

Supplementary Information

Three New Stigmatellin Derivatives Reveal Biosynthetic Insights of its Side Chain Decoration

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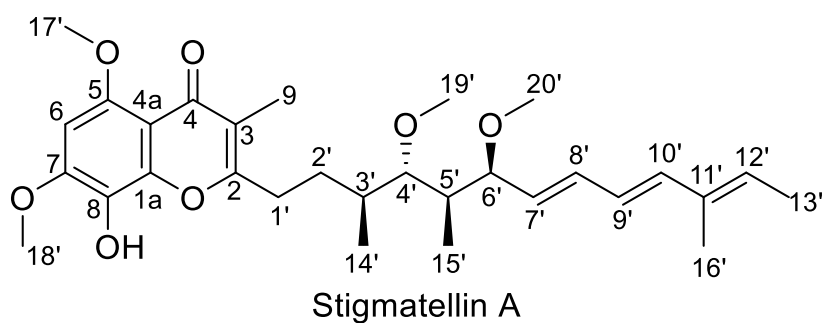
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1. Results and Discussion

Supplementary Materials 1

Table S1. Spectroscopic values for stigmatellin A (**4**) acquired in methanol- d_4 at 700 MHz.

Stigmatellin A (4)			
Position	δ_c	δ_H , [m, J (Hz)]	δ_c , type [1]
1a	148.0	-	148.0
2	165.4	-	165.4
3	117.3	-	117.3
4	179.7	-	179.6
4a	108.2	-	108.7
5	153.8	-	154.0
6	93.7	6.59 s 1H	93.8
7	152.5	-	152.6
8	128.9	-	129.1
9	10.0	1.97 s 3H	9.9
1'	30.5	2.83 m 1H 2.67 m 1H	30.6
2'	28.2	1.92 m 1H 1.56 m 1H	28.5
3'	35.5	1.73 m 1H	35.6
4'	88.5	3.20 m 3H	88.8
5'	42.9	1.66 m 1H	43.0
6'	82.4	3.88 m 3H	82.7
7'	132.5	5.57 dd 1H (7.7)	132.5
8'	134.7	6.20 m 1H	134.6
9'	126.4	6.20 m 1H	126.3
10'	138.9	6.20 m 1H	138.9
11'	135.9	-	135.9
12'	128.5	5.57 q 1H (7.7)	128.4
13'	14.0	1.75 s 3H	13.9
14'	18.3	1.14 dd 3H (3.05/6.7)	18.3
15'	10.5	0.74 d 3H (7.0)	10.7
16'	12.1	1.75 s 3H	12.0
17'	56.6	3.87 s 3H	56.8
18'	56.9	3.97 s 3H	57.0
19'	61.7	3.46 s 3H	61.6
20'	56.5	3.20 s 3H	56.5



Supplementary Materials 2

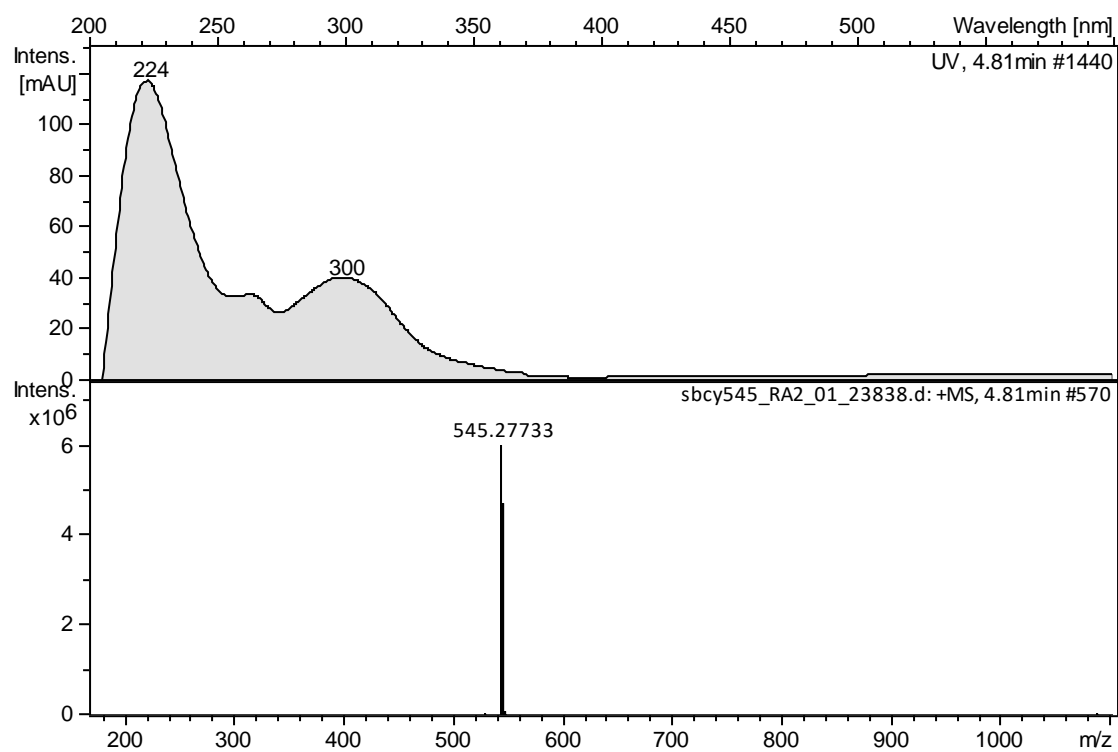


Figure S1. UV/VIS and partial ESI+MS spectra of purified stigmatellic acid (**1**).

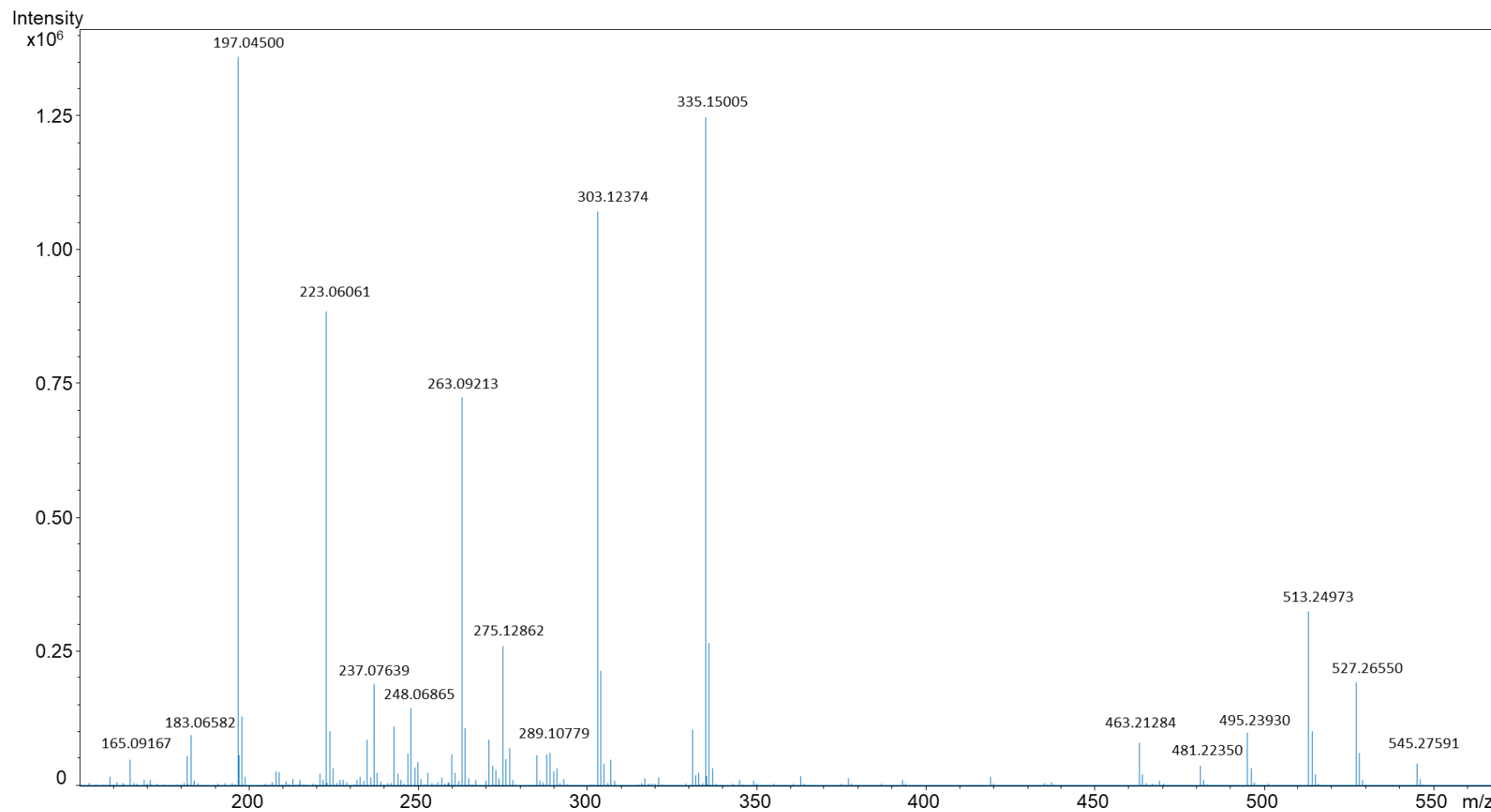


Figure S2. Fragmentation pattern in ESI+MS² experiment of stigmatellic acid (**1**).

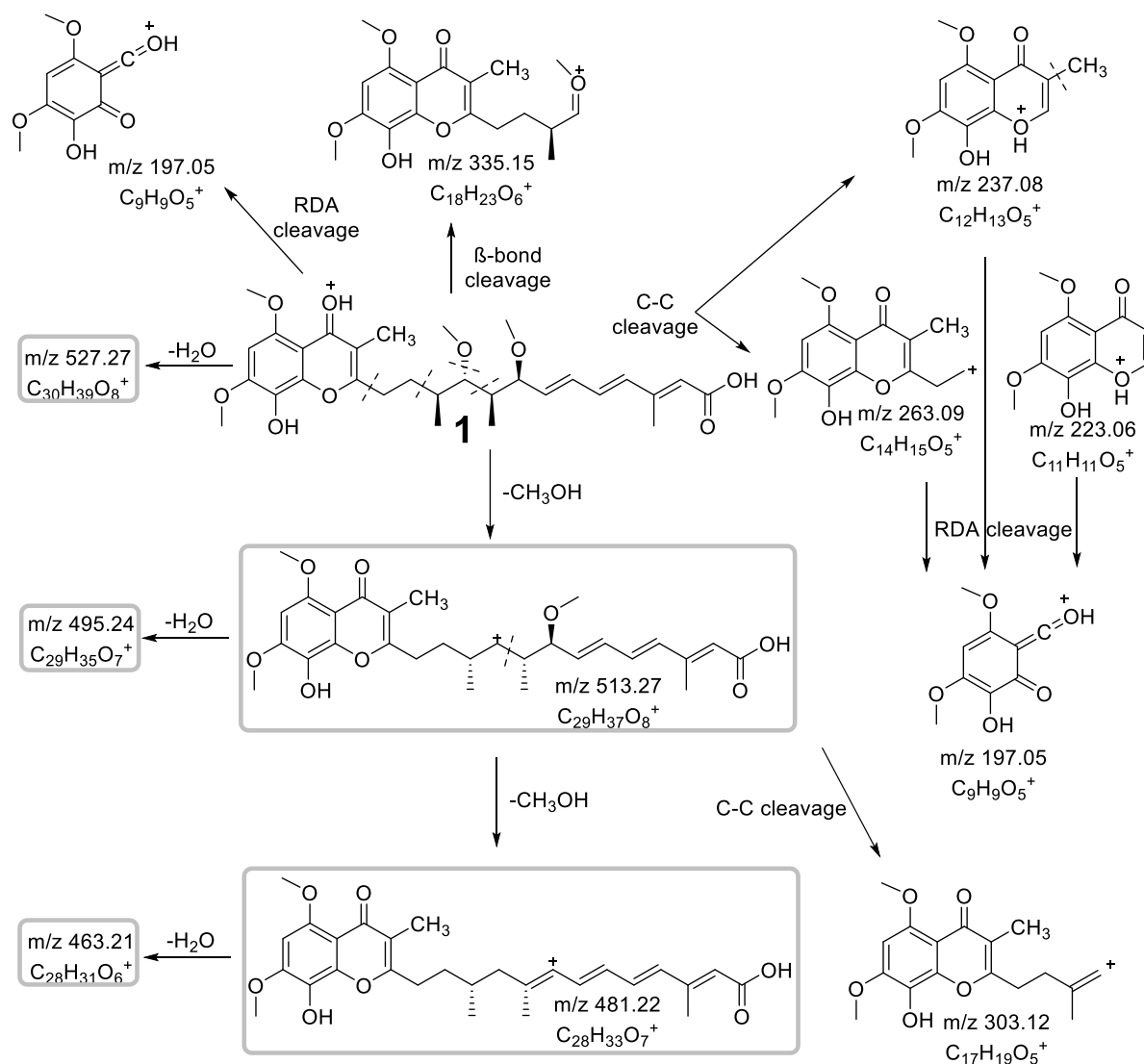
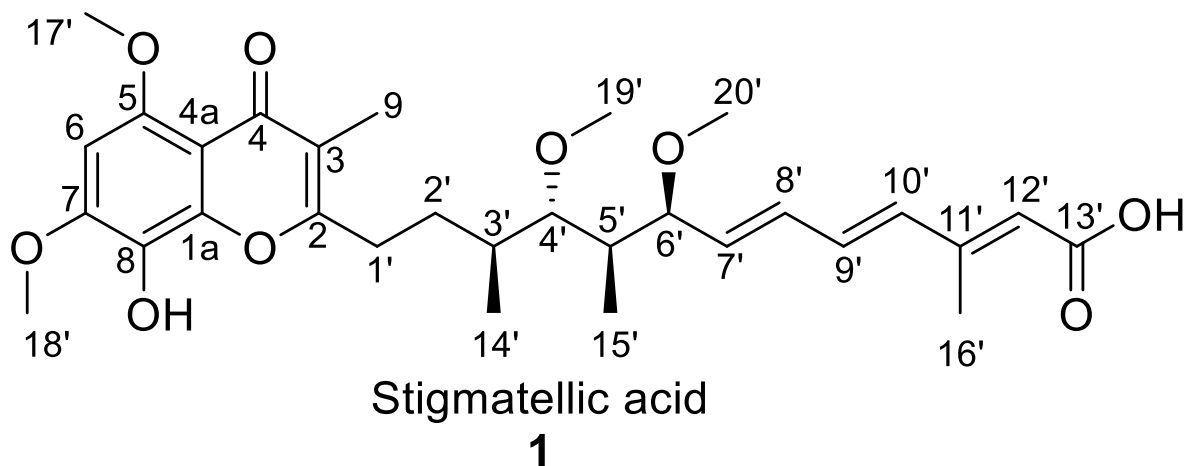


Figure S3. MS² fragmentation scheme of **1** and proposed structure of identified key ion fragments (ion fragments in grey box are specific for **1**). RDA: retro-Diels Alder.

Supplementary Materials 3

Table S2. Spectroscopic values of stigmatellic acid (**1**) acquired in methanol- d_4 at 700 MHz.

Stigmatellic acid (1)					
Position	δ_c	δ_H [m, J (Hz)]	COSY	HMBC	ROESY
1a	148.2	-	-	-	-
2	165.6	-	-	-	-
3	117.5	-	-	-	-
4	179.9	-	-	-	-
4a	108.4	-	-	-	-
5	154.0	-	-	-	-
6	93.9	6.62 s 1H	-	1a, 4a, 4, 5, 8, 7,	H-5-O-, H-7-O-
7	152.7	-	-	-	-
8	129.1	-	-	-	-
9	10.2	1.98 s 3H	-	2, 3, 4	-
1'	30.6	2.84 m 1H 2.69 m 1H	H-2'	2, 3, 2', 3'	-
2'	28.3	1.92 m 1H 1.55 m 1H	H-3'	2, 1', 3', 4' 14'	-
3'	35.6	1.71 m 1H	H-14'	1', 2', 4', 15'	-
4'	88.7	3.11 dd 1H (2.3/9.4)	H-3'	2', 3', 5', 6', 14', 15', 4'-OCH ₃ , 6'-OCH ₃	H-14', H-15'
5'	42.9	1.68 m 1H	H-15'	4', 15'	-
6'	82.4	3.94 dd 1H (2.5/7.0)	H-5', H-7'	4', 5', 7', 8', 15', 6'O-	H-3', H-5'
7'	138.3	5.86 dd 1H (7.0/15.6)	H-6', H-8'	5', 6', 9'	-
8'	133.3	6.31 dd 1H (10.5/15.3)	H-9'	6', 9', 10'	-
9'	135.2	6.71 dd 1H (10.5/15.3)	H-8', H-10'	7', 8', 11'	H-7', H-16'
10'	136.8	6.32 d 1H (15.3)	H-9'	8', 9', 11', 12', 16'	H-6', H-8', H-12'
11'	153.4	-	-	-	-
12'	121.1	5.81 s 1H	-	10', 11', 13', 16'	H-10'
13'	170.8	-	-	-	-
14'	18.4	1.15 d 3H (6.9)	H-3'	2', 3', 4'	-
15'	10.6	0.72 d 3H (7.1)	H-5'	4', 5', 6'	-
16'	14.0	2.28 d 3H (1.1)	-	10', 11', 12', 13'	-
5O-	56.8	3.88 s 3H	-	5, 6	-
7O-	57.1	3.98 s 3H	-	7	-
4'O-	62.0	3.47 s 3H	-	4'	-
6'O-	57.0	3.24 s 3H	-	6'	-



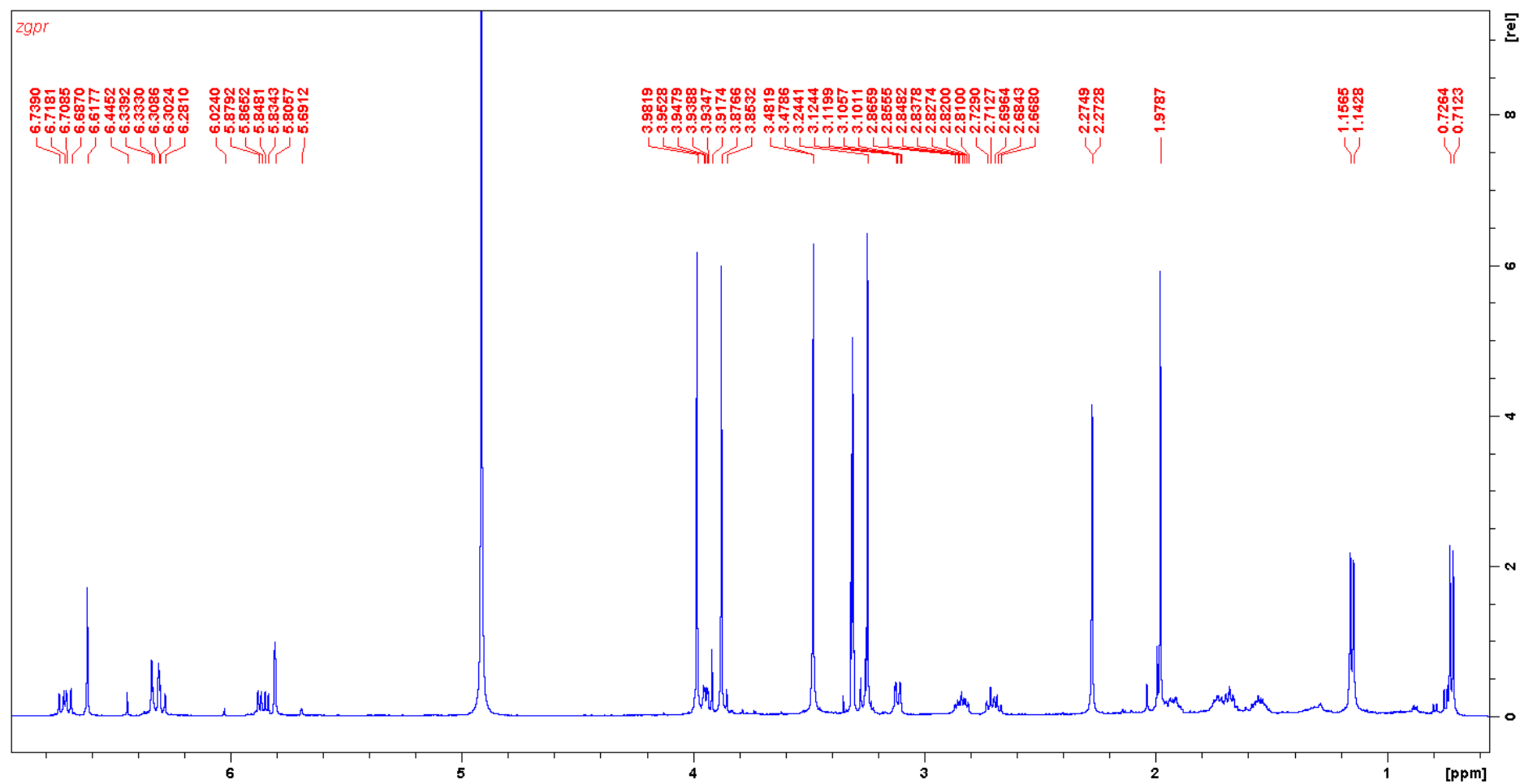


Figure S4. ^1H NMR spectrum of stigmatellic acid (**1**) in methanol- d_4 .

