Supporting Information for

Chemical Constituents from the Roots of *Angelica reflexa* That Improve Glucose-Stimulated Insulin Secretion by Regu-lating Pancreatic β-Cell Metabolism

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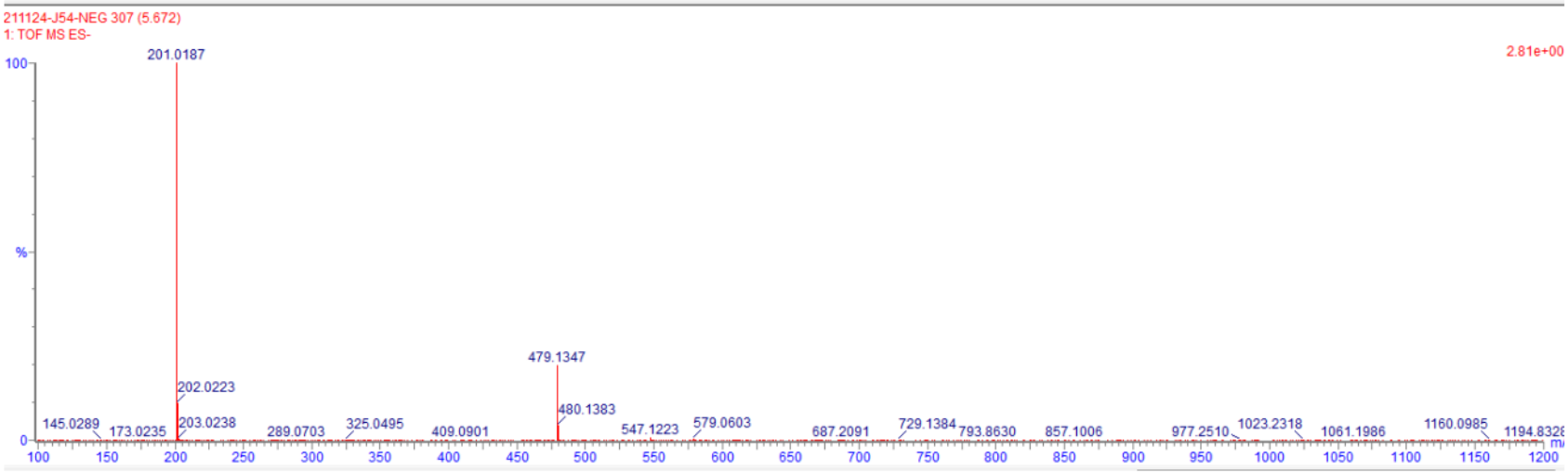
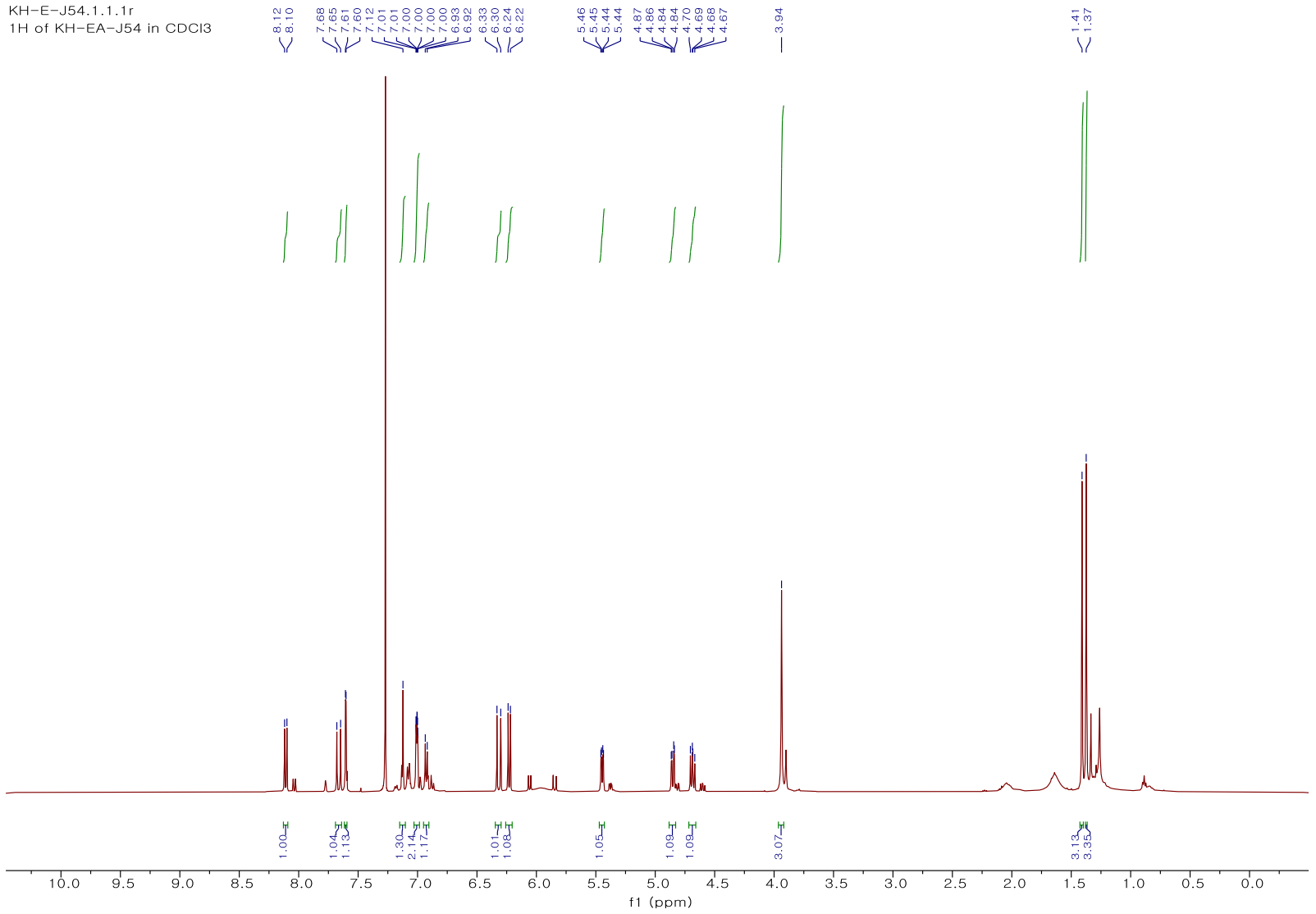
S1. HRESIMS spectrum of the new compound **1**.

