Supporting Information

Resveratrol Improves Fungal Ribosylation Capacity through a Unique Mechanism

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Structure Determination

Compound **1** was obtained as an amorphous white powder and was shown to possess a molecular formula of $C_{19}H_{20}O_7$ as determined by HR-ESI-MS (found: 383.1106, calcd.: 383.1101). The ^{1}H NMR and ^{1}H-^{1}H COSY spectra of **1** showed the presence of a 1,3,5 trisubstituted benzene ring [δ_H 6.67 (1H, br t, *J*=2.1 Hz, H-2), δ_H 6.57 (1H, br t, *J*=2.1 Hz, H-4), and δ_H 6.38 (1H, br t, *J*=2.1 Hz, H-6)], a *p*-substituted benzene ring [δ_H 7.40 (2H, d, *J*=8.8 Hz, H-2' and H-6') and δ_H 6.76 (2H, d, *J*=8.8 Hz, H-3' and H-5')] and a *trans* double bond [δ_H 6.87 (1H, d, *J*=16.4 Hz), H-7) and δ_H 7.00 (1H, d, *J*=16.4 Hz), H-8], suggesting the presence of a resveratrol moiety[1]. Additionally, a ribose residue was determined by comparing the its ^{1}H and ^{13}C NMR data with those of methyl ribofuranosides and asperflavin ribofuranoside.[1] The connection between the ribose and resveratrol was established by the key HMBC correlation from H-1″ (δ_H 5.54) to C-3 (δ_C 158.44). The sugar moiety was further determined as α-D-ribofuranose by comparison of the $J_{1'',2''}$ value (4.8 Hz) with those of the methyl-α-D-ribofuranoside $J_{1,2}$ (4.3 Hz) and methyl-D-ribofuranoside $J_{1,2}$ (1.2 Hz).[2] Thus, structure of **1** was demonstrated to be 3-*O*-α-D-ribosyl-resveratrol.

Compound **2** was obtained as an amorphous white powder, possessed the same formula as **1**. The ^{1}H NMR spectrum of **2** indicated that it was an isomer of **1**. The chemical shifts and coupling relationships of aromatic protons in **1** were almost identical to those of resveratrol, suggesting the 4-O-ribosylation, which was further supported by the HMBC correlation of H-1'' (δ 5.65) with C-4' (δ 158.1). The $J_{1'',2''}$ value (4.4 Hz) indicated the α configuration of C-1'. Thus, structure of **2** was clarified to be 4'-*O*-α-D-ribosyl-resveratrol.[2]

Compound **3**, a light yellow amorphous powder, had the molecular formula $C_{17}H_{20}O_9$, as determined by positive HR-ESI-MS (*m/z* 369.1177 $[M + H]^+$; calcd 369.1180). The ^{1}H NMR spectrum revealed a ribosyl residue evidenced from the anormeric proton at δ_H 5.54 (*J*=4.8 Hz) and five multiplets at δ_H 4.24, 4.17, 4.18 and 3.68 and 3.54. The ^{1}H NMR spectrum of **3** suggested that it was a riboside of orthosporin.[3] The ribosyl group was shown to anchor on C-6 (δ_C 165.5) by the HMBC correlation of this carbon with the anomeric proton (H-1′). Thus, the structure of **3** was established as 6-*O*-α-D-ribosyl-orthosporin.

Compound **4** was afforded as an amorphous light yellow powder. Its molecular formula was determined to be $C_{17}H_{20}O_8$ according to the protonated molecular ion at *m/z* 353.1239 (353.1236 calcd. for $C_{17}H_{21}O_8$) in its HR-ESI-MS. The ^{1}H NMR spectrum of compound **4** showed resonances assignable to a pair of *meta*-coupled aromatic protons at δ_H 6.67 (1H, d, J = 2.0 Hz, H-8) and 6.47 (1H, d, J = 2.0 Hz, H-6), a separate olefinic proton at δ_H 6.13 (1H, s, H-3), a set of protons for propyl vinyl moiety at δ_H 2.66 (2H, t, J = 7.6 Hz, H-11), 1.79 (2H, qt, J = 7.6 Hz, H-12) and 1.01 (3H, t, J = 7.4 Hz, H-13). The ^{1}H and ^{13}C NMR data of **4** were similar to those of 5,7-dihydroxy-2-propylchromone 7-*O*-β-D-glucopyranoside,[4] but their sugar moieties were different. As in case of **2**, the signals between δ_H 3.6 and 5.8 indicated the presence of a ribose residue. Similarly, the $J_{1',2'}$ value (4.4 Hz) demonstrated an α-configuration of the anormeric carbon (C-1'). Thus, structure of **4** was elucidated as 7-*O*-α-D-ribosyl-5-hydroxy-2-propylchromone.

Compound **5**, a light yellow amorphous powder, had the molecular formula $C_{15}H_{20}O_8$, as determined by its HR-ESI-MS (*m/z* 329.1230 $[M + H]^+$; calcd. 329.1231). The ^{1}H NMR spectrum of **5** indicated a 1,2,3,5-tetrasubstituted benzene ring (displaying two-protons singlets at δ_H 6.16), a propyl moiety at δ_H 3.07 (2H, t, J = 7.2 Hz, H-8), 1.68 (2H, qt, J = 7.2 Hz, H-9) and 0.92 (3H, t, J = 7.2 Hz, H-10) and a set of protons assignable for an α-D-ribosyl residue. The ^{1}H NMR signals due to benzene and propyl moieties resembled those of phlorobutyrophenone, and the symmetry of benzene ring suggested the ribosyl group was anchored on C-4. Thus, the structure of **5** was assigned as 4-*O*-α-D-ribosyl-phlorobutyrophenone.[5]

Experimental Procedures

Chemicals: Resveratrol, UDP, NAD, NMN, AMP and ADP were purchased from Aladdin. SDS was purchased from Sangon Biotech.

NMR Spectroscopy: The ^{1}H and ^{13}C NMR spectra were acquired on a Bruker Advance 400 MHz or a Bruker DRX 500 MHz NMR spectrometers equipped with a 5 mm probe head.

Phylogenetic Analysis: To identify the pgps subfamily of *Daldinia eschscolzii*, sequences of ABC transporter proteins[6] representing different subfamilies were selected (Table S4) and aligned with

*pgp*3, 6, 7 11using Clustal W.[7] A phylogenetic tree was then constructed with the alignment by the MEGA program (version 5.10) and the neighbor-joining method (Figure S1).[8]

References

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Supplementary Figures

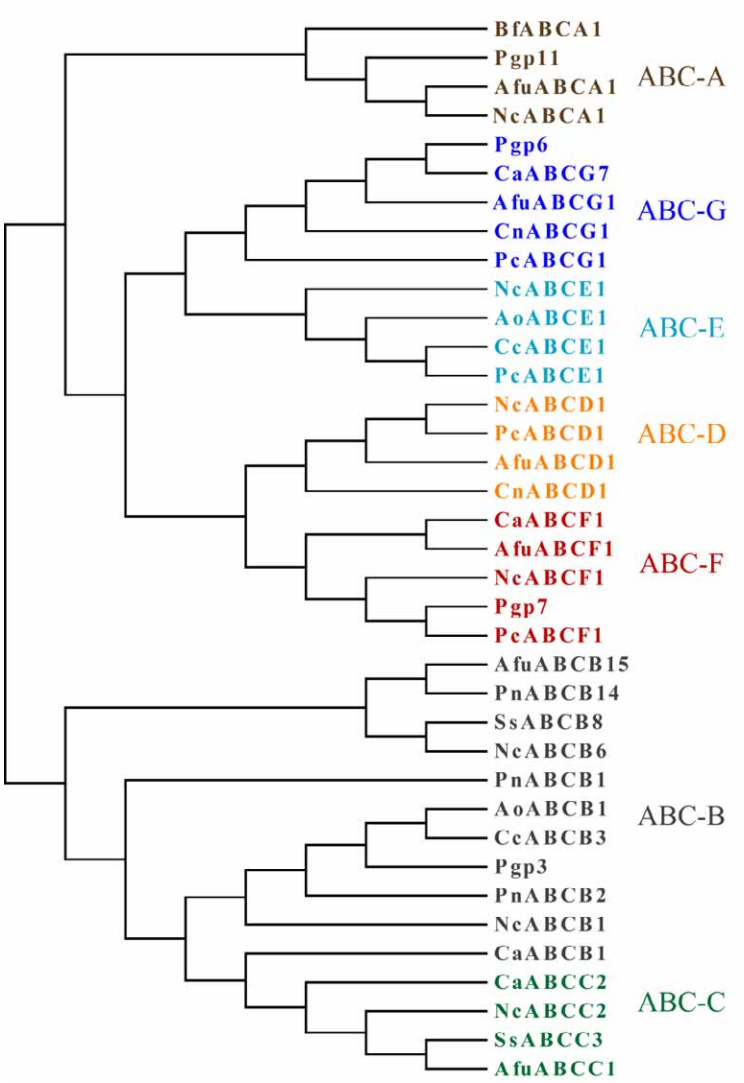


Figure S1. Phylogenetic tree of fungal ABC transporter proteins. Pgps in *D. eschscholzii* and other homologous ABC transporter proteins (details in Table S3) were aligned with Clustal W.[7] The phylogenetic tree was subsequently generated using the neighbour-joining method with MEGA 5.10[8] software package.

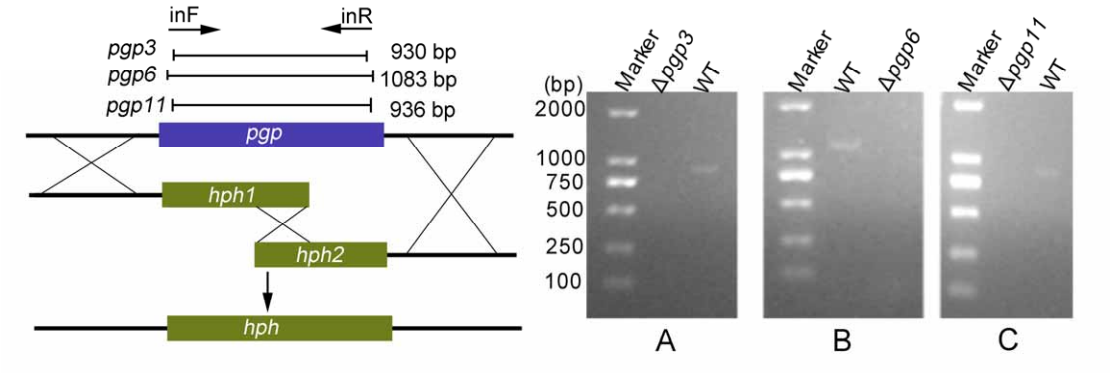


Figure S2. PCR confirmation of deletions of (A) *pgp3*, (B) *pgp6*, and (C) *pgp11* in *D. eschscholzii*. The primers (inF and inR) used for PCR analysis are list in Table S2. *pgp*, p-glycoprotein gene; *hph*, hygromycin phosphotransferase gene; Δ*pgp3*, the strain with *pgp3* gene deleted; Δ*pgp6*, the strain with *pgp6* gene deleted; Δ*pgp11*, the strain with *pgp11* gene deleted; WT, wild-type strain.

Supplementary Tables

Table S1. ^{1}H and ^{13}C NMR data of 1 and 2.

position	**1** [a]		**2** [b]	
	δ_C	δ_H (mult. *J* in Hz)	δ_C	δ_H (mult. *J* in Hz)
1	139.7		140.5	
2	106.3	6.67 (s)	105.7	6.55 (d, 2.4)
3	158.4		159.6	
4	103.0	6.38 (t, 2.0)	102.8	6.27 (t, 2.4)
5	158.9		159.6	
6	107.2	6.57 (s)	105.7	6.55 (d, 2.4)
7	125.8	6.87 (d, 16.4)	128.2	6.94 (d, 16)
8	128.4	7.00 (d, 16.4)	128.6	7.05 (d, 16)
1’	128.9		132.2	
2’	128.4	7.40 (d, 8.8)	128.4	7.51 (d, 8.8)
3’	116.0	6.76 (d, 8.4)	118.0	7.10 (d, 8.4)
4’	158.0		158.1	
5’	116.0	6.76 (d, 8.4)	118.0	7.10 (d, 8.4)
6’	128.4	7.40 (d, 8.8)	128.4	7.51 (d, 8.8)
5-OH		9.58 (s)		
4’-OH		9.42 (s)		
1’’	100.8	5.54 (d, 4.8)	101.9	5.65 (d, 4.4)
2’’	71.9	4.04 (m)	73.0	4.23 (4.4, 6.4)
3’’	69.8	3.92 (m)	70.9	4.15 (m)
4’’	86.5	3.97 (m)	87.7	4.16 (m)
5’’	62.1	3.48 (d, 4.0)	62.1	3.66 (d, 4.0)
2’’-OH		4.61 (d, 8.4)		
3’’-OH		4.85 (d, 5.2)		
5’’-OH		4.78 (t, 5.2)		

[a] In DMSO-d_6 at 400 MHz. [b] In acetone-d_6 at 500 MHz. [c] In acetone-d_6 at 400 MHz.