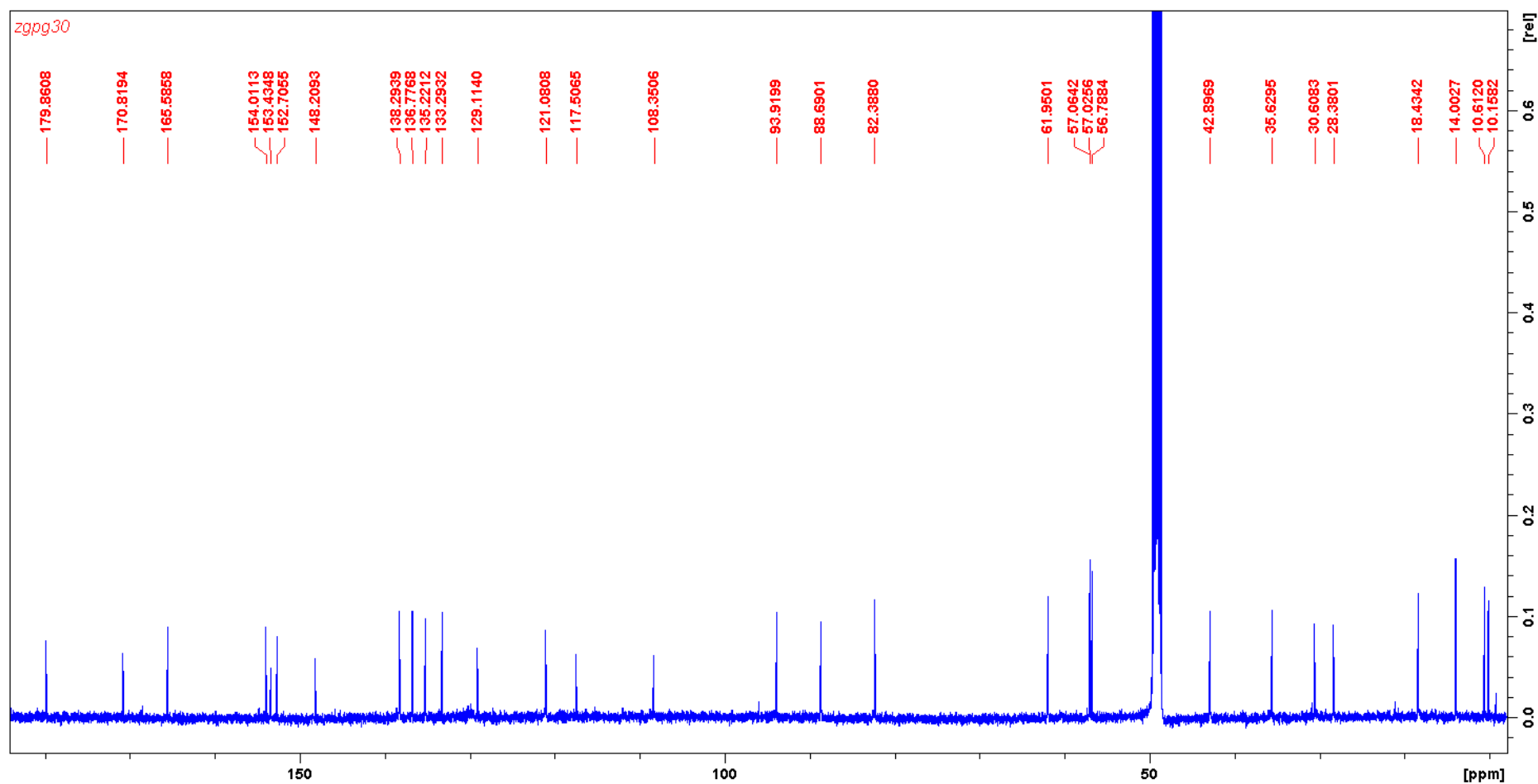


Figure S5. ^{13}C NMR spectrum of stigmatellic acid (**1**) in methanol- d_4 .

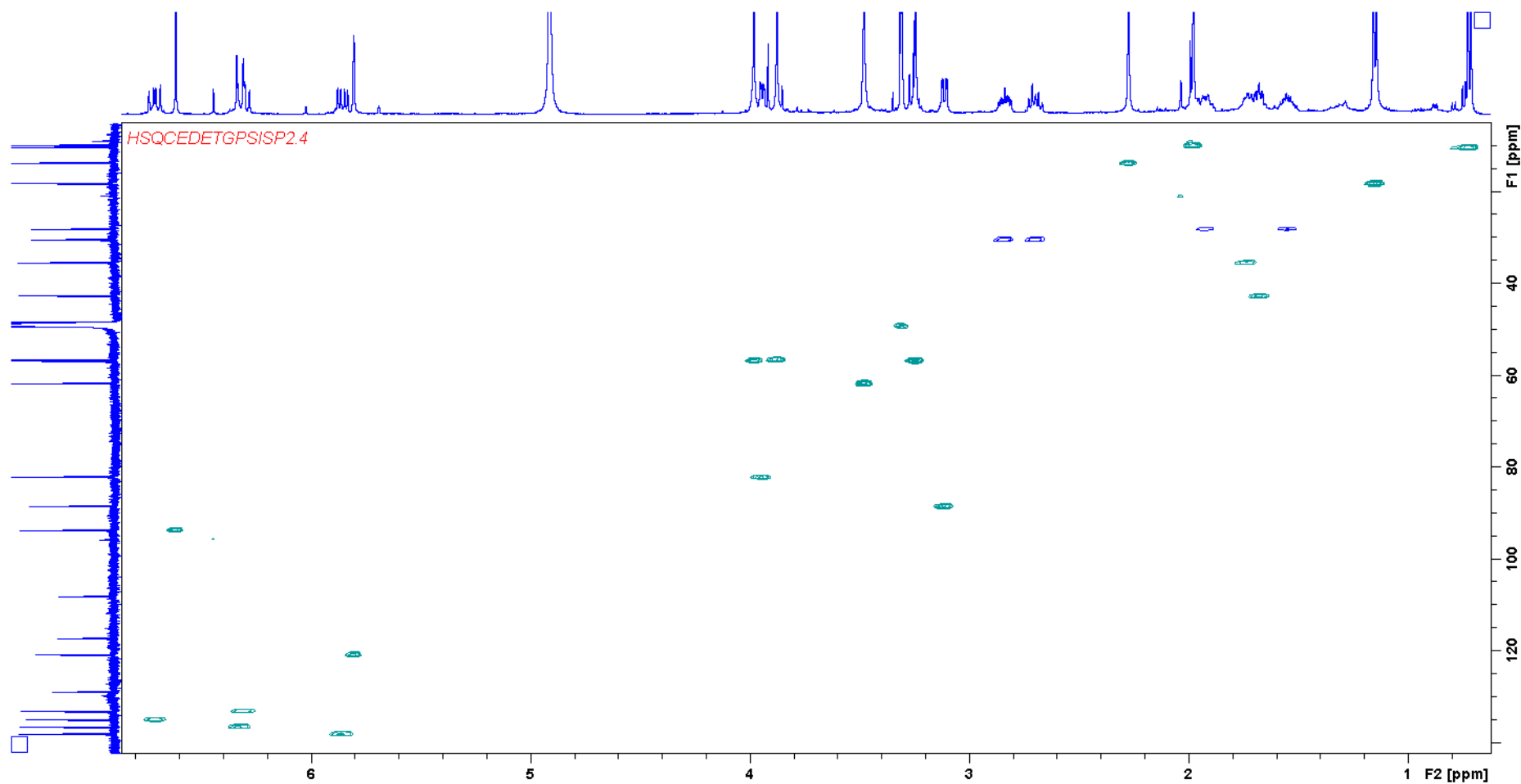


Figure S6. HSQC spectrum of stigmatellic acid (**1**) in methanol- d_4 .

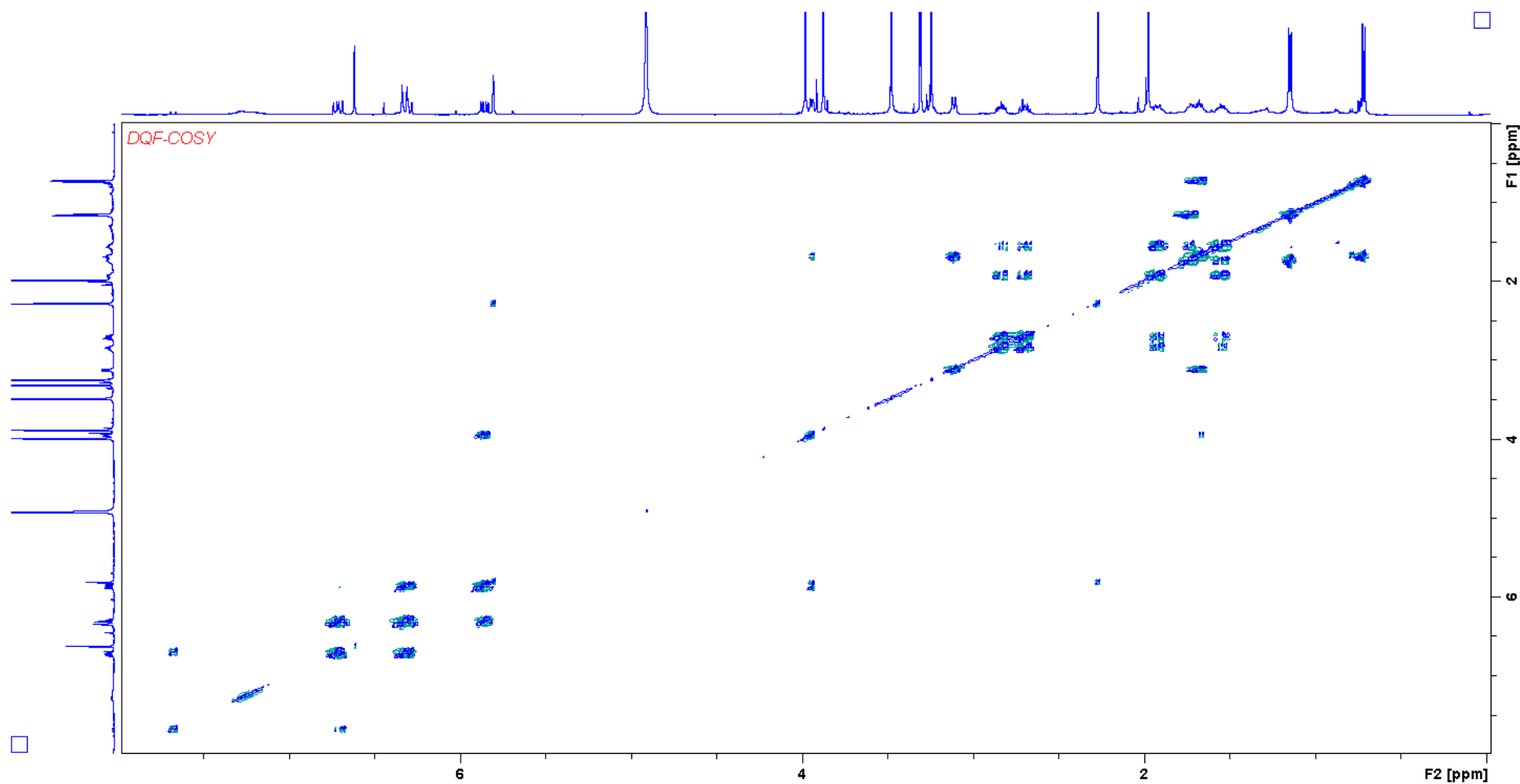


Figure S7. DQF-COSY spectrum of stigmatellic acid (**1**) in methanol- d_4 .

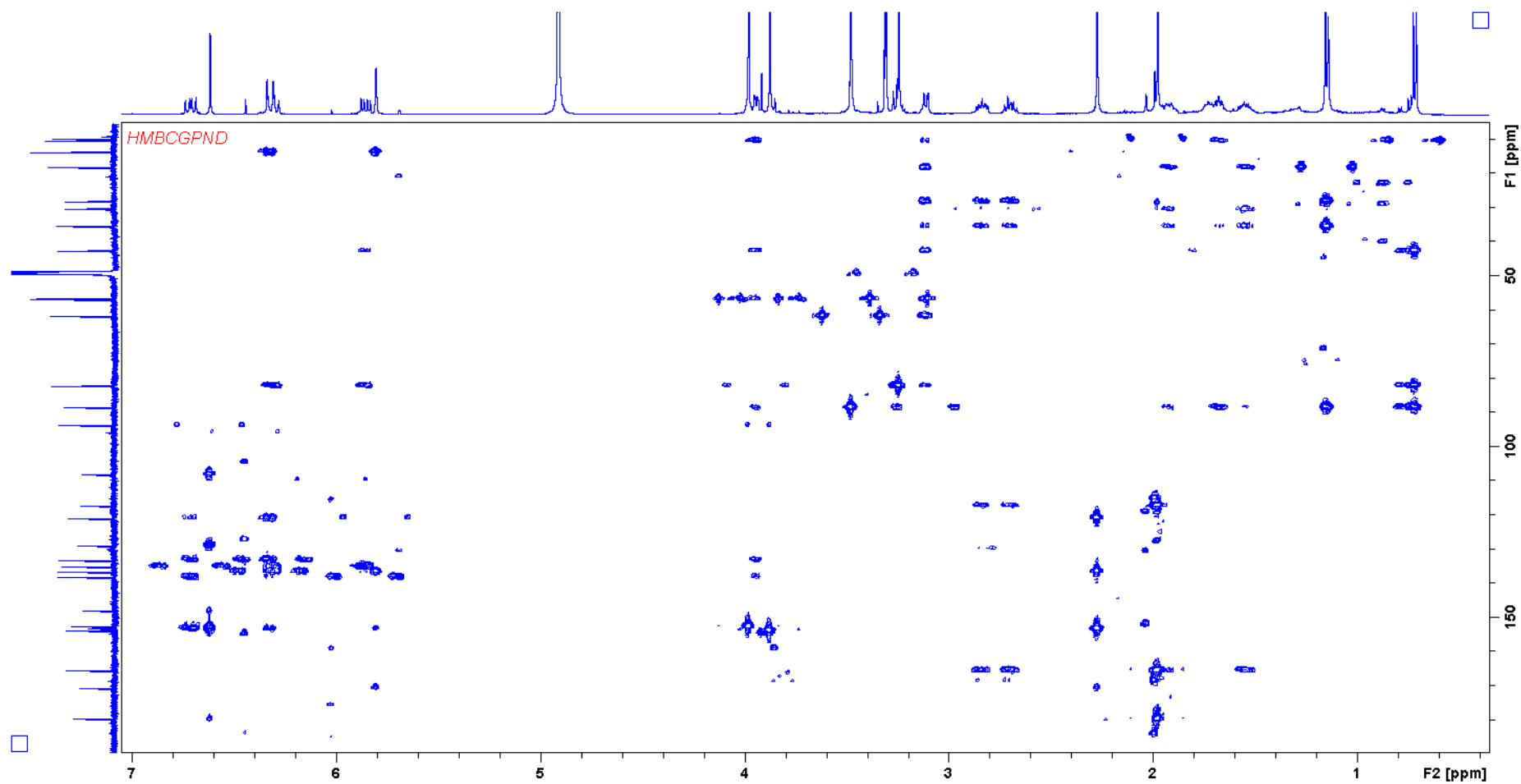


Figure S8. HMBC spectrum of stigmatellic acid (**1**) in methanol- d_4 .

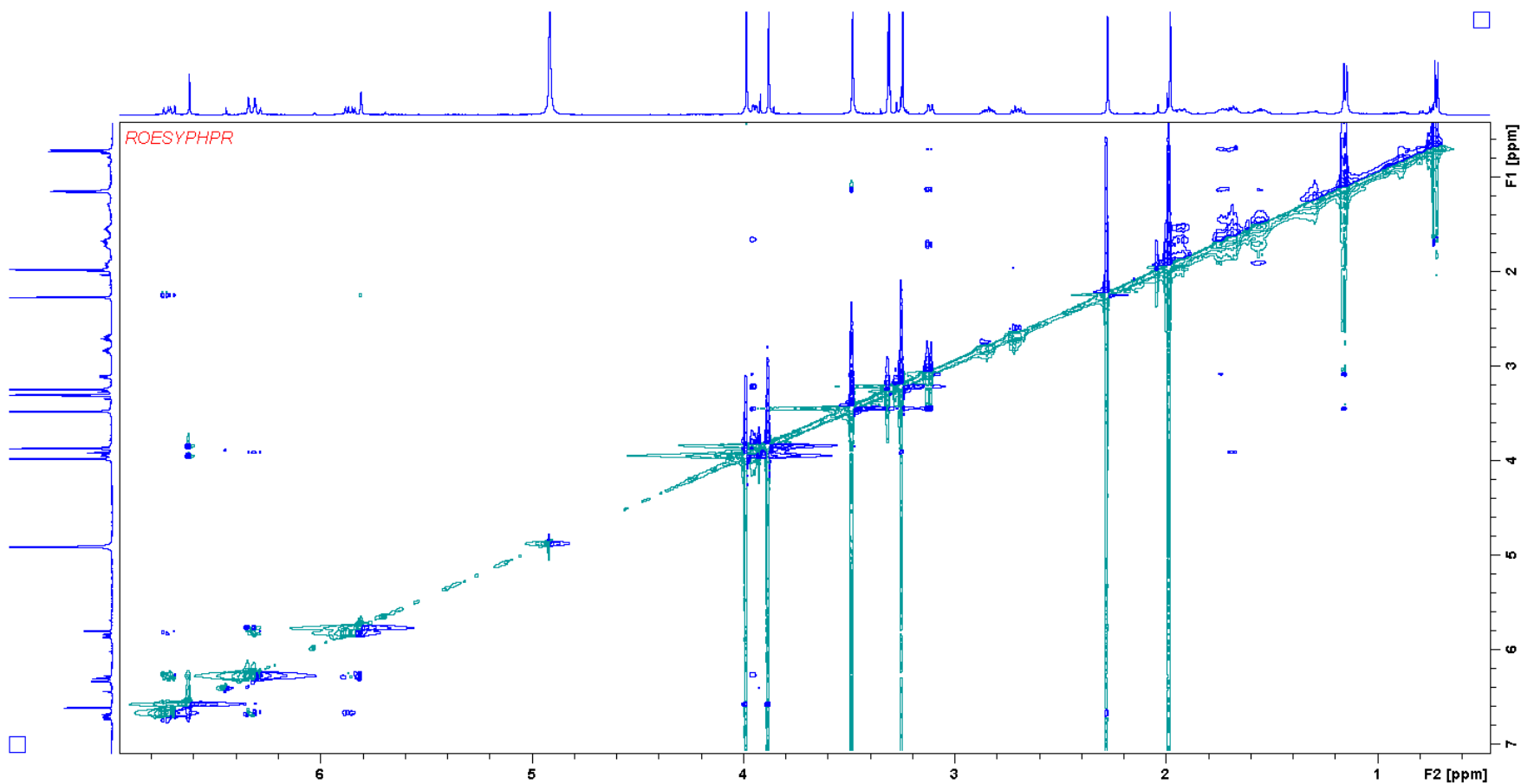


Figure S9. ROESY spectrum of stigmatellic acid (1) in methanol-d₄.

