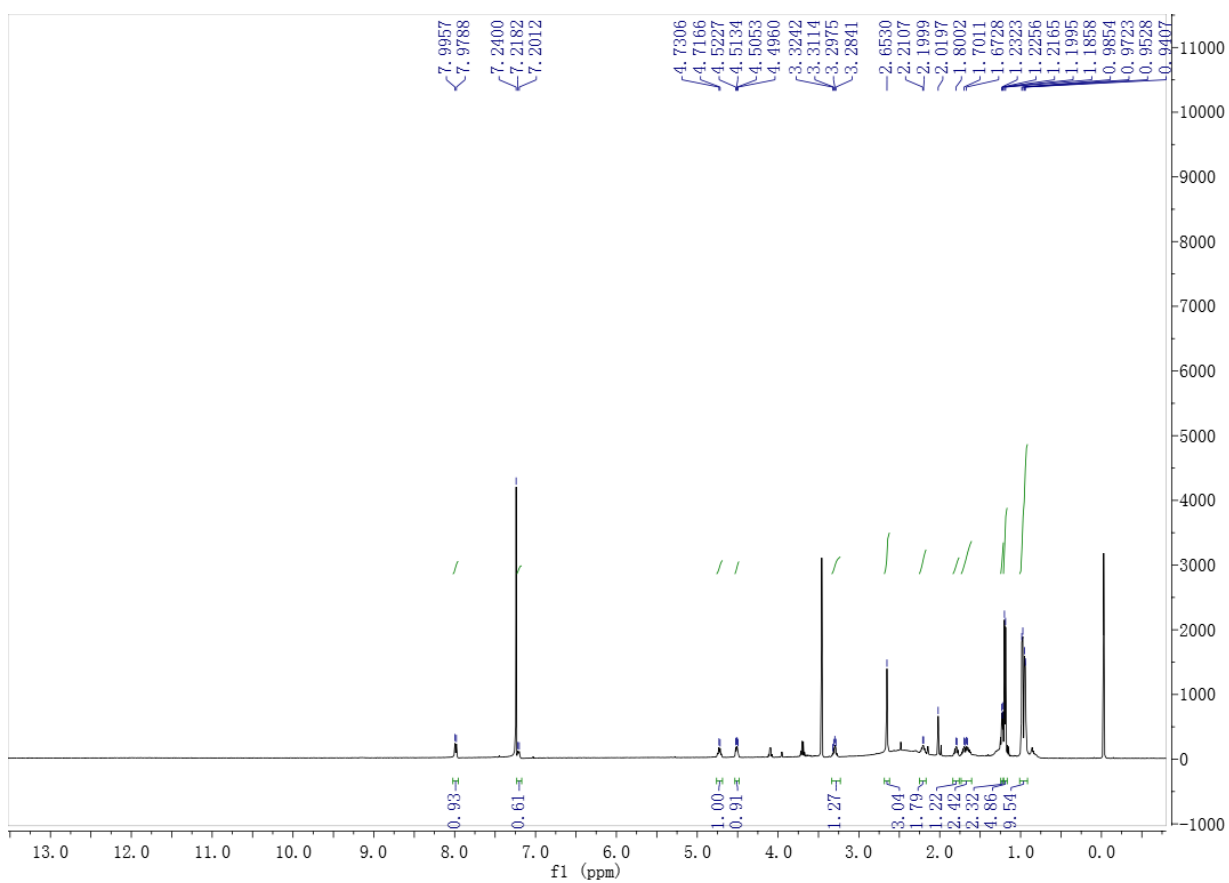


Figure S8. ^1H NMR (500 MHz, CDCl_3) spectrum of compound **1**.

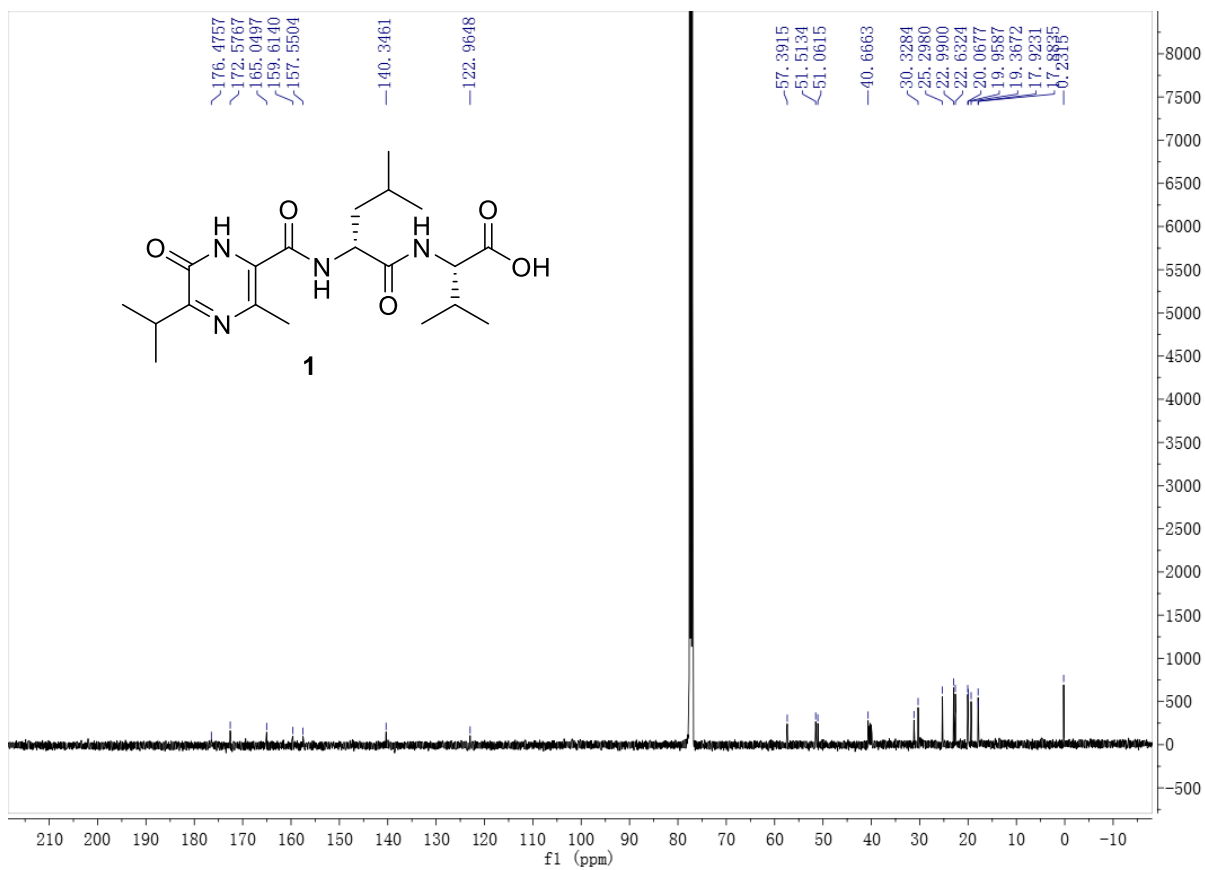


Figure S9. ^{13}C NMR (125 MHz, CDCl_3) spectrum of compound **1**.

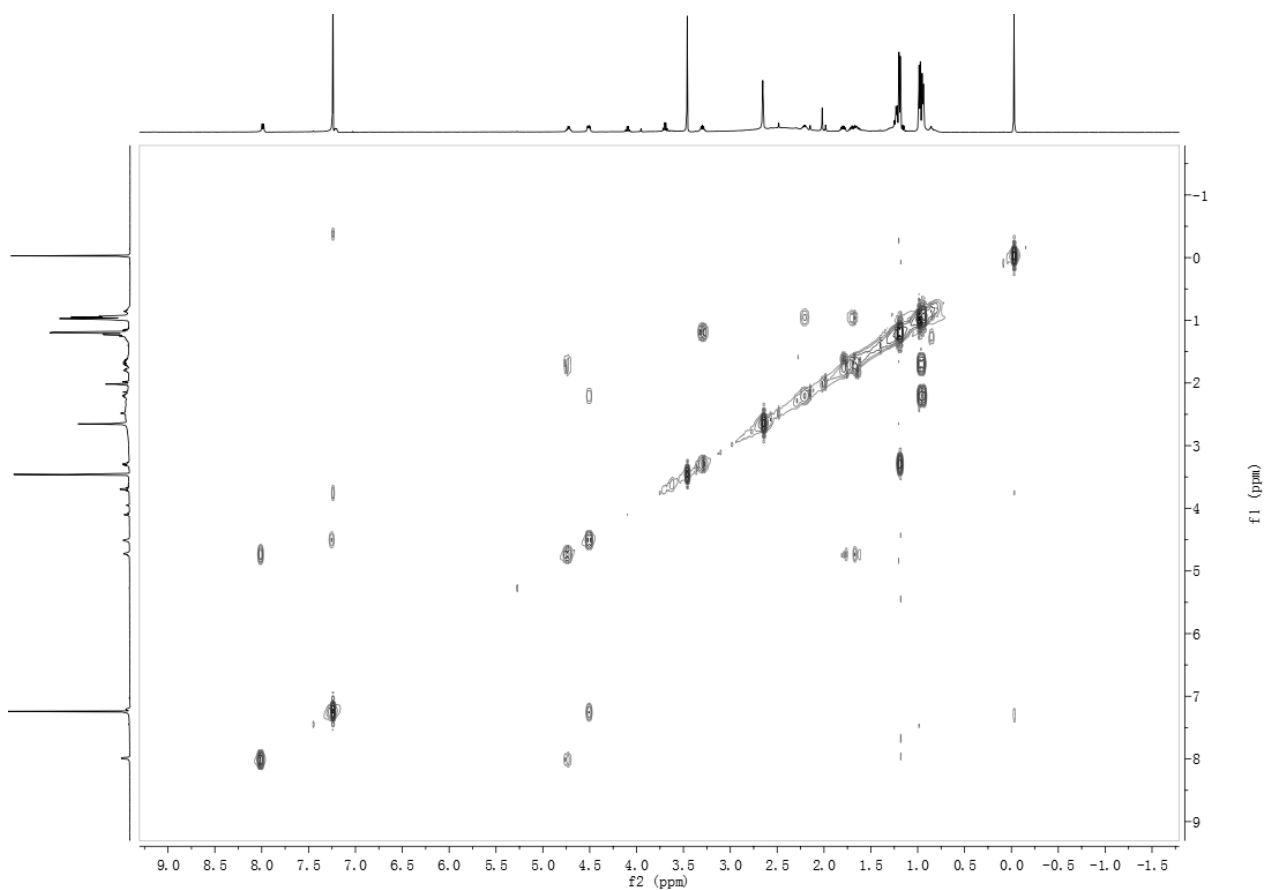


Figure S10. ^1H - ^1H COSY (500 MHz, CDCl_3) spectrum of compound **1**.

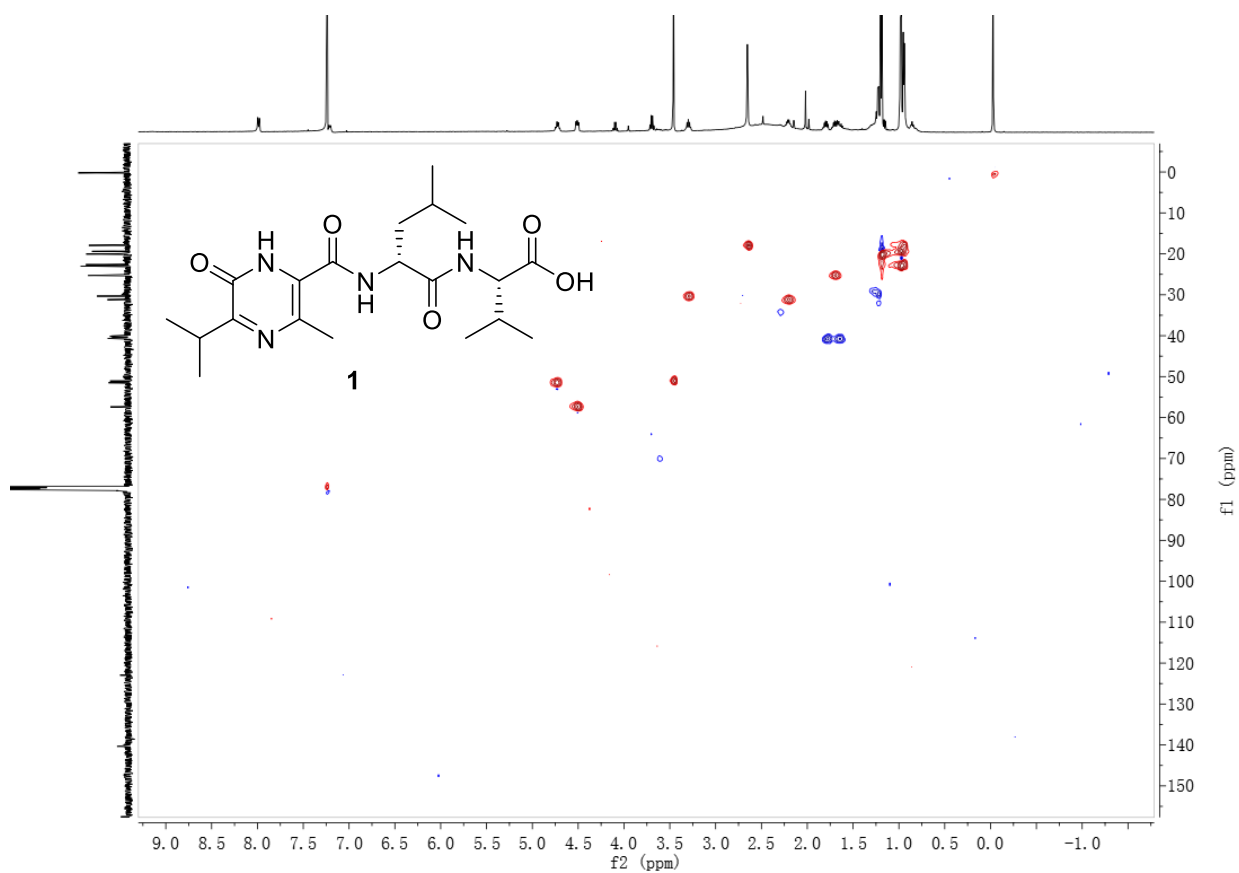


Figure S11. HSQC (500 MHz, CDCl₃) spectrum of compound **1**.