Table S2. ^{1}H and ^{13}C NMR data of 3−5 (400 MHz, acetone-d_6**).**

position	**3**		**4**		**5**
	δ_C	δ_H (mult. *J*)	δ_C	δ_H (mult. *J*)	δ_H (mult. *J*)
1	167.1				
2			171.9		
3	156.6		108.7	6.13 (s)	6.16 (s)
4	106.6	6.52 (s)	183.3		
5	104.3	6.67 (d, 2.0)	162.4		6.16 (s)
6	165.5		100.8	6.47 (d, 2.0)	
7	103.3	6.63 (d, 2.0)	164.0		
8	163.8		95.7	6.67 (d, 2.0)	3.07 (t, 7.2)
9	101.1		158.6		1.68 (qt, 7.2)
10	140.6		106.3		0.96 (t, 7.2)
11	43.7	2.60 (dd, 7.2, 14.4)	36.4	2.66 (t, 7.6)	
		2.64 (dd, 5.6, 14.4)			
12	65.5	4.18 (m)	20.8	1.79 (qt, 7.6)	
13	23.5	1.24 (d, 7.0)	13.7	1.01 (t, 7.6)	
1’	101.3	5.80 (d, 4.4)	101.5	5.78 (d, 4.4)	5.67 (d, 4.4)
2’	73.0	4.24 (dd, 4.8, 7.0)	73.1	4.29 (m)	4.22 (m)
3’	70.7	4.17 (m)	70.7	4.17 (m)	4.12 (m)
4’	88.3	4.18 (m)	88.3	4.19 (m)	4.13 (m)
5’	62.8	3.68 (dd, 3.6, 12.0)	62.9	3.70 (dd, 3.6, 12.0)	3.68 (dd, 3.6, 12.0)
		3.64 (dd, 3.6, 12.0)		3.66 (dd, 3.6, 12.0)	3.63 (dd, 3.6, 12.0)

Table S3. Primers used in this paper.

Primers for qRT-PCR	
Pgp1F	5’-AGTCTGAAAGTTGCCGAGAT-3’
Pgp1R	5’-CGTAGAACGTGAGTTGGGAG-3’
Pgp2F	5’-TGCTGGCTATGTACCTGACG-3’
Pgp2R	5’-CTAGCATAATTTGGCCGTGA-3’
Pgp3F	5’-CTGGTTAGTGCGACCCTCTG-3’
Pgp3R	5’-CTCTGCTTCCGCCTCTATGT-3’
Pgp4F	5’-GAGTTCATTTCTTCCCTTCC-3’
Pgp4R	5’-TACTGCGATTGTGATTCTGT-3’
Pgp5F	5’-CAGGGCTCTTCAGGGTCGTA-3’

Pgp5R	5’-TGTCGGGAGTAATAGGCACA-3’
Pgp6F	5’-AGTCCCATTCTTACCCTATT-3’
Pgp6R	5’-AACCGTTGTCTCATTTCATT-3’
Pgp7F	5’-ATCCCTGTTATTTCCGAGTC-3’
Pgp7R	5’-CCATCAGAGCCAAAGTAGGT-3’
Pgp8F	5’-TCGGCTGTGAAGCGATTAGA-3’
Pgp8R	5’-TGAGTATCCTCGGGCTGGTT-3’
Pgp9F	5’-GCAGGTGACAGGCTACAAGG-3’
Pgp9R	5’-GCGAAAGATAGACCGAAACG-3’
Pgp10F	5’-CCGTGCGGAGGGAGTGAC-3’
Pgp10R	5’-CGGGACGAGATGGGTAGG-3’
Pgp11F	5’-TCTACTTGCCGACCAT-3’
Pgp11R	5’-CTGCTGACTCAAGGGA-3’
Pgp12F	5’-GTCCATTCCTCCGCTACTTT-3’
Pgp12R	5’-ACTCGGGTATTCACATCCTG-3’
AT1F	5’-TCCTCTGCGAAGCGGAACT-3’
AT1R	5’-CACCCTTTAACGATGGATGAAC-3’
AT2F	5’-TTCGGCGAGCCTCTATTC-3’
AT2R	5’-TCGTCTATCGGCGTGTCC-3’
AT3F	5’-CCGACTGTGCTCTAATCTC-3’
AT3R	5’-CTGGATGCTCCCTGGTAA-3’
AT4F	5’-CGACCACGACCGACTACAA-3’
AT4R	5’-TCACCGCGATTTCCTTCT-3’
AT5F	5’-GGCAAGGCATCCAAAGCT-3’
AT5R	5’-CTCGCCAACCTCCTCCAC-3’
AT6F	5’-CCGCCGTATCAACAAGCC-3’
AT6R	5’-CATCCCAAGAAACGCCTA-3’
PT1F	5’- GCCTTACGGTTCGGGTCT-3’
PT1R	5’- TCAGCCAGTTCGCTTGTG-3’

PT2F	5’-AGAGTCGAGCGCCTATCT-3’
PT2R	5’-GCAAGGTTCTCCCTAATCC-3’
PT3F	5’-CCTGCTAAACAACGAACTAC-3’
PT3R	5’-CTTCCTTCCAACGACCAC-3’
PT4F	5’-TACCTGACTTCCCTATTCCC-3’
PT4R	5’-GCTTCCAGACCCACTATGA-3’
PT5F	5’-CGAATGGTTTATGGGTATT-3’
PT5R	5’-TTGAGGCGGTATGTTTGG-3’
PT6F	5’-AAAGCCCATCGCTACTGT-3’
PT6R	5’-TCAGCCCTTCCTCAACAA-3’
PT7F	5’-TTTACCTGGCTCTATGGG-3’
PT7R	5’-CTCGCTGTCGCTATCTGT-3’
PT8F	5’-ACCTATTGGAGGGTGCTG-3’
PT8R	5’-TGGTCGTATCCCGTTATT-3’
PT9F	5’-CCCCAACATCCCTATTCA-3’
PT9R	5’-ATGCGCTTACCAACCAAG-3’
PT10F	5’-CACAGCCGTGCTTCCATT-3’
PT10R	5’-CTCGCAAGGTCGGTCTCC-3’
18sF	5’-GTCCGAATAACCGAAGCG-3’
18sR	5’-GCCAGCGTACTGCCAAAG-3’
Actin1F	5’-GCCTACCACGATGTTCAA-3’
Actin1R	5’-ATAATGCCGAAGCGAAAG-3’
Actin2F	5’-CAGACGCTATCAACAGGA-3’
Actin2R	5’-CTCAAACCAGCAAGAATG-3’

Primers for knockout of *pgp* genes by amplification of split-marker cassettes	
Pgp3-sp1	5’-CAGGCTTACGGACACCAT-3’
Pgp3-sp2	5’-GCTCCTTCAATATCATCTTCTGCGAAAGGCAAACACCAAT -3’
Pgp3-sp3	5’-ATTGGTGTTTGCCTTTCGCAGAAGATGATATTGAAGGAGC-3’
Pgp3-sp4	5’-GCTCCATACAAGCCAACCAC-3’

Pgp3-sp5	5’- CCTTCCTCCCTTTATTTCAGA-3’
Pgp3-sp6	5’-GGCTGAGGATCTCGGAAGGGATCCTCTAGAAAGAAGGATTAC-3’
Pgp3-sp7	5’-GTAATCCTTCTTTCTAGAGGATCCCTTCCGAGATCCTCAGCC-3’
Pgp3-sp8	5’-GCGAGGTGCCGTATTCTA-3’
Pgp6-sp1	5’-CCGTGATACGTTCGTGGTA-3’
Pgp6-sp2	5’-GCTCCTTCAATATCATCTTCTGCAACCCTGGATTGAAGTG-3’
Pgp6-sp3	5’-CACTTCAATCCAGGGTTGCAGAAGATGATATTGAAGGAGC-3’
Pgp6-sp4	5’-GCTCCATACAAGCCAACCAC-3’
Pgp6-sp5	5’-CCTTCCTCCCTTTATTTCAGA-3’
Pgp6-sp6	5’-CCTATCAACGGCACTTCAGGATCCTCTAGAAAGAAGGATTAC-3’
Pgp6-sp7	5’-GTAATCCTTCTTTCTAGAGGATCCTGAAGTGCCGTTGATAGG-3’
Pgp6-sp8	5’-TTTGGACTCGCATGATAT-3’
Pgp7-sp1	5’-TGATGCCTAAATGGGACT-3’
Pgp7-sp2	5’-GCTCCTTCAATATCATCTTCTGGAACAAGGAGCCAGAATA-3’
Pgp7-sp3	5’-TATTCTGGCTCCTTGTTCCAGAAGATGATATTGAAGGAGC-3’
Pgp7-sp4	5’-GCTCCATACAAGCCAACCAC-3’
Pgp7-sp5	5’-CCTTCCTCCCTTTATTTCAGA-3’
Pgp7-sp6	5’-GAGCAAGCAGCGAGGACAGGATCCTCTAGAAAGAAGGATTAC-3’
Pgp7-sp7	5’-GTAATCCTTCTTTCTAGAGGATCCTGTCCTCGCTGCTTGCTC-3’
Pgp7-sp8	5’-CATGCCATGCGTCTGTCT-3’
Pgp11-sp1	5’-CGGCTCGTTTATTCGTCC-3’
Pgp11-sp2	5’-GCTCCTTCAATATCATCTTCTGCAGGGCTCGCAATCAGTC-3’
Pgp11-sp3	5’-GACTGATTGCGAGCCCTGCAGAAGATGATATTGAAGGAGC-3’
Pgp11-sp4	5’-GCTCCATACAAGCCAACCAC-3’
Pgp11-sp5	5’-CCTTCCTCCCTTTATTTCAGA-3’
Pgp11-sp6	5’-CTCCACGCCCACCACTTCTTGGATCCTCTAGAAAGAAGGATTAC-3’
Pgp11-sp7	5’-GTAATCCTTCTTTCTAGAGGATCCAAGAAGTGGTGGGCGTGGAG-3’
Pgp11-sp8	5’-TGGGCGGTCTTCCTTTCG-3’

Primers for diagnostic PCR of deleted *pgp* genes

Pgp3-inF	5’-GAAAGGAGCCACAAAGCG-3’
Pgp3-inR	5’-CTGCGGAAGTTCCACGAT-3’
Pgp6-inF	5’-CGCCGAGATCAGATGTTT-3’
Pgp6-inR	5’-ATTCAGTGGCACGGTTTT-3’
Pgp7-inF	5’-GCAACTGTACCTTCTCCCTT-3’
Pgp7-inR	5’-ATGCGTGCTGCTTGATGT-3’
Pgp11-inF	5’-GCAGCATTGGAAGTGAGC-3’
Pgp11-inR	5’-AAACGAGGAAGAGGTAAGG-3’

Table S4. Gene informations of ABC transporters in phylogenetic analysis.

Proposed name	Subfamily	Genome locus	Species	Genbank no.
NcABCE1	ABC-E	NCU03061	*Neurospora crassa* OR74A	EAA34633.2
AoABCE1	ABC-E	AO090038000399	*Aspergillus oryzae* RIB40	BAE64192.1
CcABCE1	ABC-E	CC1G_07665	*Coprinopsis cinerea* okayama7*130	EAU89439.2
PcABCE1	ABC-E	Pc16g04800	*Penicillium chrysogenum* Wisconsin 54-1255	CAP93150
AfuABCA1	ABC-A	Afu5g09480	*Aspergillus fumigatus* Af293	EAL91653
NcABCA1	ABC-A	NCU04021	*Neurospora crassa* OR74A	EAA28400.1
BfABCA1	ABC-A	BC1G_11159	*Botryotinia fuckeliana* B05.10	EDN32616
PnABCB1	ABC-B (FL)[α]	SNOG_00742	*Phaeosphaeria nodorum* SN15	EAT92237.1
PnABCB2	ABC-B	SNOG_02135	*Phaeosphaeria nodorum*	EAT90347.2