Supplementary Materials 4

Table S3 Alignment of KR domain sequences from the stigmatellin biosynthesis (MCy10943^T) and comparison of predicted and observed product stereochemistry. Influential residues in the sequence are shown in bold letters. Since the predicted stereospecificity of the KR domains involved in the stigmatellin biosynthesis in the myxobacterial strain *V. cumulatum* MCy10943^T is – according to previously identified sequence motifs within KR domains [3] – identical to the homologs in the myxobacterial strain *S. aurantiaca* Sg a15 (**Table S7**), the absolute configuration of **1** and **3** might resemble the absolute configuration of **4**.

Gene	Module	Loop region	Catalytic region	KR type	Pred.	Obs.
<i>stiA</i>	1	HAAGLLDDGTVLQL	SSSASLVGMPGQGNYAAANA	B	active (C ^S)	C=C (<i>E</i>)
<i>stiB</i>	2	HAAGVLDDGVLLRQ	SSMASALGSRGQGNYAAANA	B	C ^S –OH	C=C (<i>E</i>)
<i>stiC</i>	3	HAAGVVQDGALLRQ	SSAASLLGPRGQGNYAAGNA	?	active	C=C (<i>E</i>)
<i>stiD</i>	4	HAAGVAHPRSLVEL	SSGSALMSSPMLGGYAAANS	?	active	C ^S –OH
<i>stiE</i>	5	HSVVLLDDGVLLKQ	SSLASMLGAPGQGNYTAAGA	B1	active	C ^S –OH
<i>stiF</i>	6	HSAGVLDDGVLRQ	SSVASLFGSASQGNYAAANAF	B	active (C ^S)	CH ₂
<i>stiH</i>	7	HTGGPWTVRASREL	SSVASVWGSGLSHHAAAH	---	inactive	C=O

Table S4 Alignment of KR domain sequences from the stigmatellin biosynthesis (Sg a15) and comparison of predicted and observed product stereochemistry. Influential residues in the sequence are shown in bold letters.

Gene	Module	Loop region	Catalytic region	KR type	Pred.	Obs.
<i>stiA</i>	1	HAAGLLDDGTVLQL	SSAASLVGIPGQGNYAAGNA	B	active (C ^S)	C=C (<i>E</i>)
<i>stiB</i>	2	HAAGVLDDGVLLRQ	SSMASALGSRGQGNYAAANA	B	C ^S –OH	C=C (<i>E</i>)
<i>stiC</i>	3	HAAGVVQDGALLRQ	SSAASLLGPRGQGNYAAGNA	?	active	C=C (<i>E</i>)
<i>stiD</i>	4	HAAGVANPKPLADL	SSGSALMSSPLLGGYAAANAF	?	active	C ^S –OH
<i>stiE</i>	5	HSVVLLDDGVLLKQ	SSLASMLGAPGQGNYTAAGA	B1	active	C ^S –OH
<i>stiF</i>	6	HSAGVLDDGVLRQ	SSIASMFGSASQGNYAAANAF	B	active (C ^S)	CH ₂
<i>stiH</i>	7	HAGGAWTPRASRD	SSVASVWGSGLSHHAAAH	---	inactive	C=O

Supplementary Materials 5

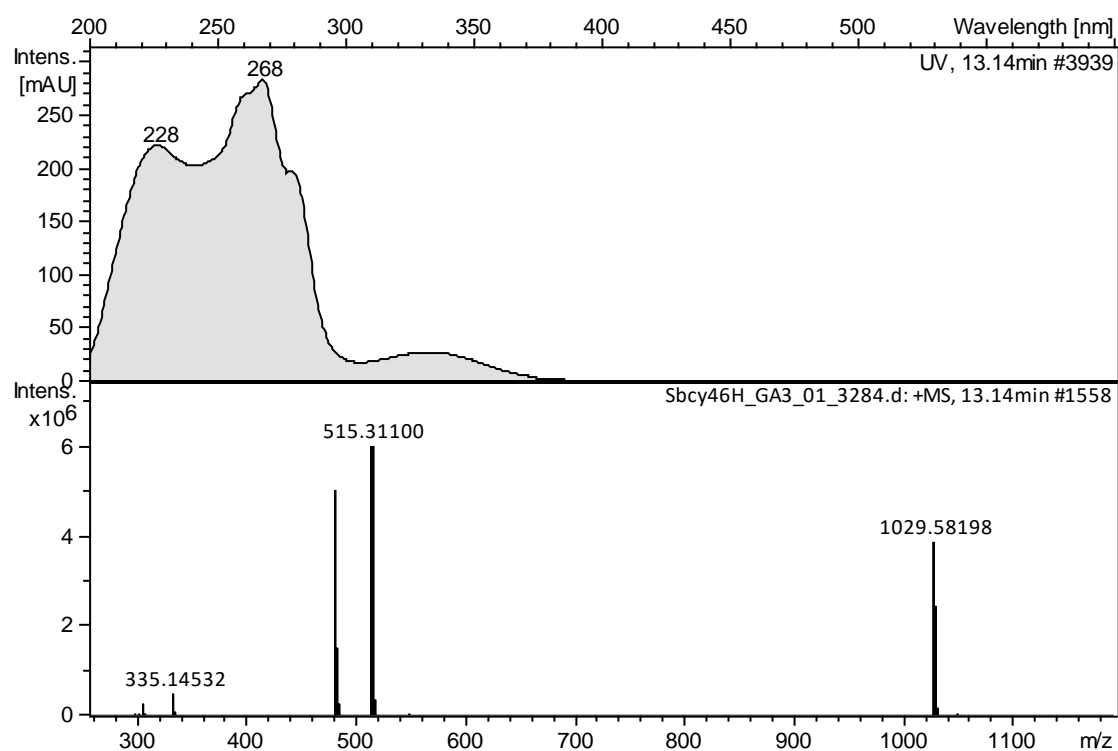


Figure S10. UV/VIS and partial ESI+MS spectra of purified *iso*-methoxy stigmatellin (**2**).

Supplementary Materials 6

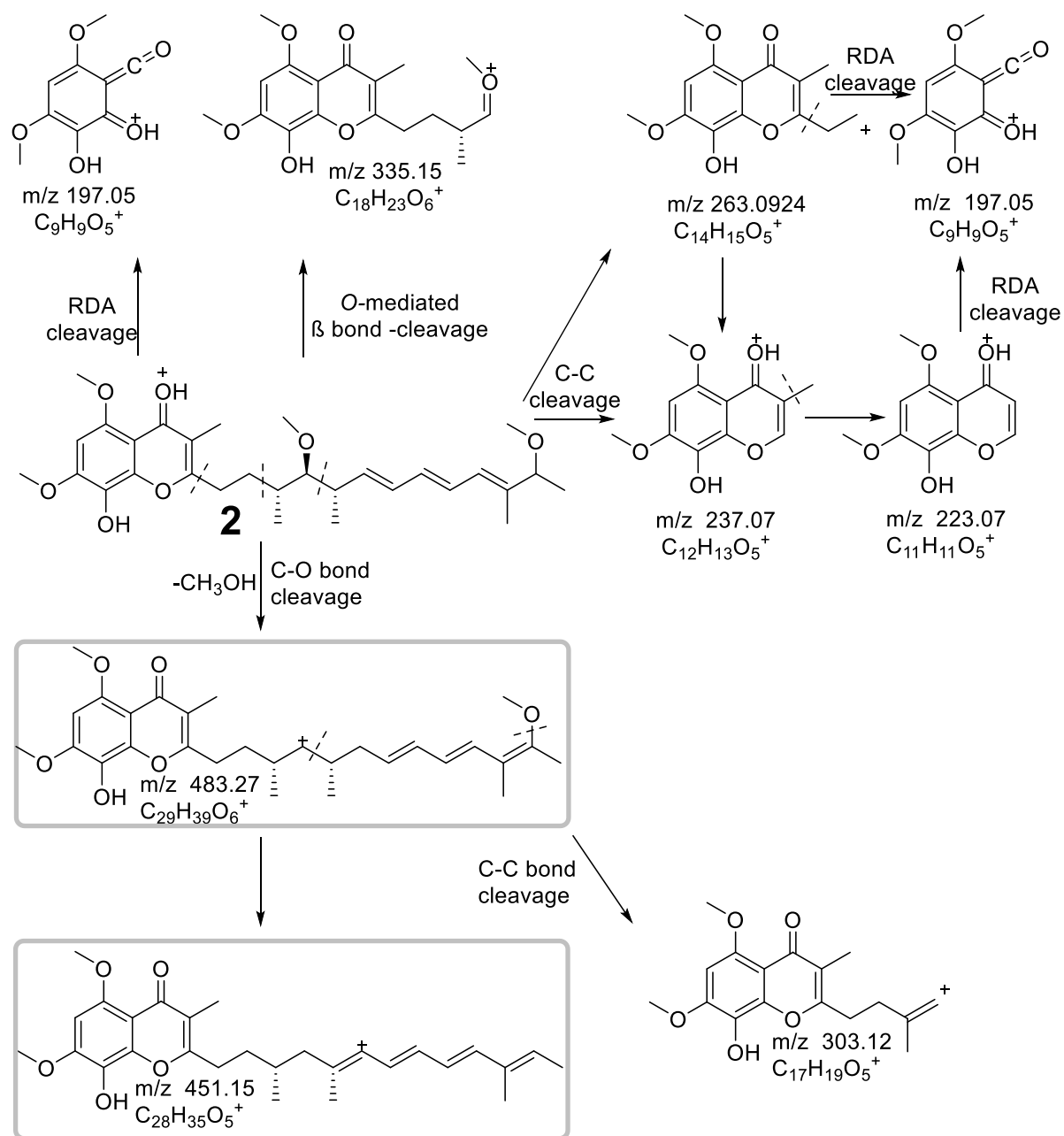


Figure S11. MS² fragmentation scheme of **2** and proposed structure of identified key ion fragments (ion fragments in grey box have been observed specifically for **2** and **4**). RDA: retro-Diels Alder.

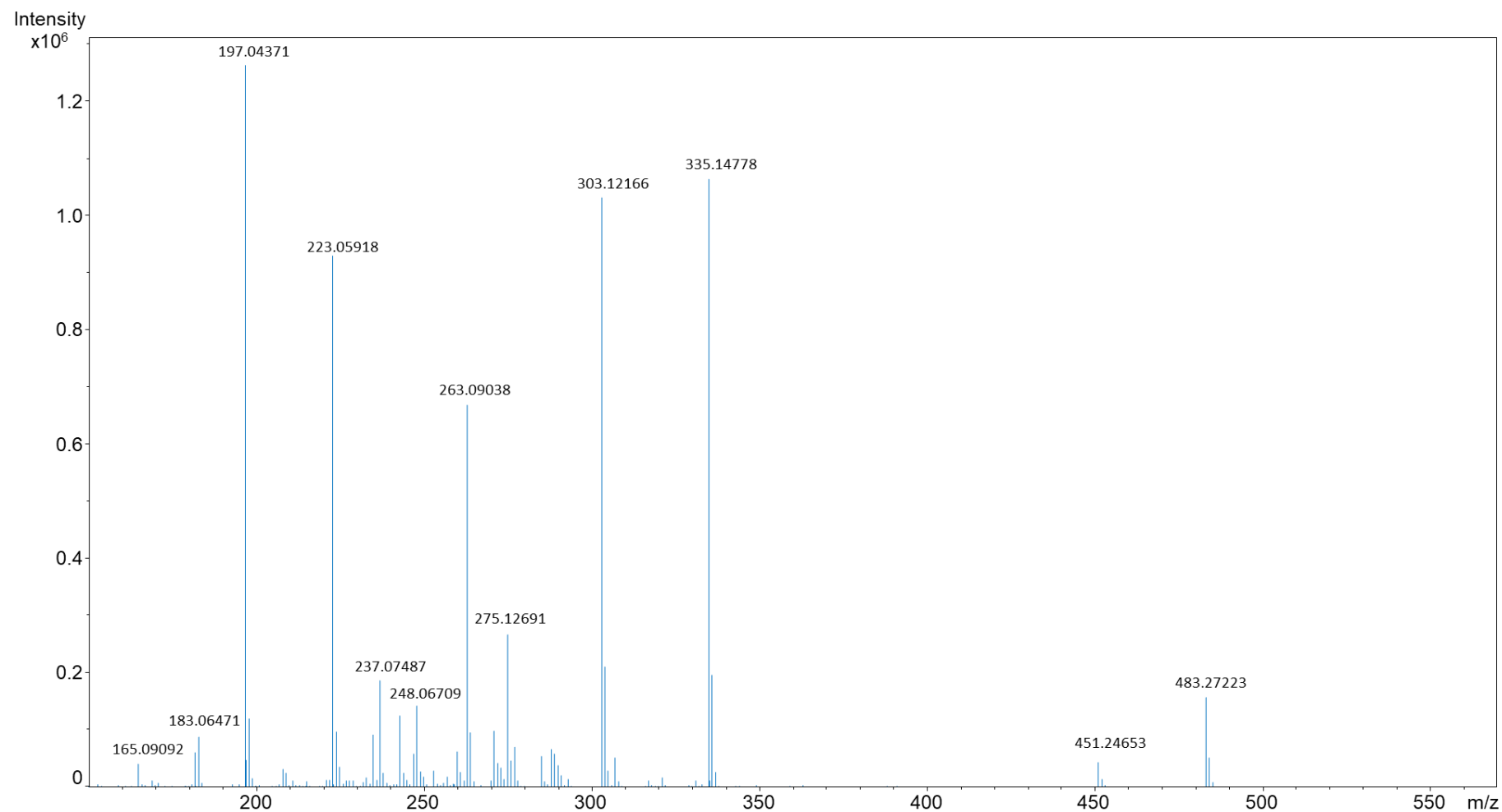


Figure S12. Fragmentation pattern in ESI+MS² experiment of *iso*-methoxy stigmatellin A (2).

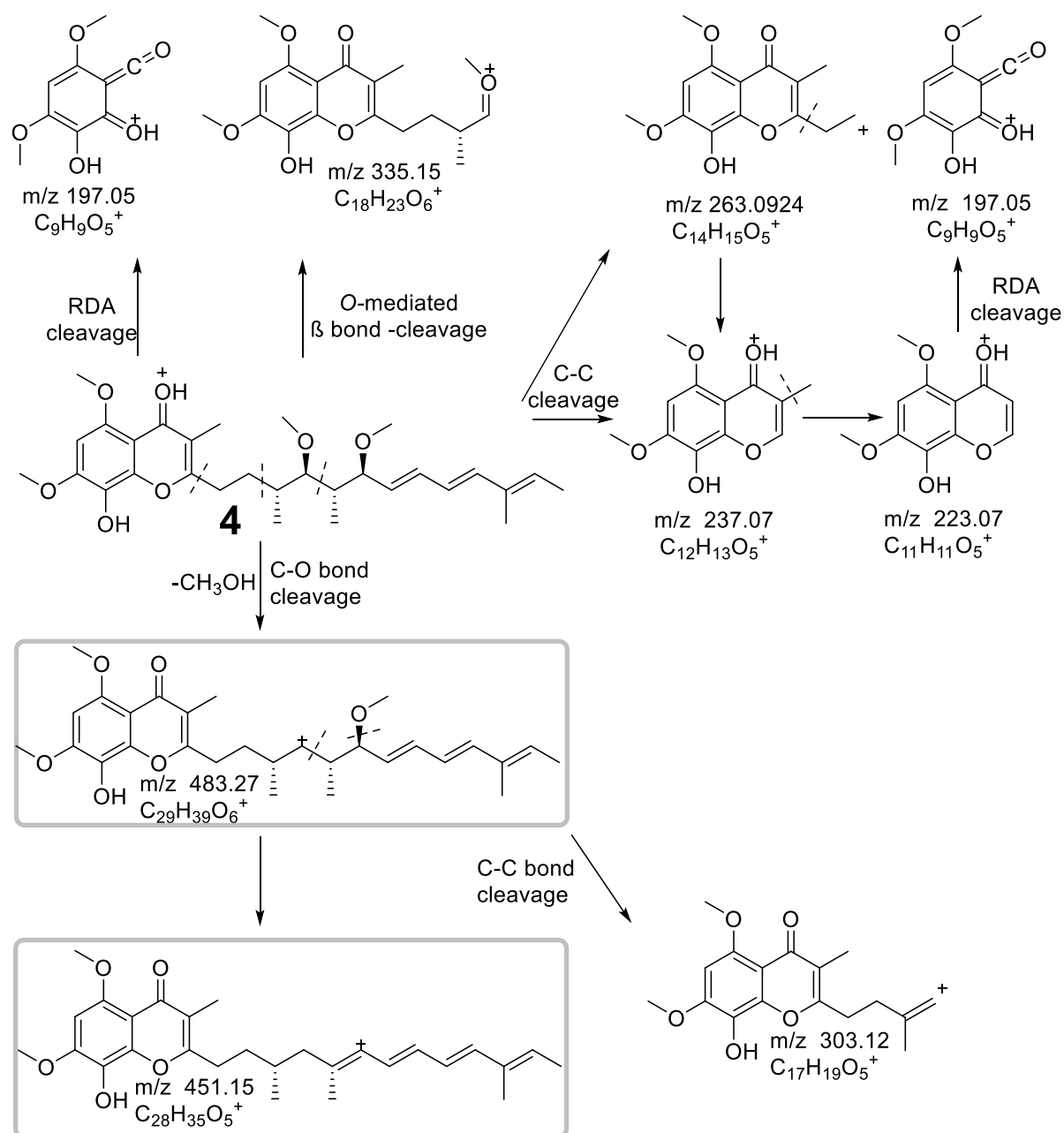


Figure S13. MS² fragmentation scheme of **4** and proposed structure of identified key ion fragments (ion fragments in grey box have been observed specifically for **2** and **4**). RDA: retro-Diels Alder.