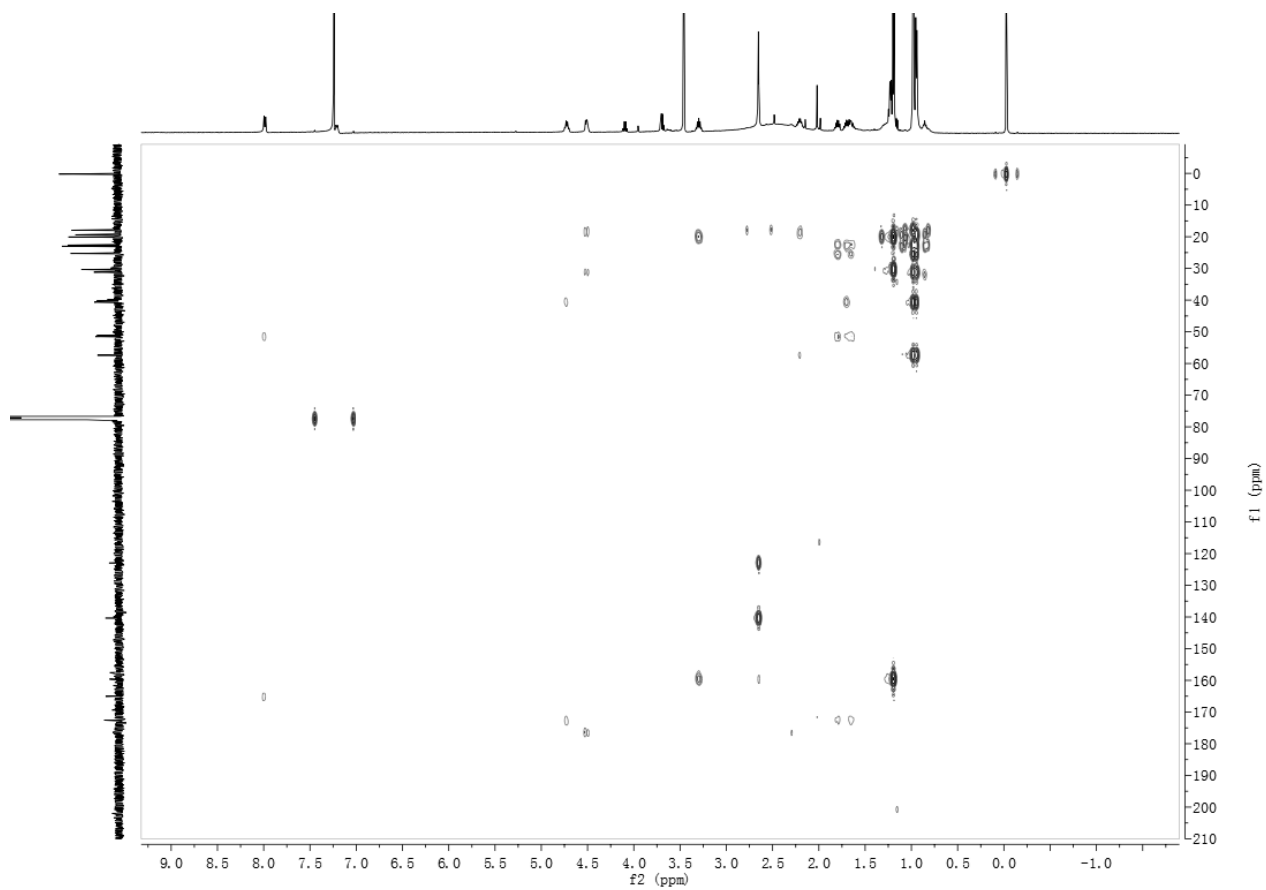


Figure S12. HMBC (500 MHz, CDCl₃) spectrum of compound **1**.

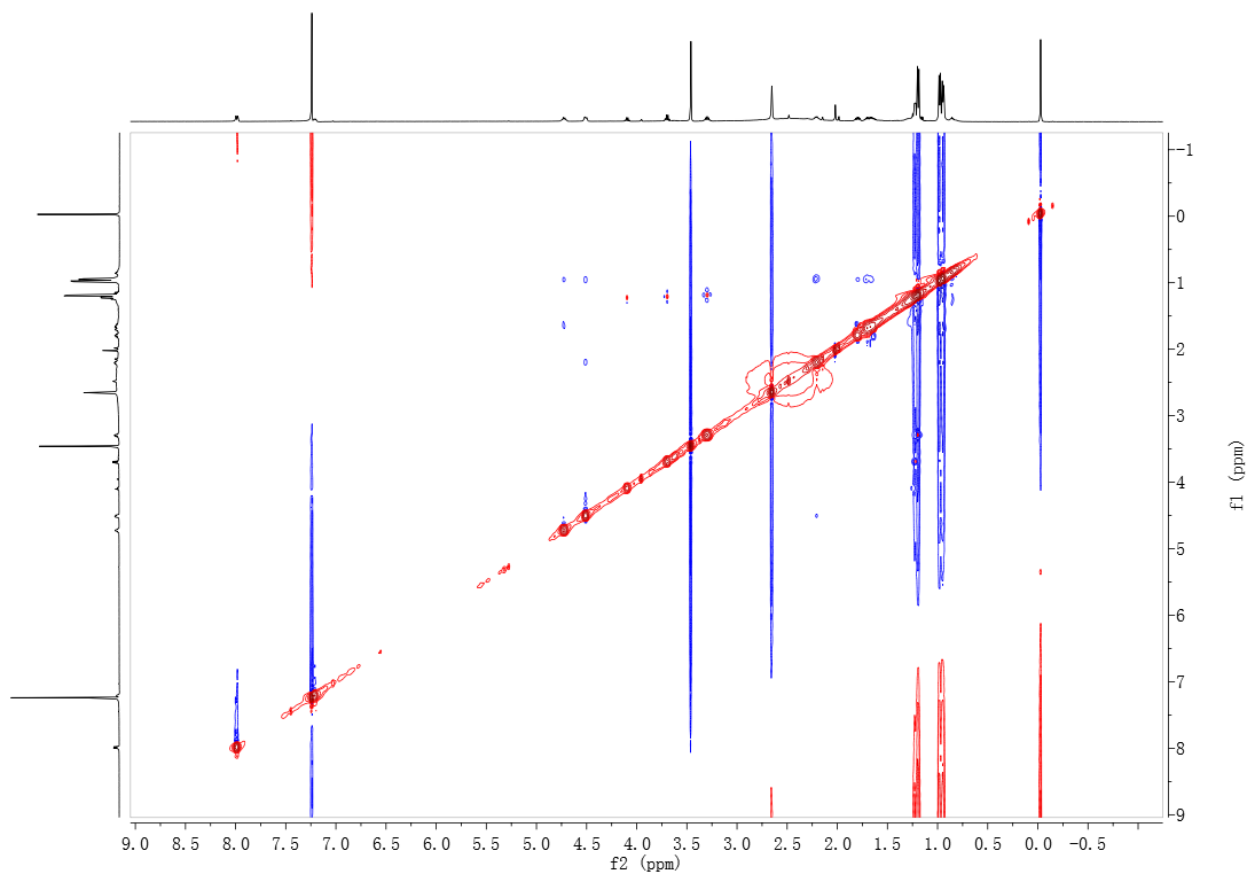


Figure S13. ROESY (500 MHz, CDCl_3) spectrum of compound **1**.

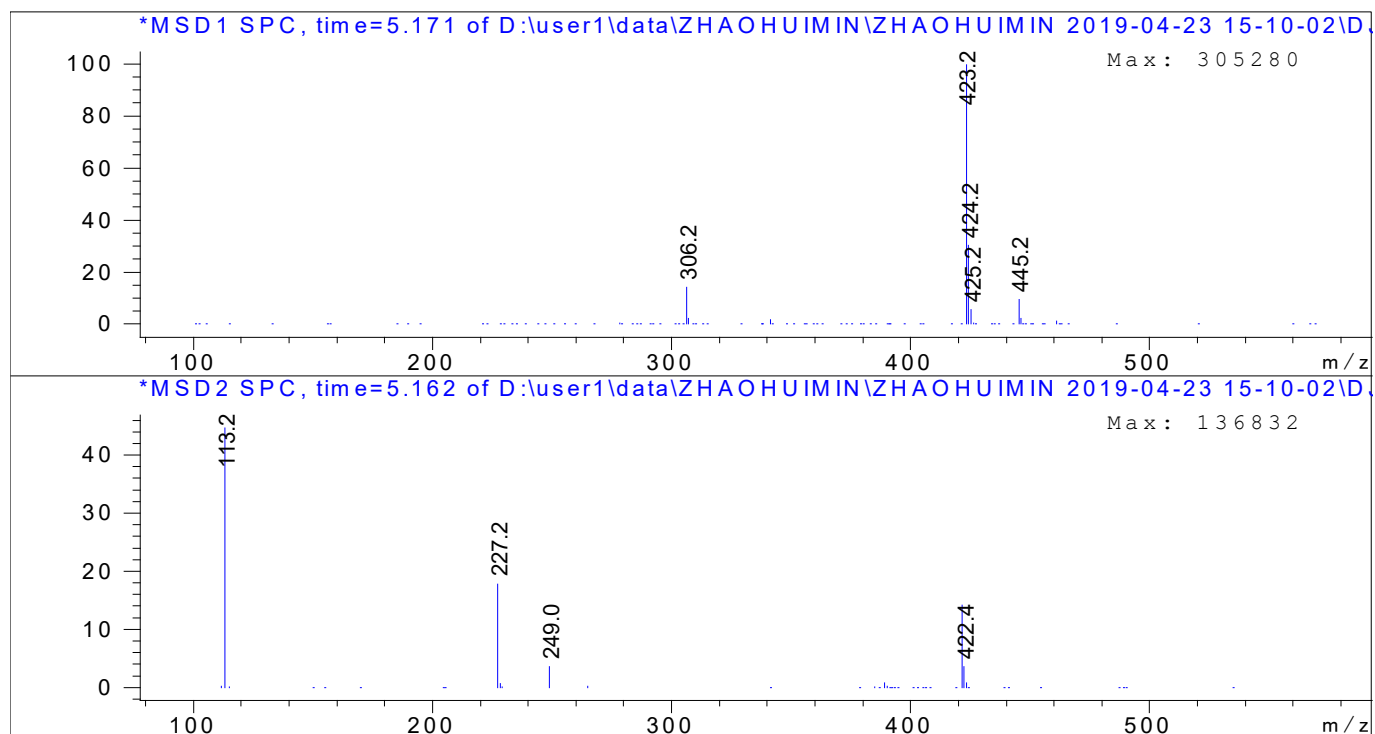
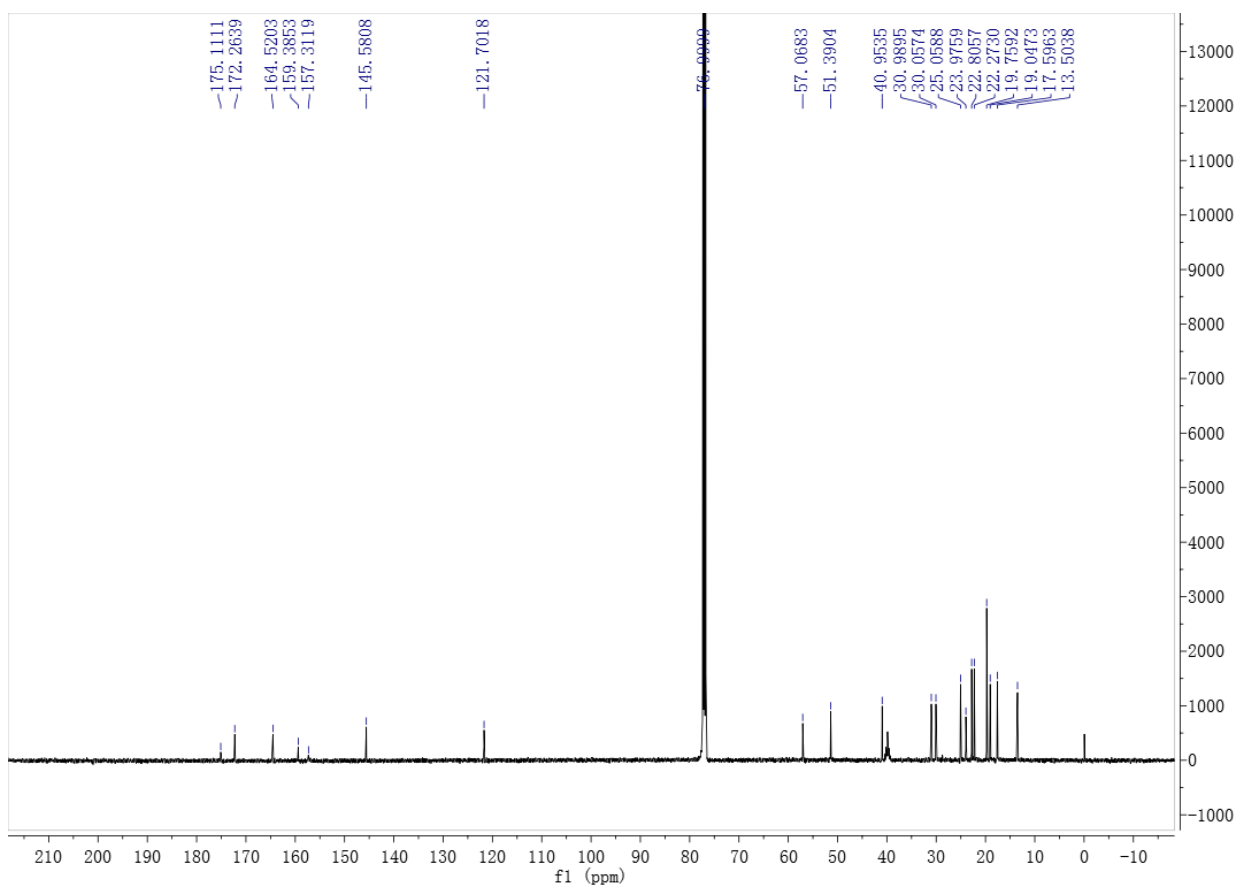
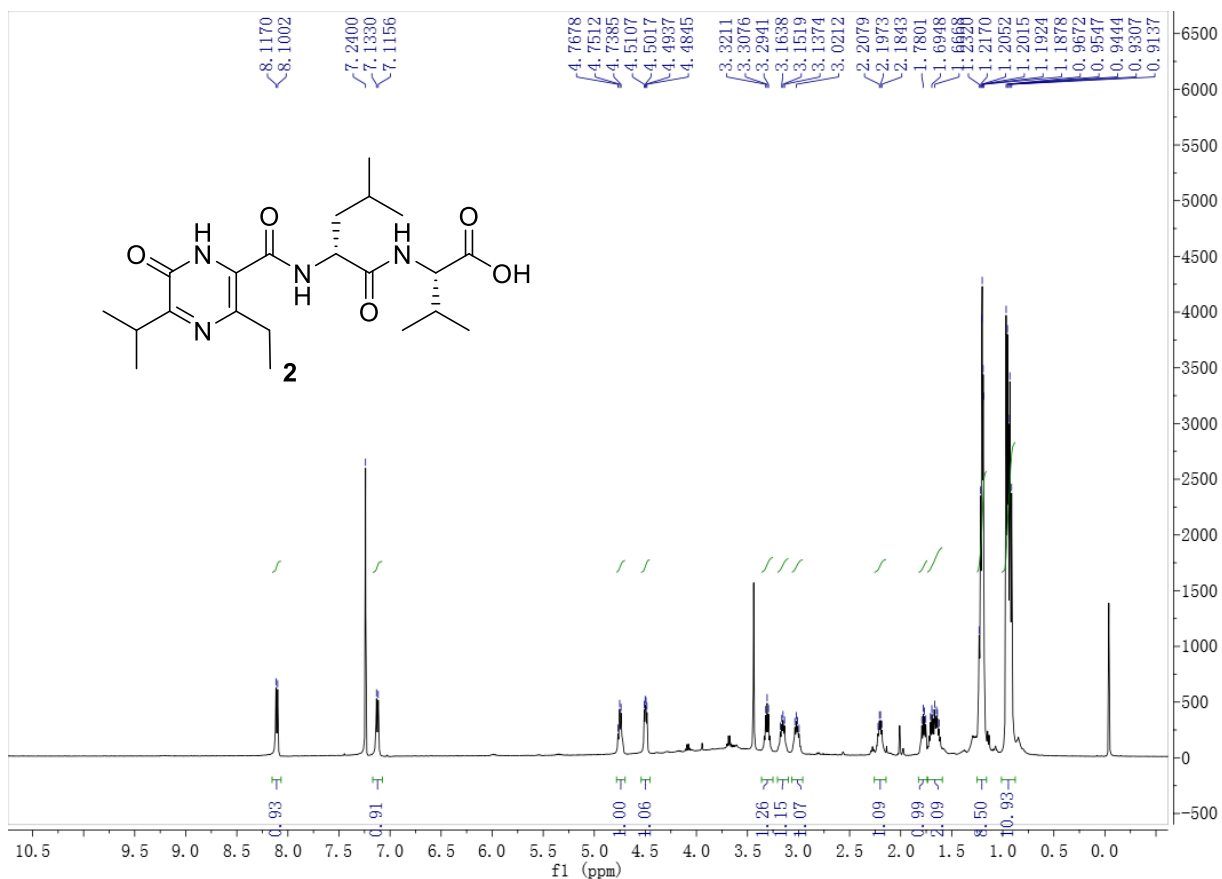


Figure S14. (+) and (-)-ESI-MS of compound **2**.