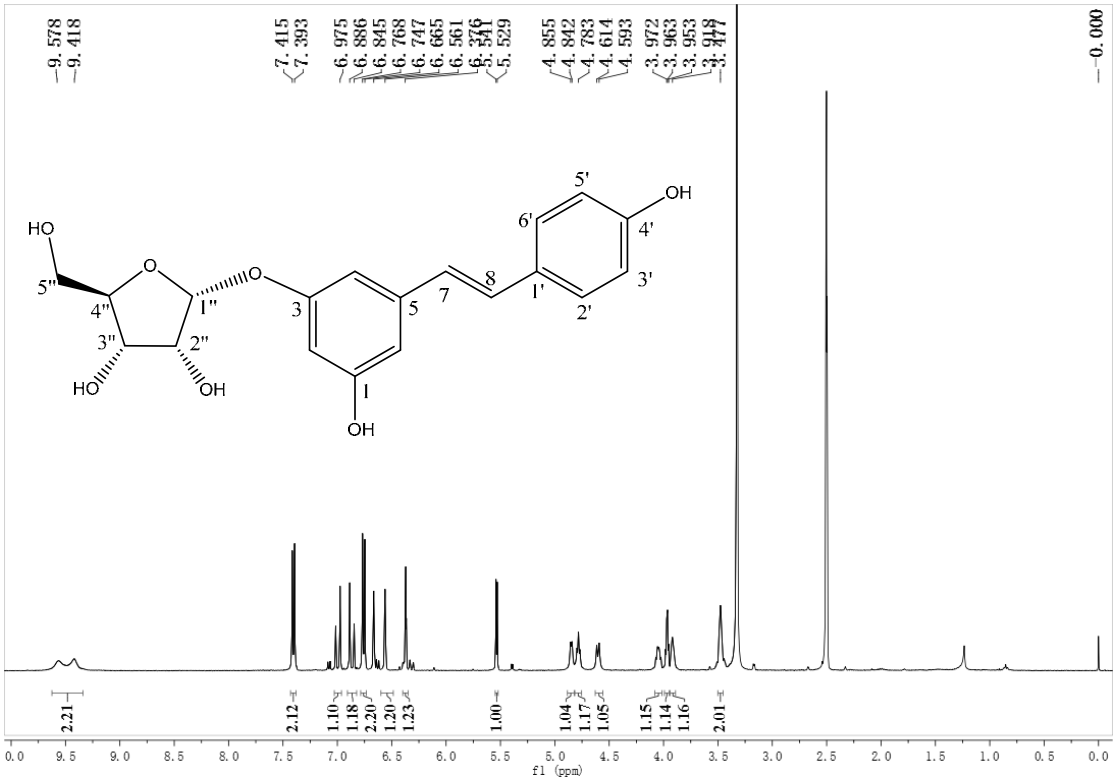
	(FL) [α]		SN15	
NcABCB1	ABC-B	NCU06011	*Neurospora crassa*	EAA29583.1
	(FL) [α]		OR74A	
AoABCB1	ABC-B	AO090001000021	*Aspergillus oryzae*	BAE56585.1
	(FL) [α]		RIB40	
CcABCB3	ABC-B	CC1G_04855	*Coprinopsis cinerea*	EAU80745.2
	(FL) [α]		okayama 7*130	
CaABCB1	ABC-B	CaO19.7440	*Candida albicans*	EAK97097.1
	(FL) [α]		SC5314	
AfuABCB15	ABC-B	Afu6g12870	*Aspergillus fumigatus*	EAL89127.1
	(HT)[β]		Af293	
PnABCB14	ABC-B	SNOG_15856	*Phaeosphaeria nodorum*	EAT76694.2
	(HT) [β]		SN15	
SsABCB8	ABC-B	SS1G_03201	*Sclerotinia sclerotiorum*	EDO00728.1
	(HT) [β]		1980_UF-70	
NcABCB6	ABC-B	NCU00010	*Neurospora crassa*	EAA27761.2
	(HT) [β]		OR74A	
SsABCC3	ABC-C	SS1G_05336	*Sclerotinia sclerotiorum*	EDO02859.1
			1980 UF-70	
AfuABCC1	ABC-C	Afu1g10390	*Aspergillus fumigatus*	EAL90367.2
			Af293	
CaABCC2	ABC-C	CaO19.5100	*Candida albicans*	EAK98674.1
			SC5314	
NcABCC2	ABC-C	NCU03591	*Neurospora crassa*	EAA31399.1
			OR74A	
NcABCD1	ABC-D	NCU01751	*Neurospora crassa*	EAA27938.1
			OR74A	
PcABCD1	ABC-D	Pc13g11640	*Penicillium*	CAP92233.1
			chrysogenum Wisconsin	

			54-1255	
CnABCD1	ABC-D	CNA06310	*Cryptococcus neoformans* var. *neoformans* JEC21	AAW41159.1
AfuABCD1	ABC-D	Afu1g04780	*Aspergillus fumigatus* Af293	EAL88189.1
CaABCF1	ABC-F	CaO19.2183	*Candida albicans* SC5314	EAK97015.1
NcABCF1	ABC-F	NCU04051	*Neurospora crassa* OR74A	EAA28430.1
AfuABCF1	ABC-F	Afu1g16440	*Aspergillus fumigatus* Af293	EAL90972.1
PcABCF1	ABC-F	Pc12g06650	*Penicillium chrysogenum* Wisconsin 54-1255	CAP80292.1
CaABCG7	ABC-G	CaO19.5958	*Candida albicans* SC5314	EAL04461.1
AfuABCG1	ABC-G	Afu1g14330	*Aspergillus fumigatus* Af293	EAL90765.1
CnABCG1	ABC-G	CNA07090	*Cryptococcus neoformans* var. *neoformans* JEC21	AAW41207.1
PcABCG1	ABC-G	Pc12g00190	*Penicillium chrysogenum* Wisconsin 54-1255	CAP79646.1

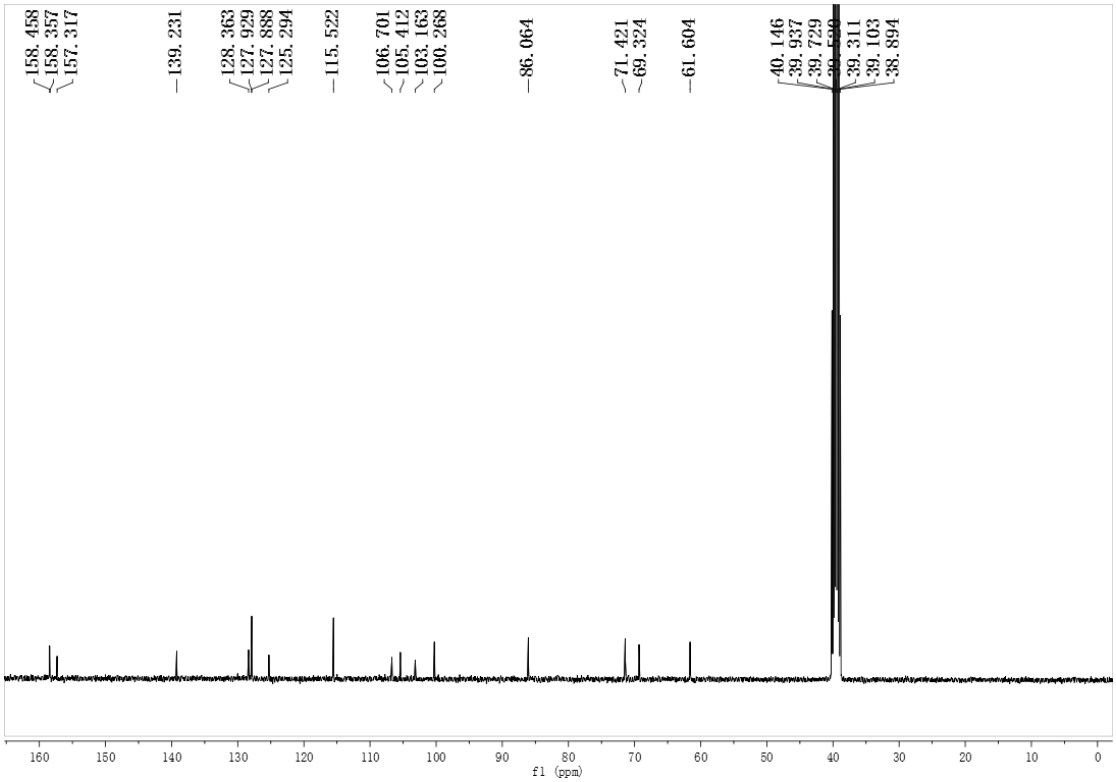
[α] Full-size ABC-B protein. [β] Half-size ABC-B protein.

NMR Spectra

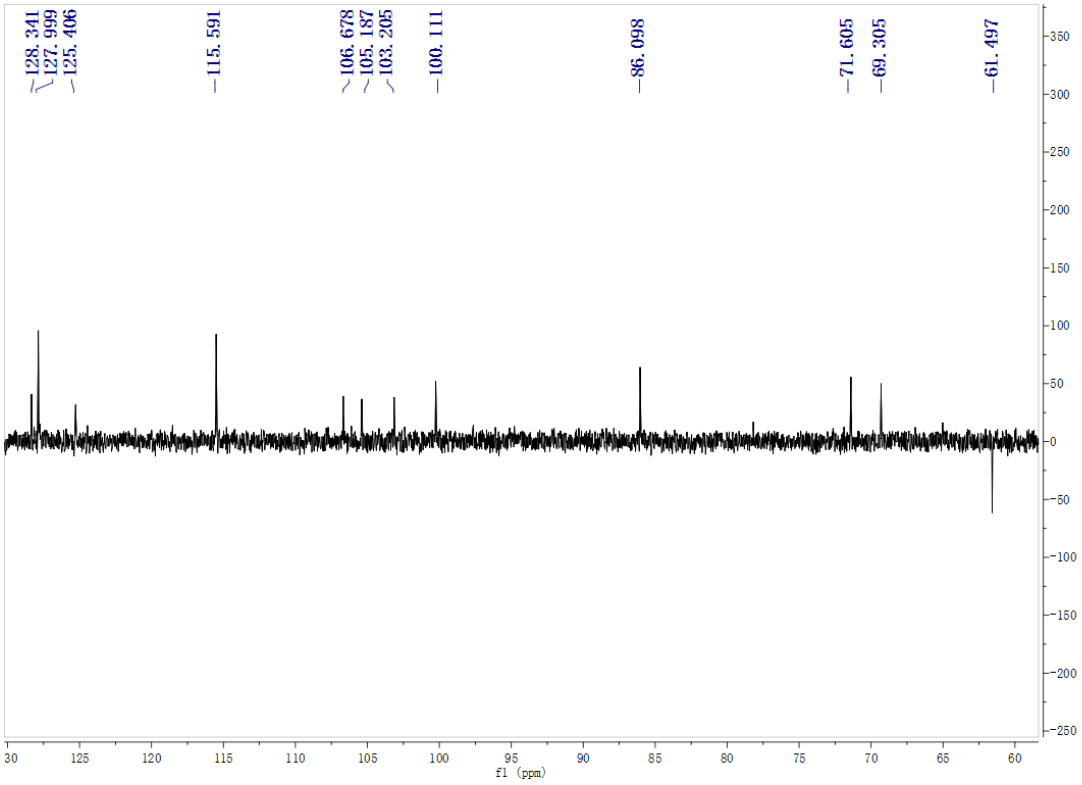
^{1}H NMR spectrum of **1**.



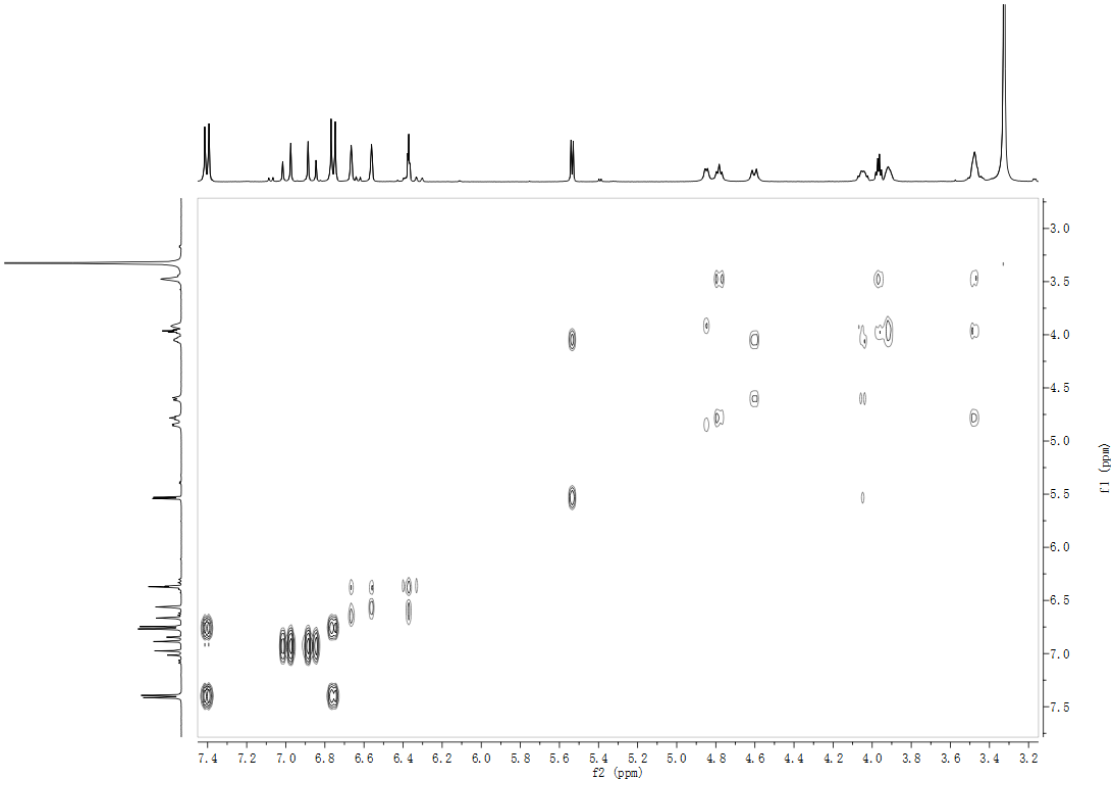
^{13}C NMR spectrum of **1**.