Single Mass Analysis
Tolerance = 30.0 PPM / DBE: min = -1.5, max = 50.0
Element prediction: Off
Number of isotope peaks used for i-FIT = 3
Monoisotopic Mass, Even Electron Ions
62 formula(e) evaluated with 1 results within limits (up to 20 closest results for each mass)
Elements Used:

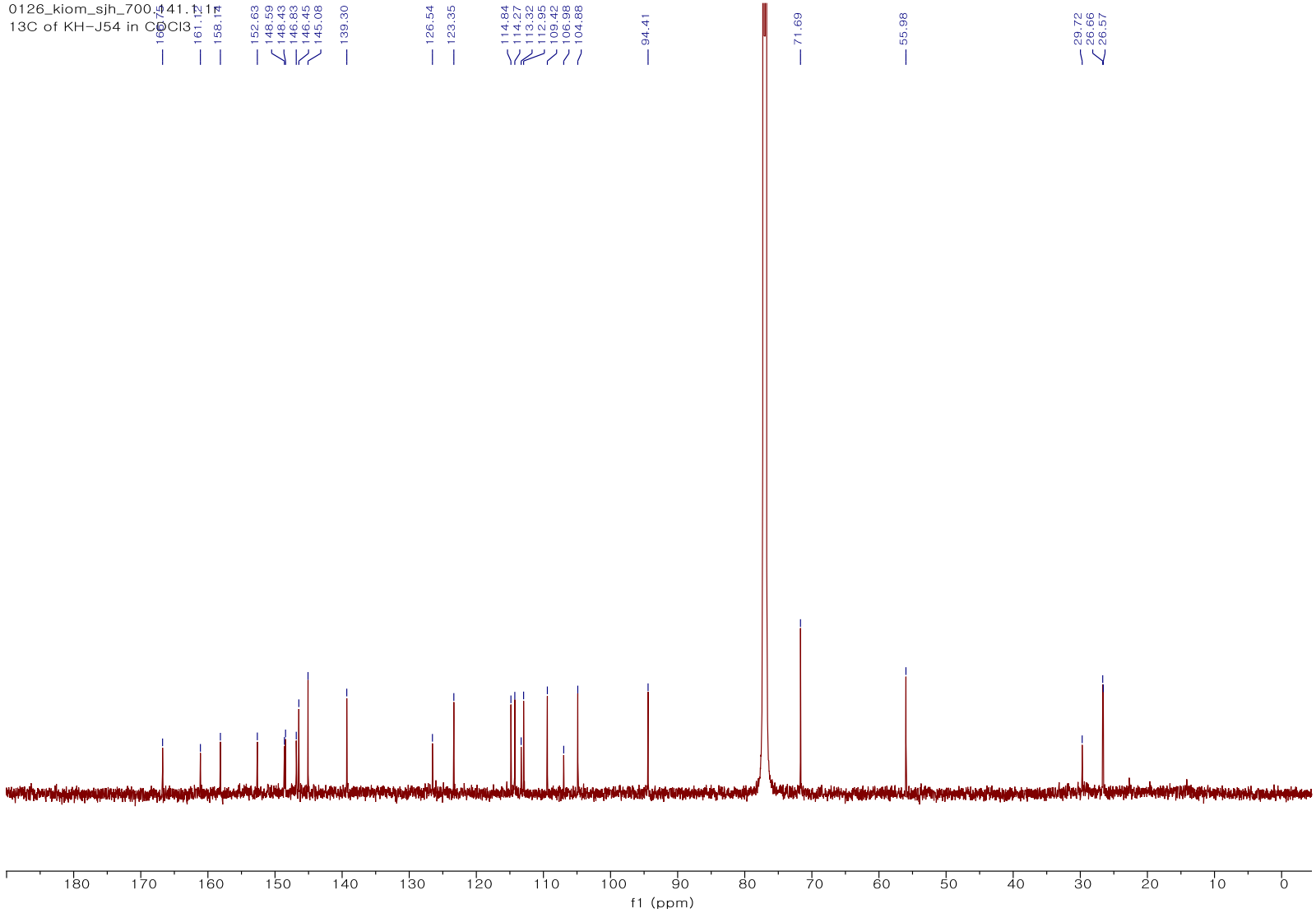
Mass	Calc. Mass	mDa	PPM	DBE	Formula	i-FIT	i-FIT Norm	Fit Conf %	C	H	O
479.1347	479.1342	0.5	1.0	15.5	C26 H23 O9	85.4	n/a	n/a	26	23	9



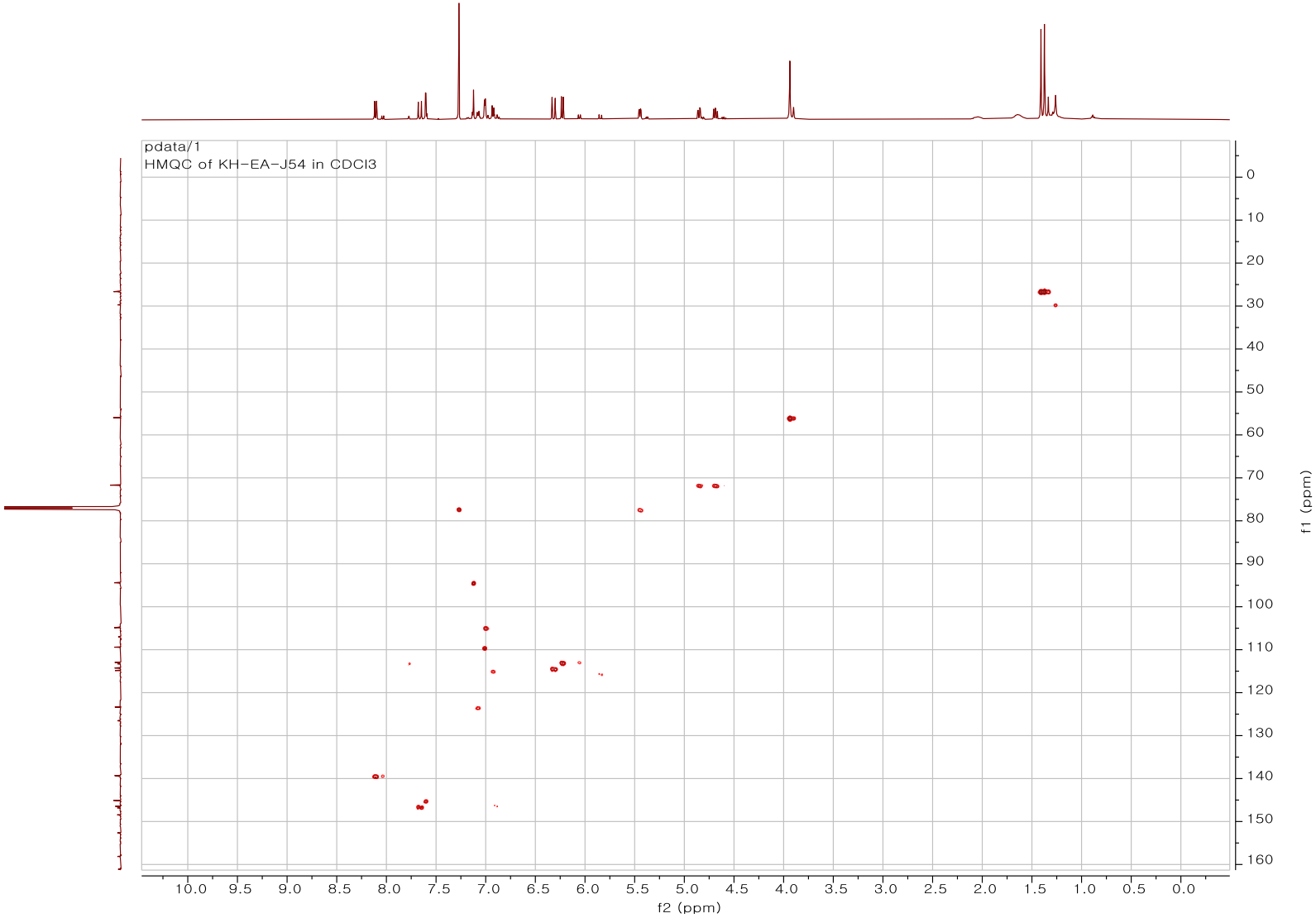
S2. ^{1}H NMR spectrum (600 MHz, $CDCl_3$) of the new compound **1**.