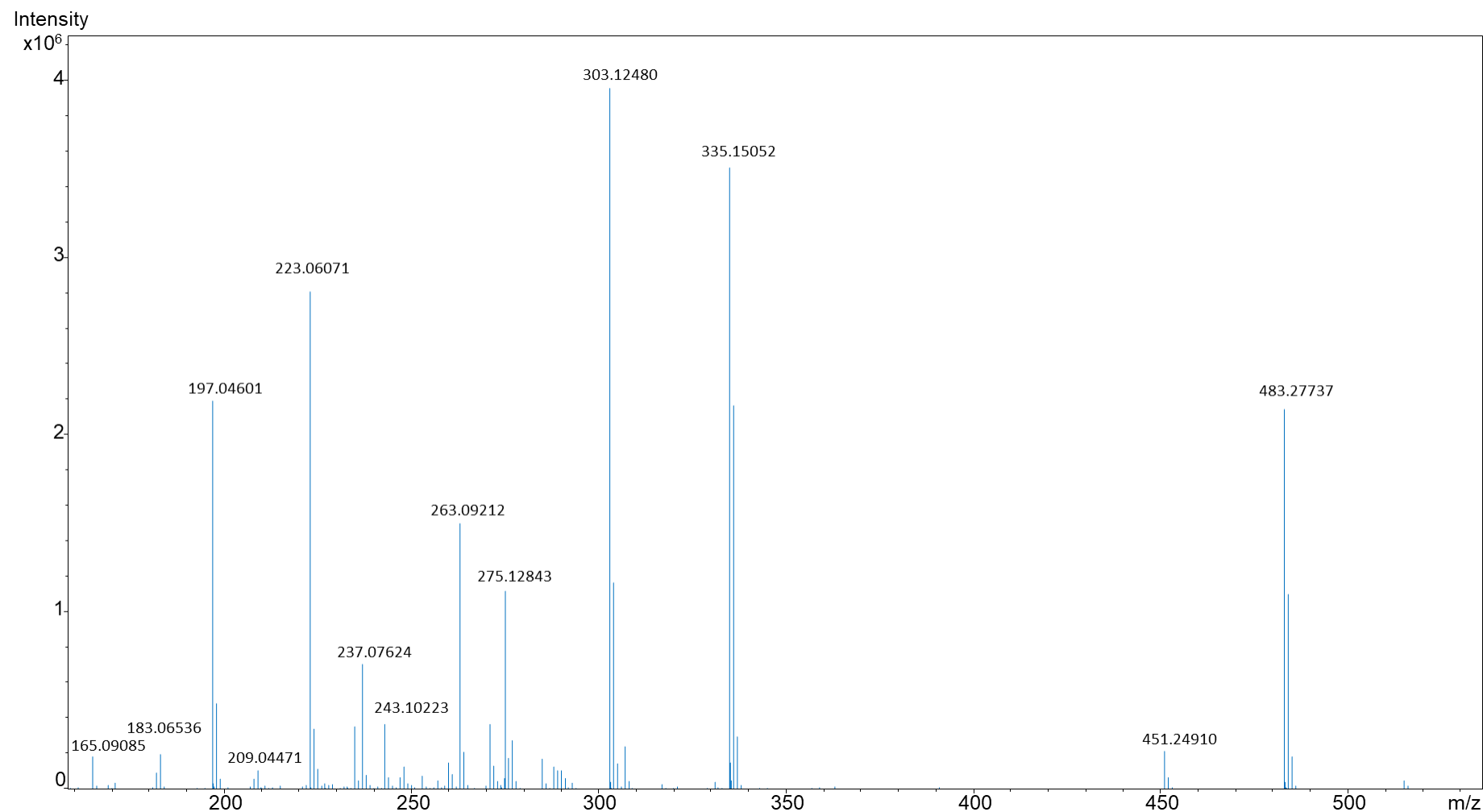
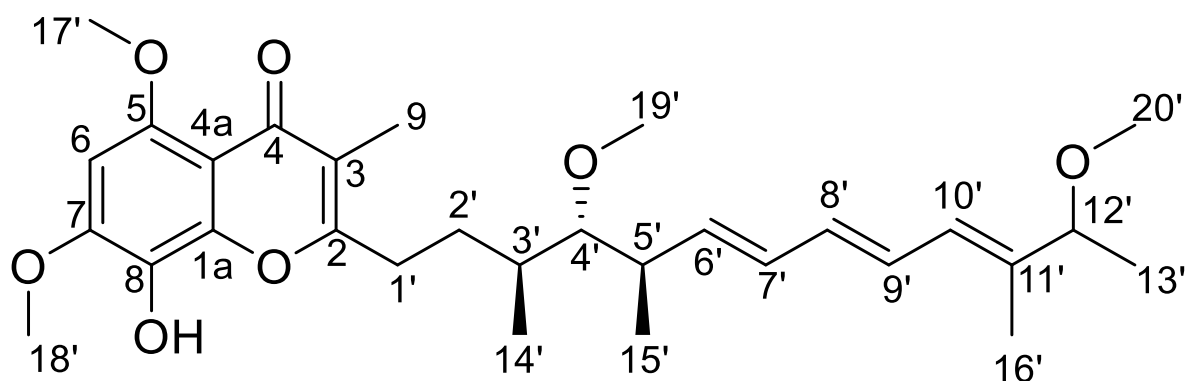


Figure S14. Fragmentation pattern in ESI+MS² experiment of stigmatellin A (**4**).

Supplementary Materials 7

Table S5. Spectroscopic values for *iso*-methoxy stigmatellin (**2**) acquired in methanol- d_4 at 700 MHz.

<i>Iso</i> -methoxy-stigmatellin (2)				
Position	δ_c	δ_H [m, J (Hz)]	COSY	HMBC
1a	148.1	-	-	-
2	165.5	-	-	-
3	117.2	-	-	-
4	179.7	-	-	-
4a	108.2	-	-	-
5	153.9	-	-	-
6	93.8	6.62 s 1H	-	4a,5,7 8, 1a,
7	152.5	-	-	-
8	128.9	-	-	-
9	9.9	1.98 s 3H	-	1', 2, 3,4
1'	30.6	2.84 m 1H 2.69 m 1H	H-2'	2',3', 2,3
2'	30.4	2.06 m 1H 1.56 m 1H	H-3'	1', 3', 4',14',
3'	37.2	1.67 m 1H (1.1)	H-14'	1',2', 4',14'
4'	91.6	2.86 m 1H	H-3',H-5'	2', 3', 5', 6', 4'-O-, 14',15'
5'	41.3	2.51 m 1H	H-6'	4', 6',7',15'
6'	137.7	5.69 m 1H	H-7'	4',5',7',8',15'
7'	132.1	6.14 dd 1H	H-6',H-8'	5', 6',8',9'
8'	127.7	6.36 m 1H	H-7,H-9'	6', 7',9',10'
9'	134.5	6.14,m, 1H	H-8',H-10'	7',8',10', 11'
10'	128.4	6.01, d, 1H(11.0)	H-9'	8',9',11',12',16'
11'	138.7	-	-	-
12'	83.9	3.37 s 1H (6.4)	H-13'	10',11',12'-O-,13',16',
13'	20.3	1.21 dd 3H (0.5/6.4)	H-12'	11';12'
14'	16.8	1.01 d 3H (6.5)	H-3'	2',3',4',
15'	18.4	1.04 d 3H (6.9)	H-5'	4',5', 6'
16'	11.1	1.67 d 3H (1.1)	-	10',11',12',13'
5O-	56.6	3.88 s 3H	-	5
7O-	56.9	4.00 s 3H	-	7
4'O-	61.7	3.45 s 3H	-	4'
6'O-	56.1	3.17 s 3H	-	12'



Iso-methoxy-stigmatellin A
2

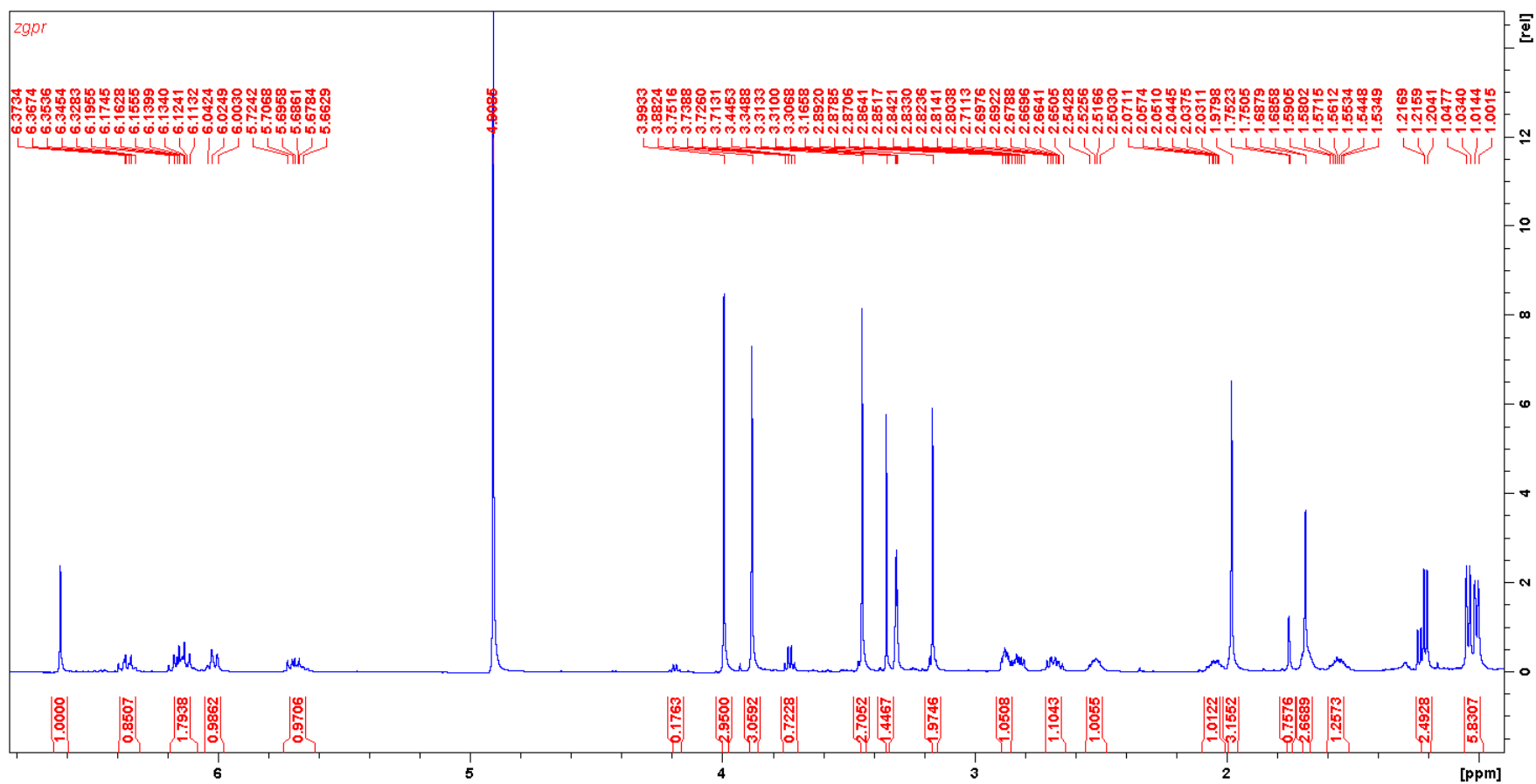


Figure S15. ^1H NMR of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

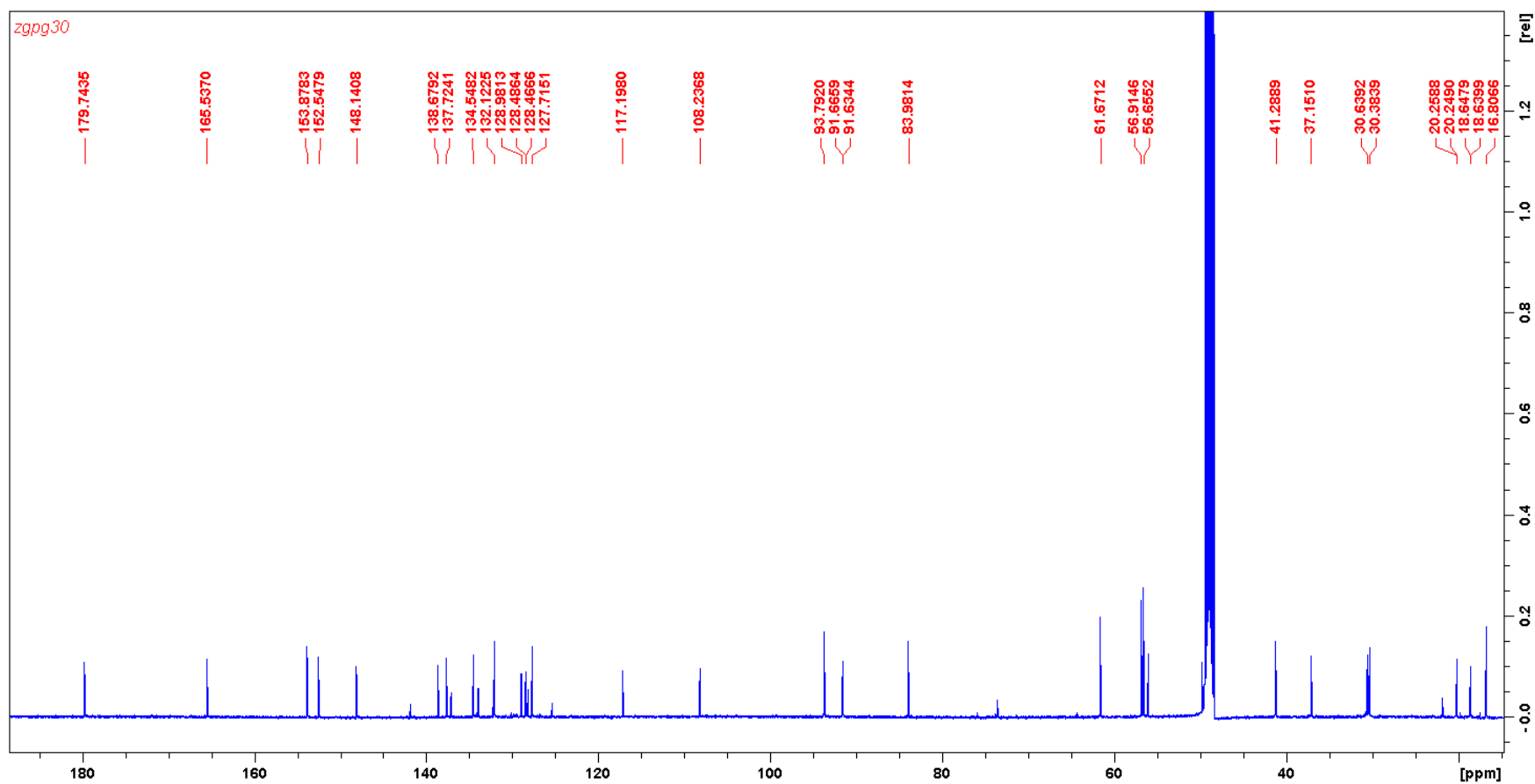


Figure S16. ^{13}C NMR of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

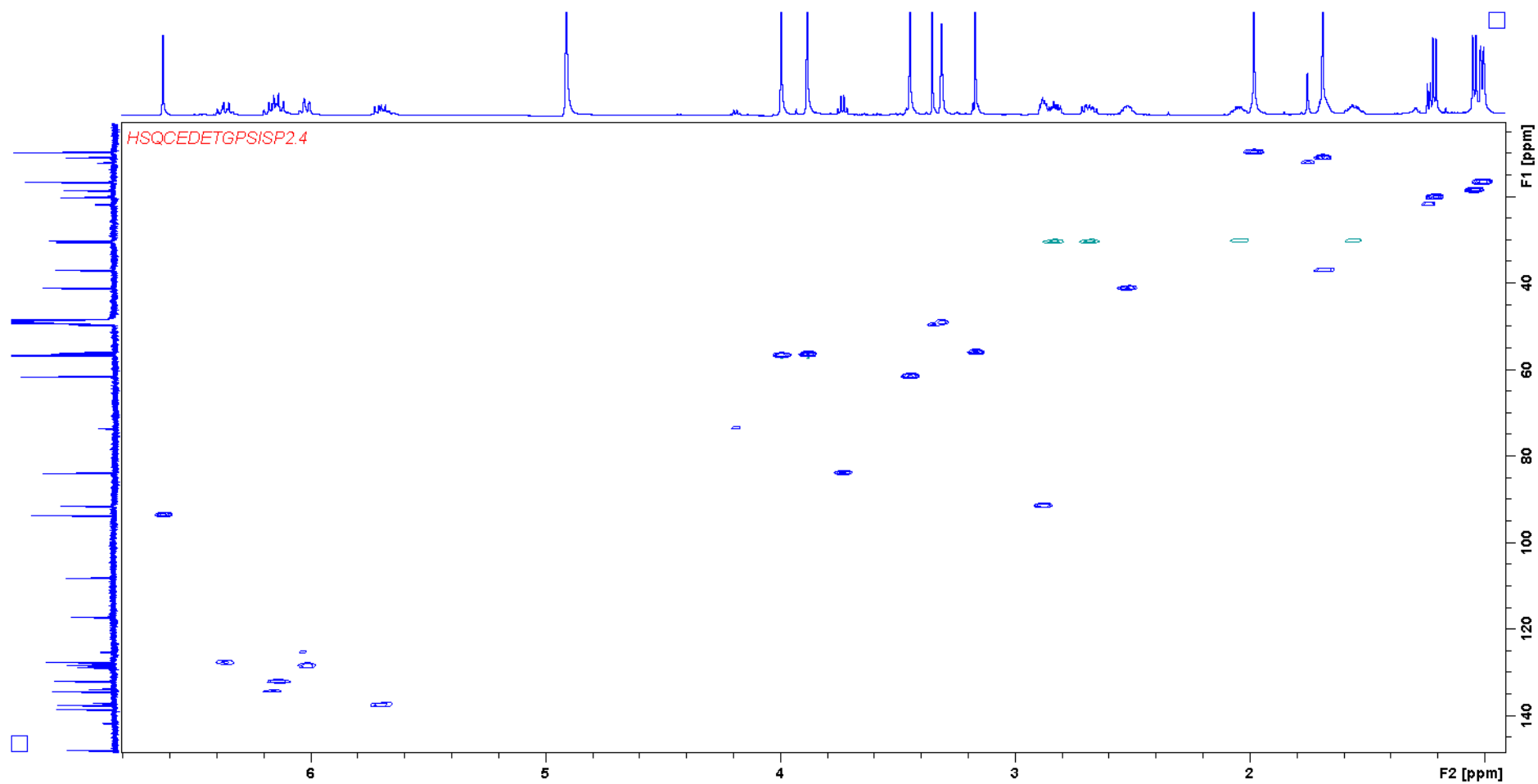


Figure S17. HSQC spectrum of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