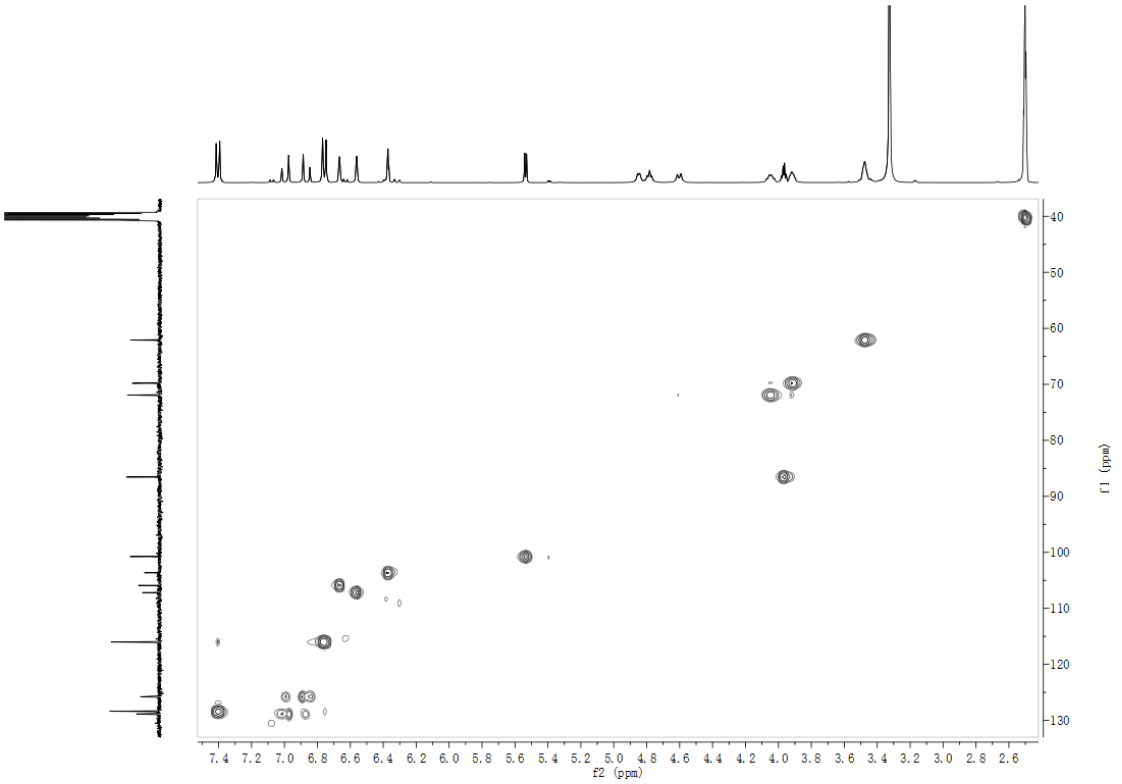
DEPT 135 spectrum of **1**.



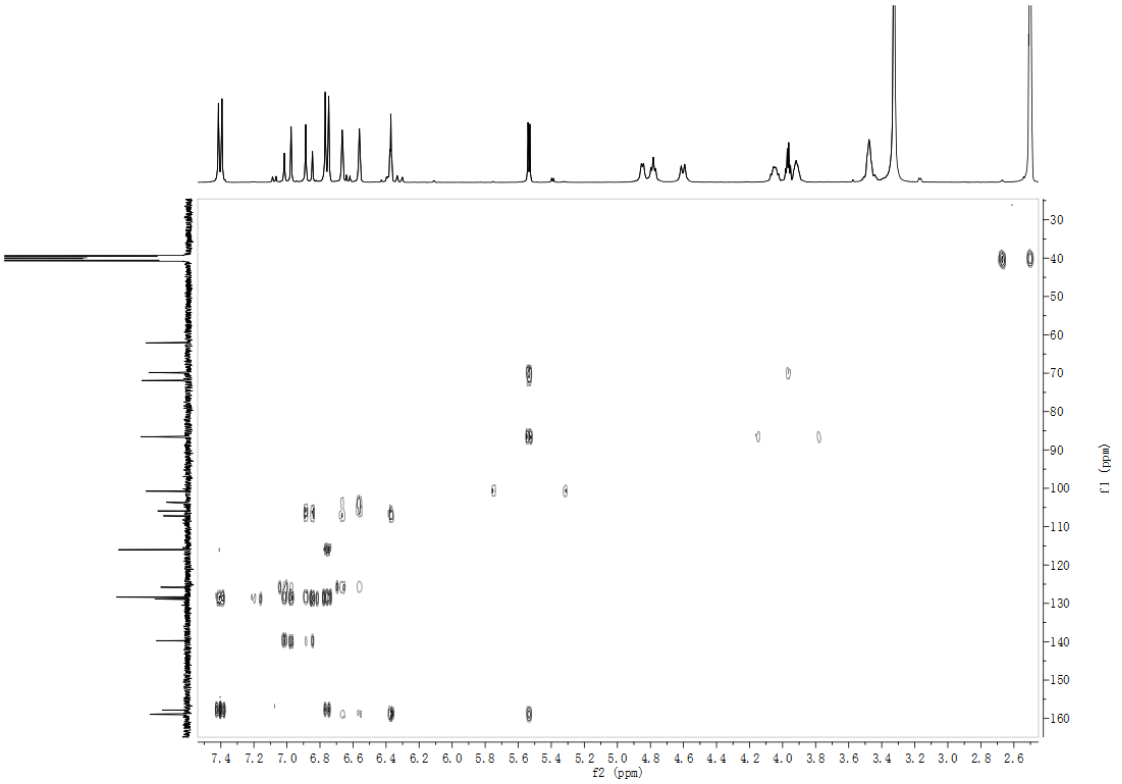
^{1}H-^{1}H COSY spectrum of **1**.



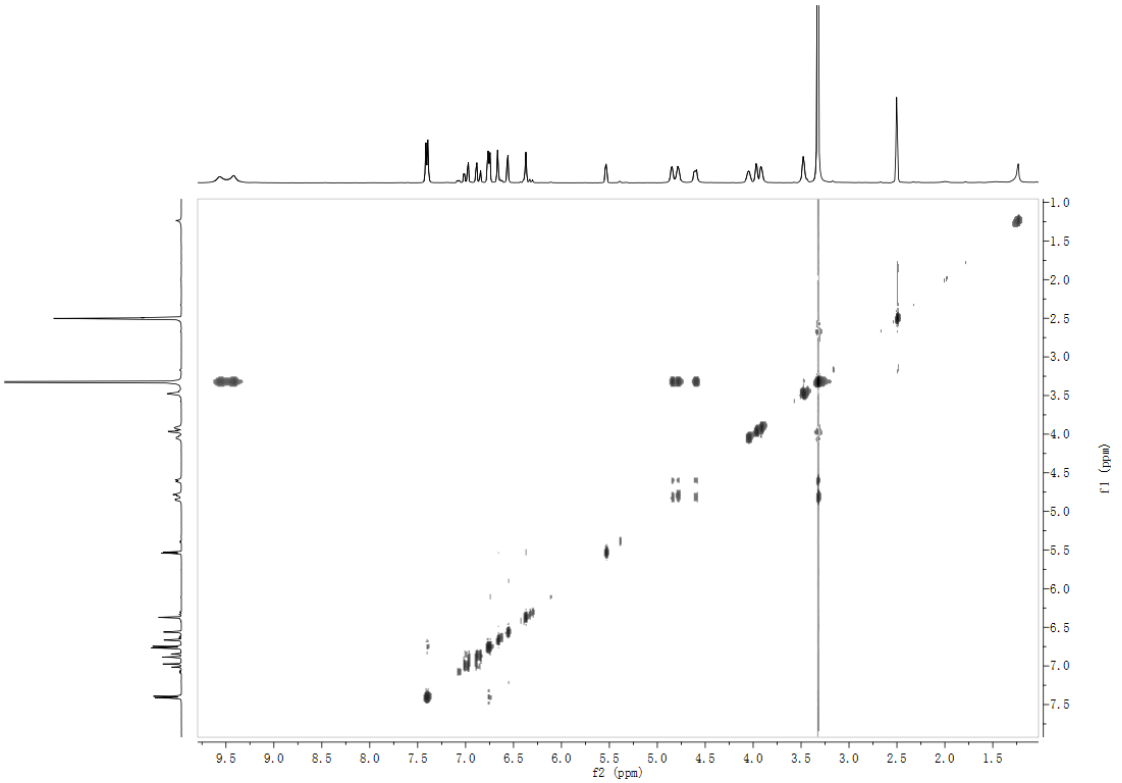
HMQC spectrum of **1**.



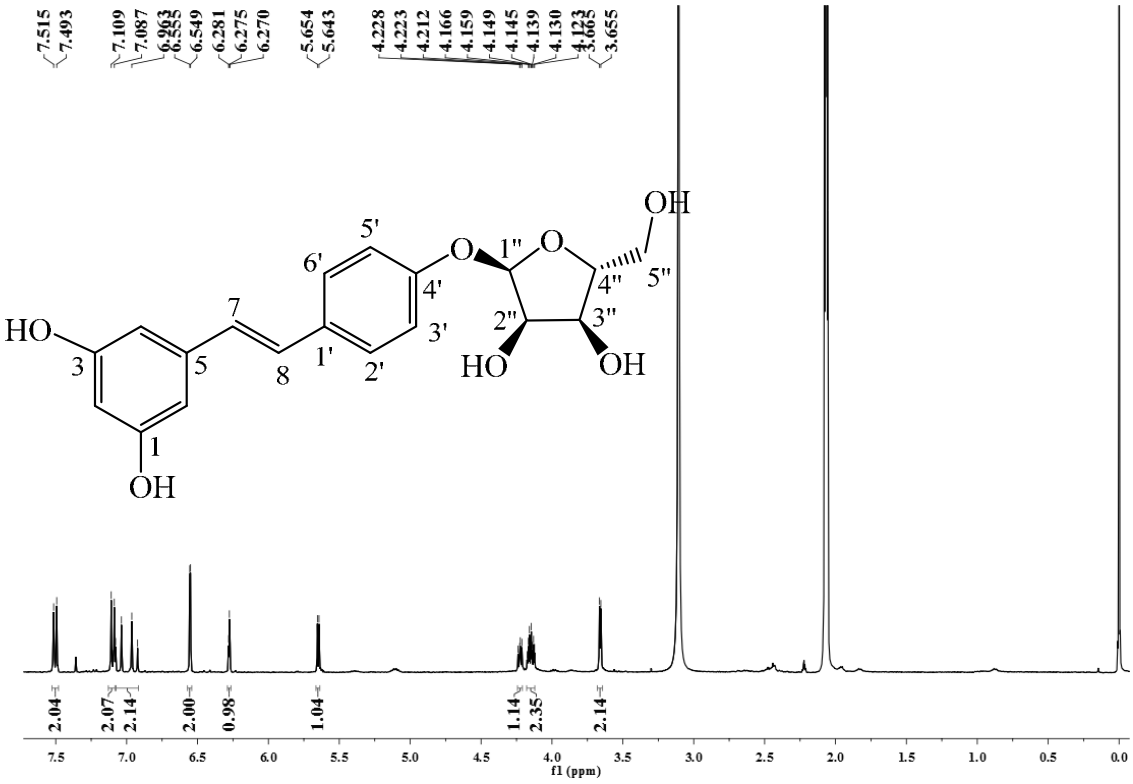
HMBC spectrum of **1**.