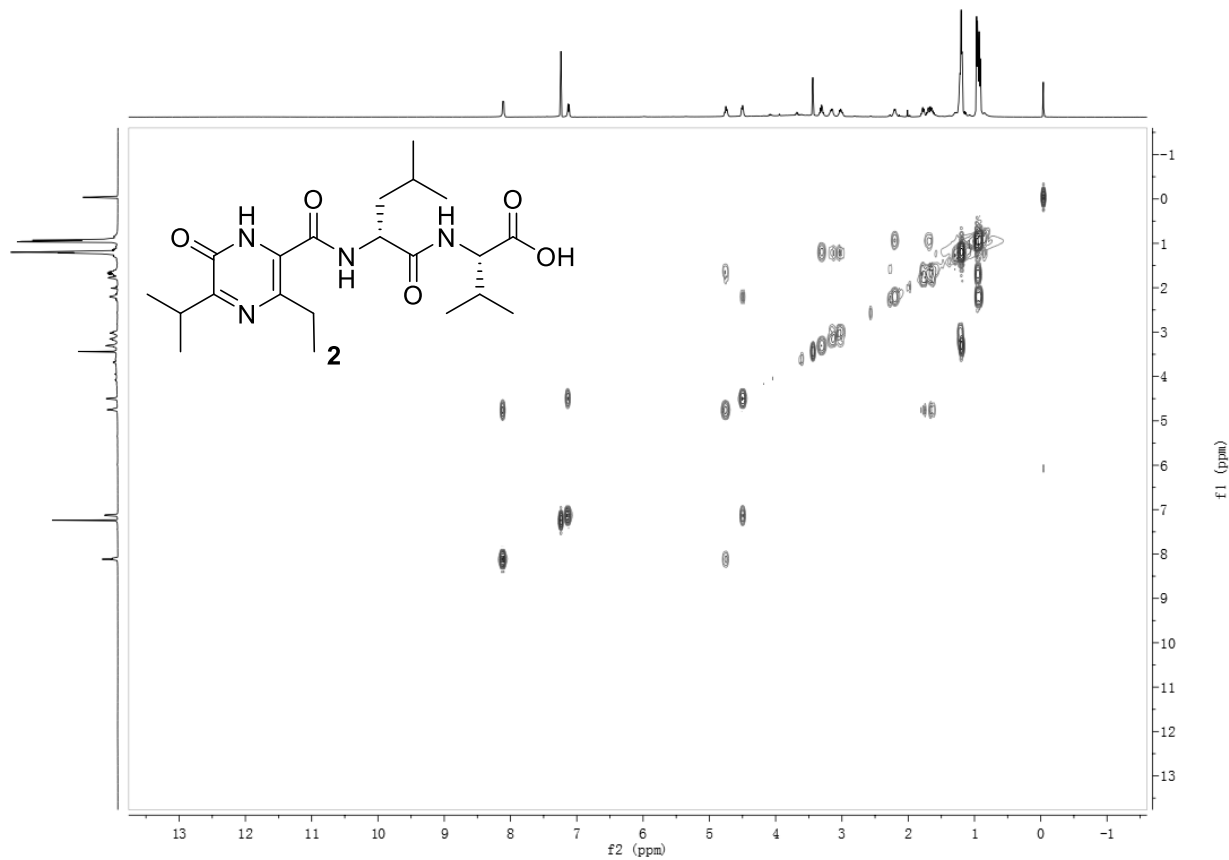


Figure S19. ^1H - ^1H COSY (500 MHz, CDCl_3) spectrum of compound **2**.

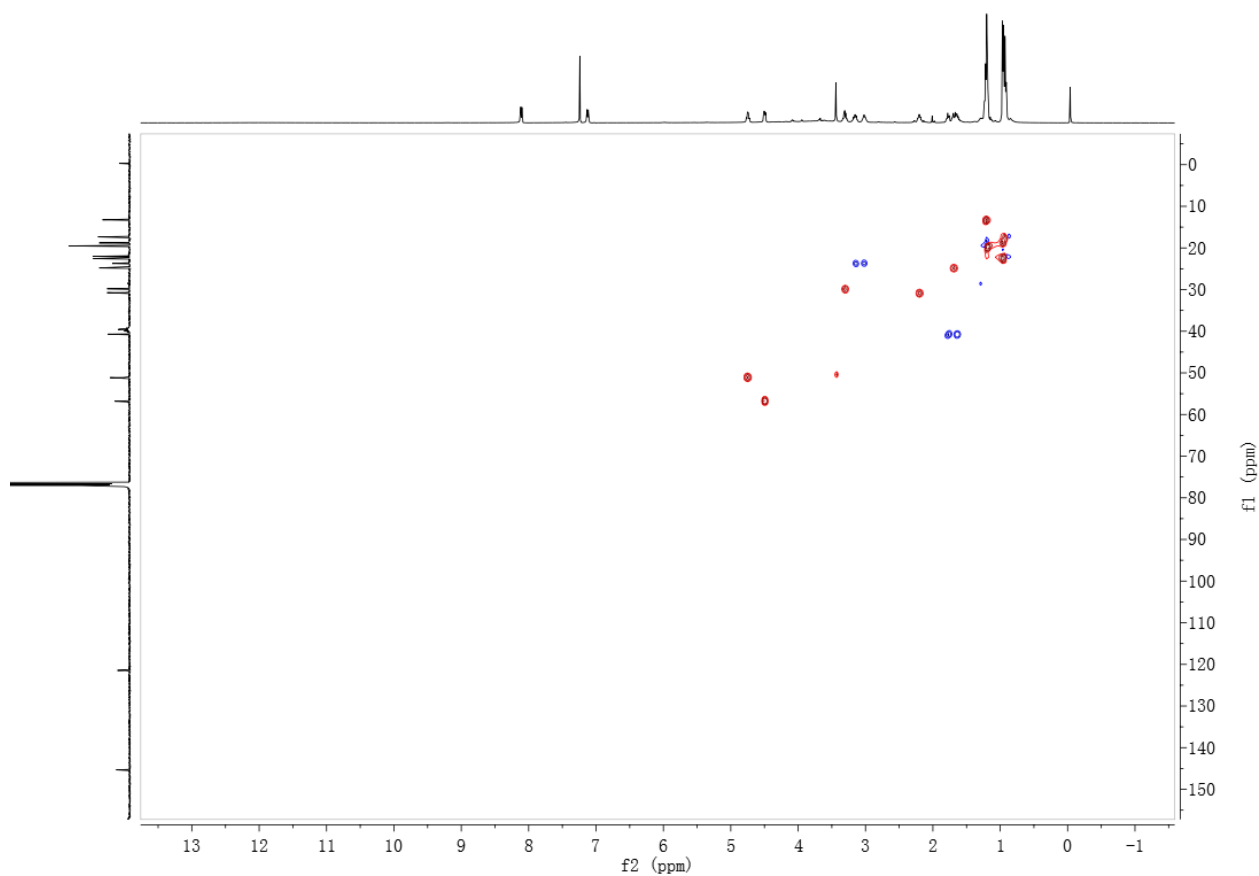


Figure S20. HSQC (500 MHz, CDCl_3) spectrum of compound **2**.

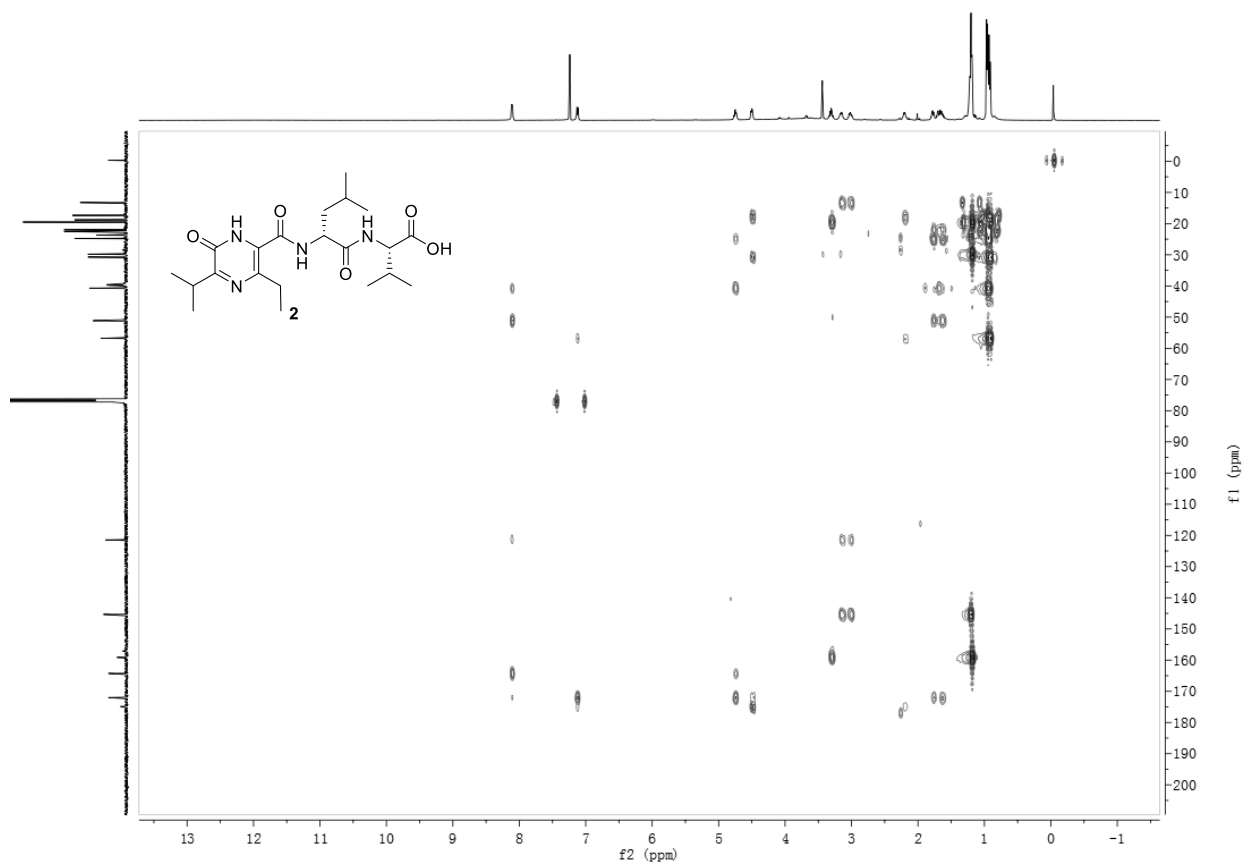


Figure S21. HMBC (500 MHz, CDCl₃) spectrum of compound **2**.

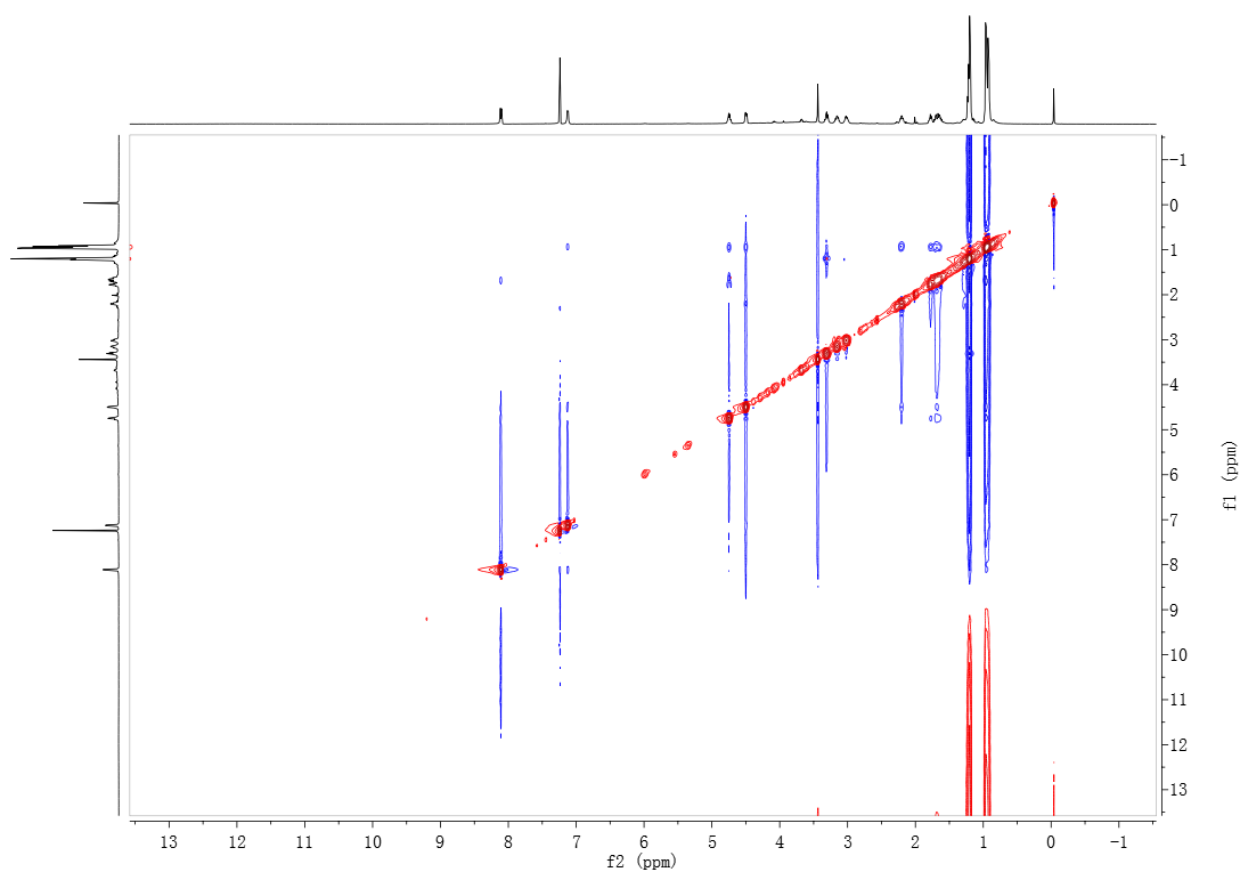


Figure S22. ROESY (500 MHz, CDCl₃) spectrum of compound **2**.