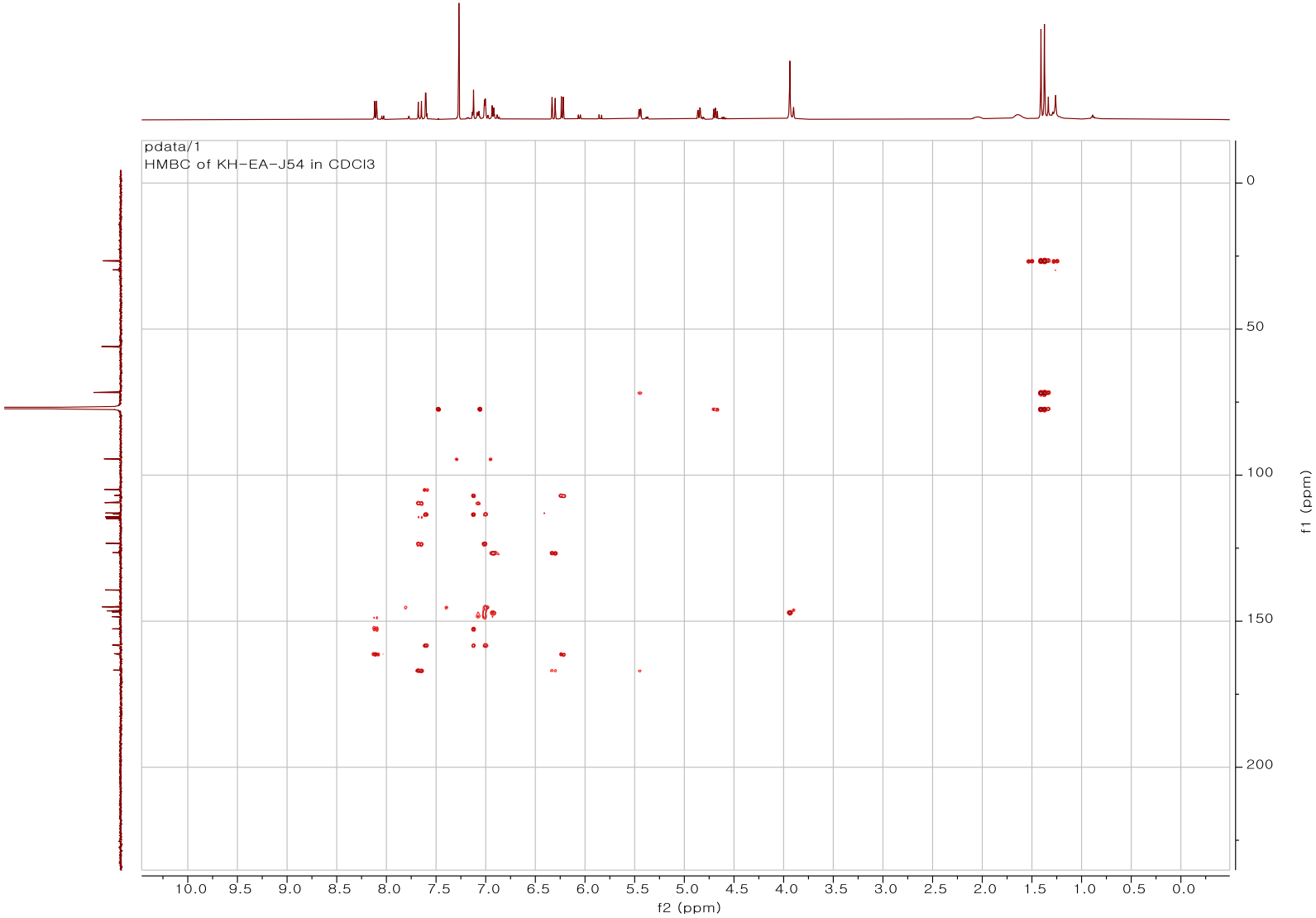
S3. ^{13}C NMR spectrum (150 MHz, $CDCl_3$) of the new compound **1**.