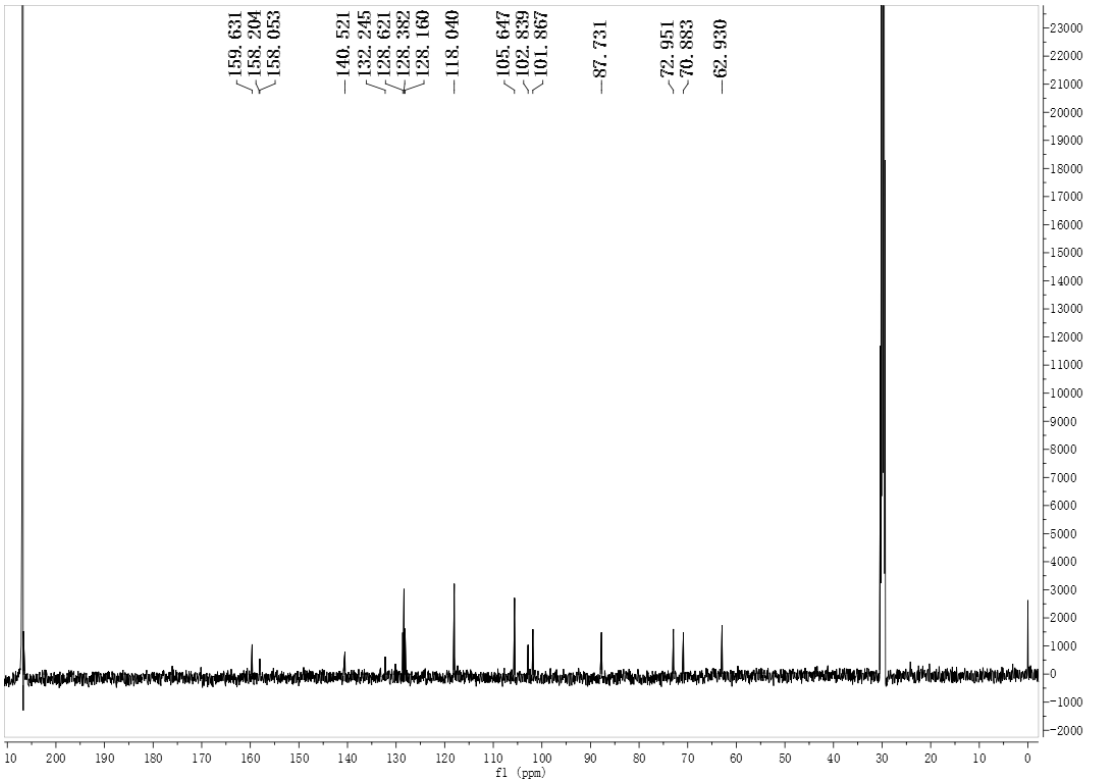
NOESY spectrum of **1**.



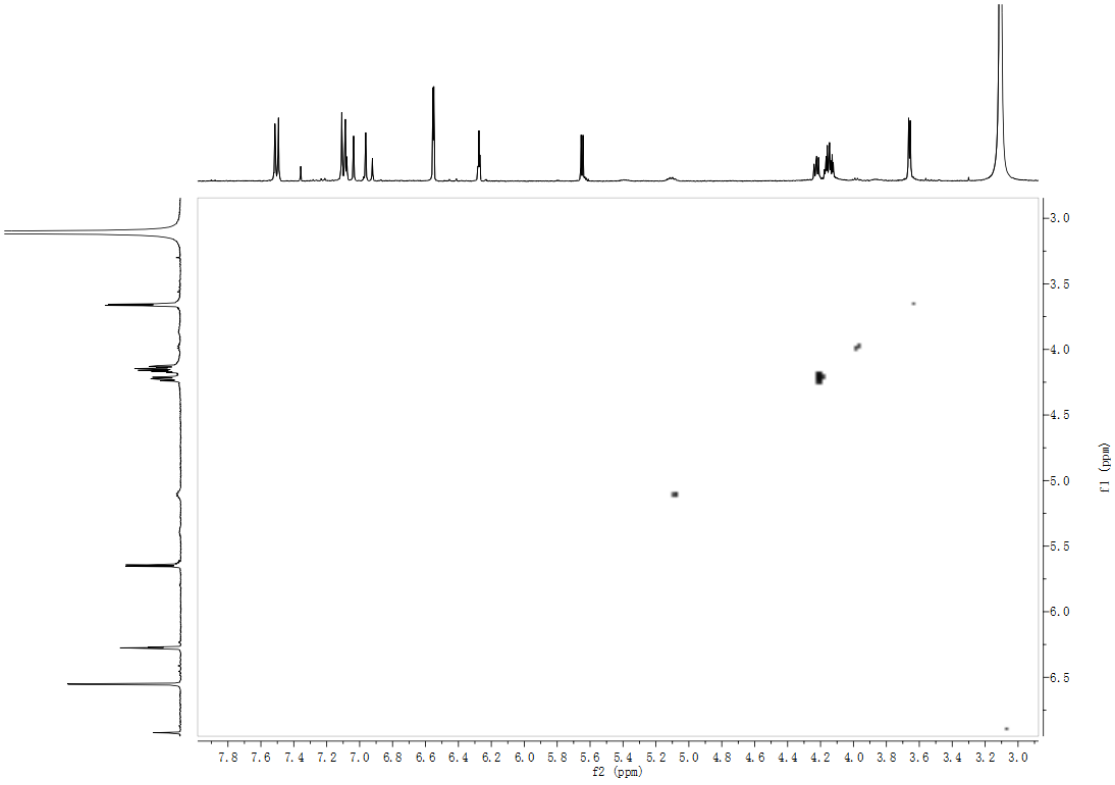
^{1}H NMR spectrum of **2**.



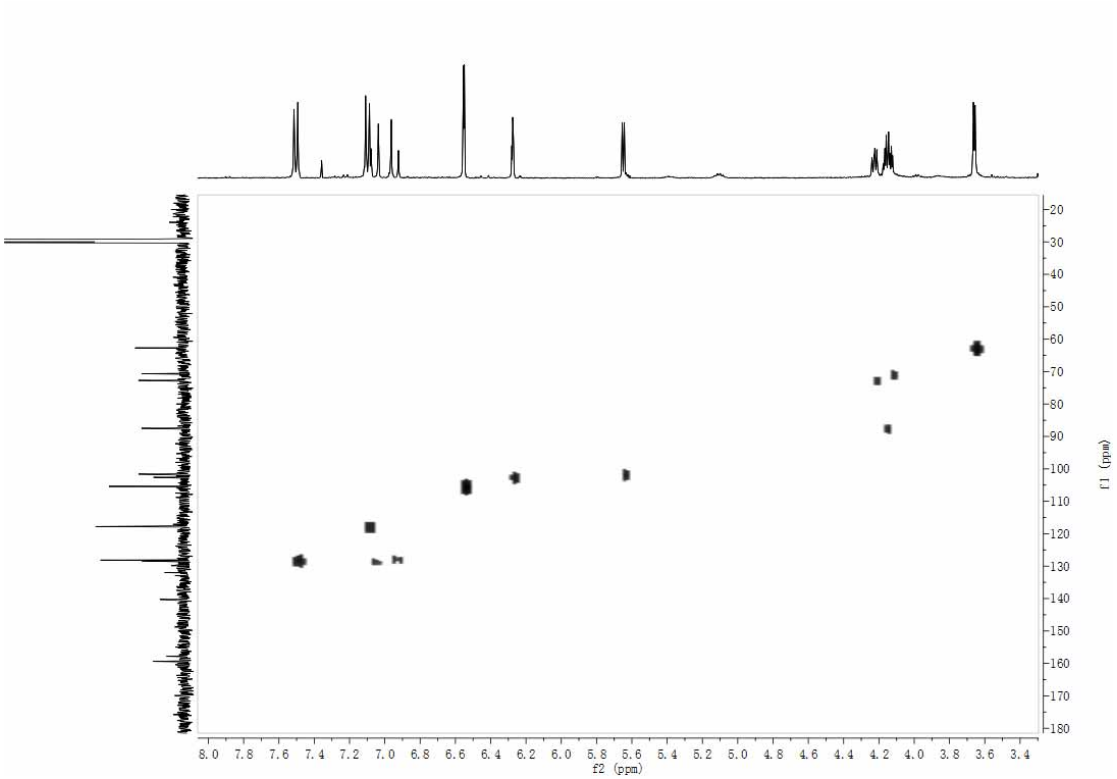
^{13}C NMR spectrum of **2**.



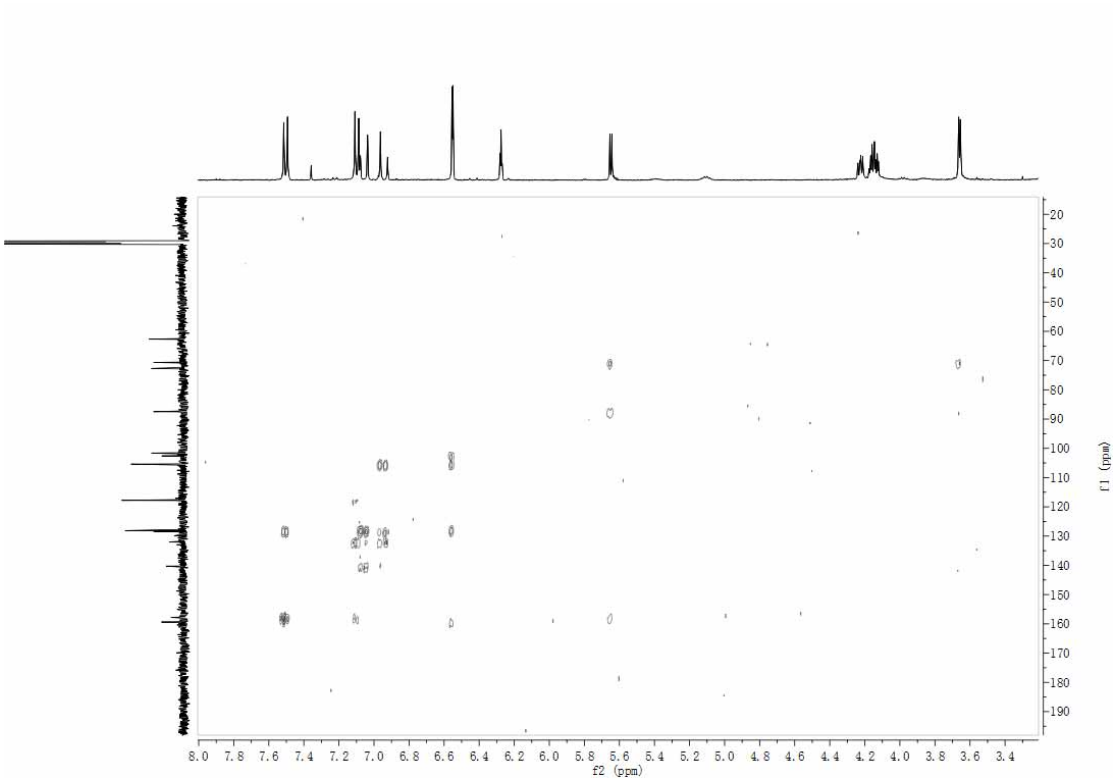
^{1}H-^{1}H COSY spectrum of **2**.



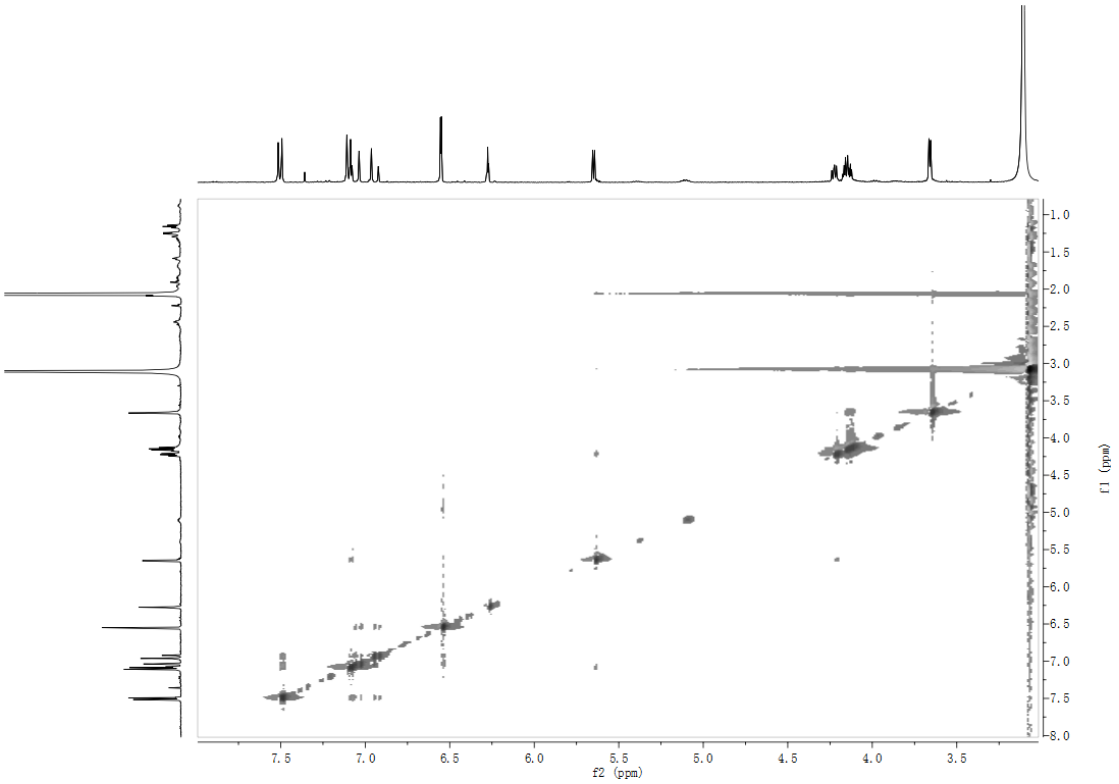
HMQC spectrum of **2**.