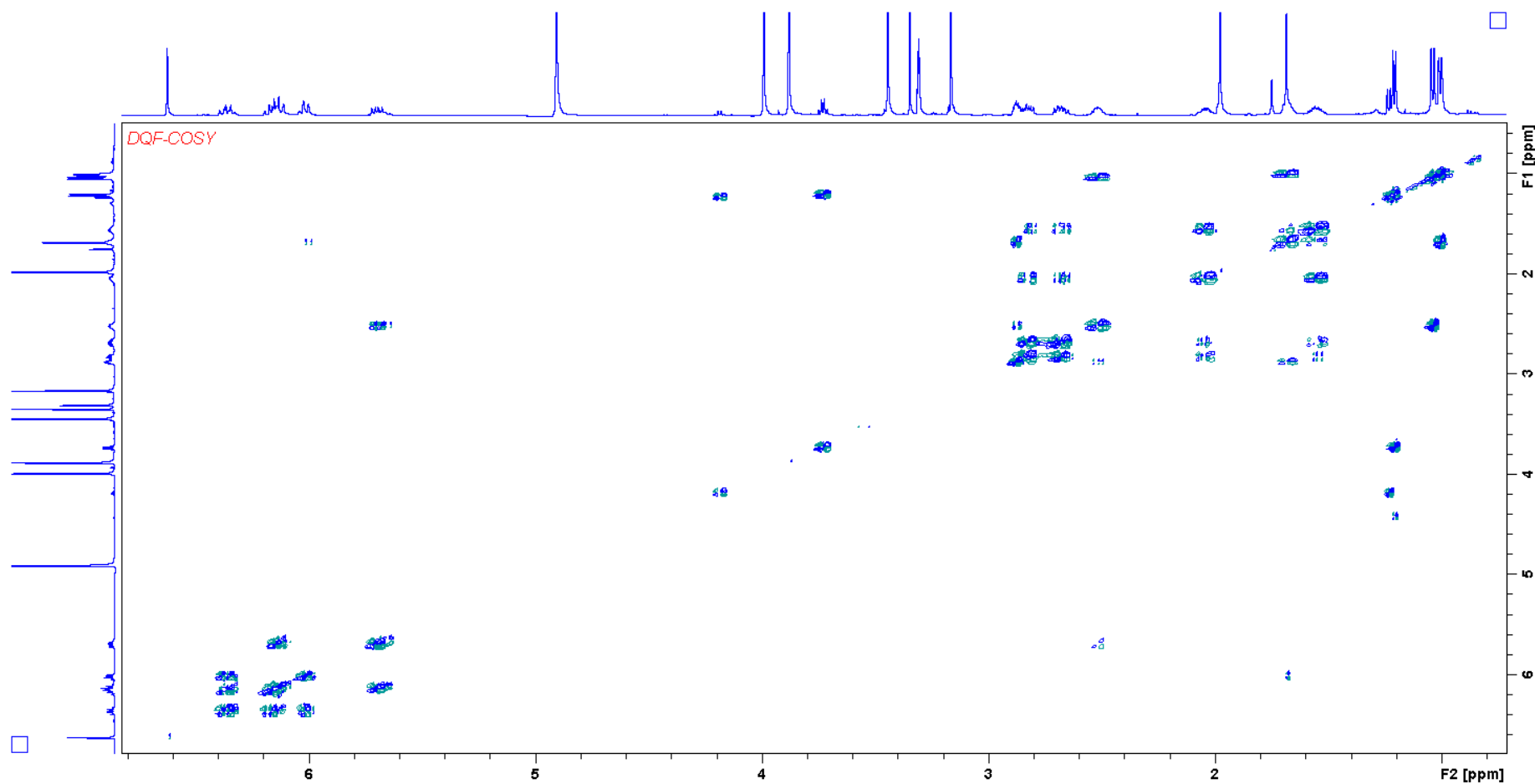


Figure S18: DQF-COSY spectrum of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

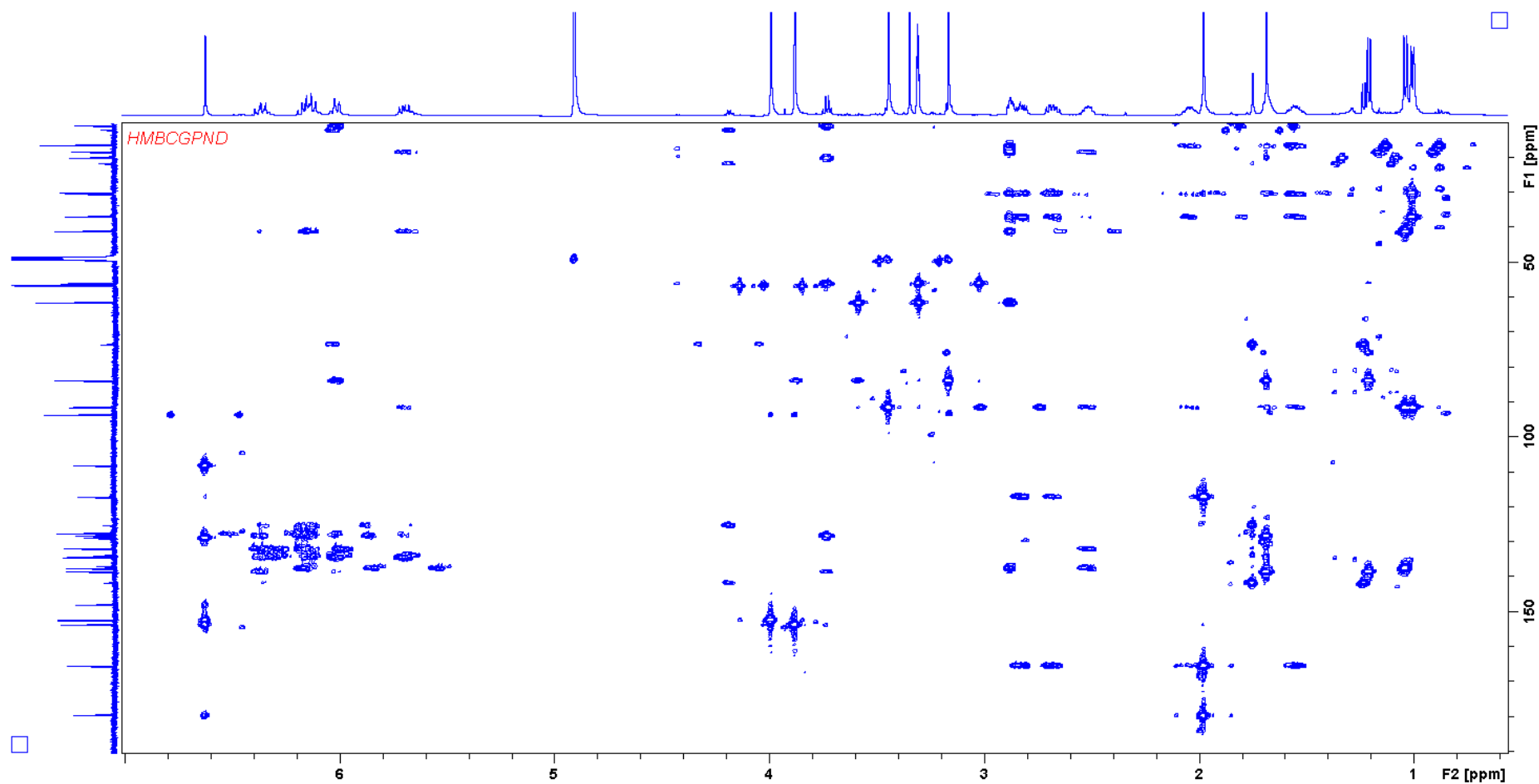


Figure S19. HMBC spectrum of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

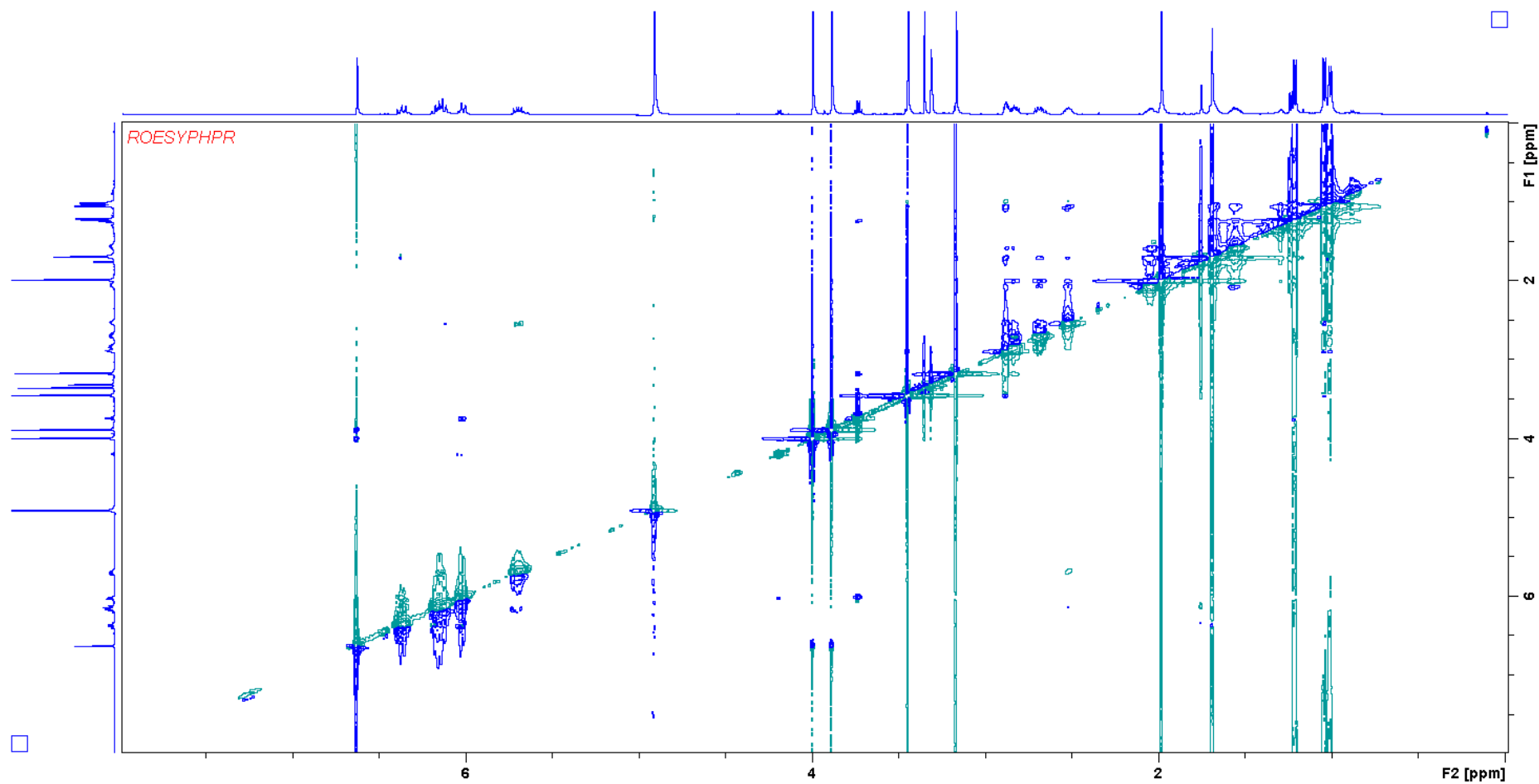


Figure S20. ROESY spectrum of *iso*-methoxy stigmatellin A (**2**) in methanol- d_4 .

Supplementary Materials 8

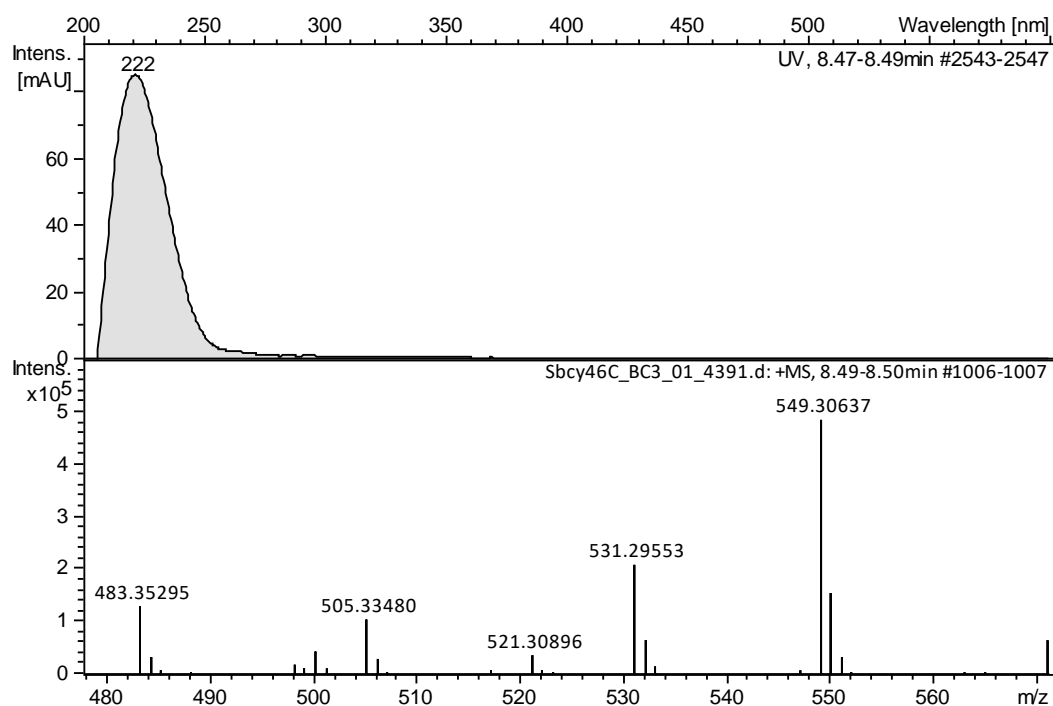


Figure S21. UV/VIS and partial ESI+MS spectra of purified stigmatellin C (isomer 1, 3).

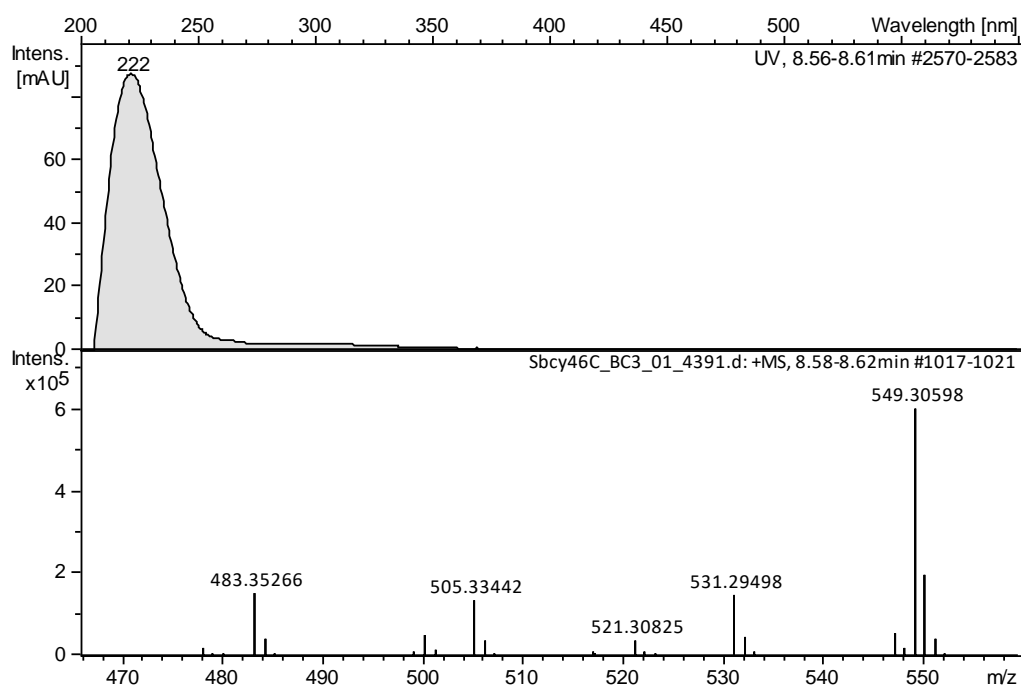


Figure S22. UV/VIS and partial ESI+MS spectra of purified stigmatellin C (isomer 2, 3).

Chemical reaction scheme showing the fragmentation pathways of compound **3** (m/z 531.30, C₃₀H₄₃O₈⁺).

Fragmentation pathways and resulting ions:

- Top Left:** RDA cleavage of compound **3** yields an ion with m/z 197.04 (C₉H₉O₅⁺).
- Top Center:** O-mediated β bond cleavage of compound **3** yields an ion with m/z 335.15 (C₁₈H₂₃O₆⁺).
- Top Right:** RDA cleavage of compound **3** yields an ion with m/z 263.0924 (C₁₄H₁₅O₅⁺).
- Top Far Right:** RDA cleavage of the m/z 263.0924 ion yields an ion with m/z 197.05 (C₉H₉O₅⁺).
- Bottom Left:** C-C cleavage of compound **3** yields an ion with m/z 237.07 (C₁₂H₁₃O₅⁺).
- Bottom Center:** C-C cleavage of the m/z 237.07 ion yields an ion with m/z 223.07 (C₁₁H₁₁O₅⁺).
- Bottom Right:** RDA cleavage of the m/z 223.07 ion yields an ion with m/z 197.05 (C₉H₉O₅⁺).
- Bottom Far Right:** RDA cleavage of the m/z 223.07 ion yields an ion with m/z 197.05 (C₉H₉O₅⁺).
- Bottom Left (Loss of H₂O):** Loss of H₂O from compound **3** yields an ion with m/z 513.30 (C₃₀H₄₁O₇⁺).
- Bottom Center (Loss of CH₃OH):** Loss of CH₃OH from compound **3** yields an ion with m/z 499.26 (C₂₉H₃₉O₇⁺).
- Bottom Far Left:** C-C cleavage of the m/z 499.26 ion yields an ion with m/z 467.24 (C₂₈H₃₅O₆⁺).
- Bottom Far Right:** C-C cleavage of the m/z 499.26 ion yields an ion with m/z 303.12 (C₁₇H₁₉O₅⁺).

S28

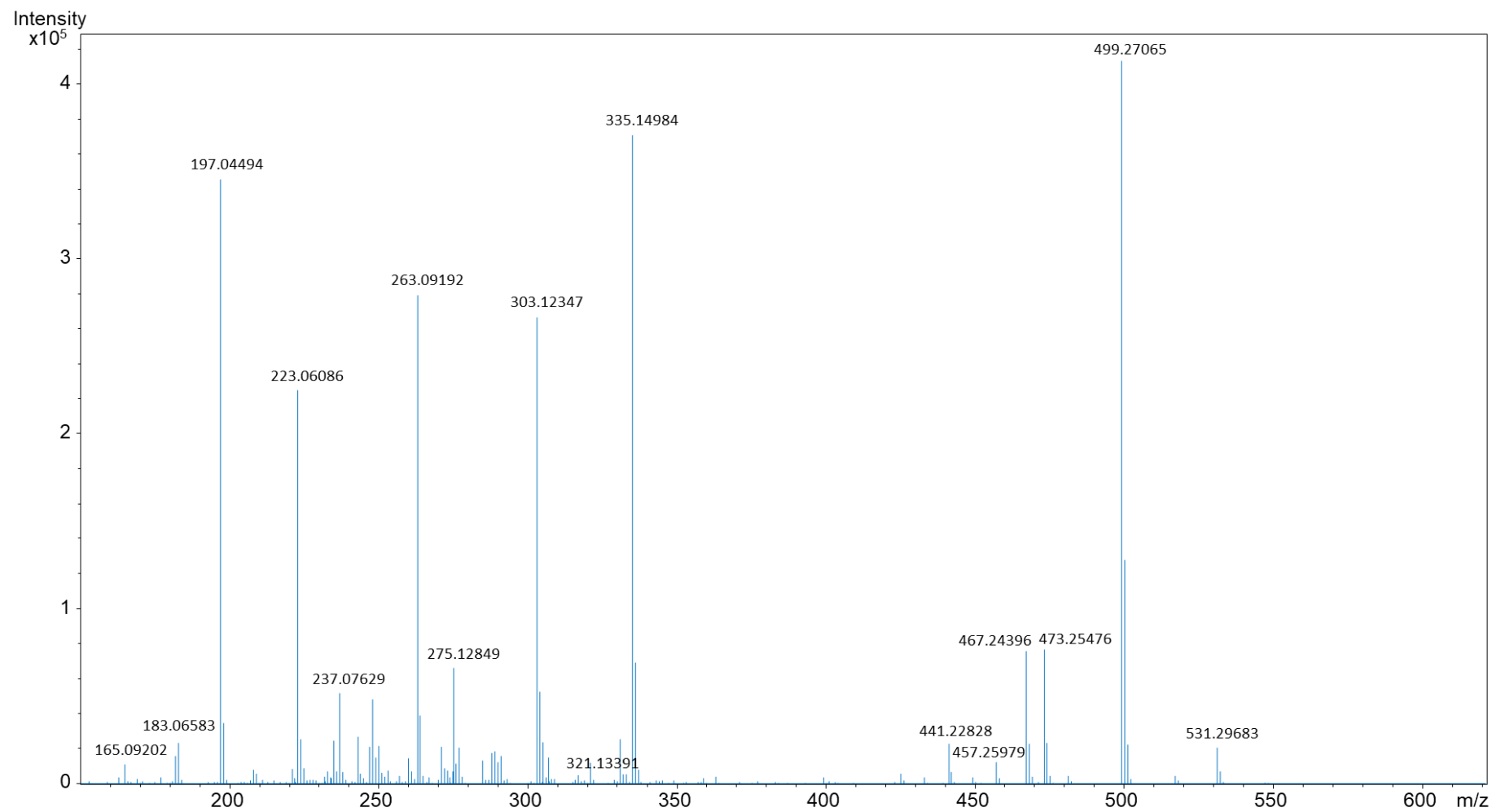


Figure S24. Fragmentation pattern in ESI+MS² experiment of stigmatellin C (isomer 1, **3**).