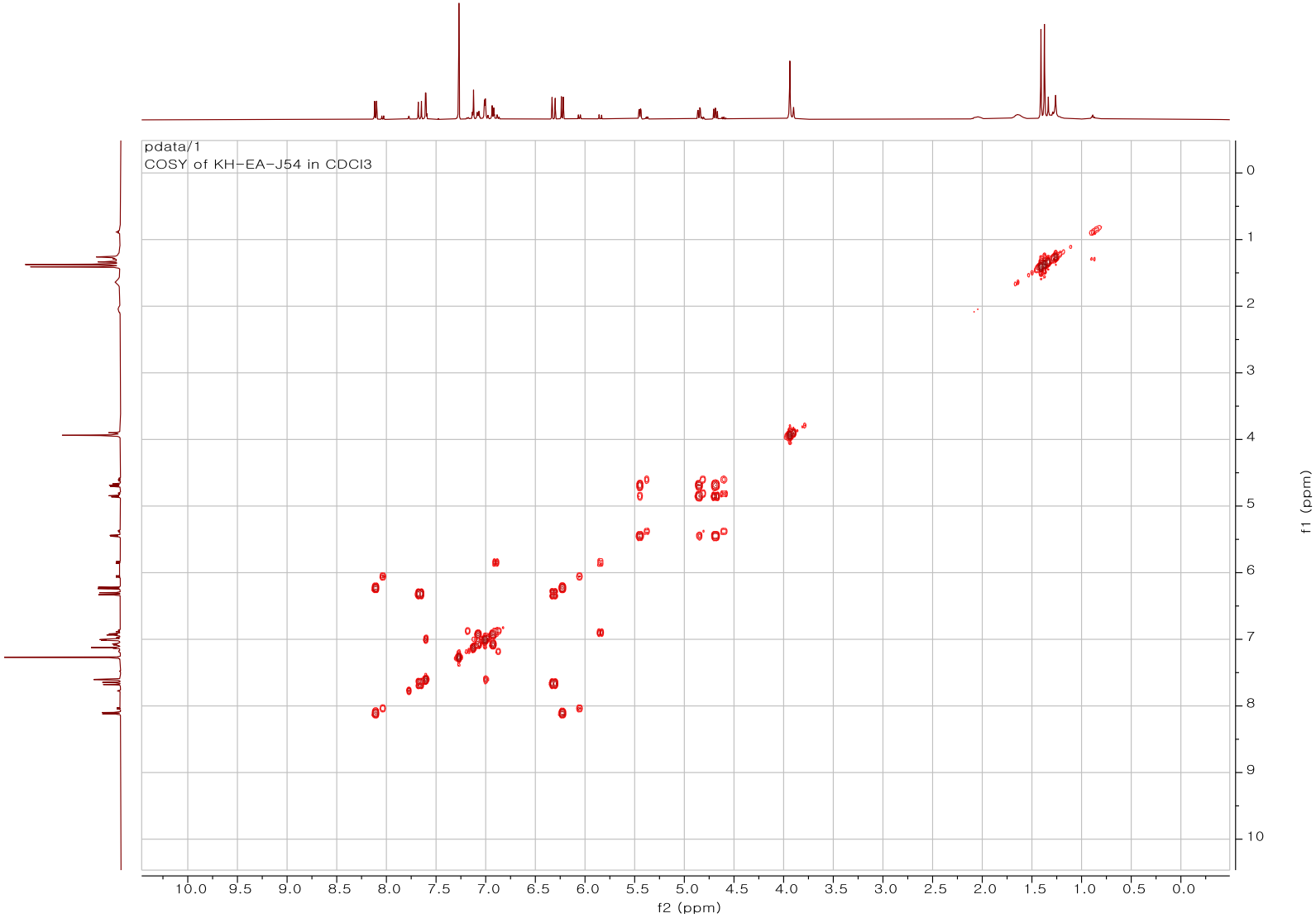
S4. HSQC spectrum of the new compound **1**.



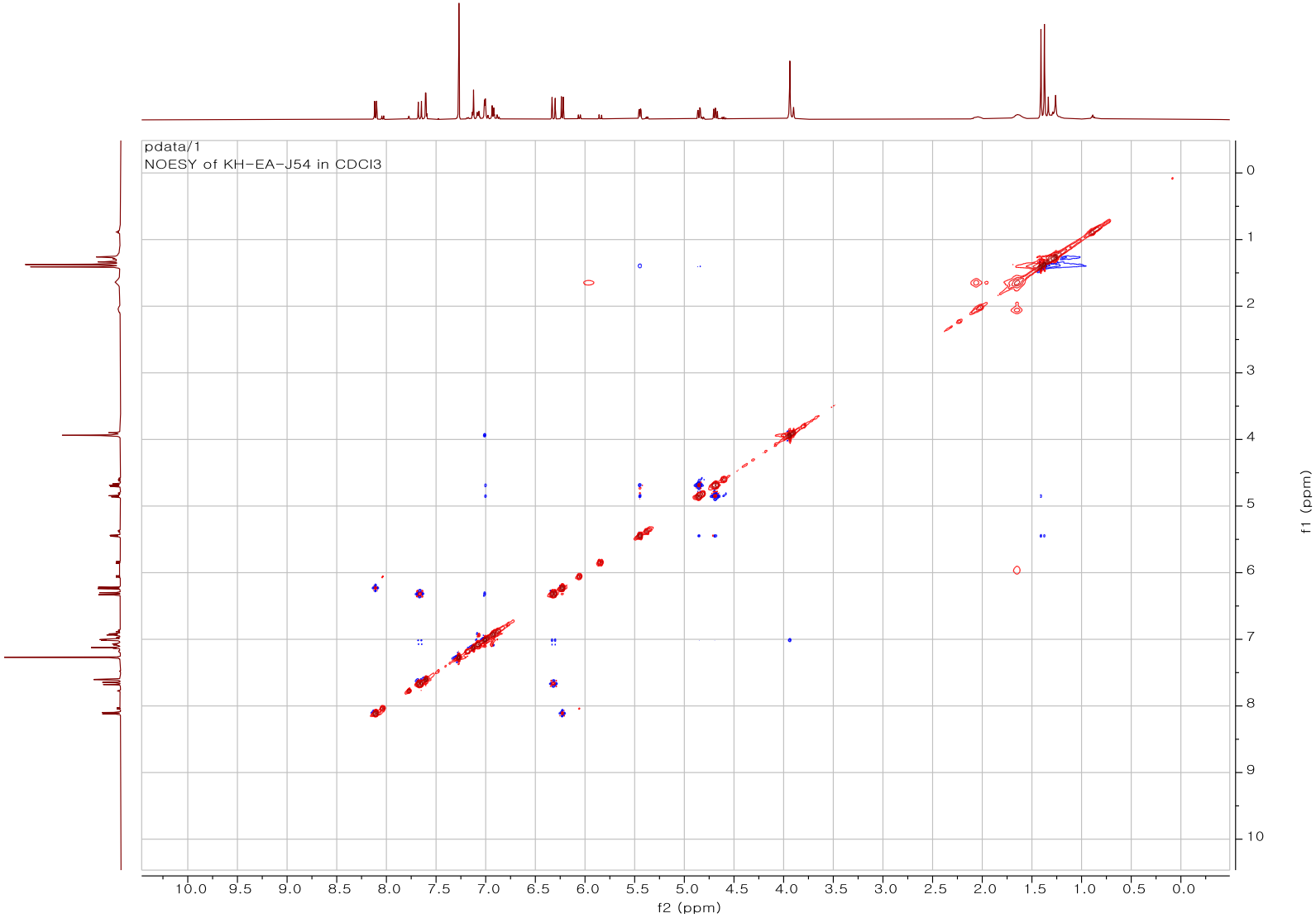
S5. HMBC spectrum of the new compound **1**.