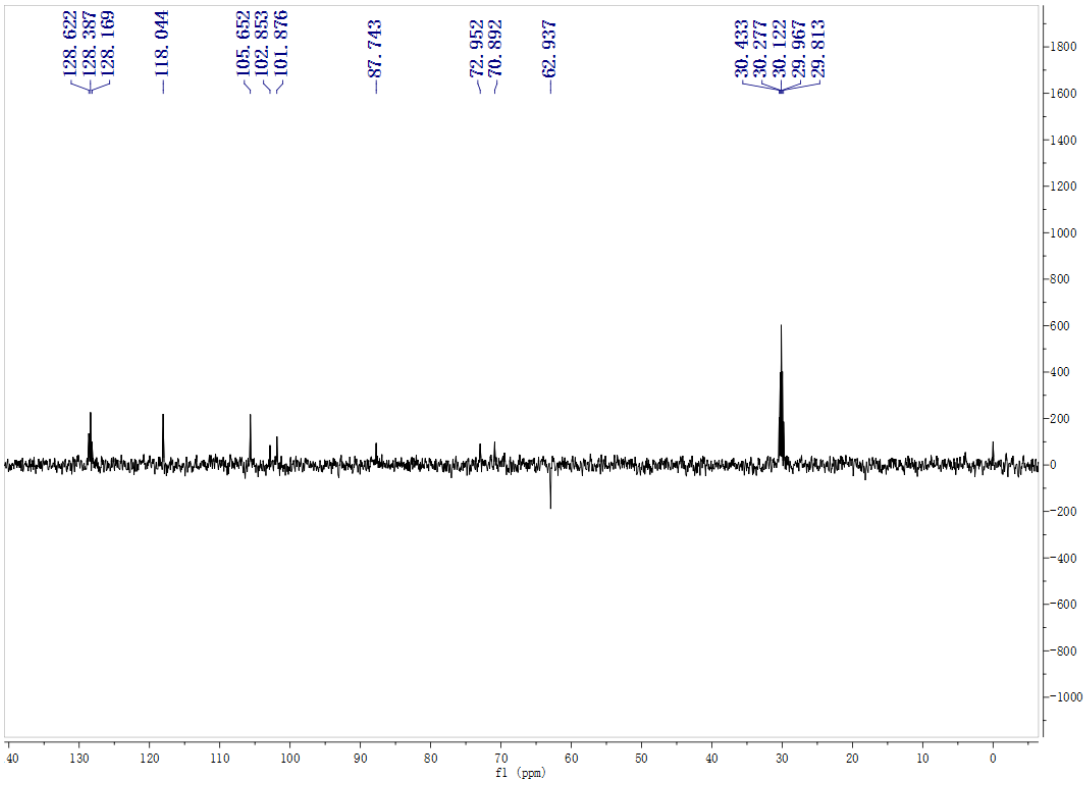
HMBC spectrum of **2**.



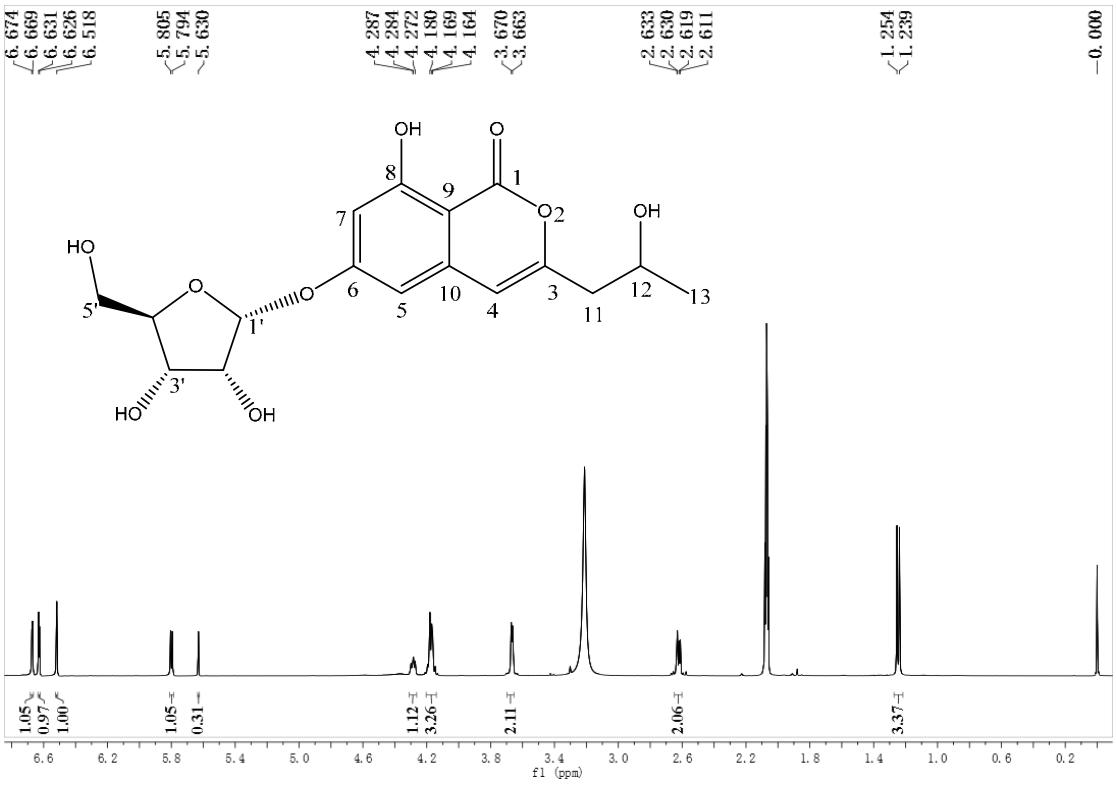
NOESY spectrum of **2**.



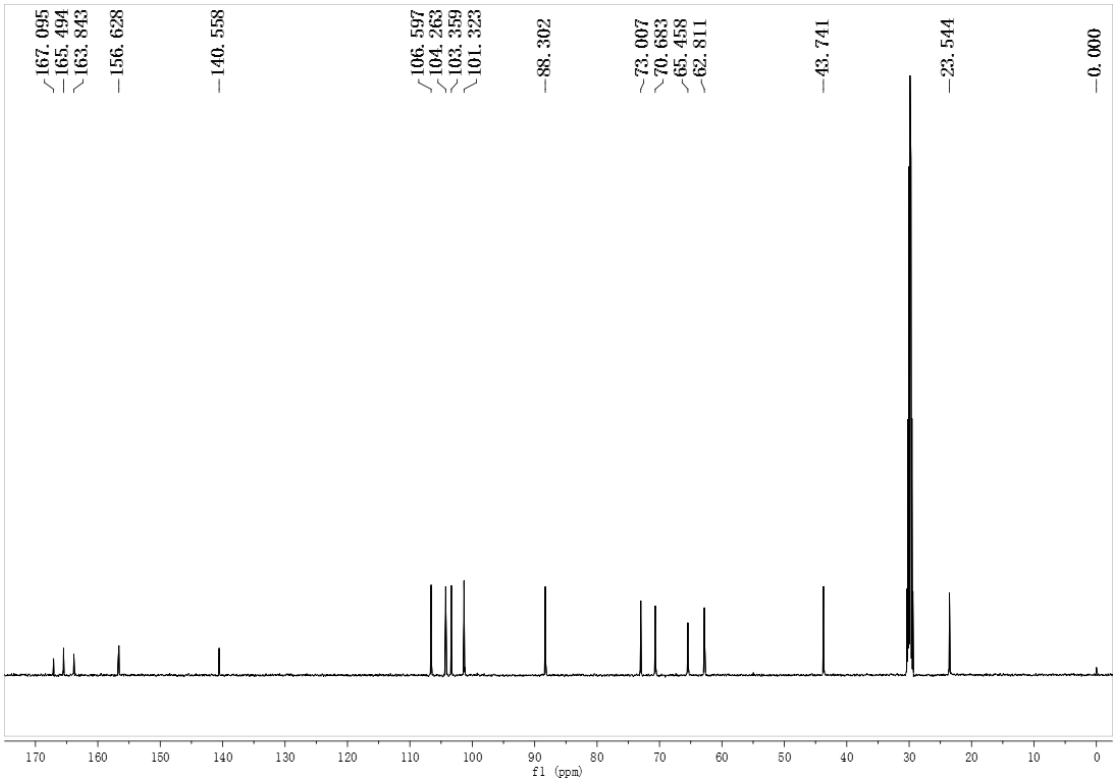
DEPT 135 spectrum of **2**.



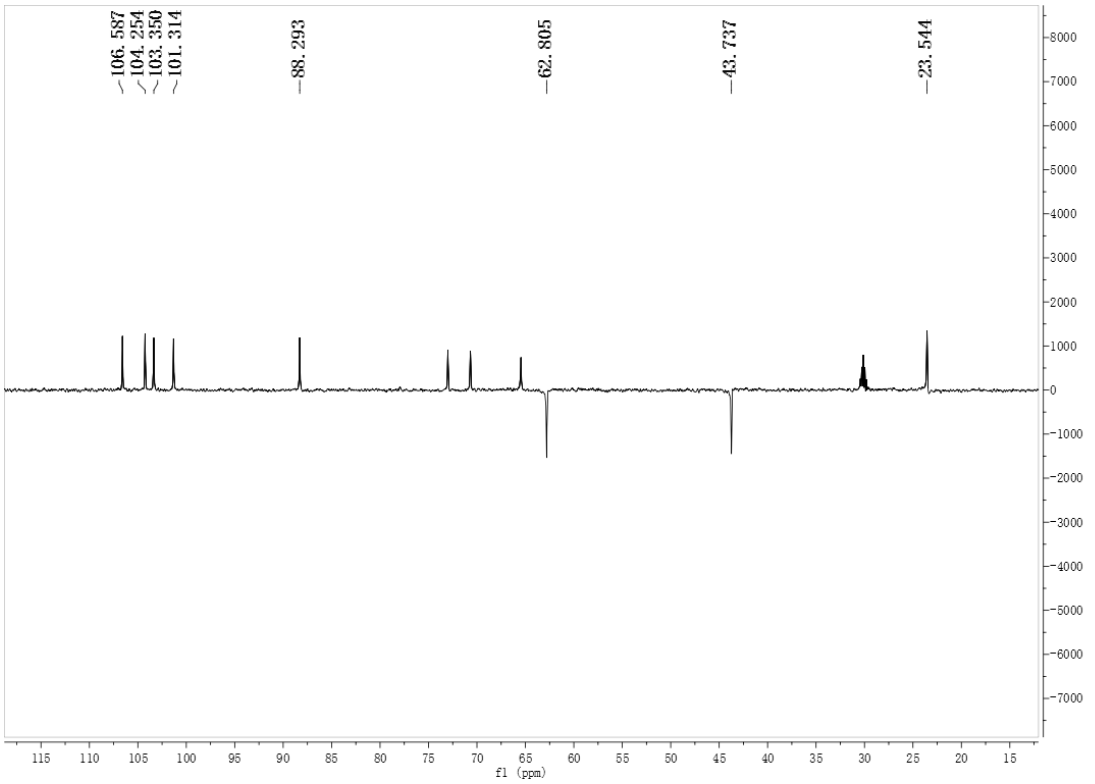
^{1}H NMR spectrum of **3**.



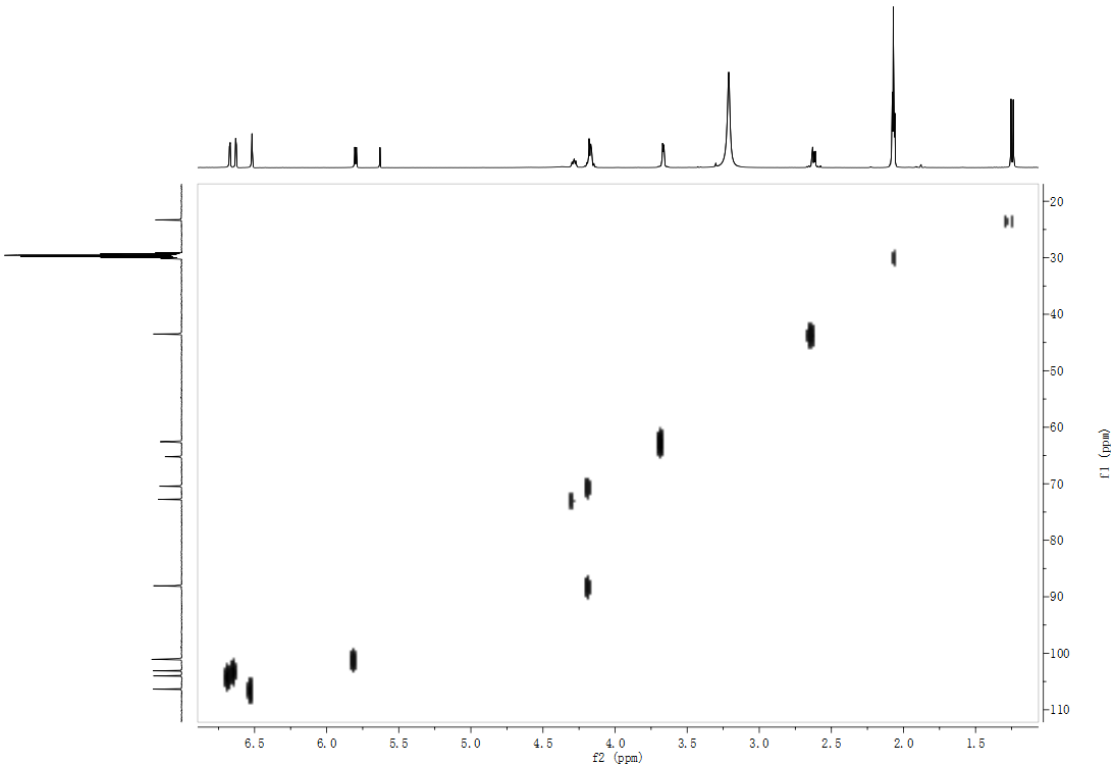
^{13}C NMR spectrum of **3**.