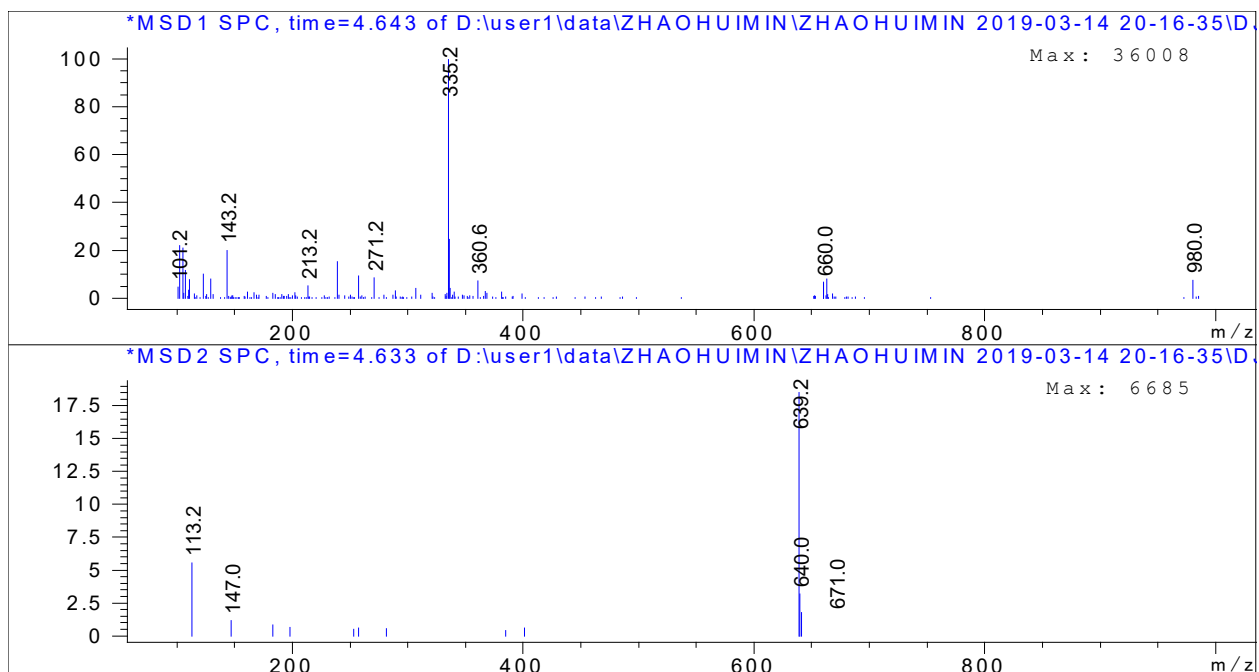


Figure S23. (+) and (-)-ESI-MS of compound 3.

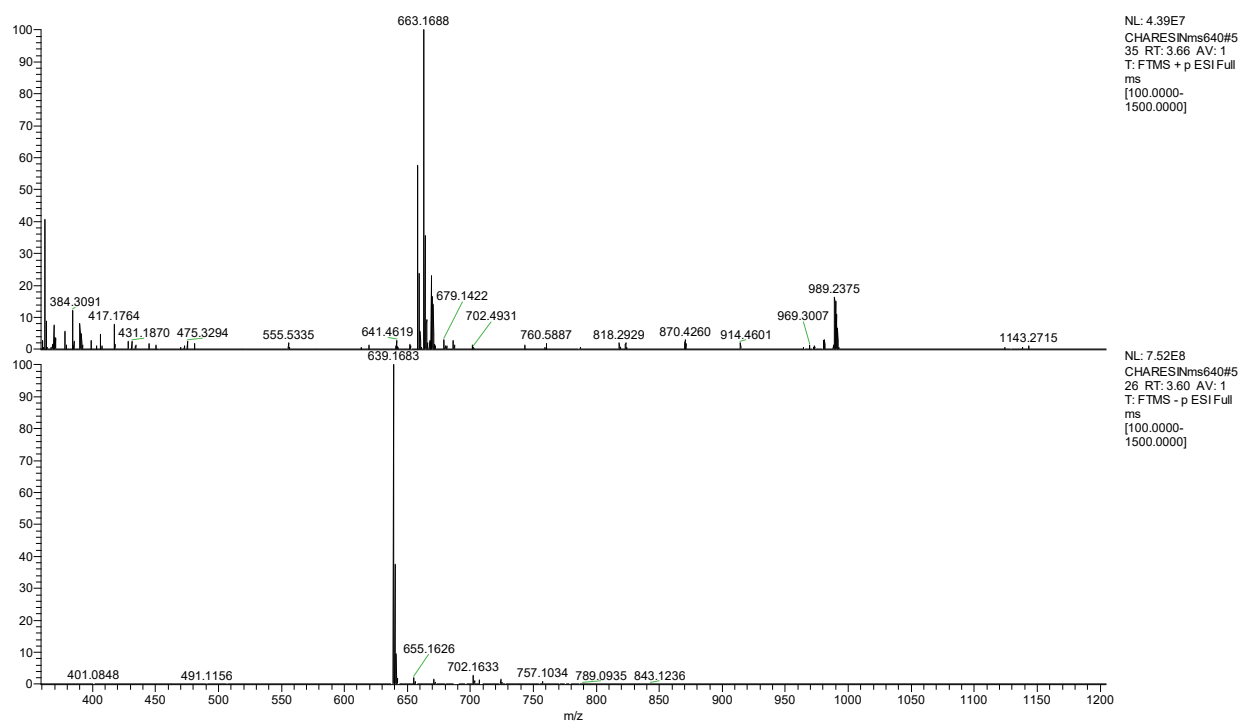


Figure S24. HRESI-MS spectrum of compound 3.

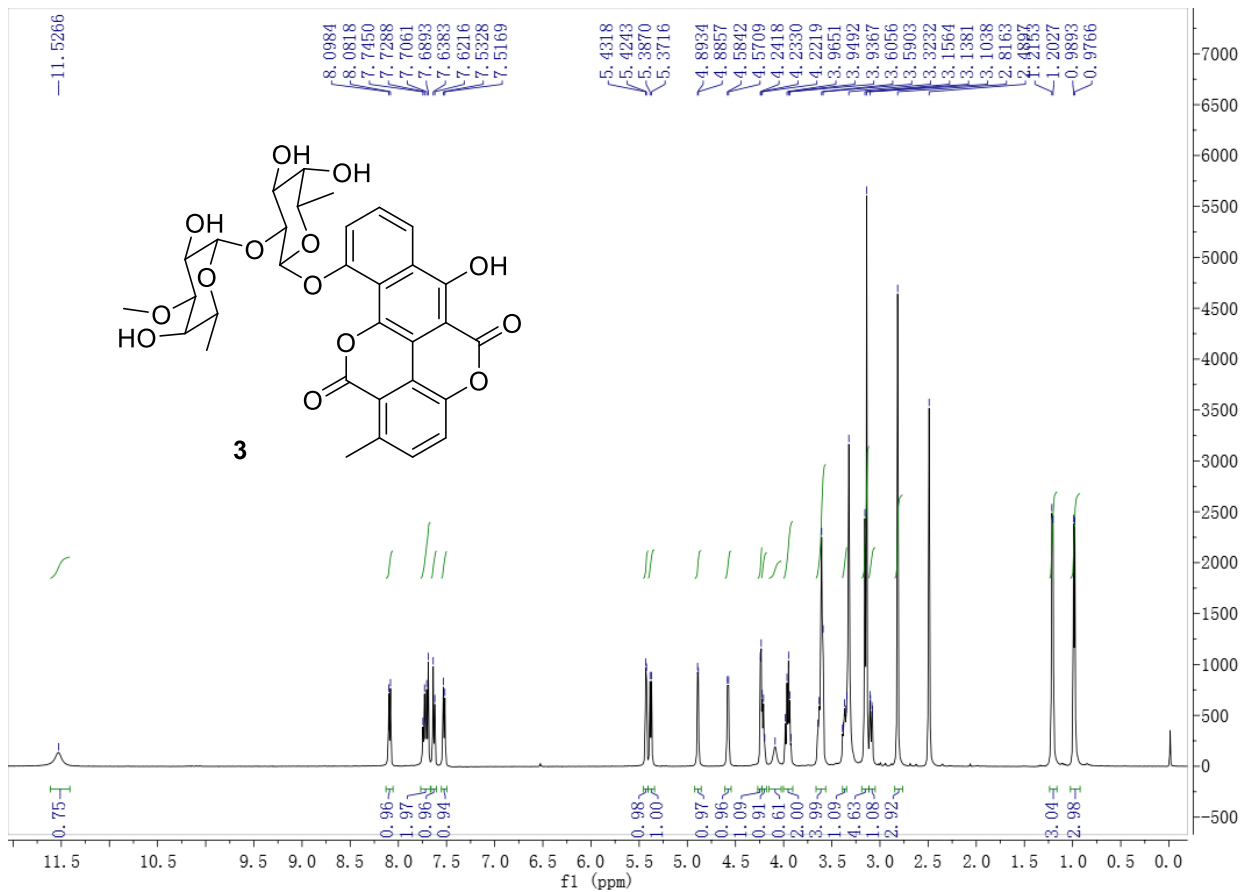


Figure S25. $^1\text{H NMR}$ (500 MHz, $\text{DMSO-}d_6$) spectrum of compound **3**.

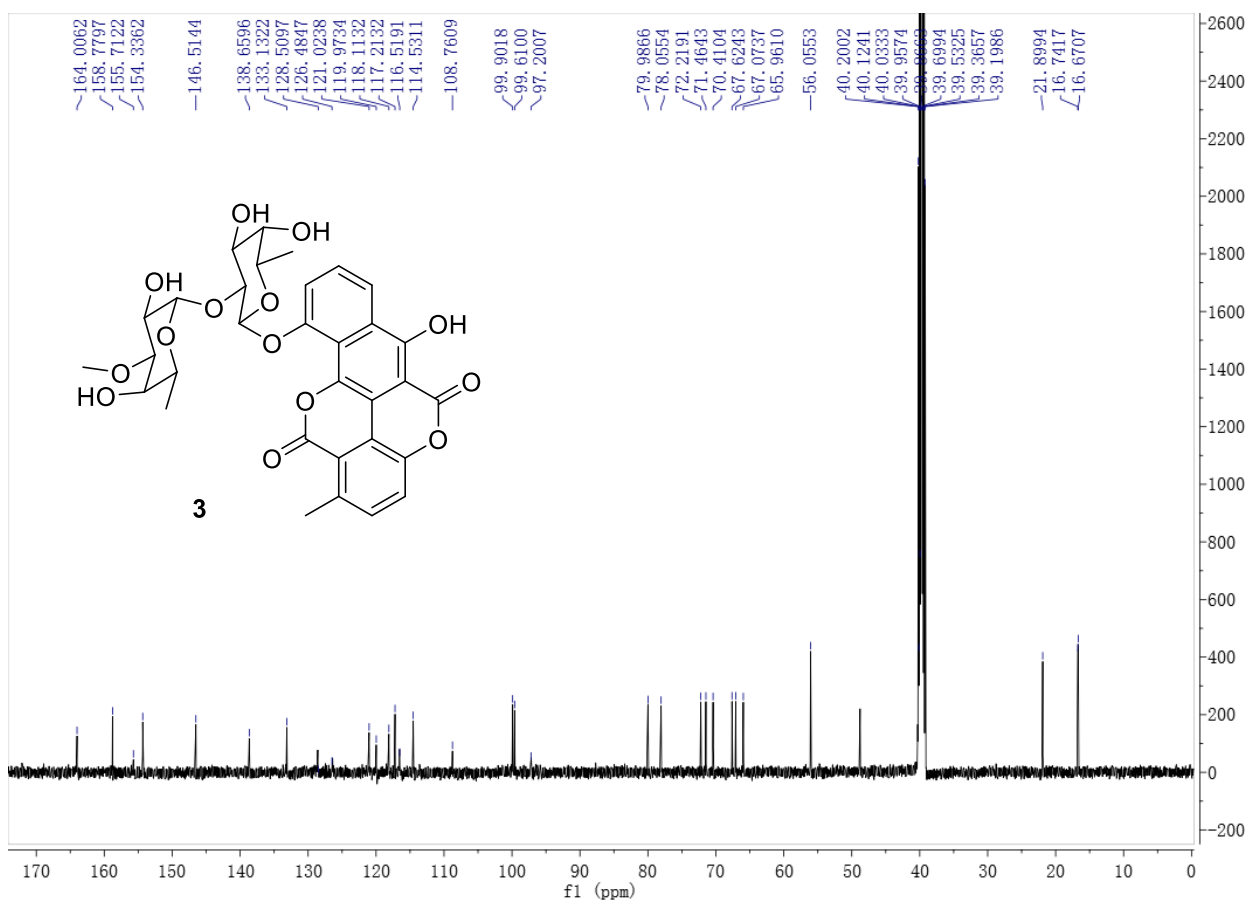


Figure S26. $^{13}\text{C NMR}$ (125 MHz, $\text{DMSO-}d_6$) spectrum of compound **3**.

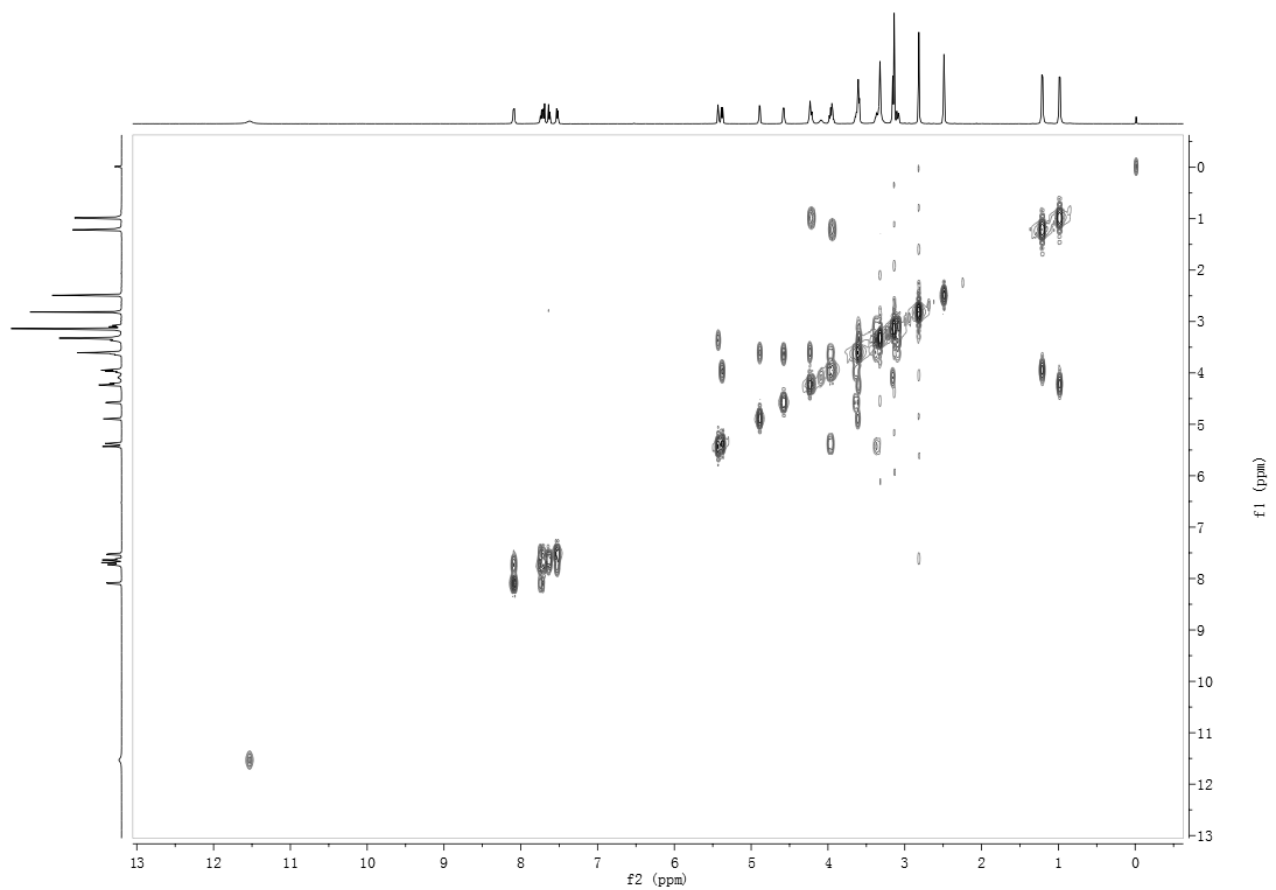


Figure S27. ¹H-¹H COSY (500 MHz, DMSO-*d*₆) spectrum of compound **3**.