S6. COSY spectrum of the new compound **1**.



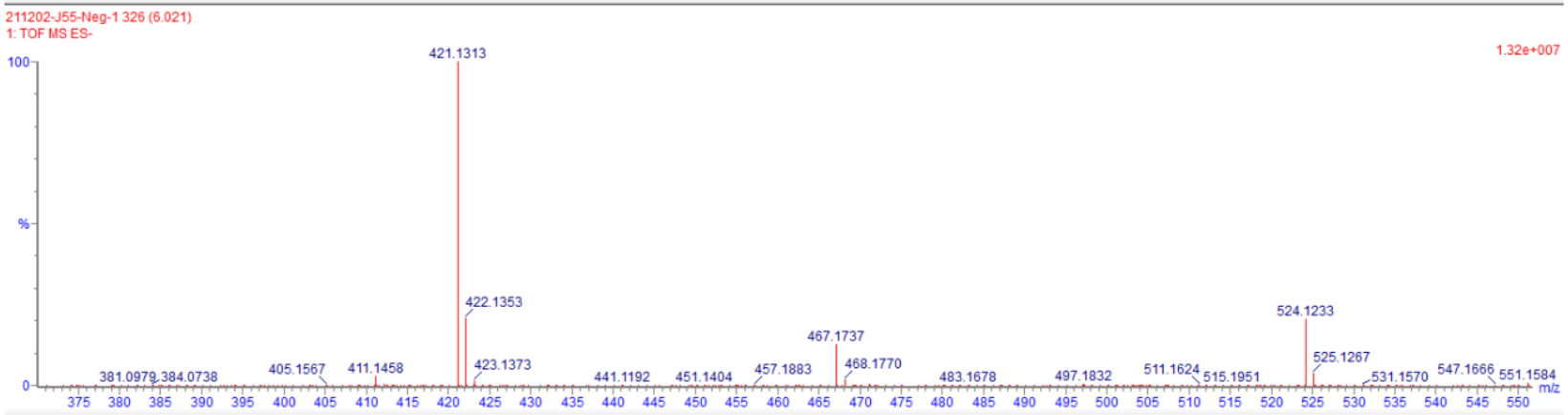
S7. NOESY spectrum of the new compound **1**.



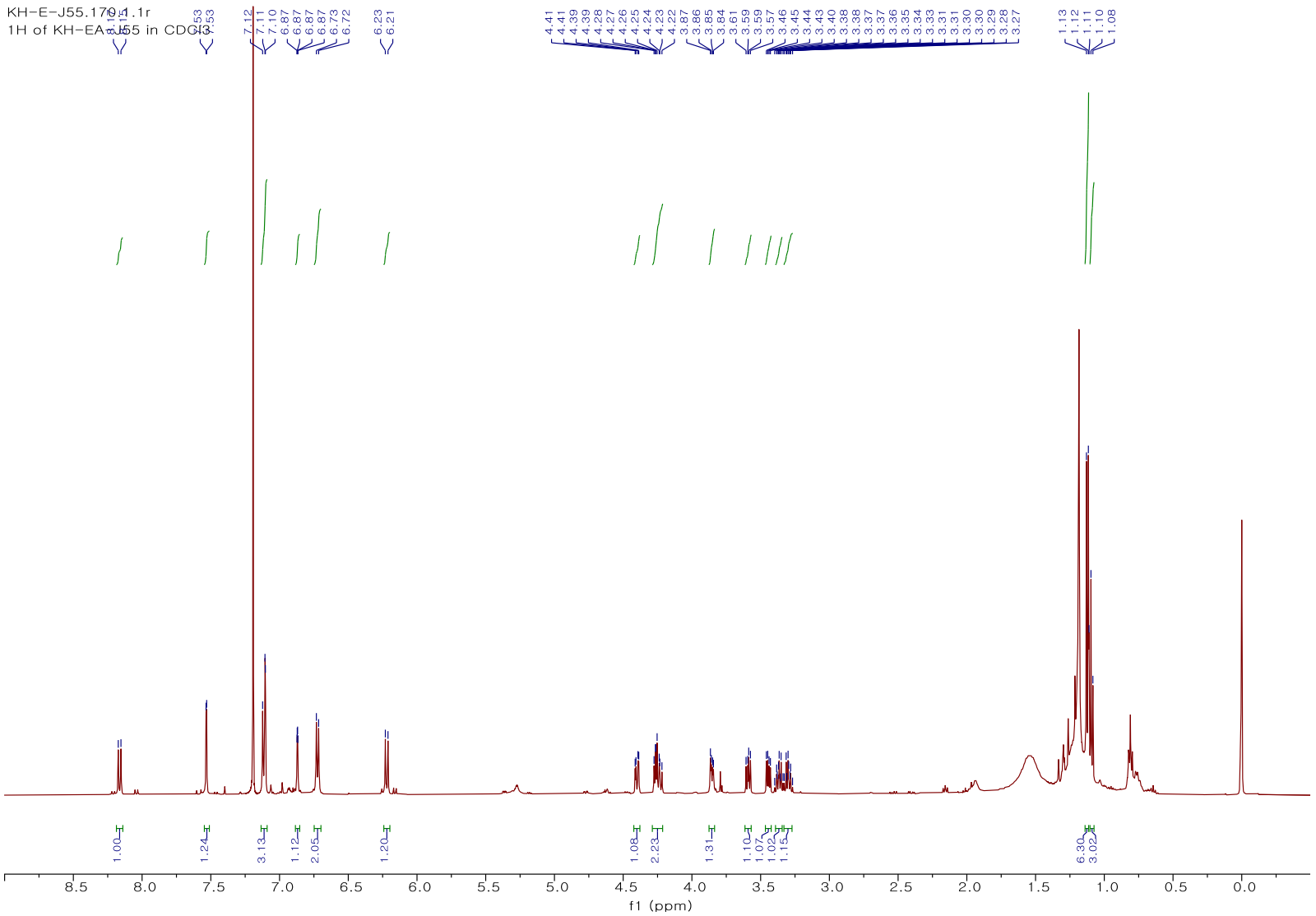
S8. HRESIMS spectrum of the new compound **2**.