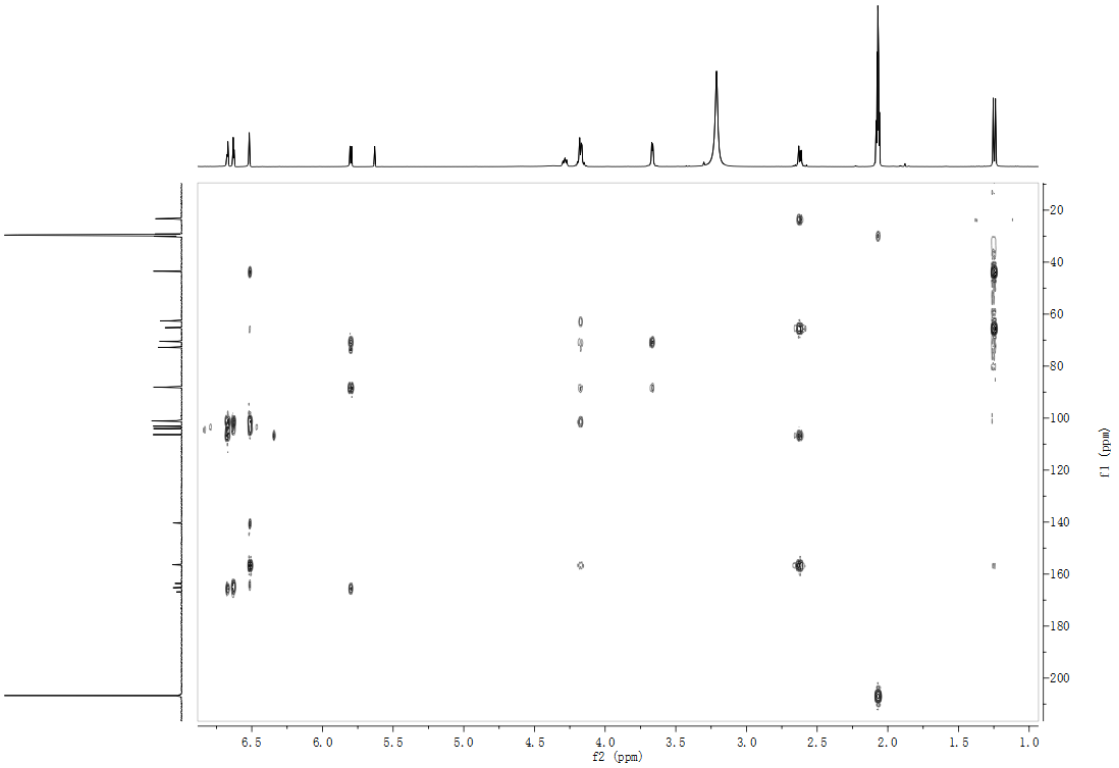
DEPT 135 spectrum of **3**.



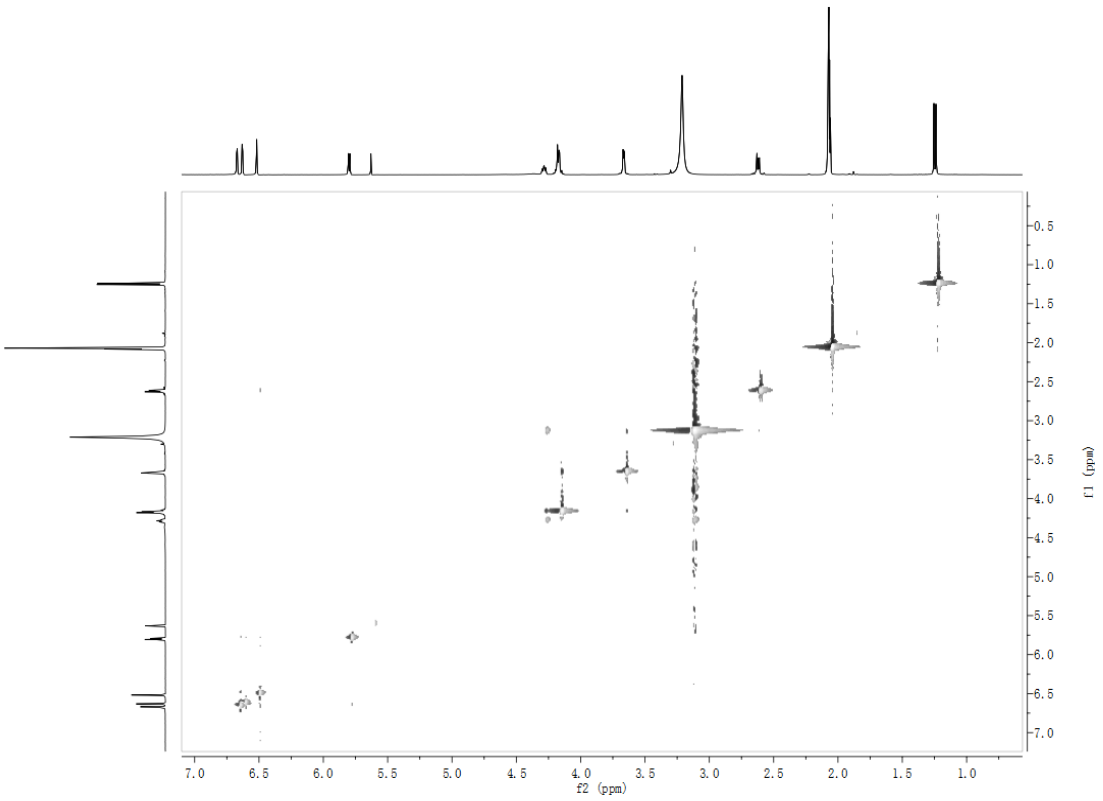
HMQC spectrum of **3**.



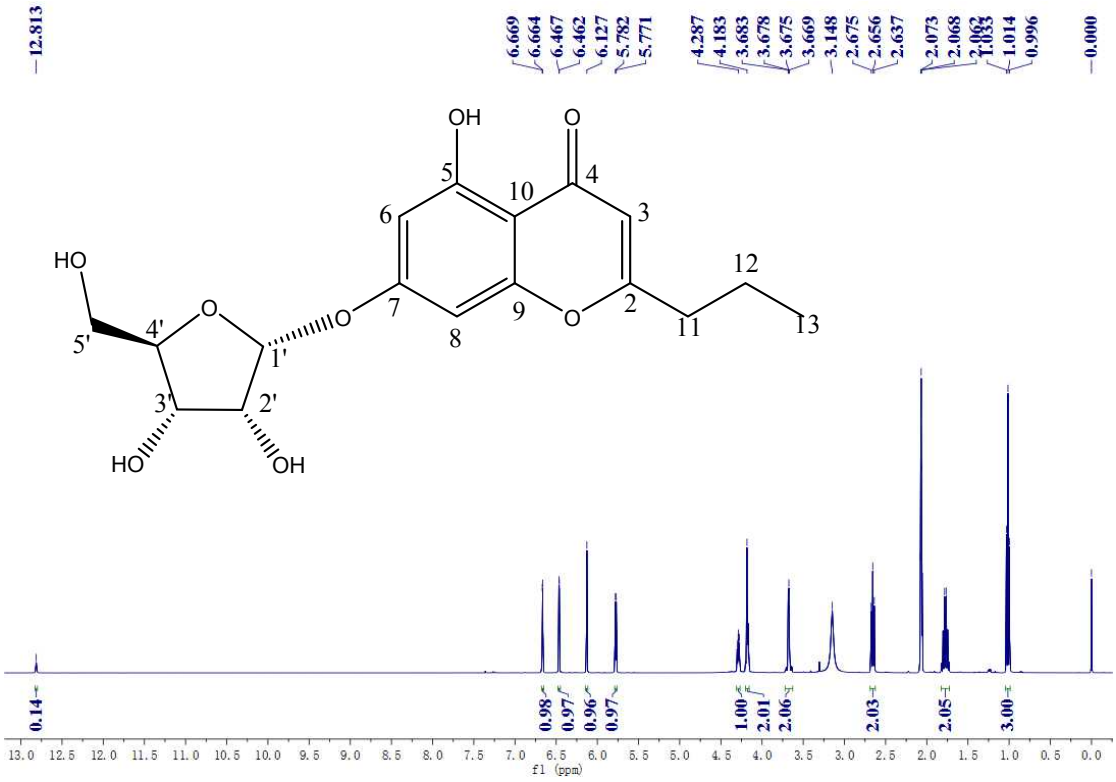
HMBC spectrum of **3**.



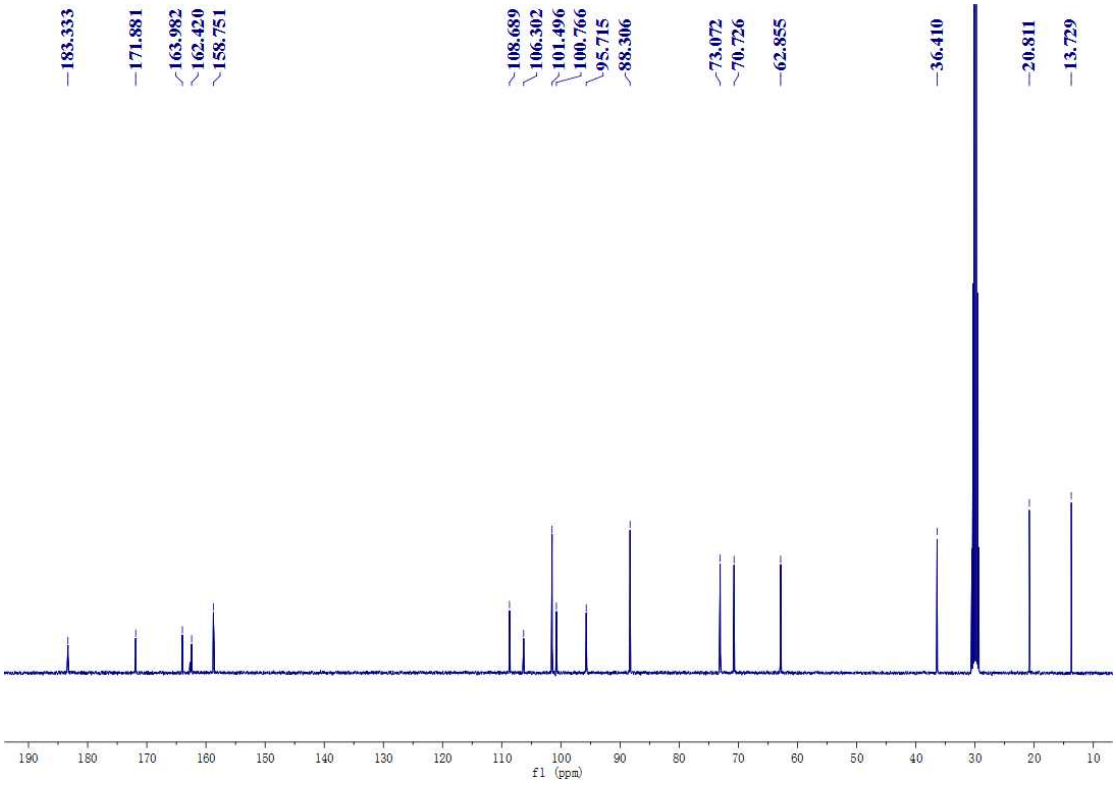
NOESY spectrum of **3**.