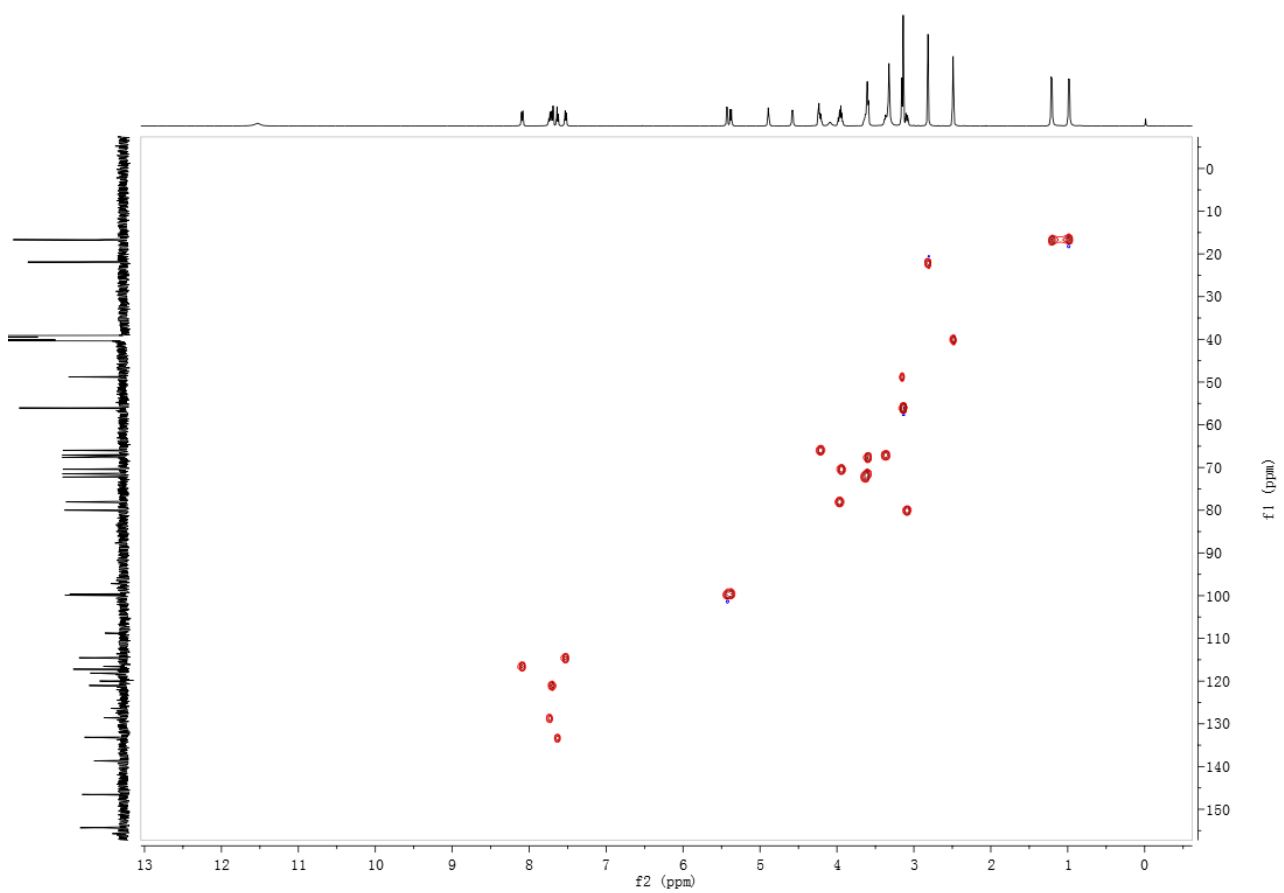


Figure S28. HSQC (500 MHz, DMSO-*d*₆) spectrum of compound **3**.

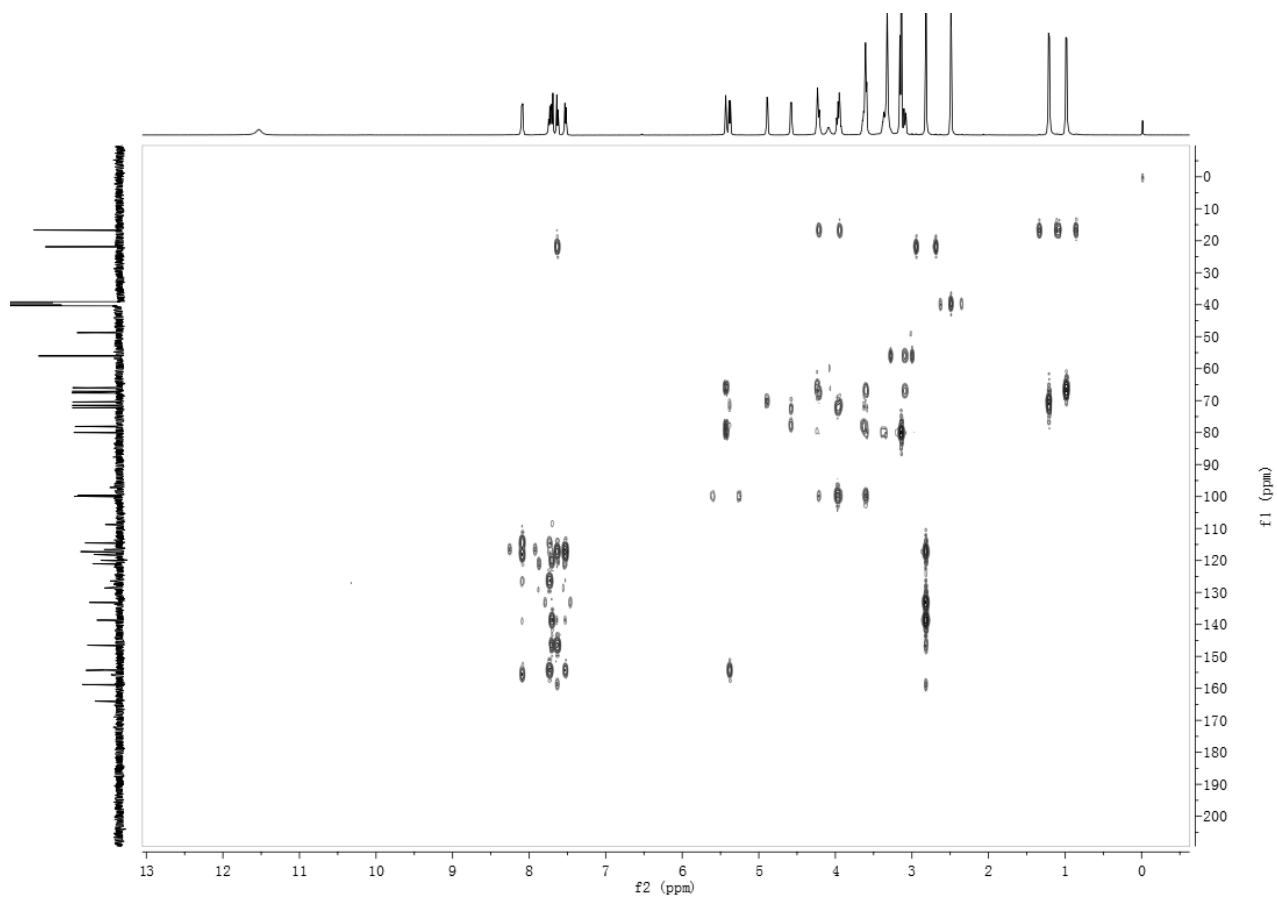


Figure S29. HMBC (500 MHz, DMSO- d_6) spectrum of compound 3.

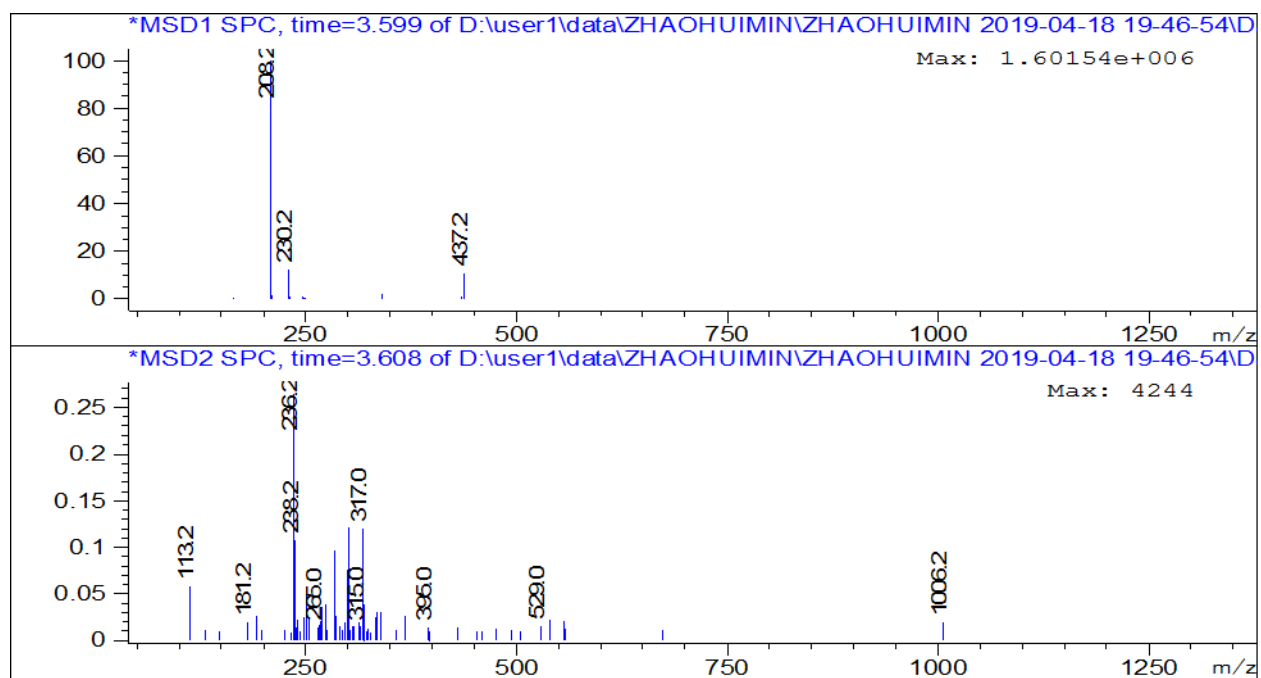


Figure S30. (+) and (-)-ESI-MS of compound 4.

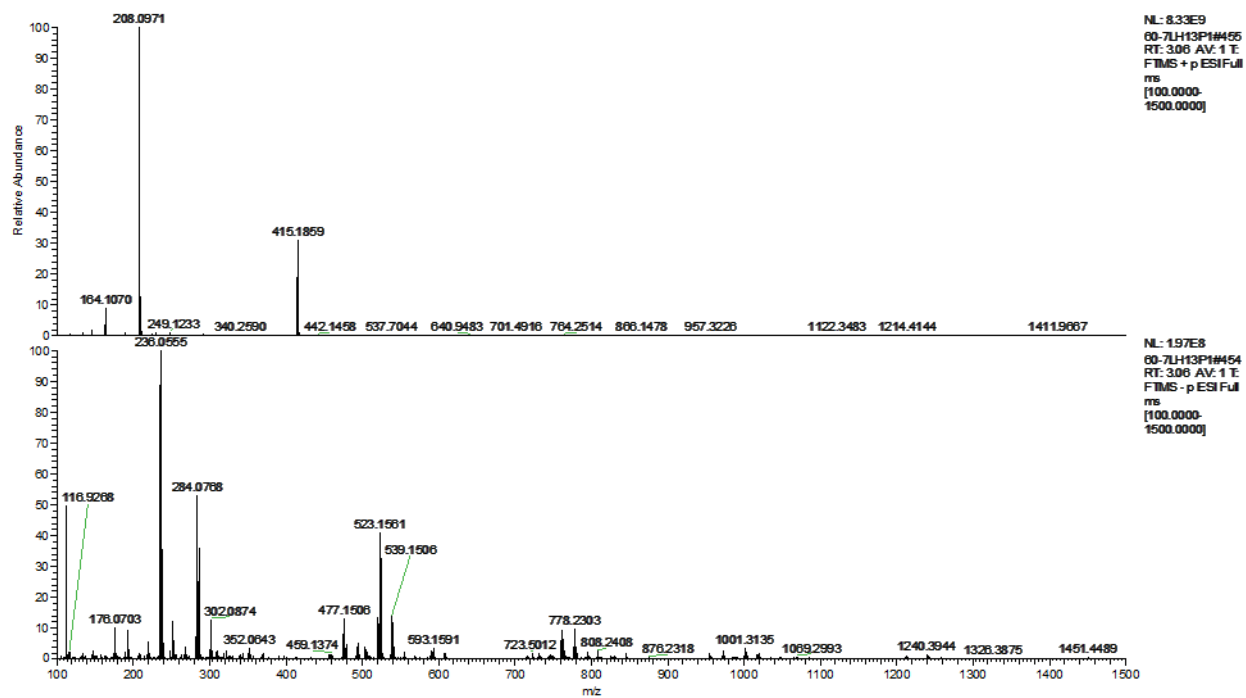


Figure S31. HRESI-MS spectrum of compound **4**.