Single Mass Analysis
Tolerance = 50.0 PPM / DBE: min = -1.5, max = 50.0
Element prediction: Off
Number of isotope peaks used for i-FIT = 3
Monoisotopic Mass, Even Electron Ions
46 formula(e) evaluated with 4 results within limits (up to 20 closest results for each mass)
Elements Used:

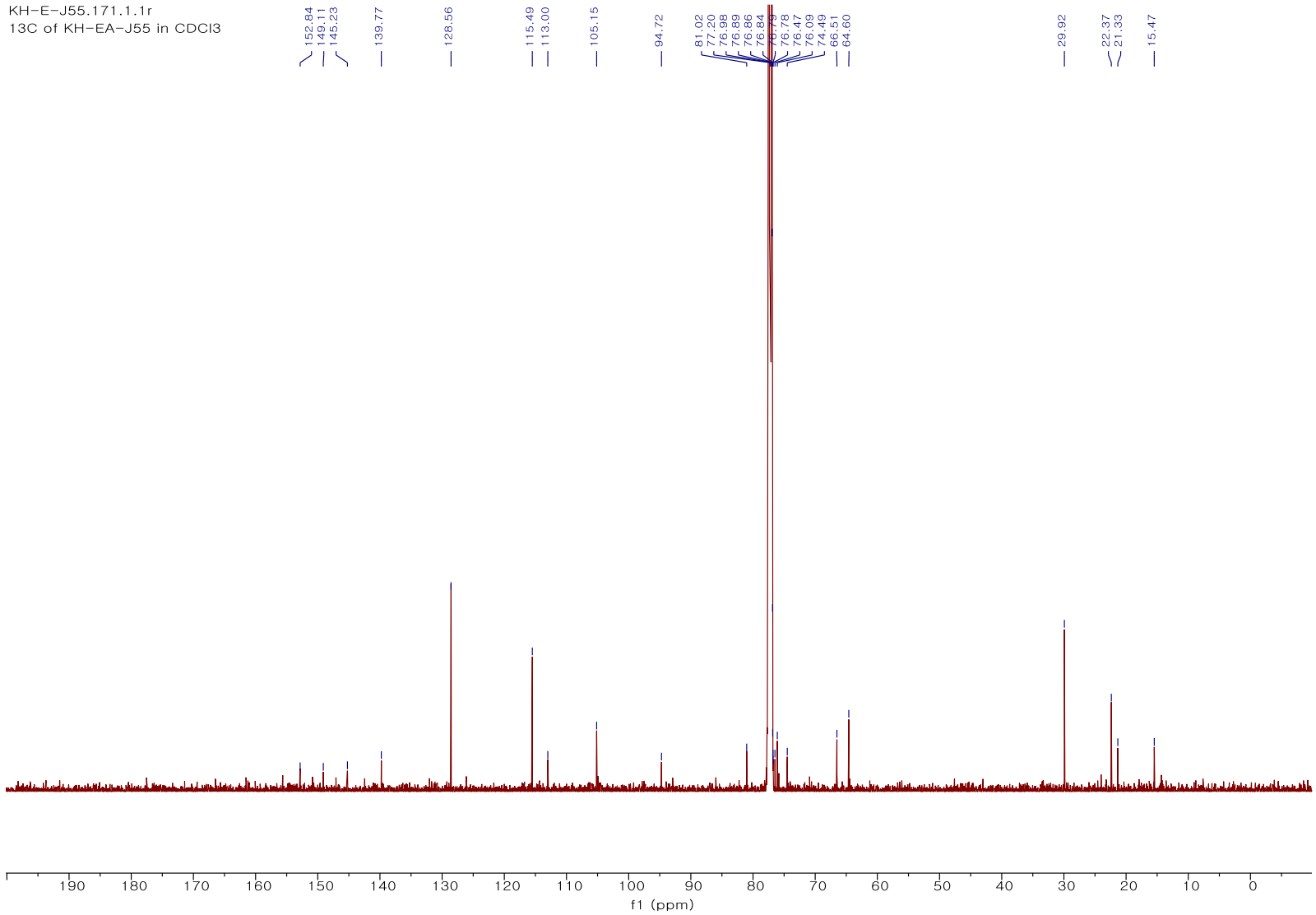
Mass	Calc. Mass	mDa	PPM	DBE	Formula	i-FIT	i-FIT Norm	Fit Conf %	C	H	O
467.1737	467.1706	3.1	6.6	13.5	C26 H27 O8	115.4	0.643	52.56	26	27	8
	467.1858	-12.1	-25.9	17.5	C30 H27 O5	115.9	1.124	32.50	30	27	5
	467.1917	-18.0	-38.5	8.5	C23 H31 O10	117.3	2.525	8.01	23	31	10
	467.1553	18.4	39.4	9.5	C22 H27 O11	117.4	2.670	6.93	22	27	11