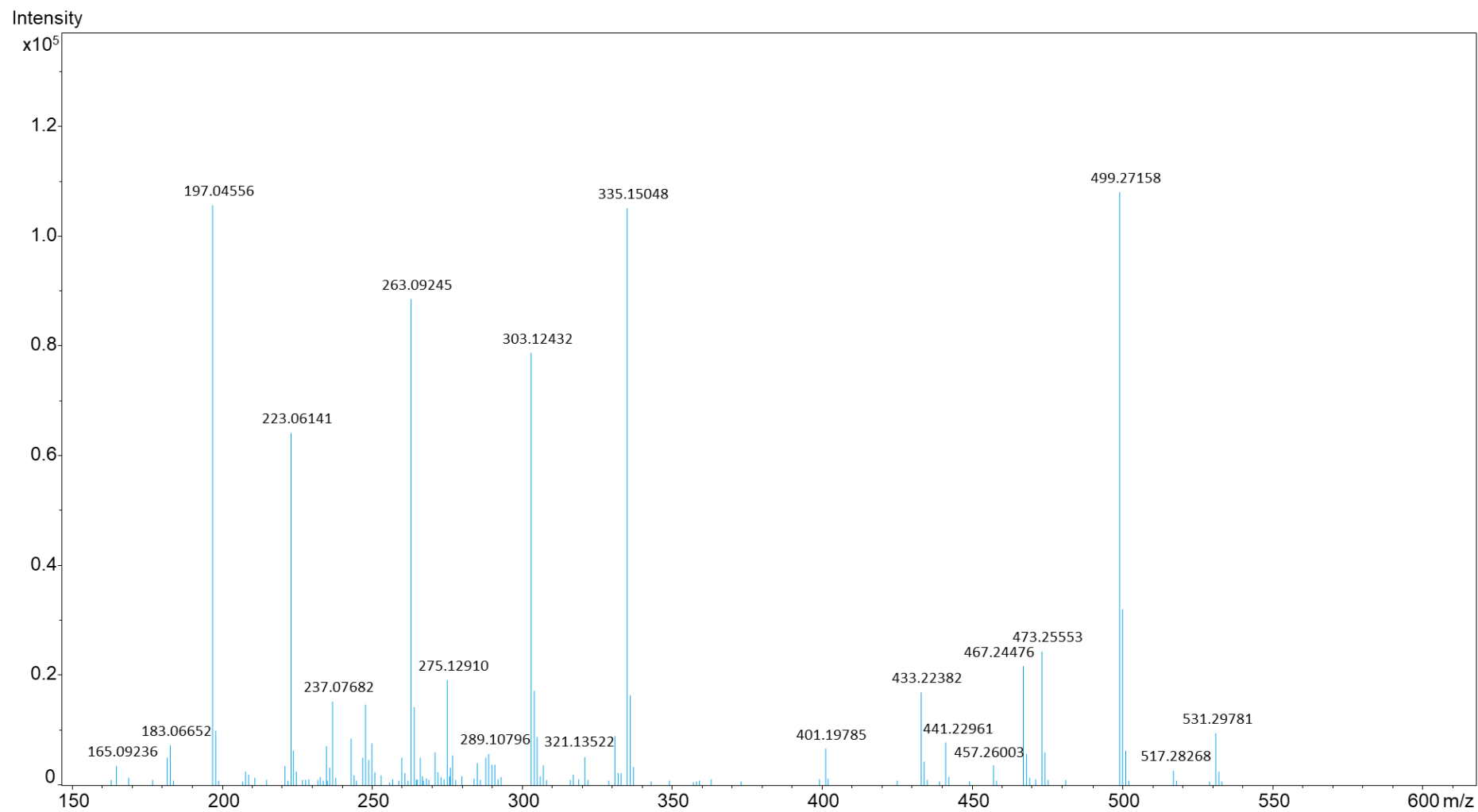
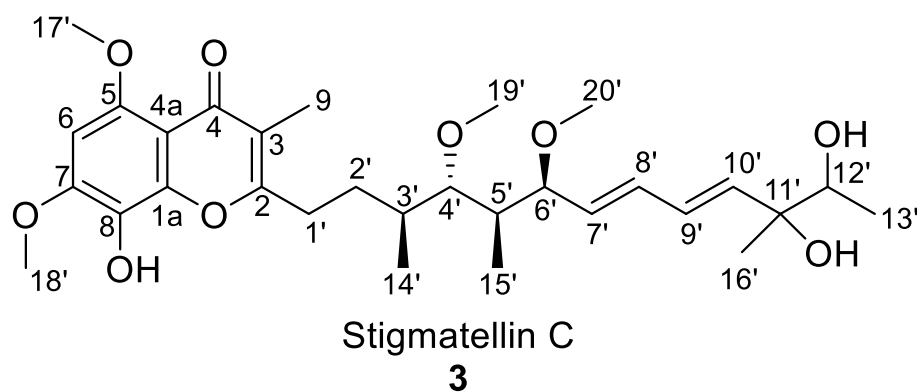


Figure S25. Fragmentation pattern in ESI+MS² experiment of stigmatellin C (isomer 2, 3).

Supplementary Materials 10

Table S6. Spectroscopic values for stigmatellin C (**3**) acquired in methanol- d_4 at 700 MHz.

Stigmatellin C (3)				
Position	δ_C	δ_H [m, J (Hz)]	COSY	HMBC
1a	148.1	-	-	-
2	165.5	-	-	-
3	117.3	-	-	-
4	179.7	-	-	-
4a	108.2	-	-	-
5	153.9	-	-	-
6	93.8	6.63 s 1H	-	4a, 5, 7, 8
7	152.6	-	-	-
8	129.6	-	-	-
9	10.0	1.98 s 3H	-	2, 3, 4, 1', 2'
1'	30.5	2.84 m 1H 2.70 m 1H	H-2'	2, 3, 2', 3'
2'	28.3	1.88 m 1H 1.55 m 1H	H-3'	1', 3', 4', 14'
3'	35.5	1.73 m 1H	H-2', H-4', H-14'	2', 14'
4'	88.5	3.11 dd 1H (2.3/9.4)	H-4', H-5'	2', 3', 4'-OCH ₃ , 5', 6', 14', 15'
5'	42.9	1.66 m 1H	H-4'', H-6', H-15'	4', 15'
6'	82.4	3.88 dd 1H	H-5', H-7'	4', 5', 7', 8', 15', 6'-OCH ₃
7'	133.4	5.60 dd 1H (7.4/15.2)	H-8'	5', 6', 8', 9'
8'	133.8/133.9	6.20 dd 1H (10.5/15.3)	H-7', H-9'	6', 9', 10'
9'	129.6	6.31 ddd 1H (3.3/4.9/7.2/15.4)	H-10'	8', 9', 10'
10'	138.9/139.1	5.81 dd 1H (15.3/20.2)	H-9'	9', 10', 11', 16'
11'	76.3/76.2	-	-	-
12'	74.9/74.8	3.56 s 1H (3.8/6.5)	H-13'	10', 11', 13', 16'
13'	17.8	1.10 dd 3H (6.5/10.5)	-	11', 12', 16'
14'	18.2	1.14 d 3H (6.8)	H-3'	2', 3', 4'
15'	10.3	0.73 d 3H (7.1)	H-5'	4', 5'
16'	23.2	1.24 d 3H (2.1/7.8)	-	9', 10', 11', 12'
5O-	56.7	3.88 s 3H	-	5
7O-	56.9	4.00 s 3H	-	7
4'O-	61.7	3.47 s 3H	-	4'
6'O-	56.6	3.22 s 3H	-	6'



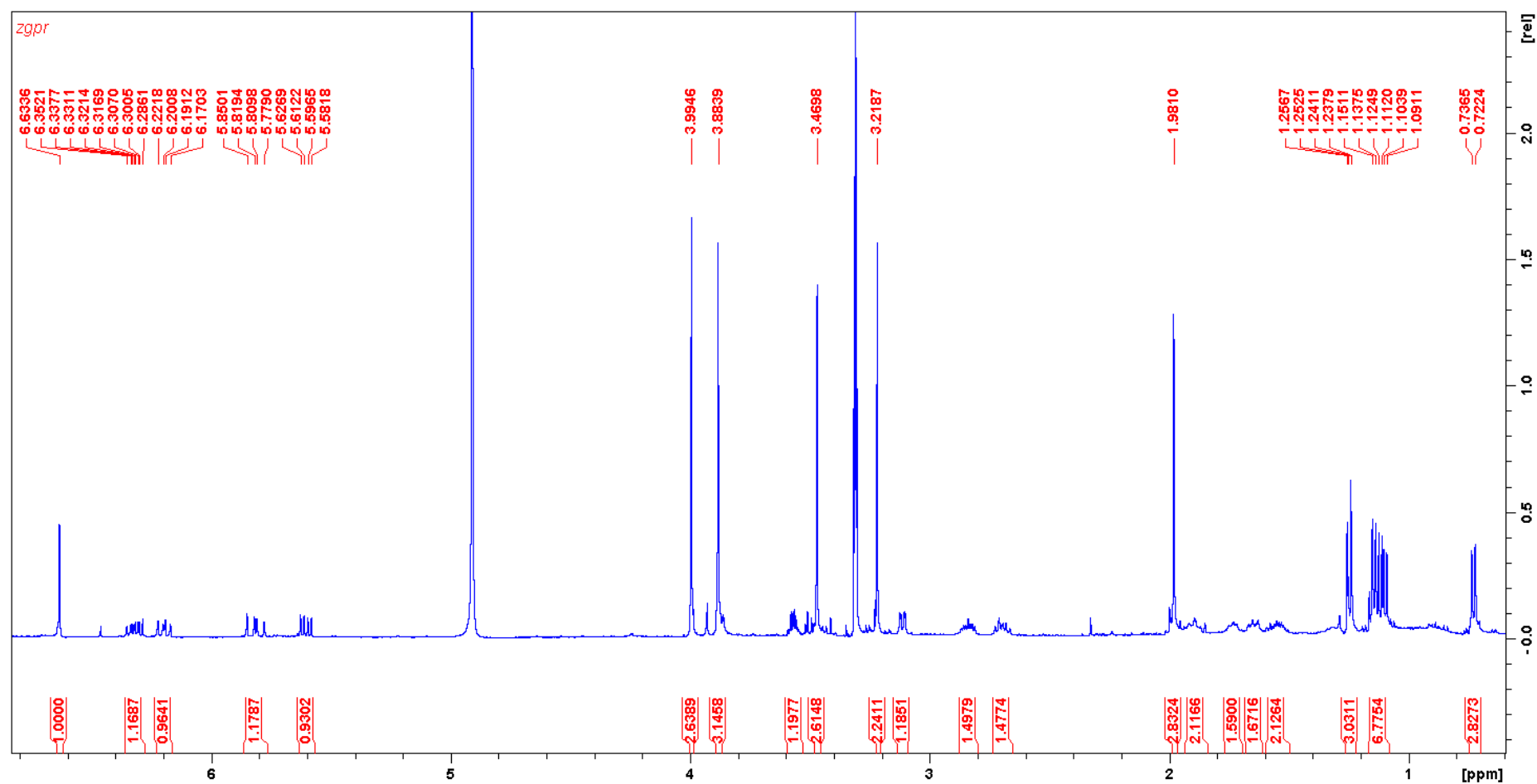


Figure S26. ¹H NMR spectrum stigmatellin C (**3**) in methanol-d₄.

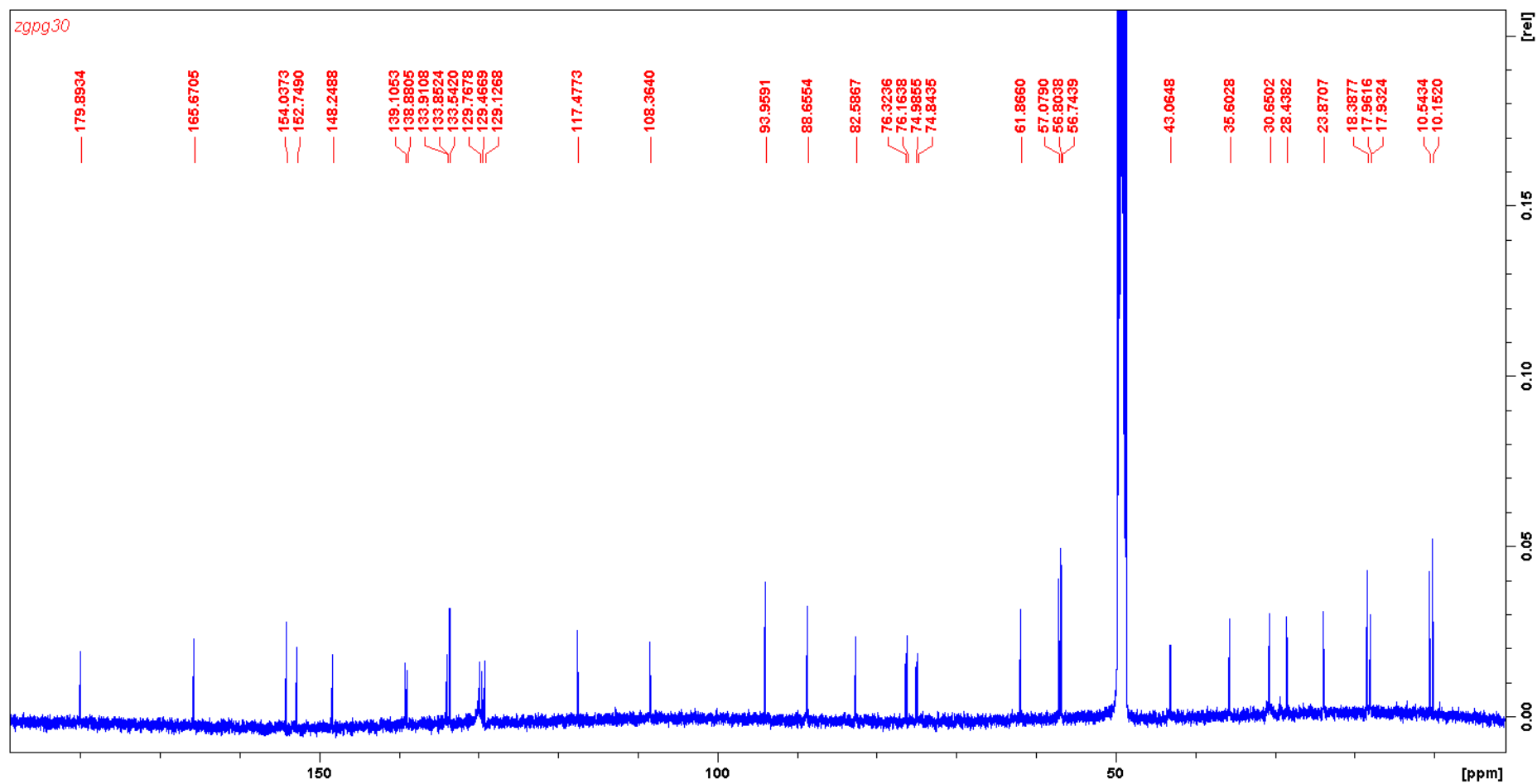


Figure S27. ^{13}C NMR spectrum of stigmatellin C (**3**) in methanol- d_4 .

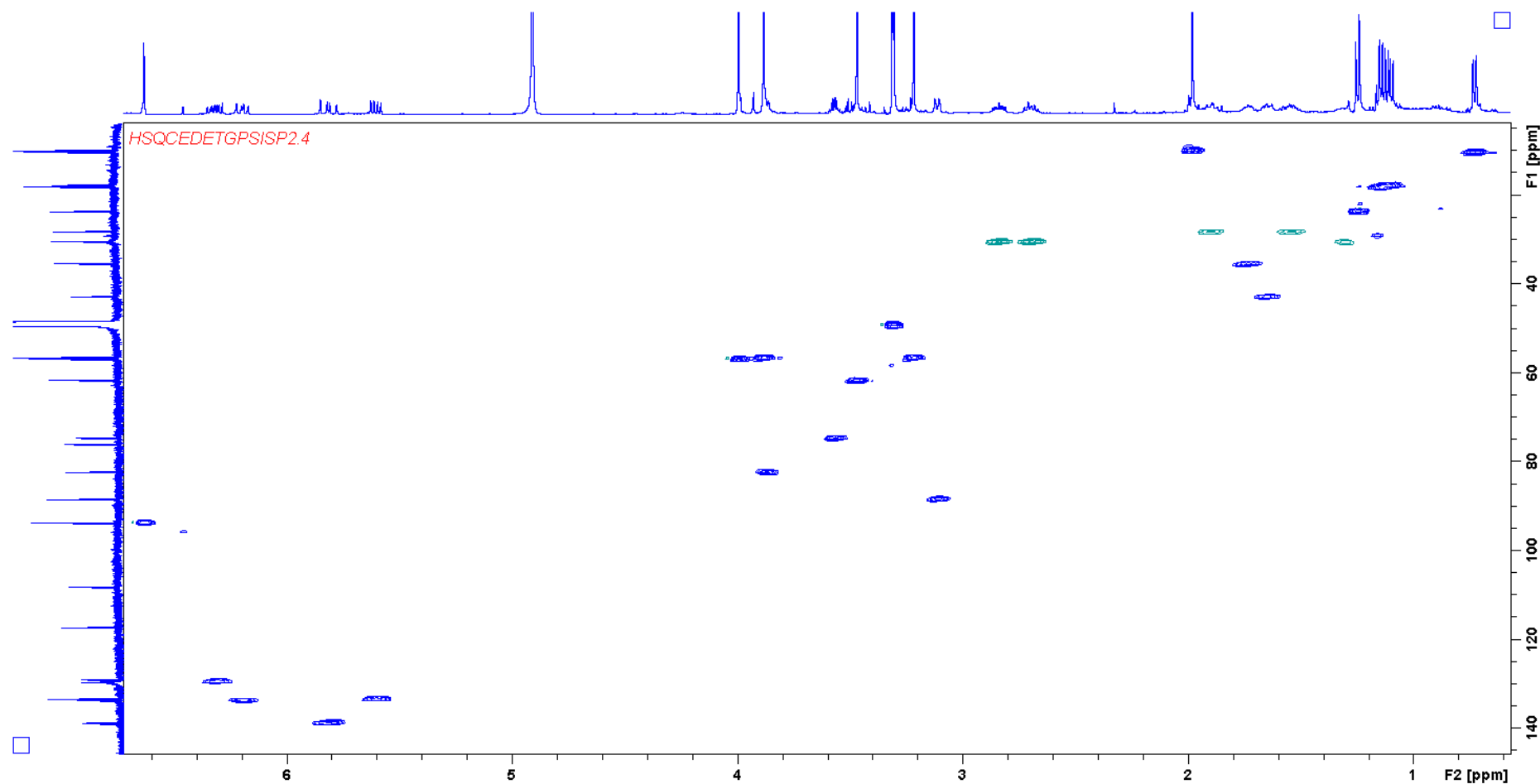


Figure S28. HSQC spectrum of stigmatellin C (**3**) in methanol- d_4 .