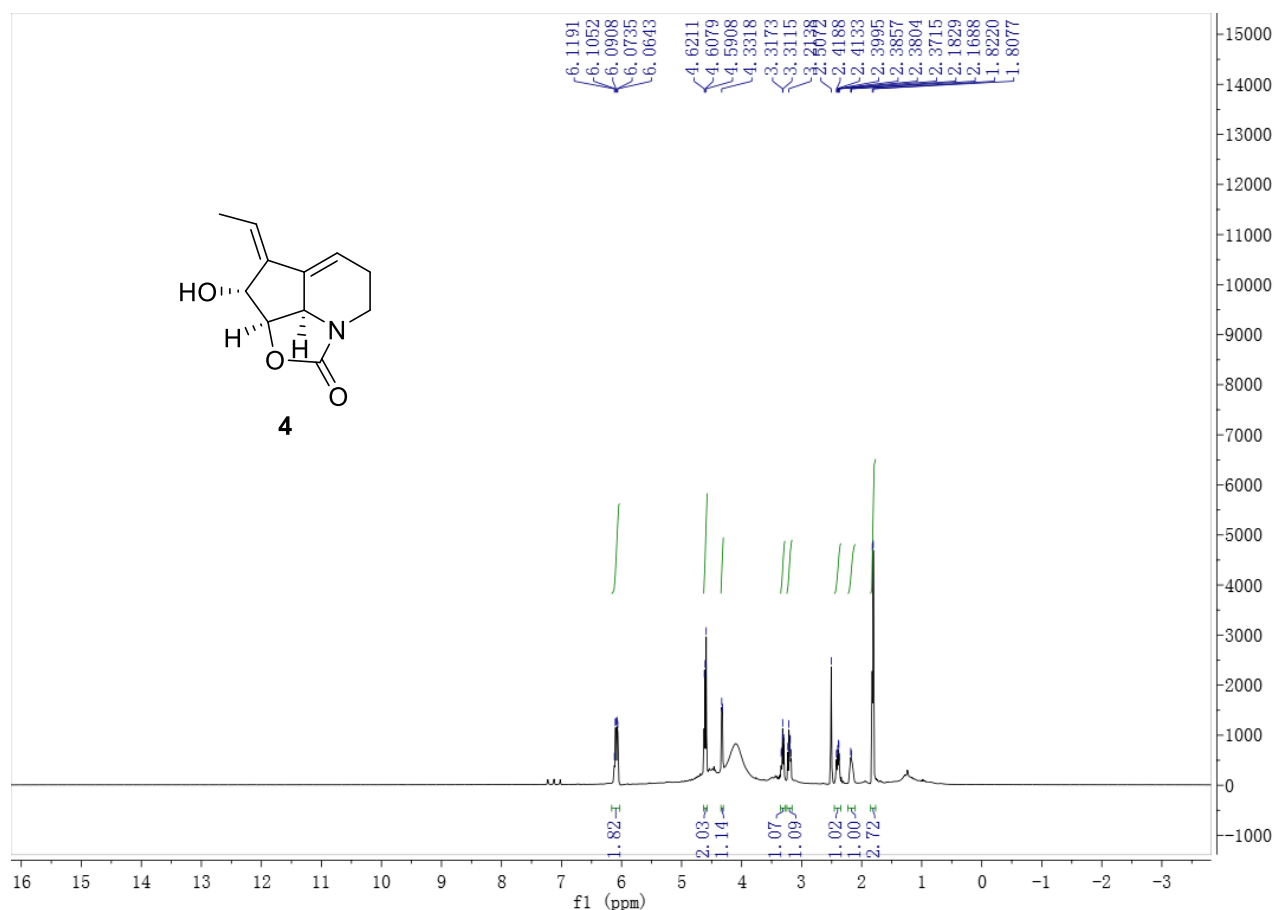


Figure S32. ^1H NMR (500 MHz, $\text{DMSO}-d_6$) spectrum of compound **4**.

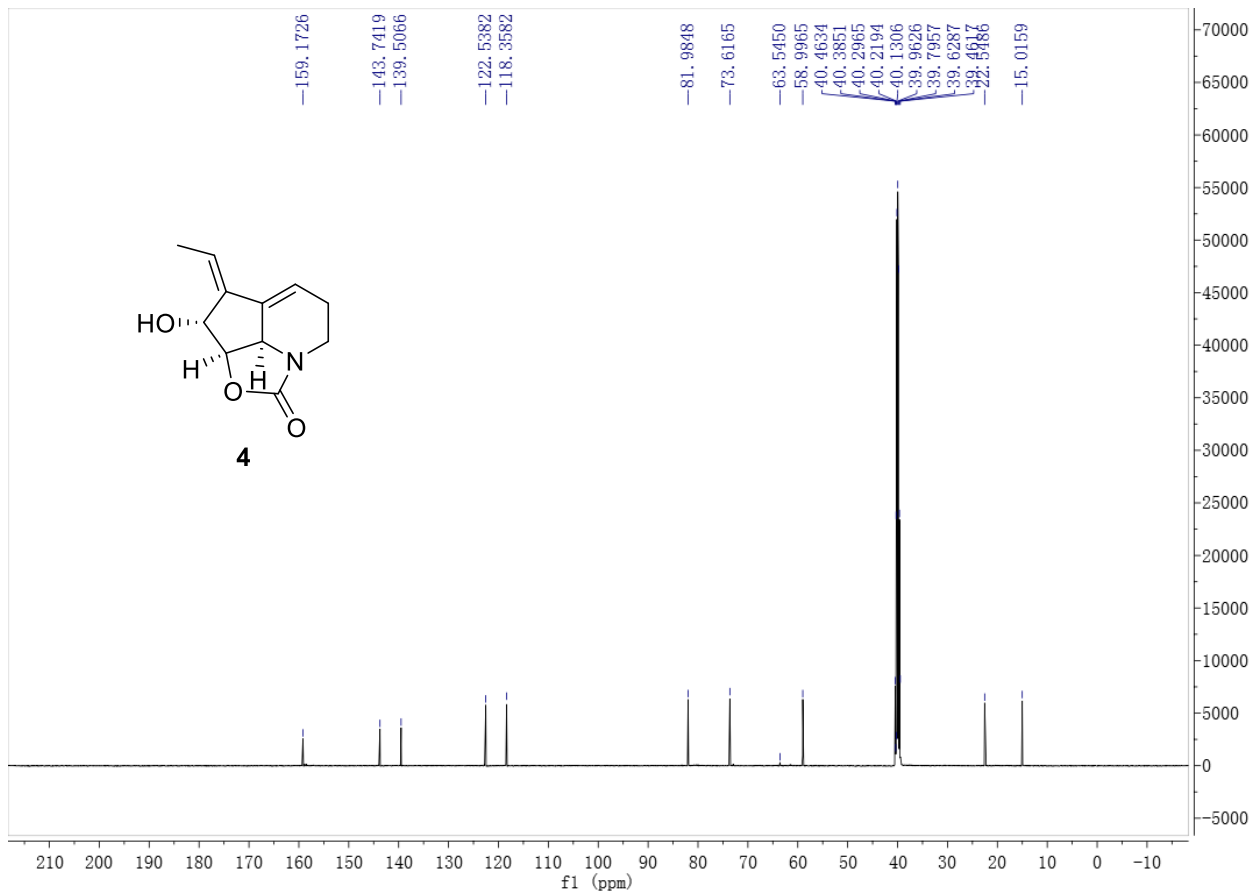


Figure S33. ^{13}C NMR (125 MHz, $\text{DMSO-}d_6$) spectrum of compound **4**.

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Different Inj Volume from Sample Entry! Actual Inj Volume : 1.000 µl
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Last changed : 5/27/2019 9:17:15 AM by SYSTEM

Current Mass Spectra

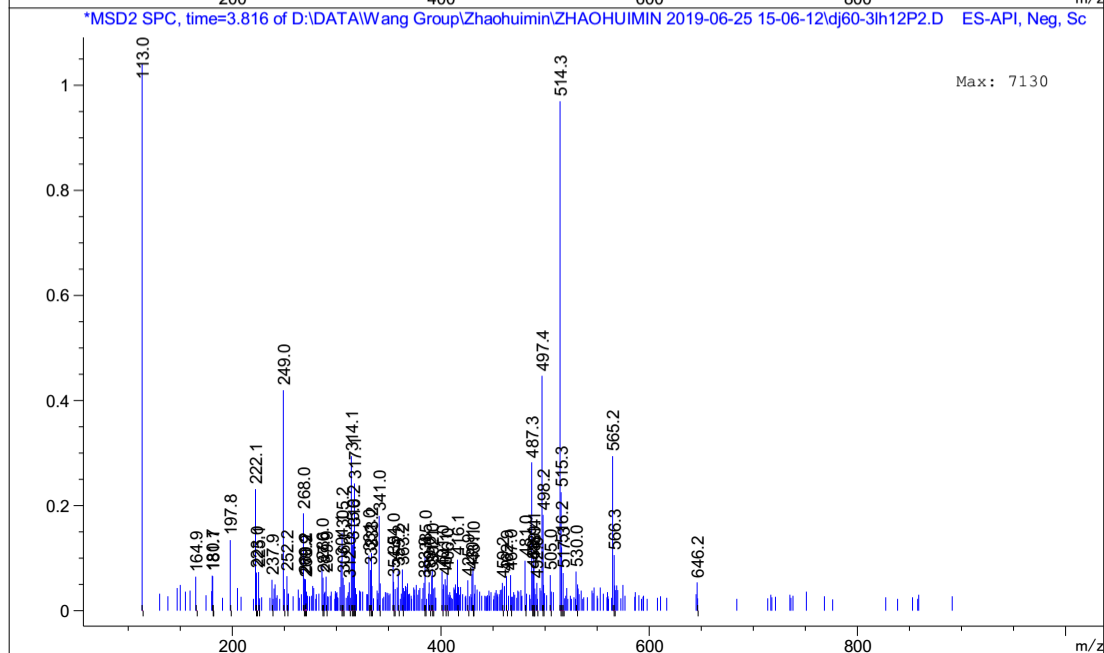
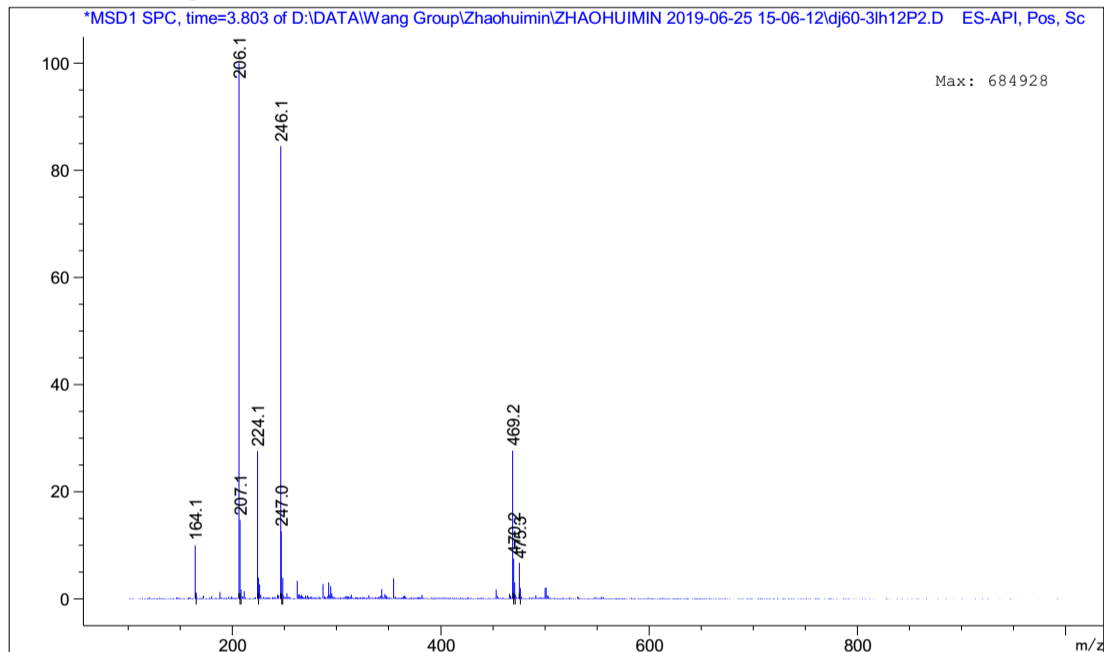


Figure S34. (+) and (-)-ESI-MS of compound 5.

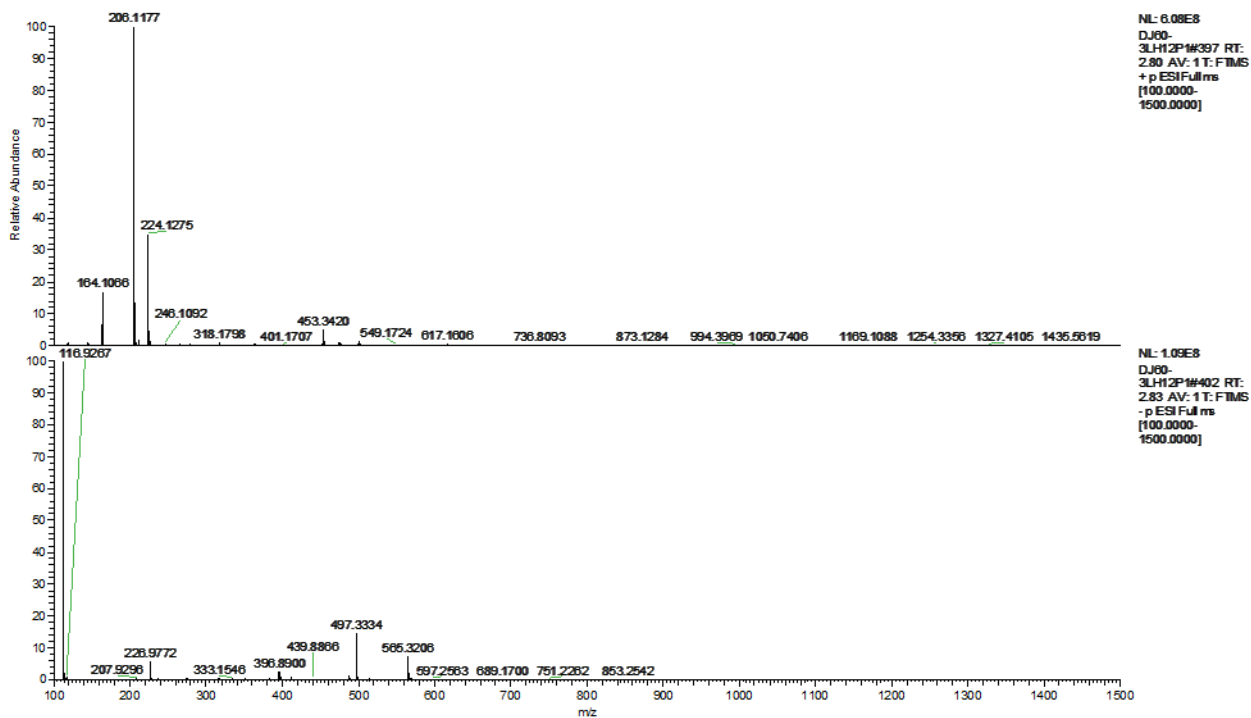


Figure S35. HRESI-MS spectrum of compound **5**.