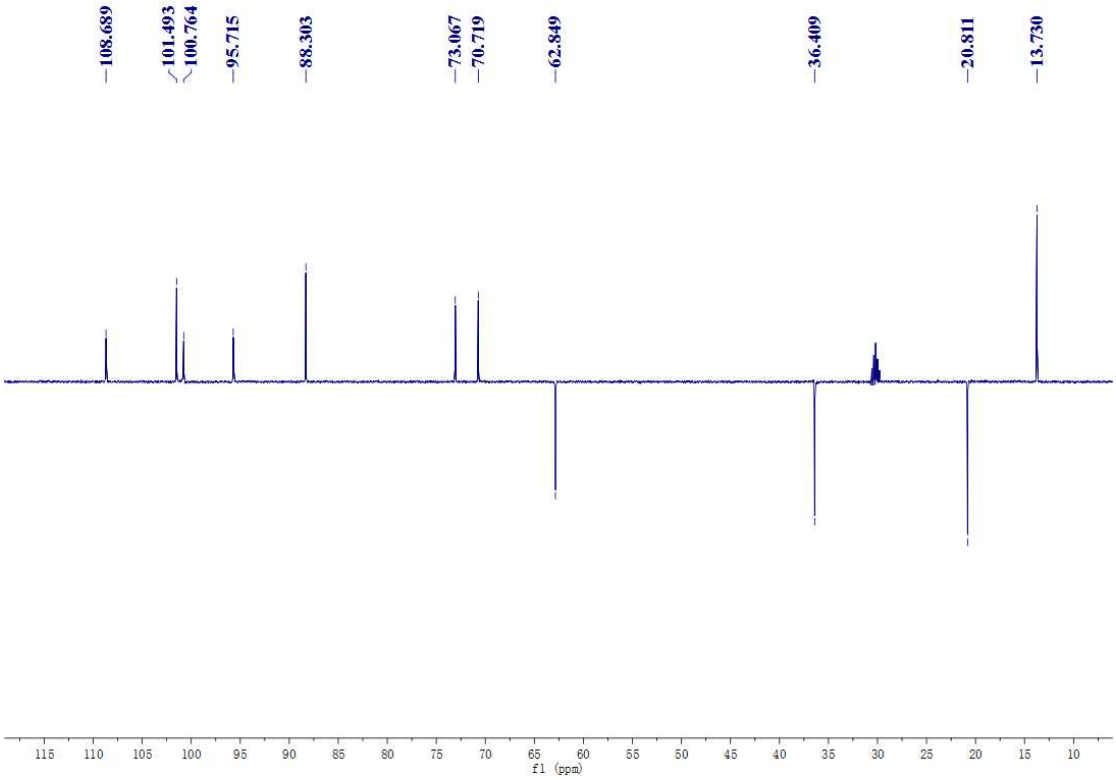
^{1}H NMR spectrum of **4**.



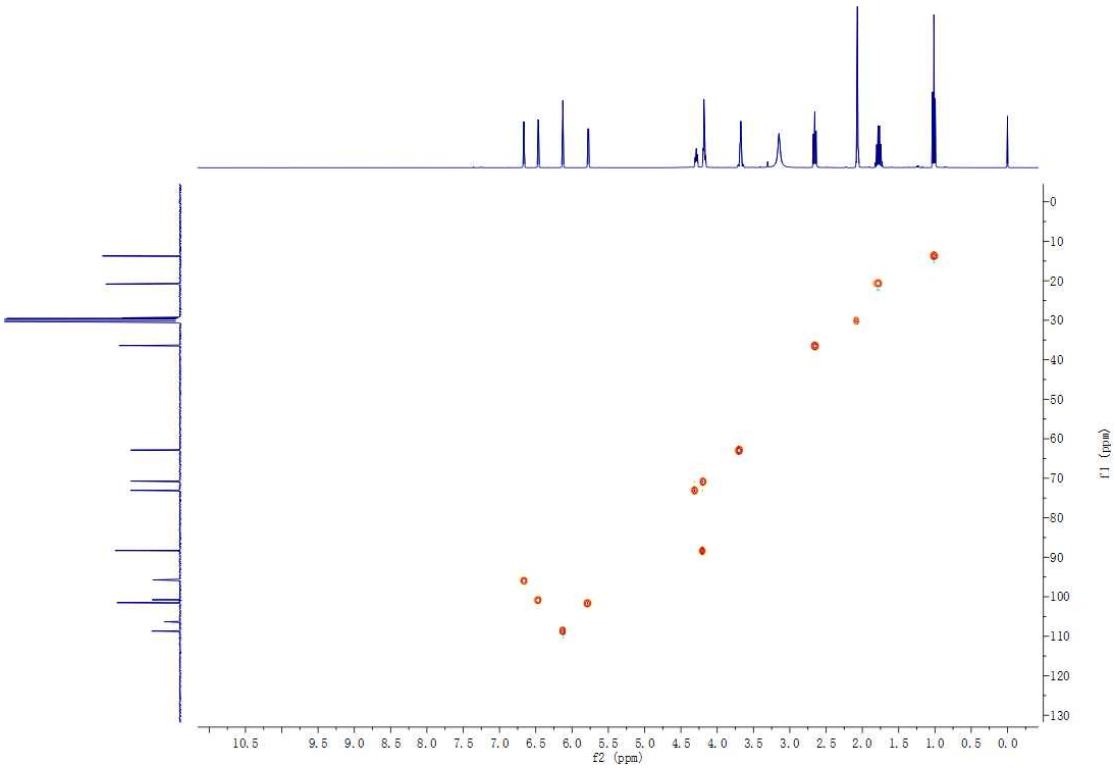
^{13}C NMR spectrum of **4**.



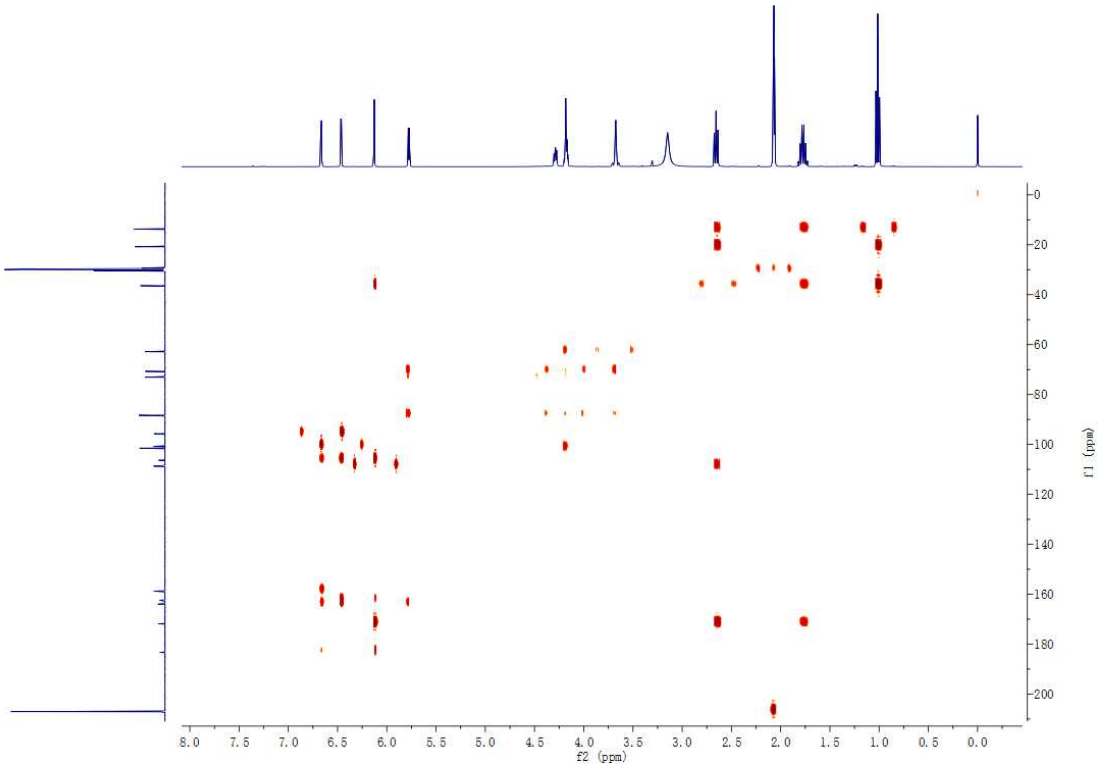
DEPT spectrum of **4**.



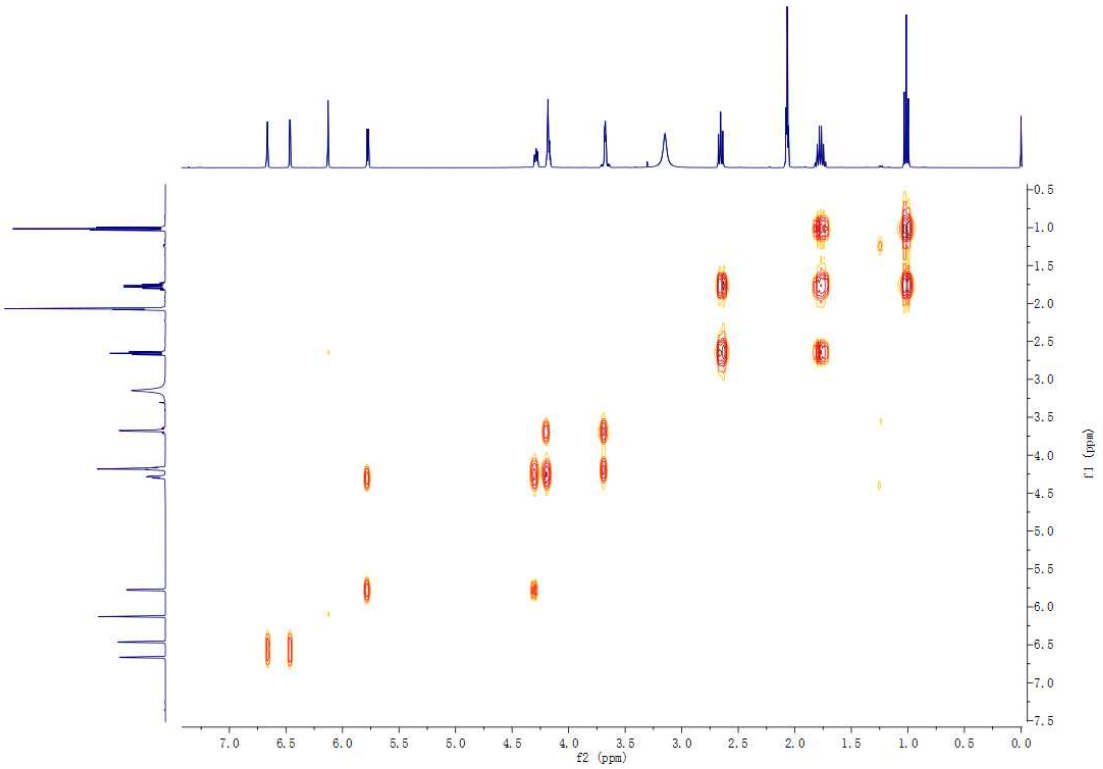
HSQC spectrum of **4**.



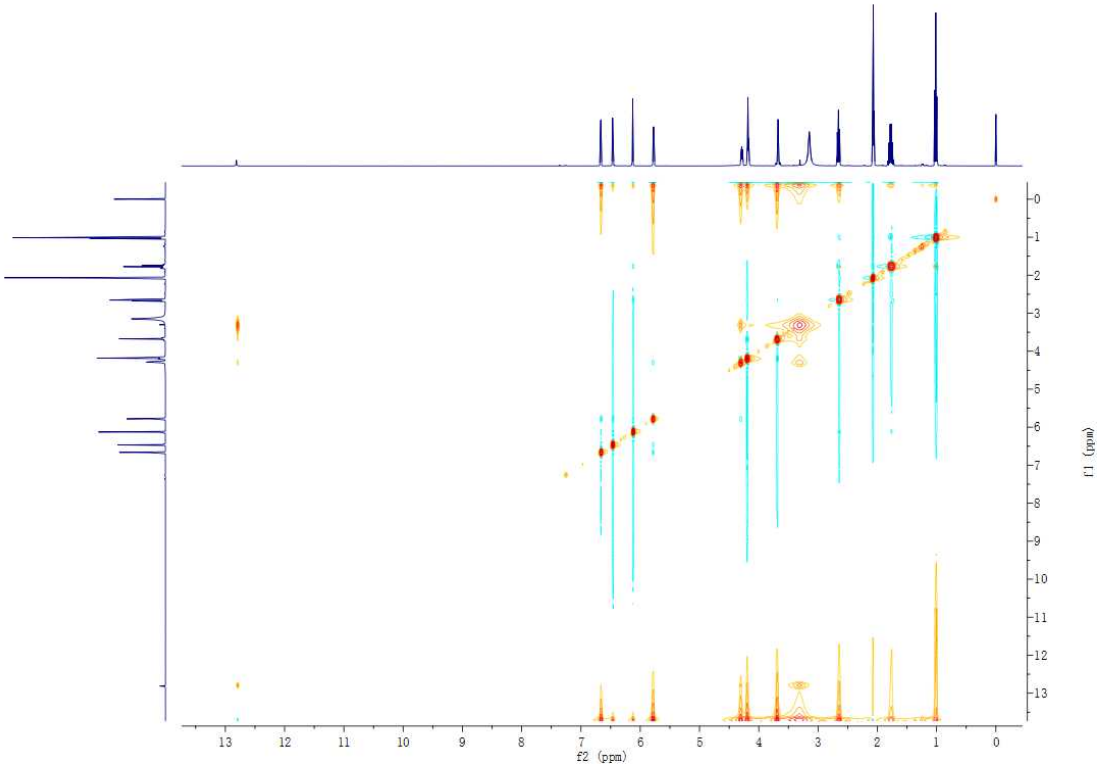
HMBC spectrum of **4**.



H-H COSY spectrum of **4**.



NOE spectrum of **4**.



^{1}H NMR spectrum of **5**.