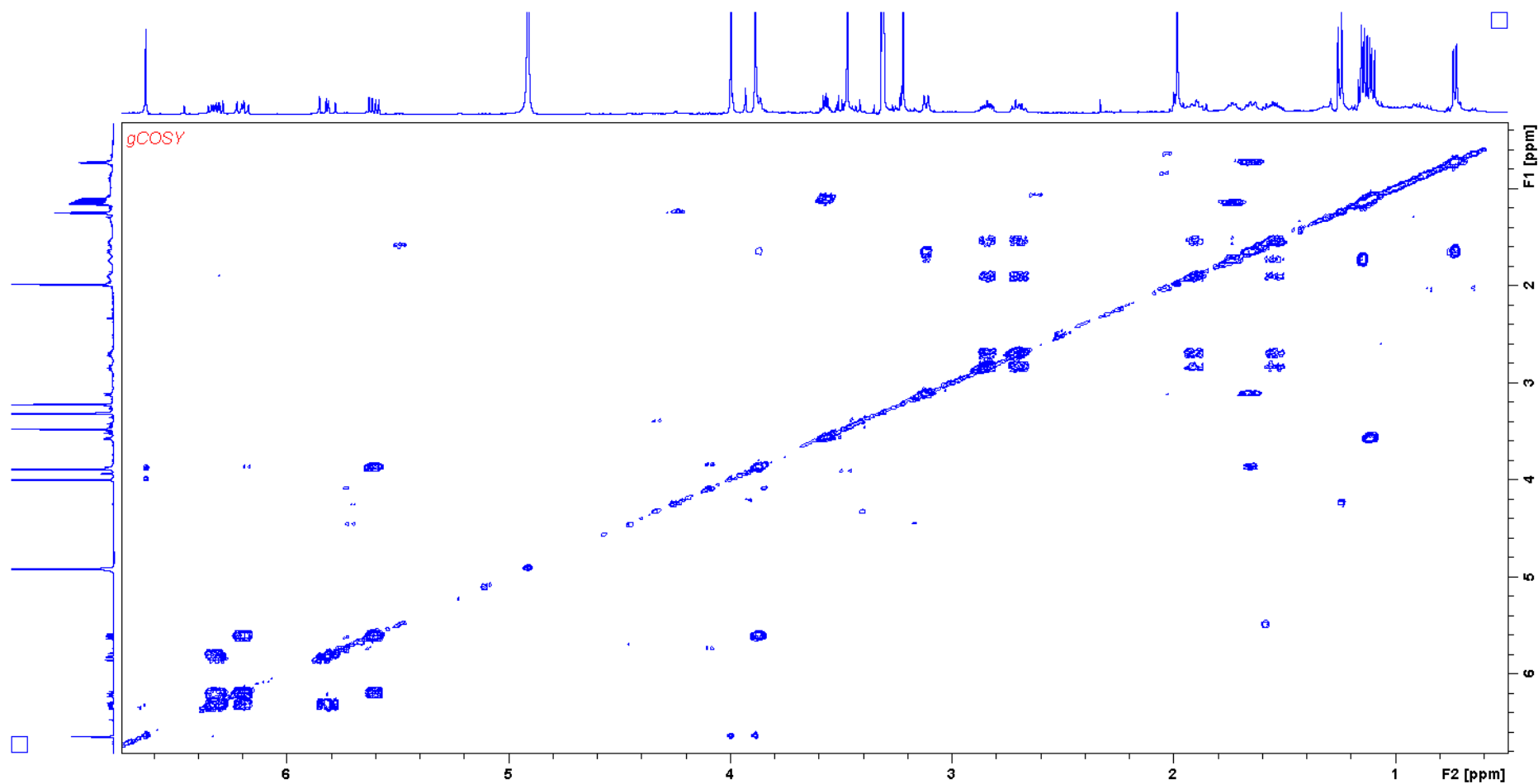


Figure S29. g-COSY spectrum of stigmatellin C (**3**) in methanol- d_4 .

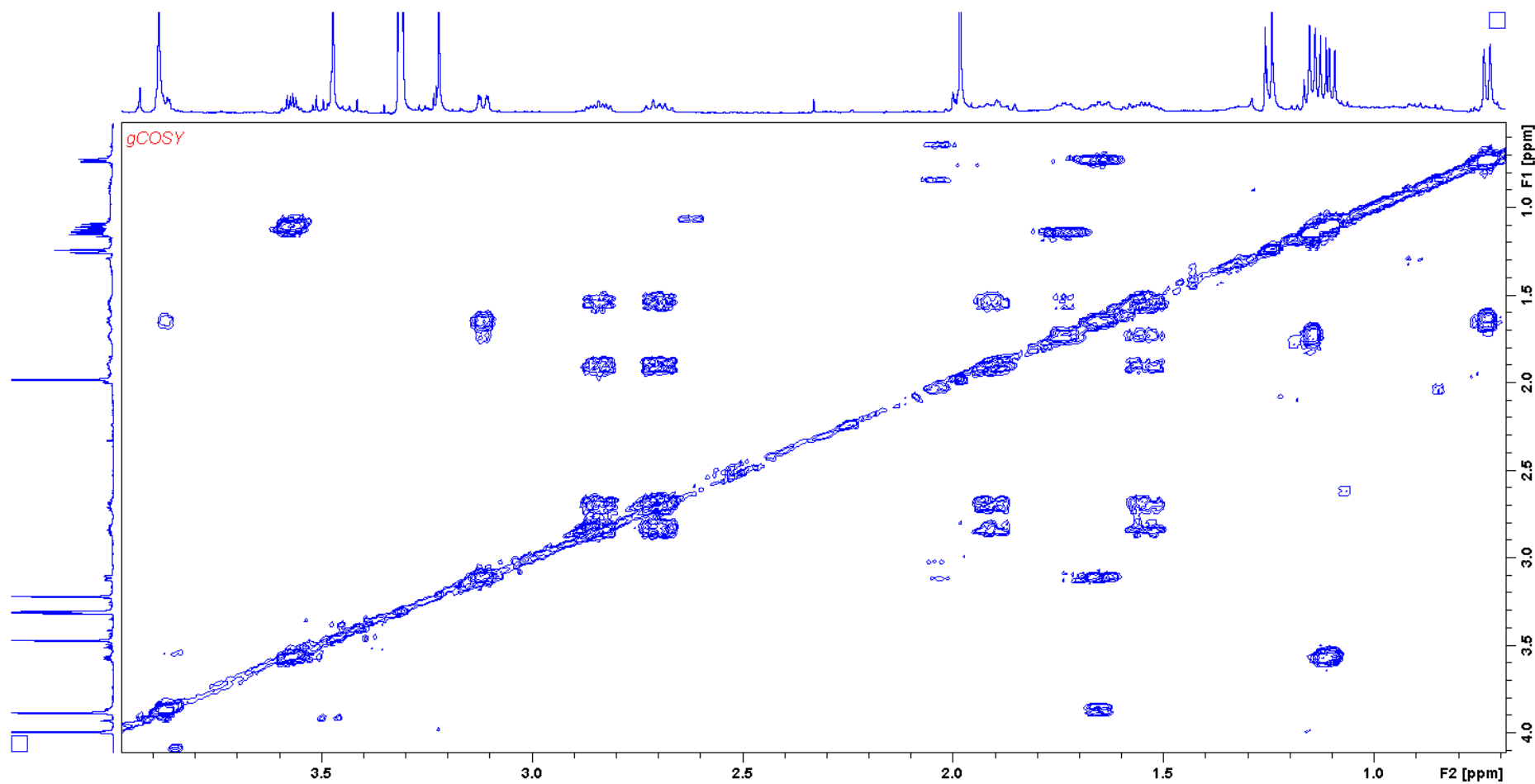


Figure S30. g-COSY spectrum (expanded) of stigmatellin C (**3**) in methanol- d_4 .

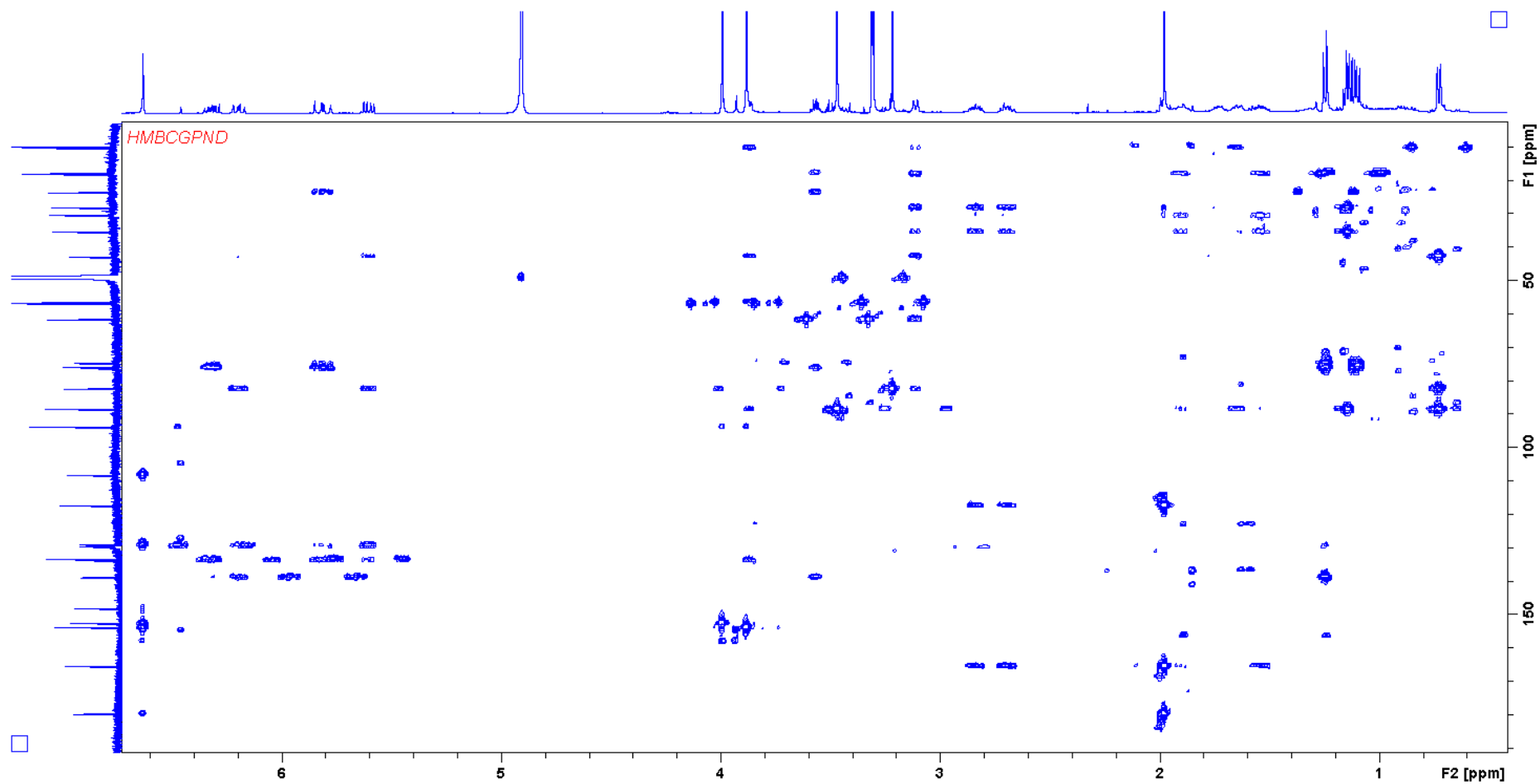


Figure S31. HMBC spectrum of stigmatellin C (**3**) in methanol- d_4 .

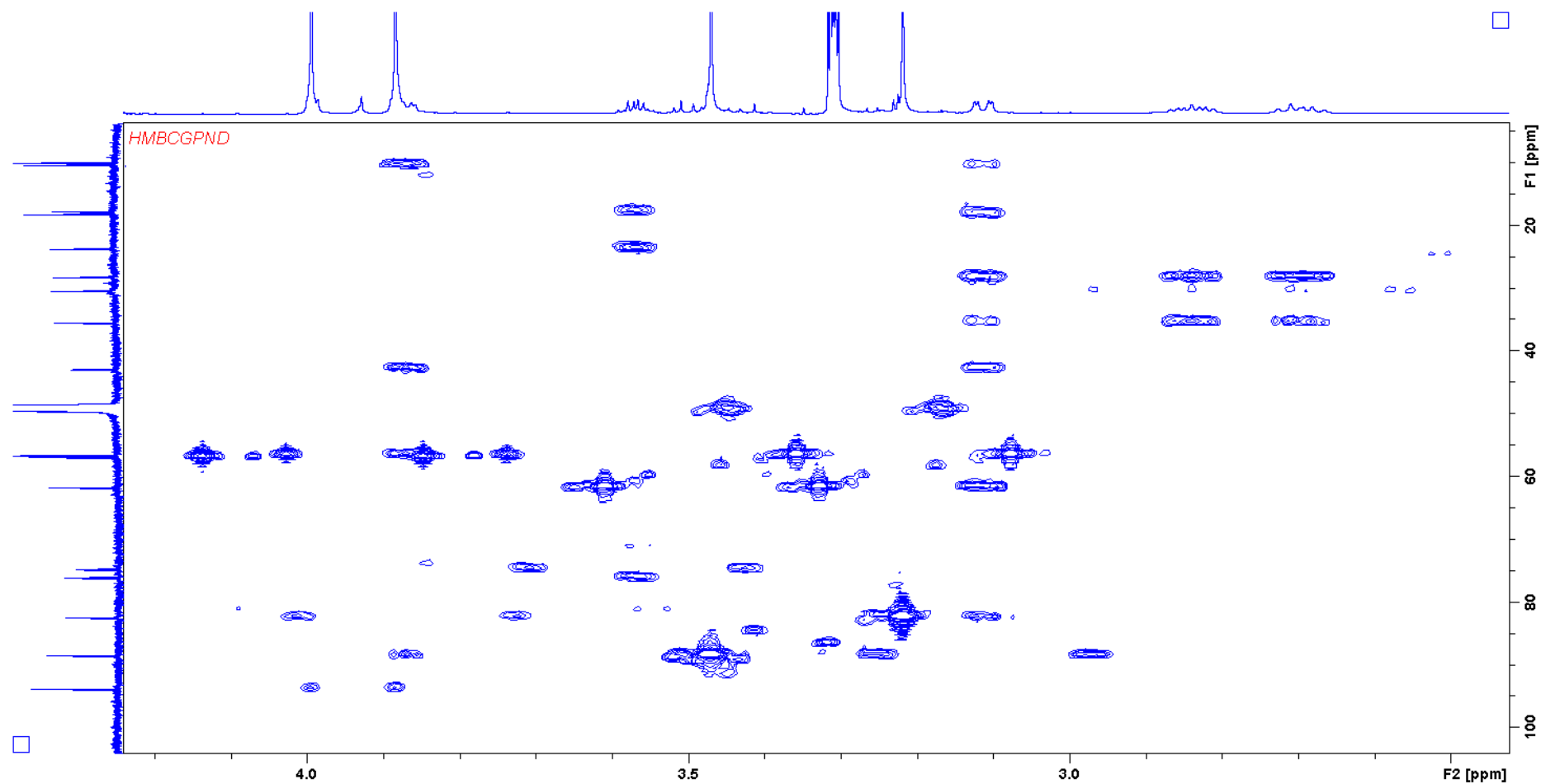


Figure S32. HMBC spectrum (expanded) of stigmatellin C (**3**) in methanol- d_4 .

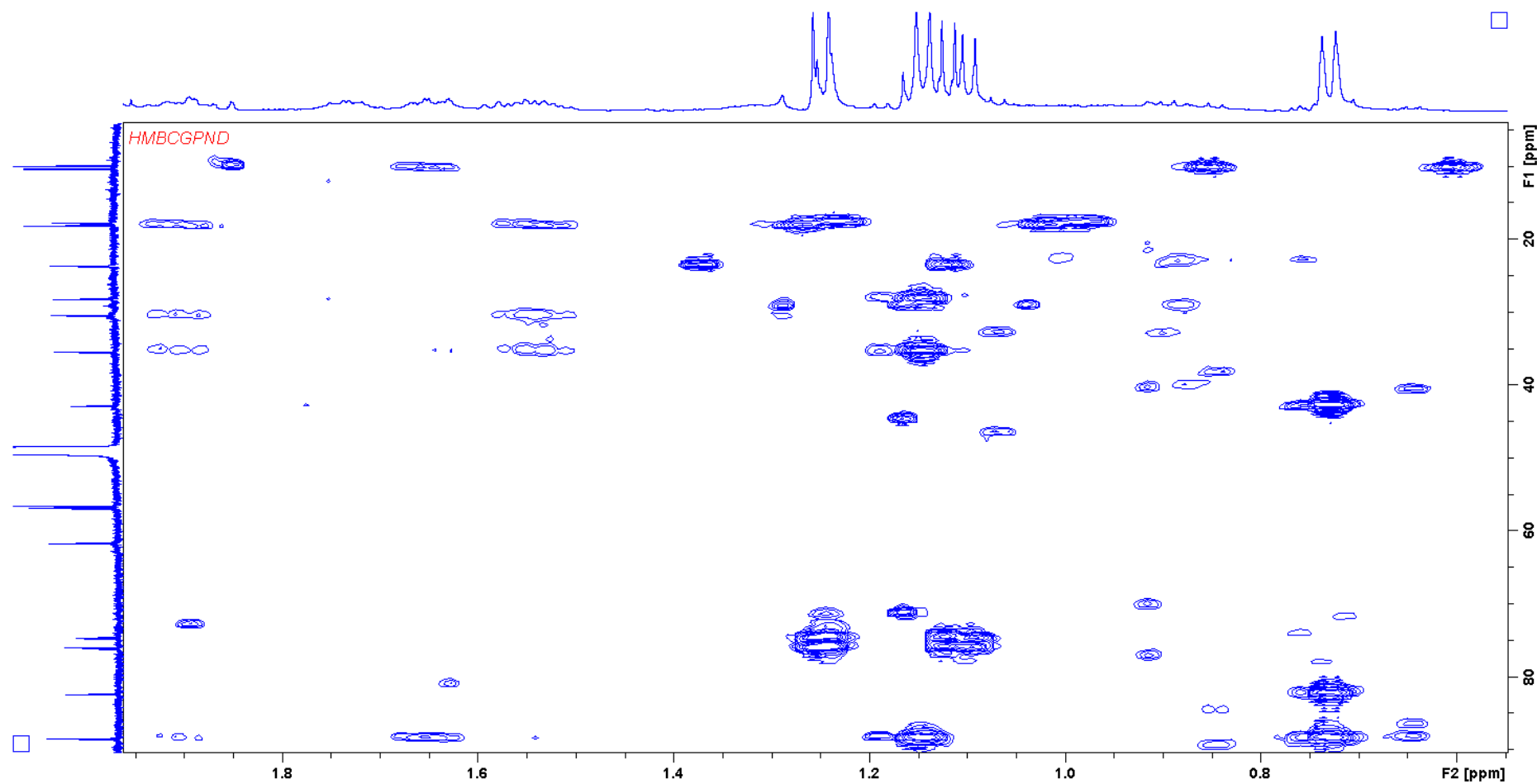


Figure S33. HMBC spectrum (expanded) of stigmatellin C (**3**) in methanol- d_4 .