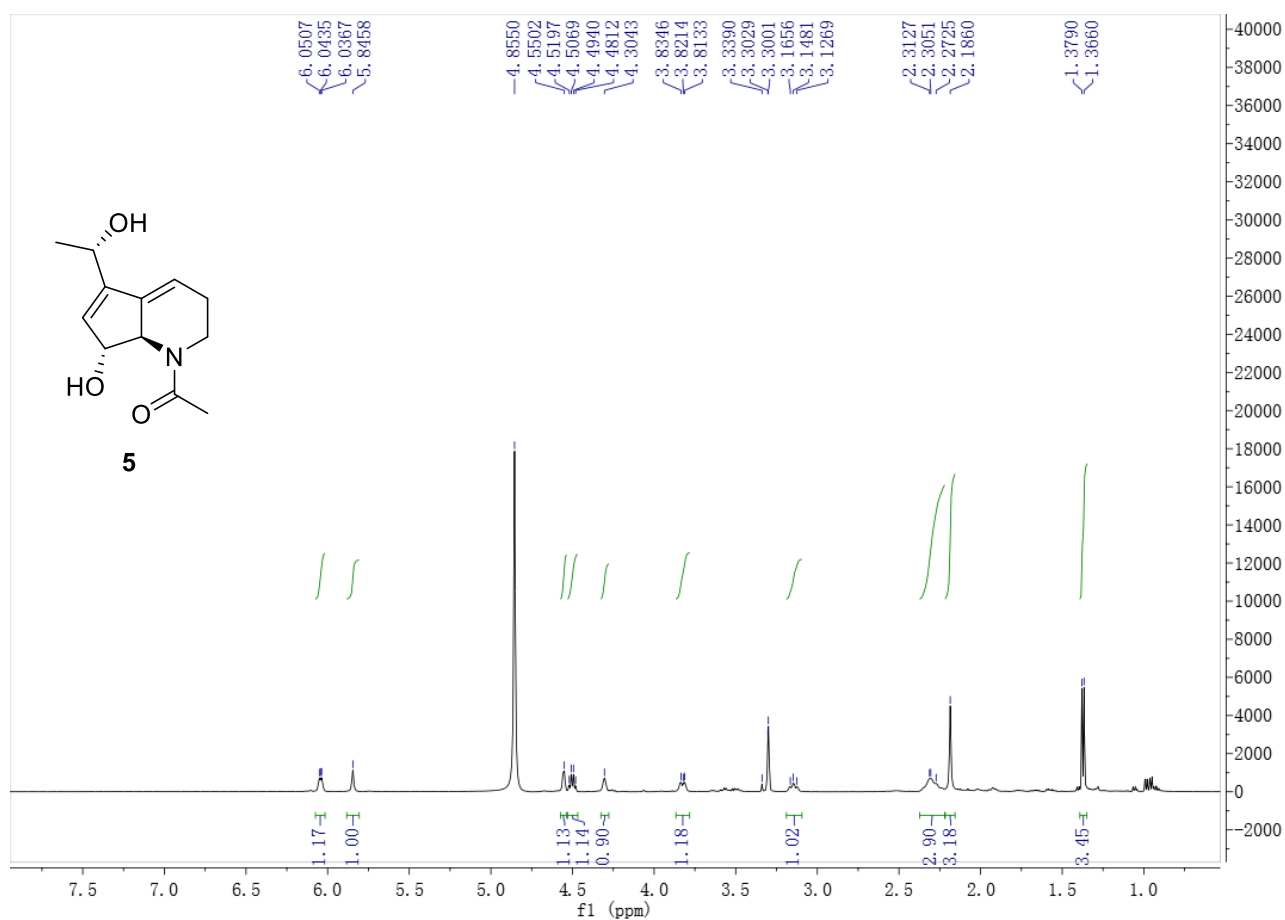


Figure S36. ^1H NMR (500 MHz, CDOD_3) spectrum of compound **5**.

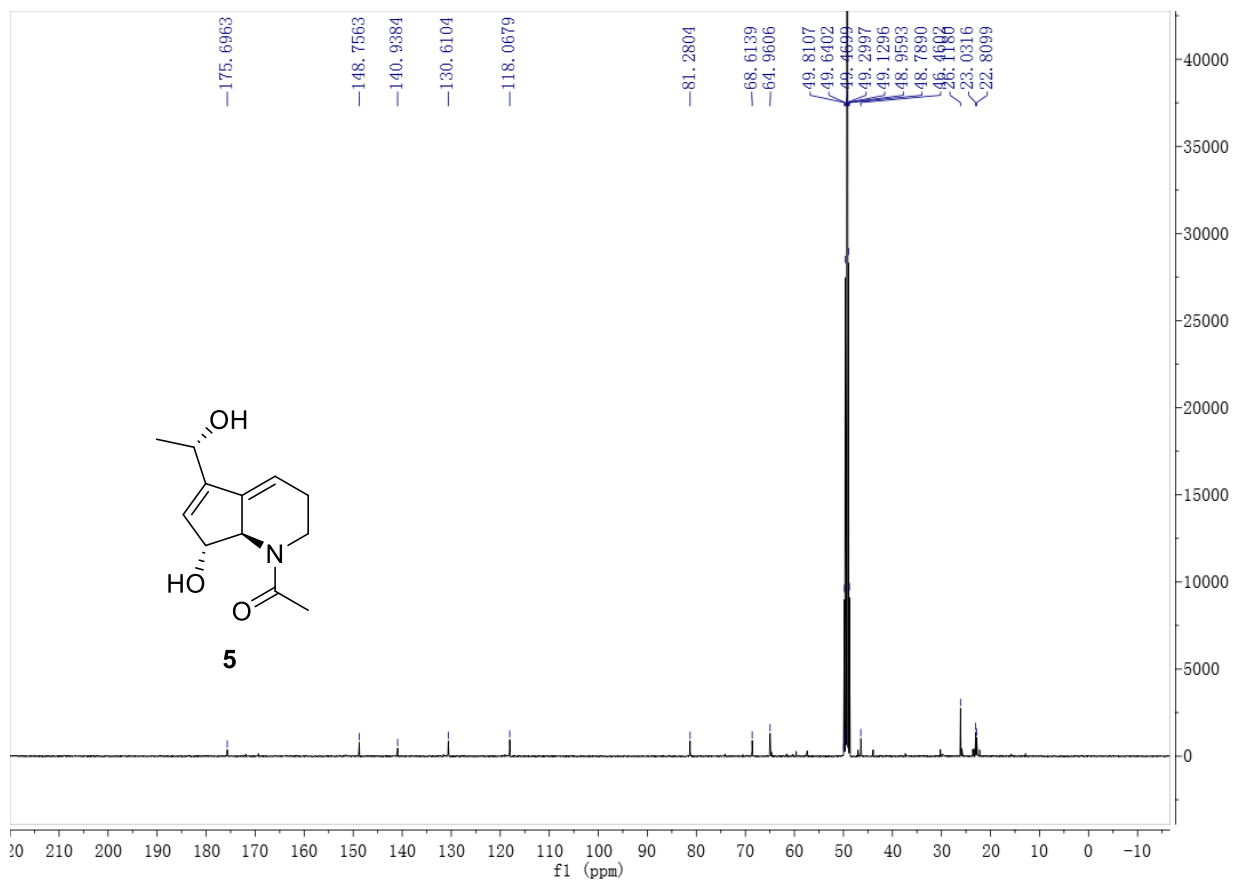


Figure S37. ¹³C NMR (125 MHz, CDOD₃) spectrum of compound **5**.

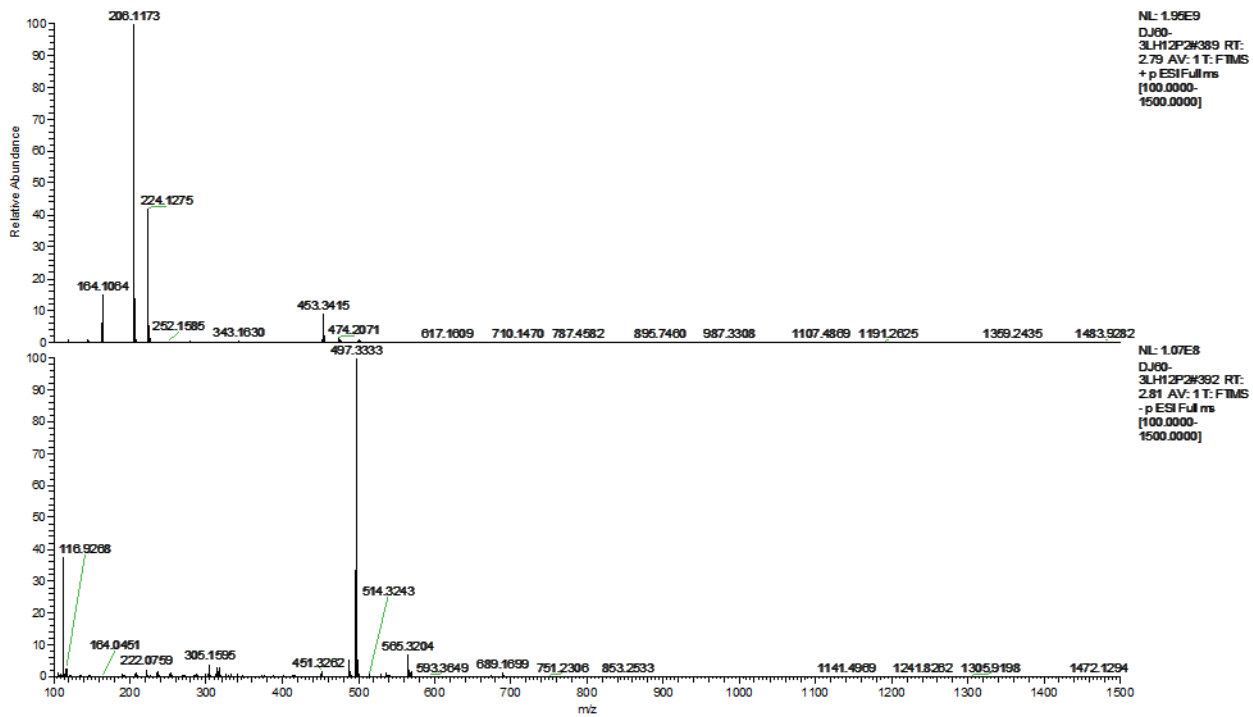


Figure S39. HRESI-MS spectrum of compound **6**.

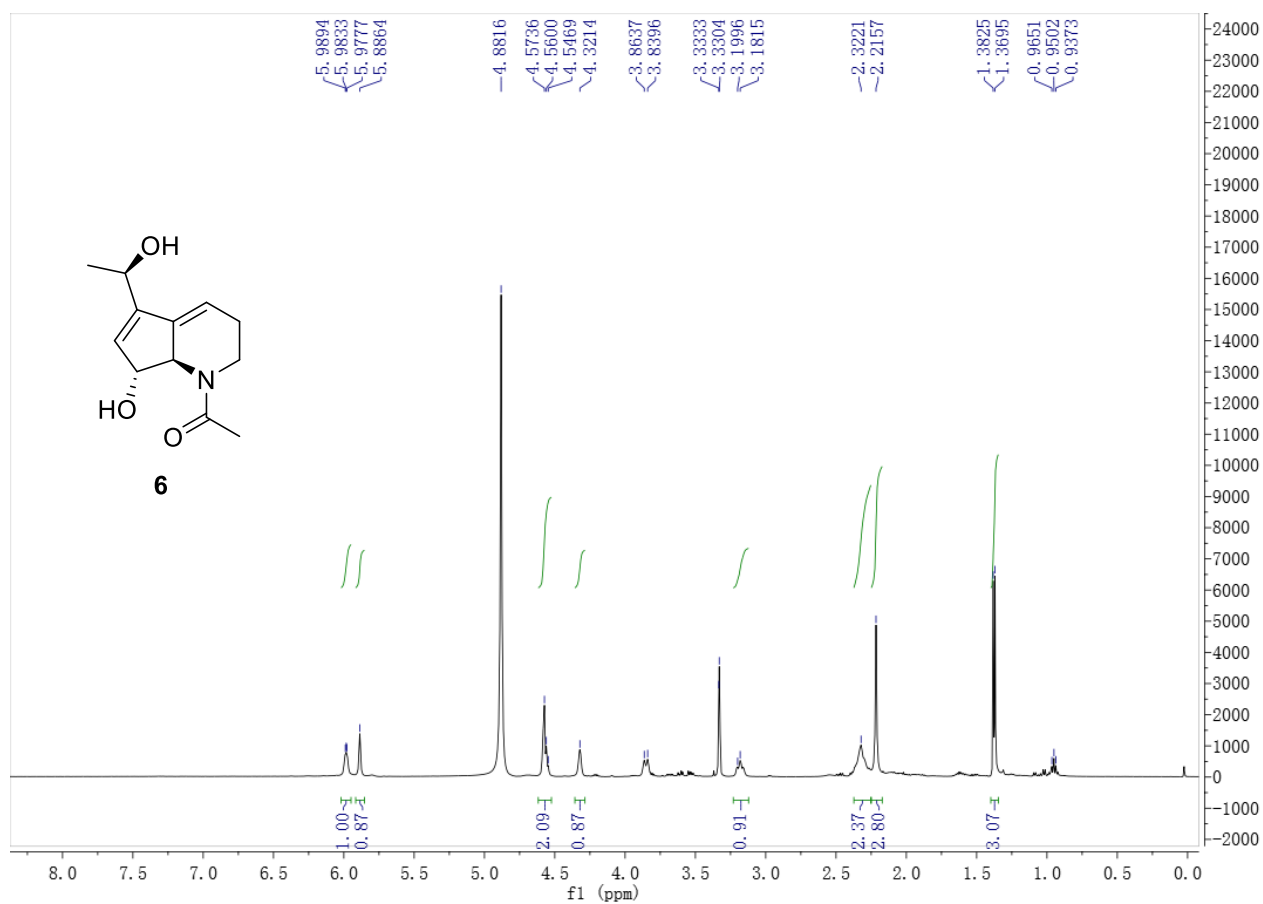


Figure S40. ^1H NMR (500 MHz, CDOD_3) spectrum of compound **6**.