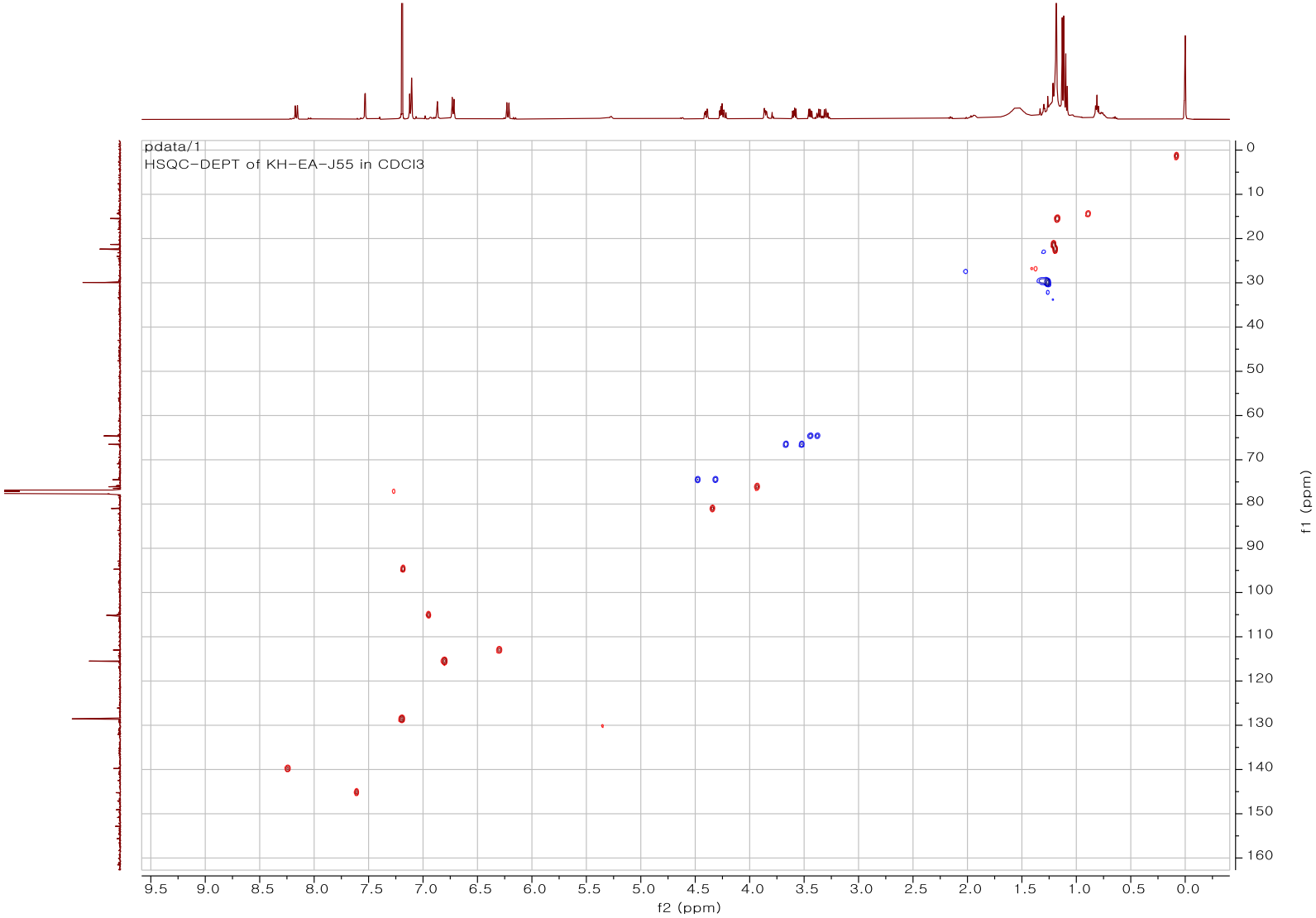
S9. ^{1}H NMR spectrum (600 MHz, $CDCl_3$) of the new compound **2**.



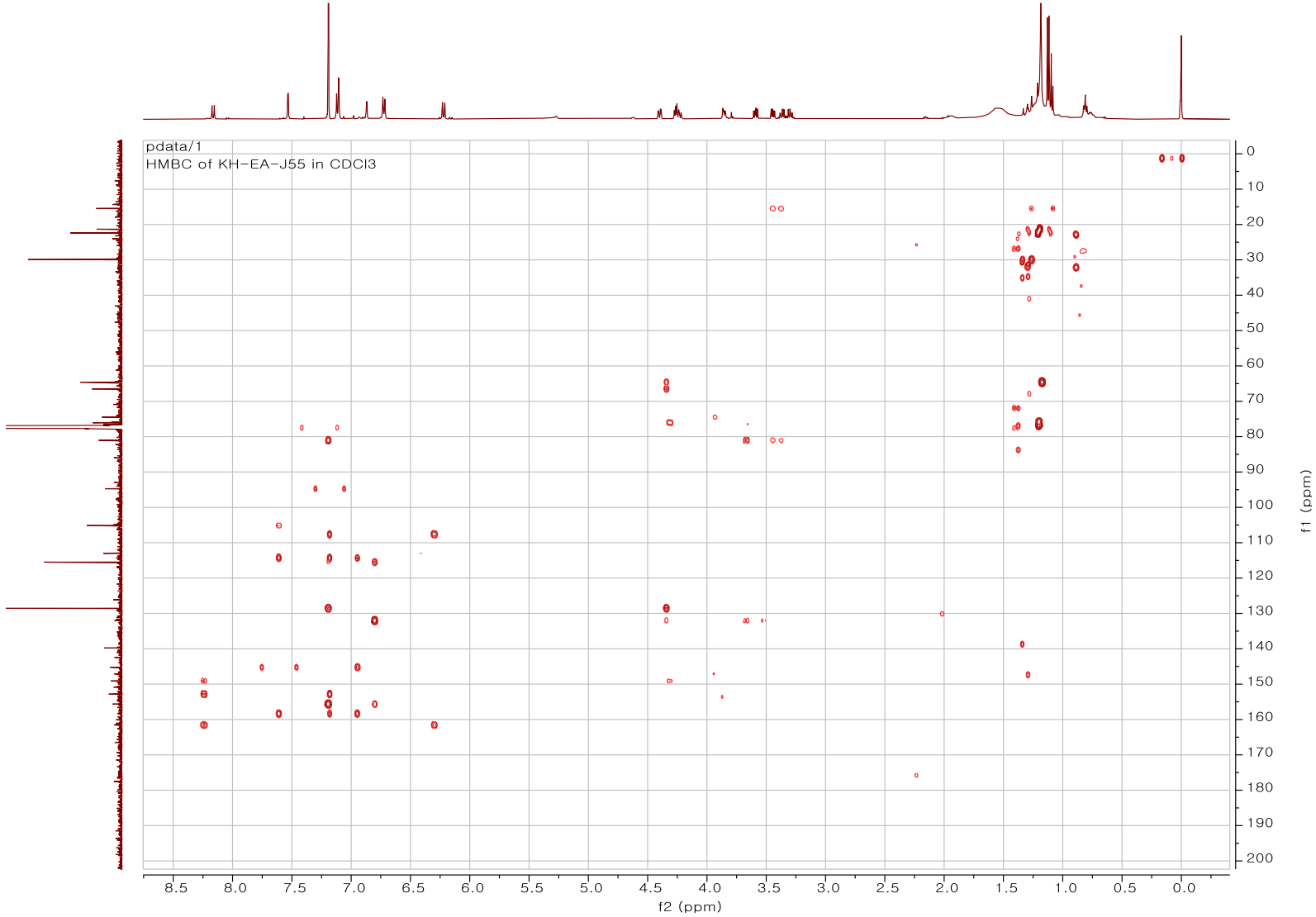
S10. ^{13}C NMR spectrum (150 MHz, $CDCl_3$) of the new compound **2**.