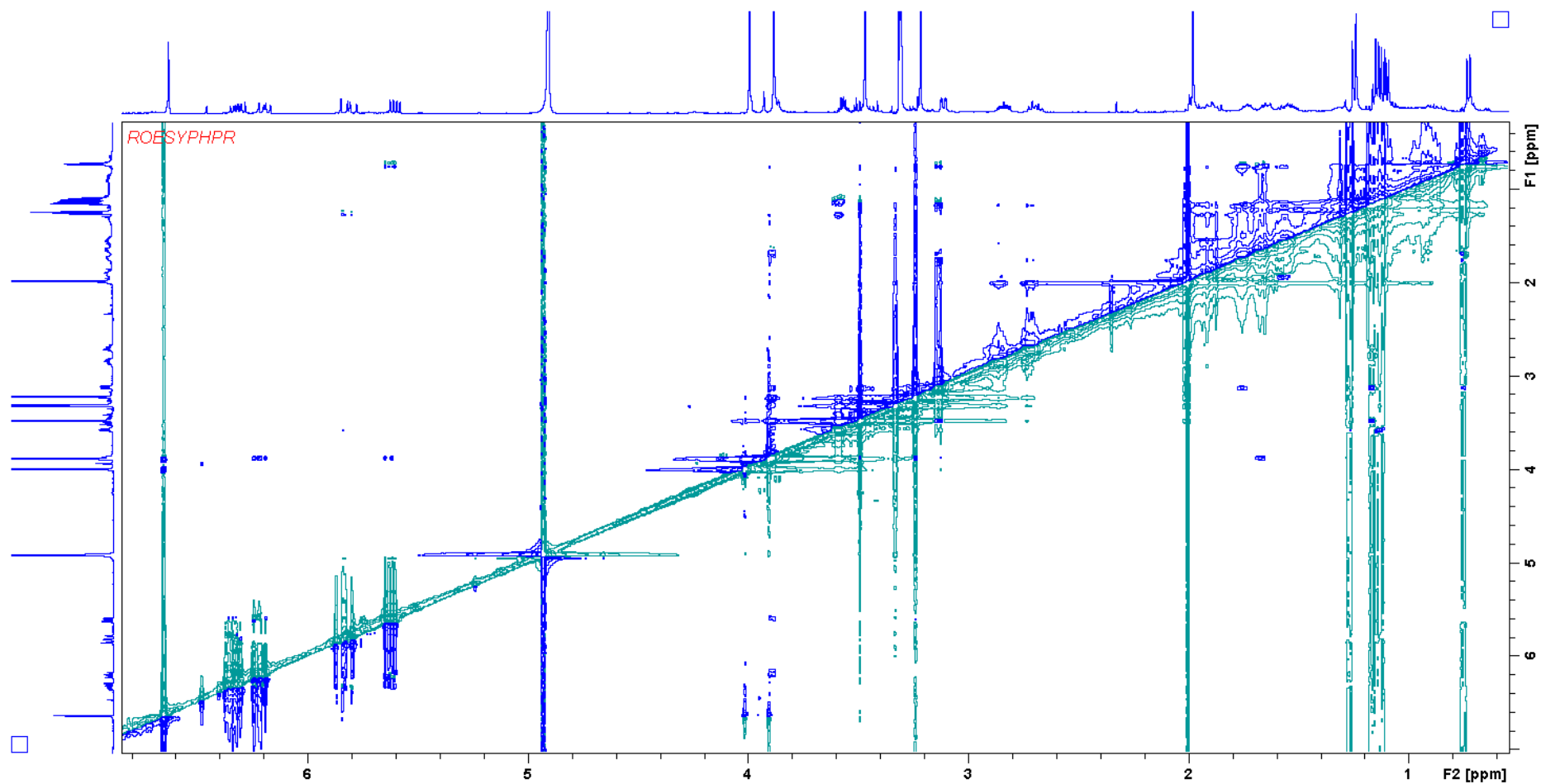


Figure S34. ROESY phpr spectrum of stigmatellin C (**3**) in methanol- d_4 .

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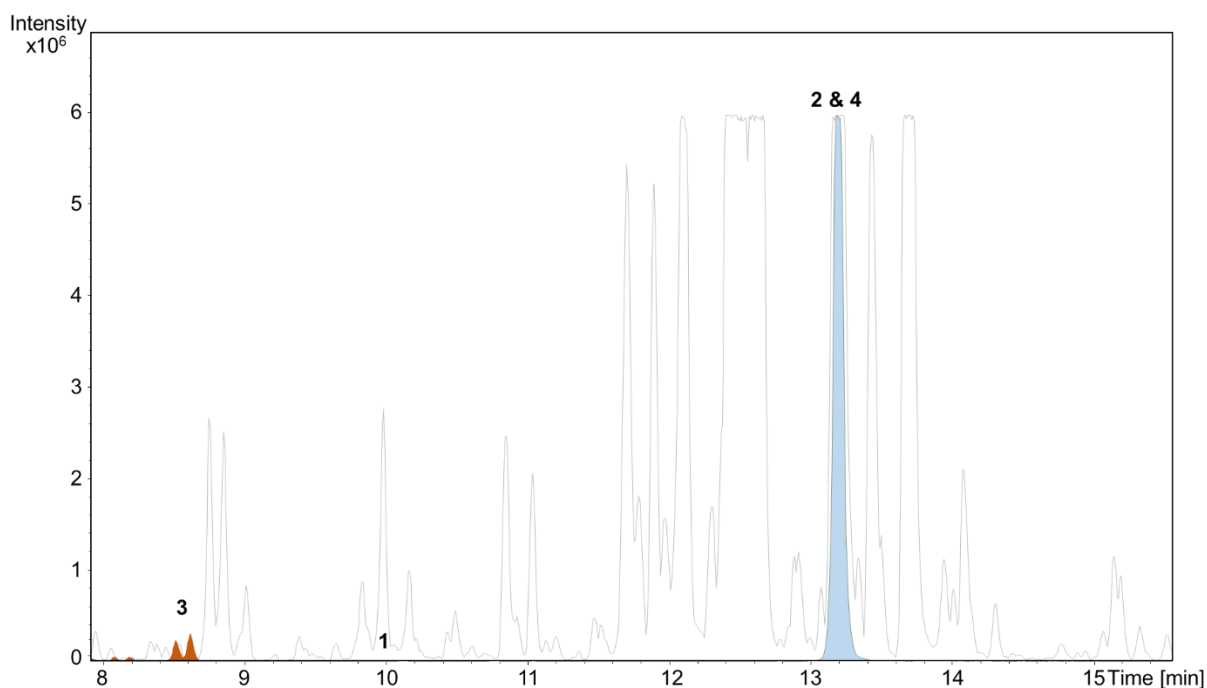


Figure S35. High performance liquid chromatography–mass spectrometry base peak chromatogram (HPLC–MS BPC) (grey) and extracted ion chromatograms (EICs) of **1** ($[M+H]^+$ 545.2755 m/z, green (not visible)), **2** ($[M+H]^+$ 515.3004 m/z, blue), **3** ($[M+H]^+$ 549.3064 and 549.3060 m/z, brown), and **4** ($[M+H]^+$ 545.2755 m/z, blue) from *Stigmatella aurantiaca* Sg a15.

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Table S7. Predicted functions of the encoded proteins by the stigmatellin BGC from *Vitiosangium cumulatum* MCy10943^T.

Gene	Size (aa)	Deduced function	Closest homolog ¹	Coverage/Identity (%)	Sg a15 homolog
<i>orf1</i>	308	DUF2381 family protein	WP_083682780.1	92/83	---
<i>orf2</i>	393	Serine/Threonine Protein Kinase	WP_204220004.1	99/92	---
<i>orf3</i>	134	Transcriptional regulator	WP_204220003.1	72/86	---
<i>orf4</i>	123	Transcriptional regulator	WP_204220002.1	100/89	---
<i>orf5</i>	458	HNH/ENDO VII superfamily nuclease	WP_204220001.1	93/93	---
<i>orf6</i>	203	Hypothetical protein	WP_203410745.1	96/75	---
<i>orf7</i>	122	Hypothetical protein	MBN1207532.1	82/84	---
<i>orf8</i>	1209	Helicase	WP_149184102.1	97/43	---
<i>orf9</i>	1097	Hypothetical protein	WP_230650848.1	97/32	---
<i>orf10</i>	388	Hypothetical protein	NQT93121.1	96/30	---
<i>orf11</i>	203	Hypothetical protein	WP_095987131.1	99/67	---
<i>stiA</i>	2364	PKS biosynthesis ACP-KS-AT-AT-DH-KR-ACP	AAK57190.1	99/49	99/79
<i>stiB</i>	1588	PKS biosynthesis KS-AT-KR-ACP	WP_203404417.1	97/53	100/82
<i>stiC</i>	1880	PKS biosynthesis KS-AT-DH-KR-ACP	WP_194142736.1	99/47	99/81
<i>stiD</i>	1932	PKS biosynthesis KS-AT-OMT-KR-ACP	WP_075010838.1	98/50	100/83
<i>stiE</i>	1925	PKS biosynthesis KS-AT-OMT-KR-ACP	WP_063796277.1	96/56	100/84
<i>stiF</i>	2212	PKS biosynthesis KS-AT-DH-ER-KR-ACP	BAZ29707.1	98/48	99/84
<i>stiG</i>	1402	PKS biosynthesis KS-AT-DH-ACP	NOT56266.1	87/51	100/81
<i>stiH</i>	1597	PKS biosynthesis KS-AT-DH-ACP	WP_196523766.1	95/48	99/79
<i>stiJ1</i>	1045	PKS biosynthesis KS-AT-ACP	MBD1836177.1	87/58	99/84
<i>stiJ2</i>	180	PKS biosynthesis	MBW4628907.1	99/28	99/78
<i>stiK</i>	256	PKS biosynthesis tailoring O-Methyltransferase	MBA2429587.1	100/51	100/85
<i>stiL1</i>	306	PKS biosynthesis tailoring Cytochrome P450 enzyme	WP_104977779.1	79/43	82/82
<i>stiL2</i>	230	PKS biosynthesis tailoring Cytochrome P450 enzyme	CTS25513.1	79/43	82/82
<i>orf12</i>	374	Transport	WP_108074850.1	100/95	---
<i>orf13</i>	911	Transport	WP_108074851.1	99/93	---
<i>orf14</i>	345	Transport	WP_108074852.1	95/88	---
<i>orf15</i>	530	Transport	WP_108074853.1	100/89	---
<i>orf16</i>	701	Glycogen debranching enzyme	MBC7855611.1	95/62	---
<i>orf17</i>	365	ATP-dependent 6-phosphofructokinase	WP_043407704.1	100/96	---
<i>orf18</i>	326	Glucokinase	WP_108074855.1	95/91	---
<i>orf19</i>	359	D-arabitol-phosphate dehydrogenase	WP_233262020.1	100/93	---
<i>orf20</i>	486	Pyruvate Kinase	WP_108074856.1	100/92	---
<i>orf21</i>	350	Hydroxyacid dehydrogenase	PTL78120.1	100/93	---
<i>orf22</i>	124	Hypothetical protein	WP_108074858.1	85/91	---

¹For stiA–stiL2 the second closest homolog was denoted.

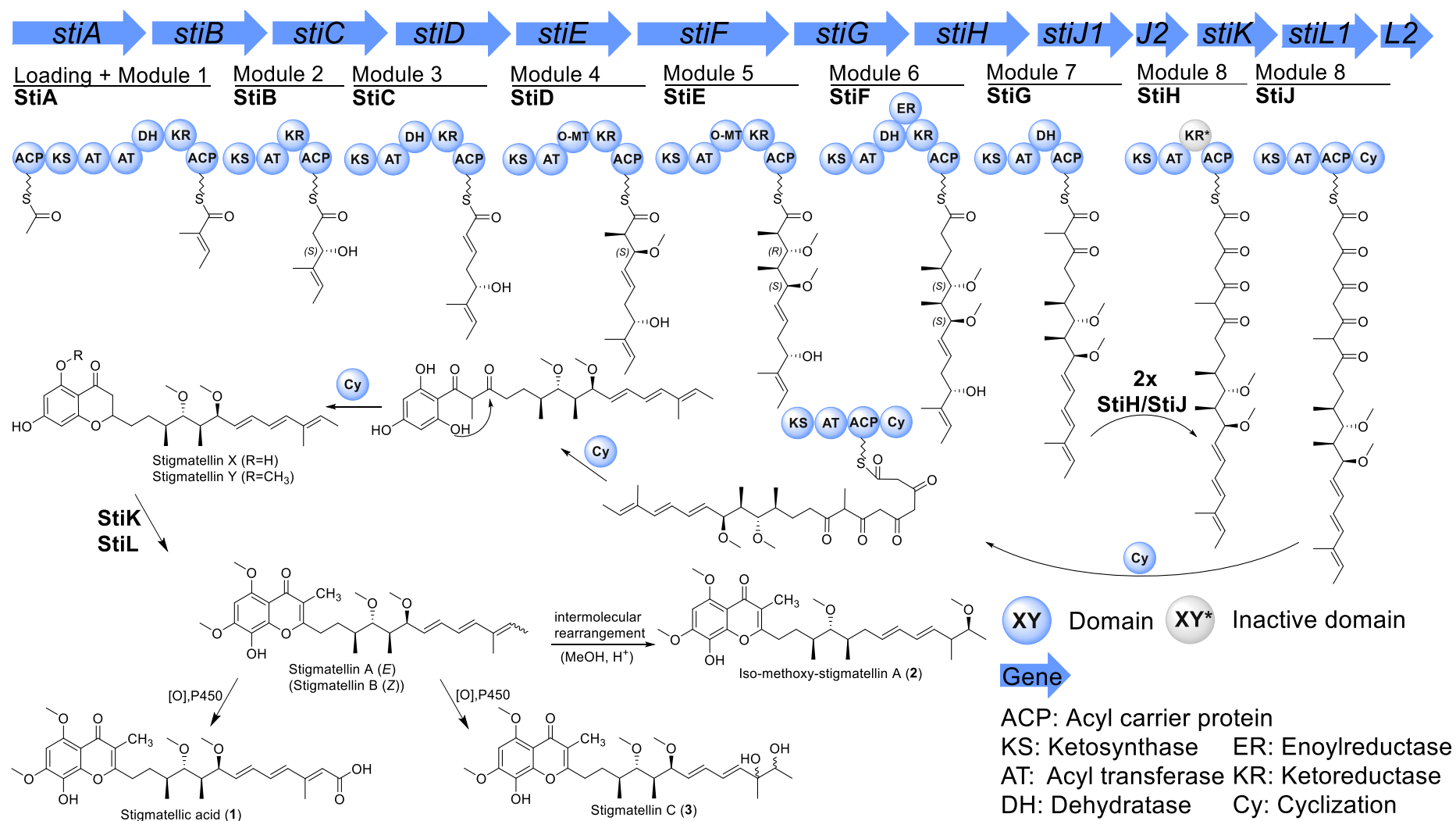


Figure S36. Genetic organization of the Stigmatellin BGC from *Vitosangium cumulatium* MCy10943^T and the proposed model of the biosynthesis leading to 1–3. The stereochemical assignment of the linear biosynthetic intermediates bound to the assembly line was assigned based on the absolute configuration of 1–3. Scheme adapted from Gaitatzis et al. [1] and Wenzel et al. [2]

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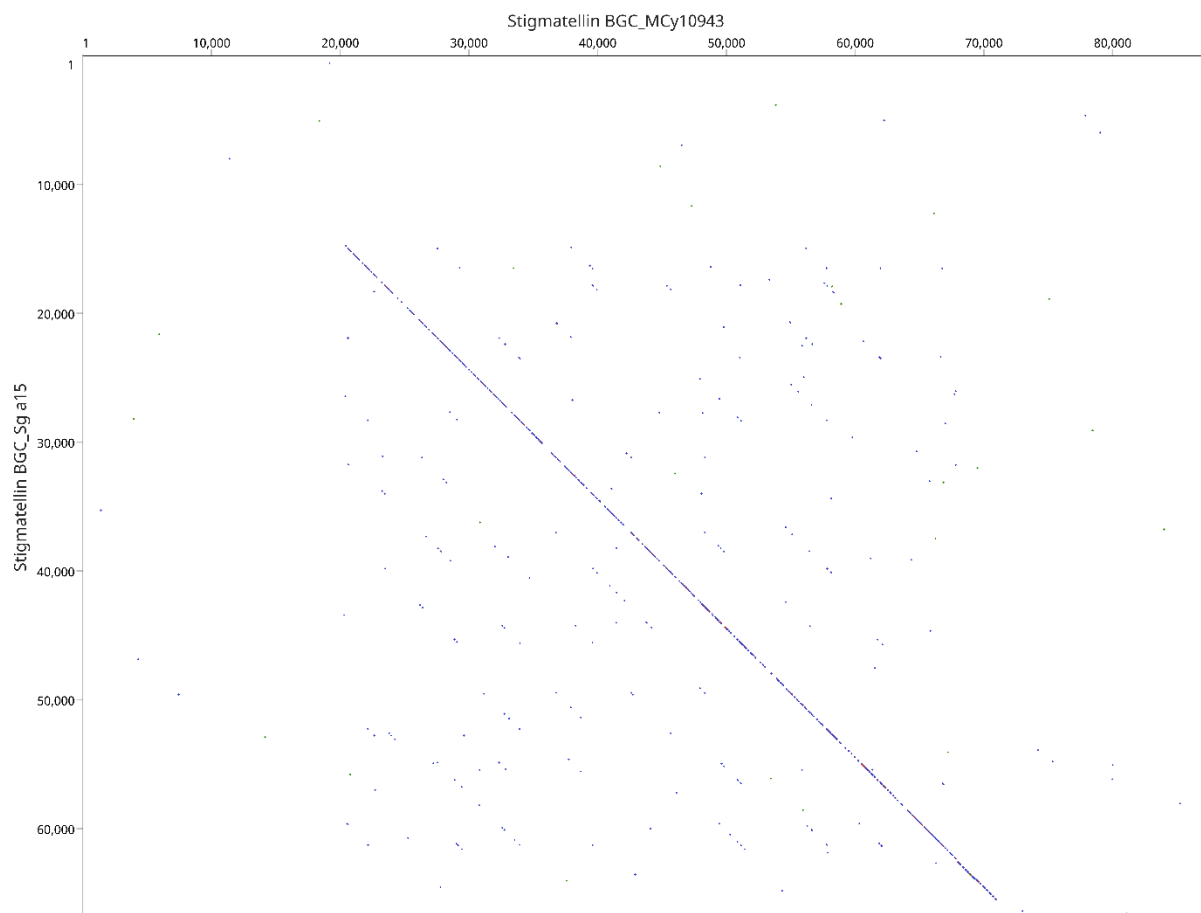


Figure S37. Dotplot of the entire herein identified stigmatellin BGC from *Vitiosangium cumulatum* MCy10943^T (GenBank: ON210143, 87854 bp) and the previously characterized BGC from Sg a15 (MIBiG: BGC0000153, 66808 bp). The blue diagonal line indicates the conserved genetic region responsible for the biosynthesis of stigmatellin in both producer strains (*stiA*–*stiL*), while the surrounding area is different and does not show similarity to each other (no visible lines indicate any similarity between *orf1*–22 (MCy10943) and *orf1*–8 (Sg a15)).

2. References

1. Gaitatzis, N.; Silakowski, B.; Kunze, B.; Nordsiek, G.; Blöcker, H.; Höfle, G.; Müller, R. The biosynthesis of the aromatic myxobacterial electron transport inhibitor stigmatellin is directed by a novel type of modular polyketide synthase. *J. Biol. Chem.* **2002**, *277*, 13082–13090.
2. Wenzel, S.C.; Müller, R. Myxobacteria - unique microbial secondary metabolite factories. In *Comprehensive Natural Products Chemistry II, Vol 2: Structural Diversity II - Secondary Metabolite Sources, Evolution and Selected Molecular Structures*; Moore, B.S., Ed.; Elsevier: Oxford, 2010; pp 189–222.
3. Keatinge-Clay, A.T. A Tylosin Ketoreductase Reveals How Chirality is Determined in Polyketides. *Chem. Biol.* **2007**, *14*, 898–908.