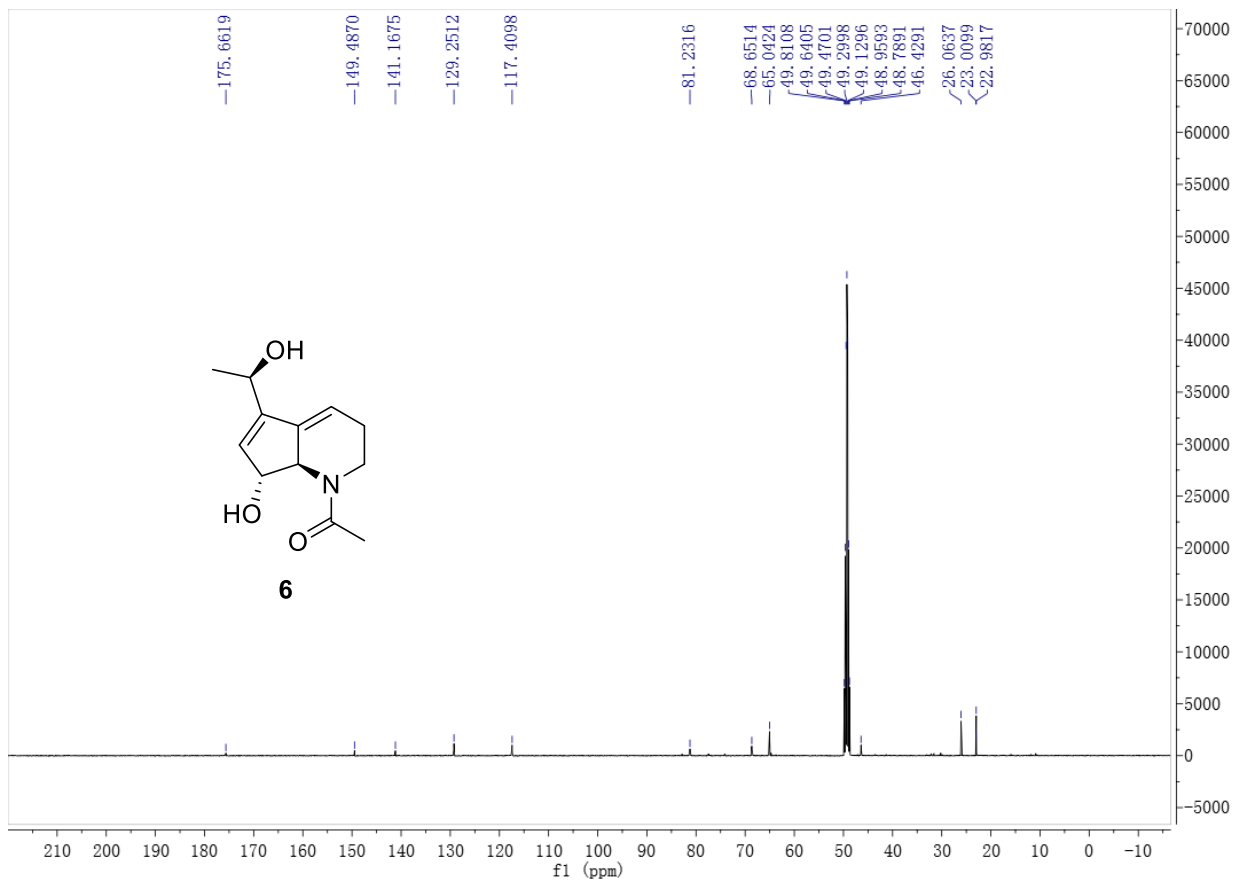


Figure S41. ¹³C NMR (125 MHz, CDOD₃) spectrum of compound **6**.

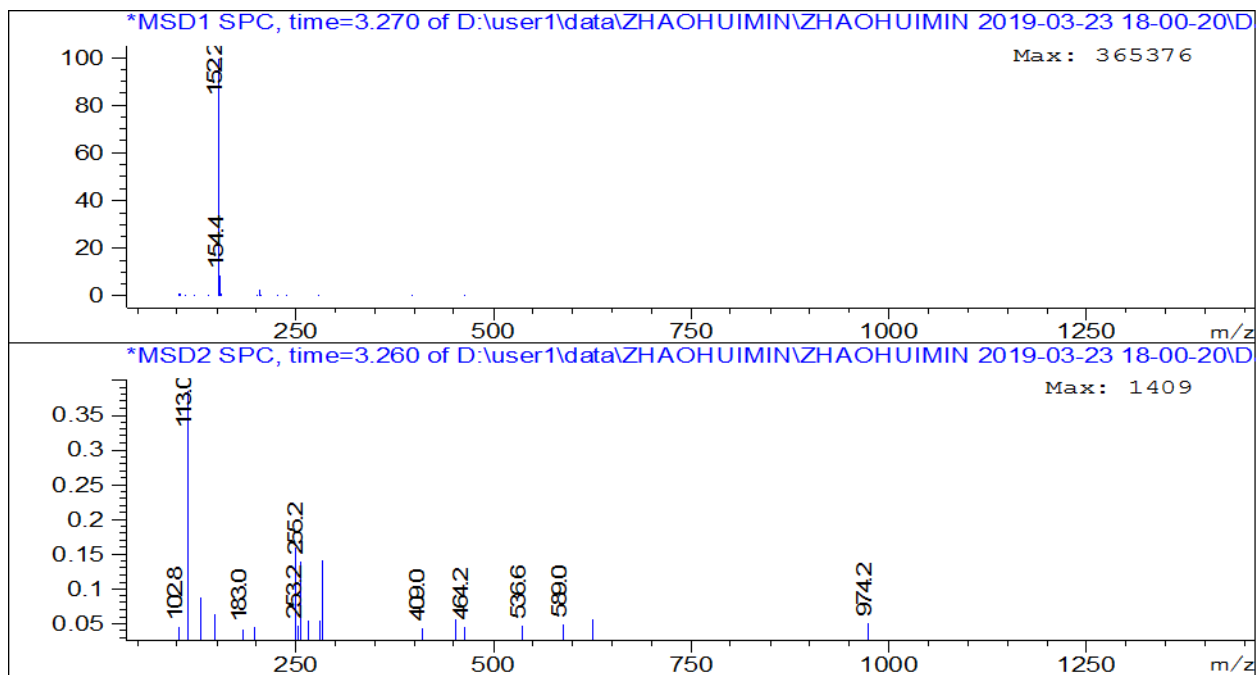


Figure S42. (+) and (-)-ESI-MS of compound **7**.

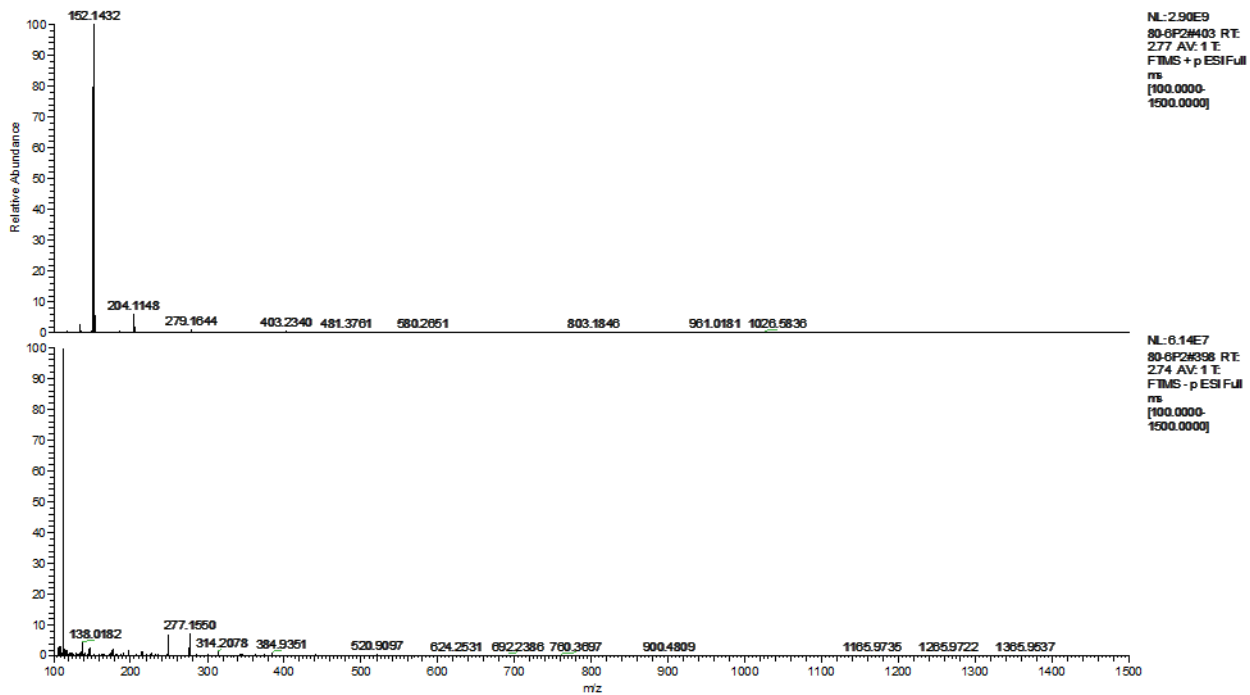


Figure S43. HRESI-MS spectrum of compound 7.

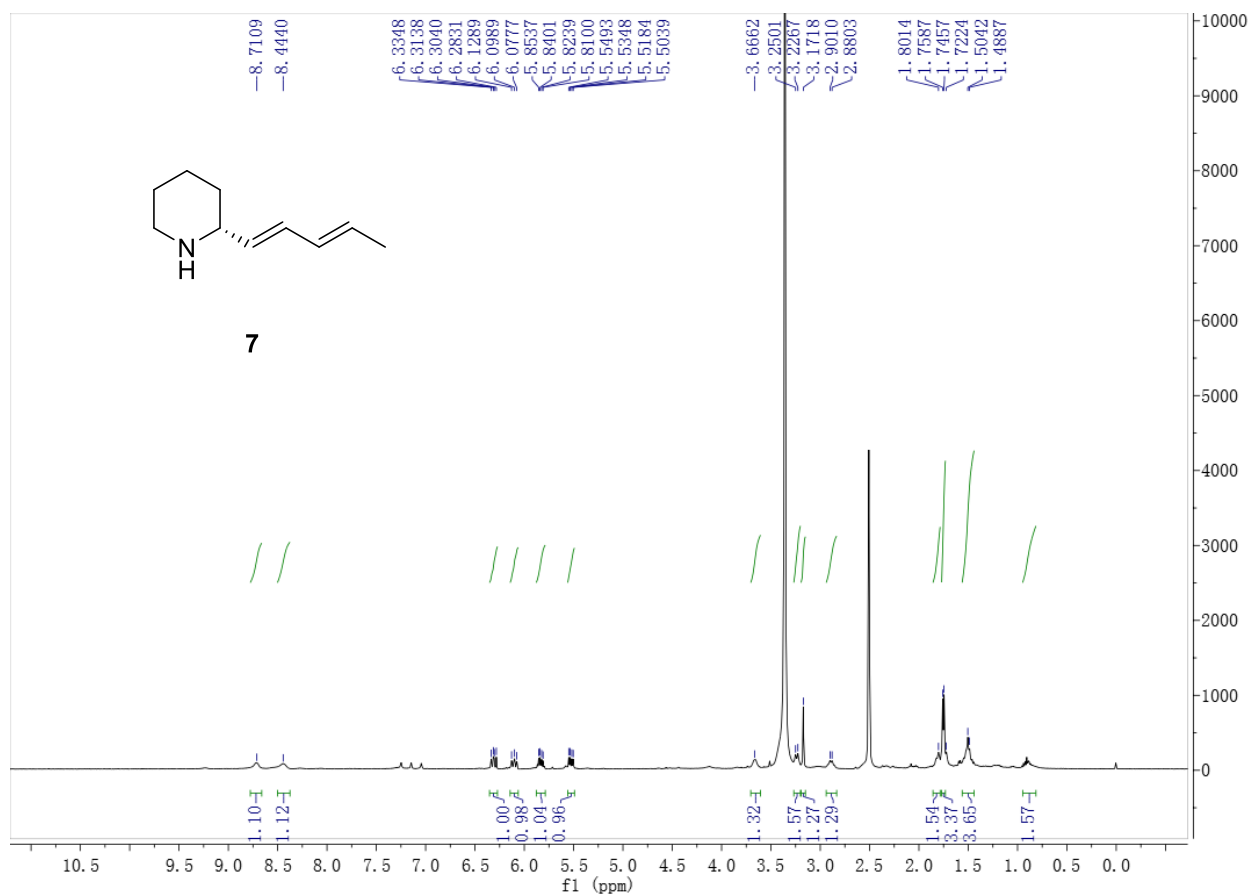


Figure S44. ^1H NMR (500 MHz, $\text{DMSO-}d_6$) spectrum of compound 7.

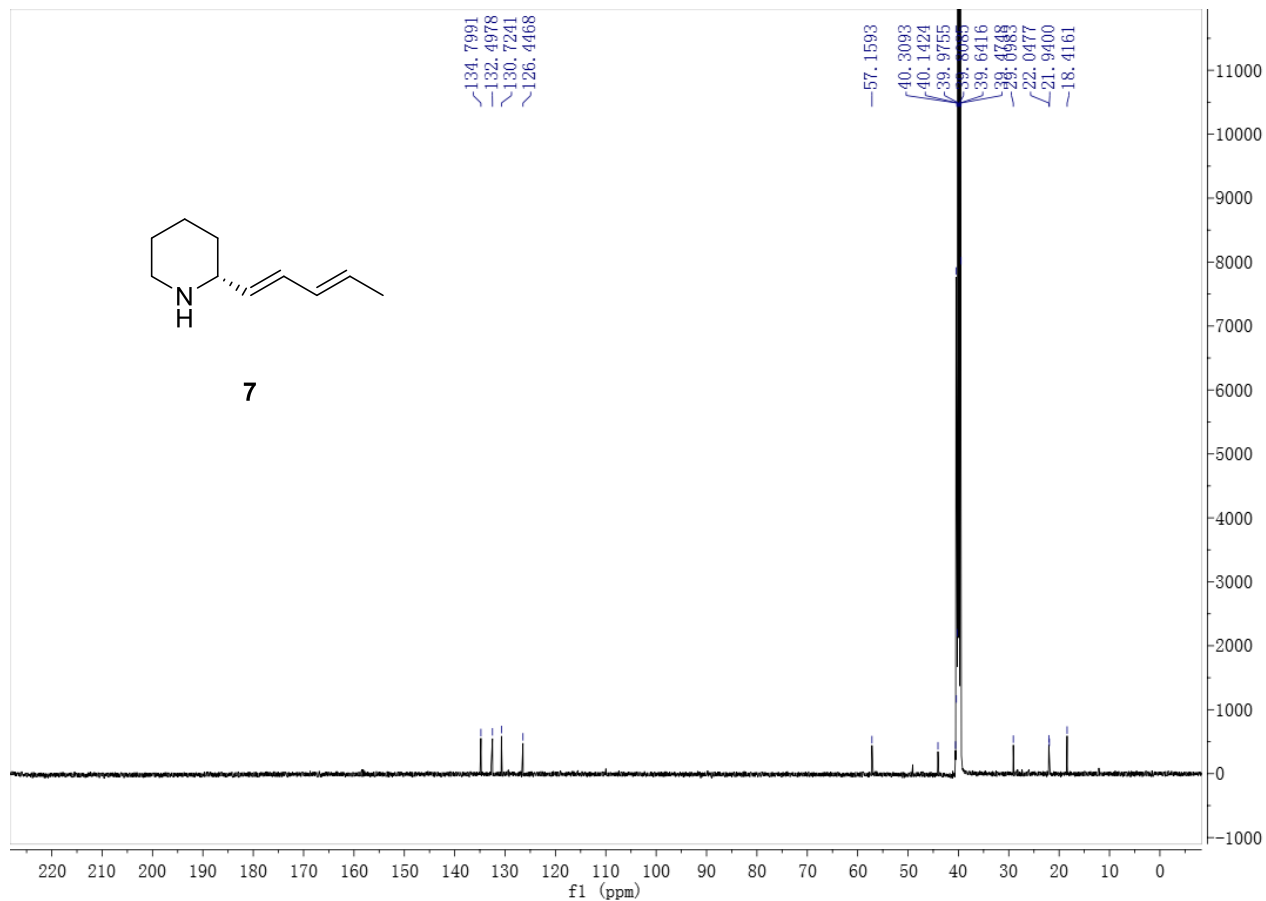


Figure S45. ^{13}C NMR (125 MHz, DMSO- d_6) spectrum of compound 7.