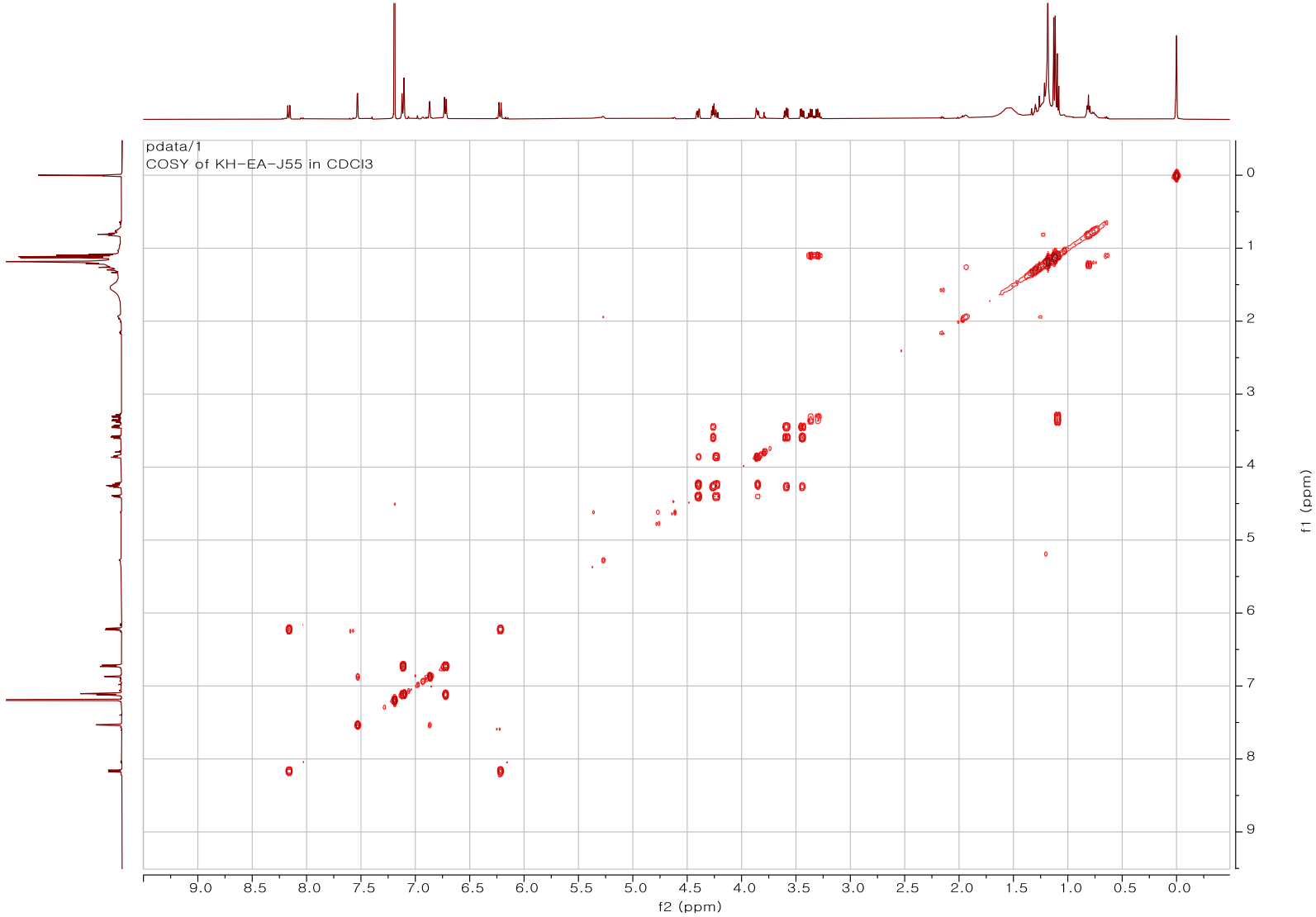
S11. HSQC spectrum of the new compound **2**.



S12. HMBC spectrum of the new compound **2**.



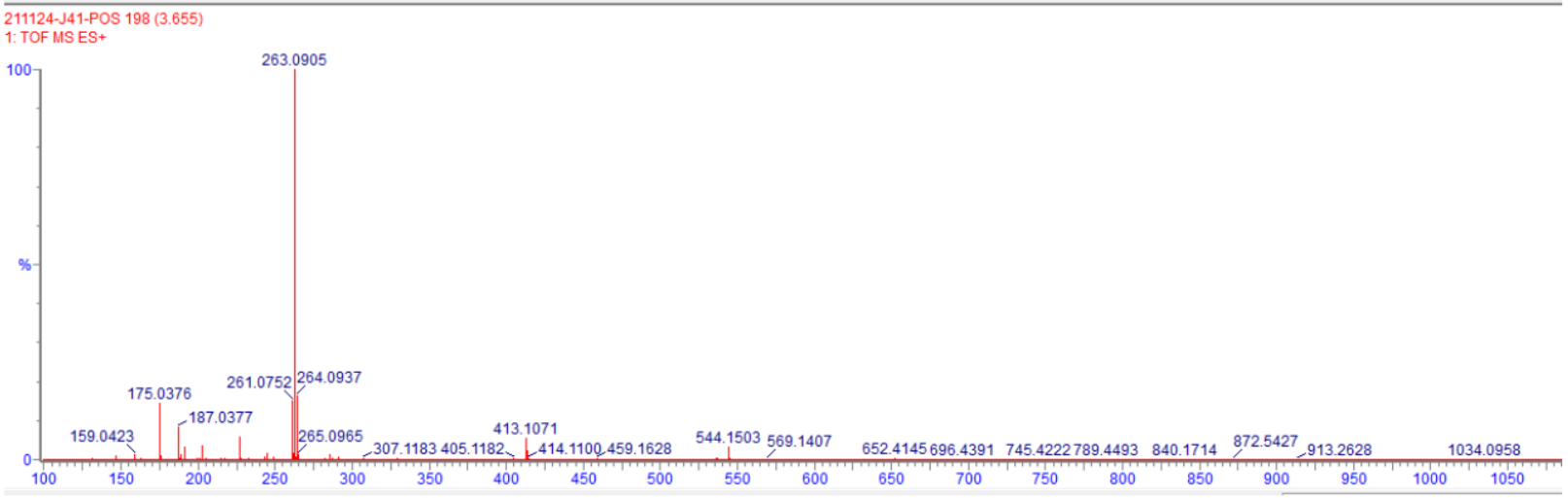
S13. COSY spectrum of the new compound **2**.



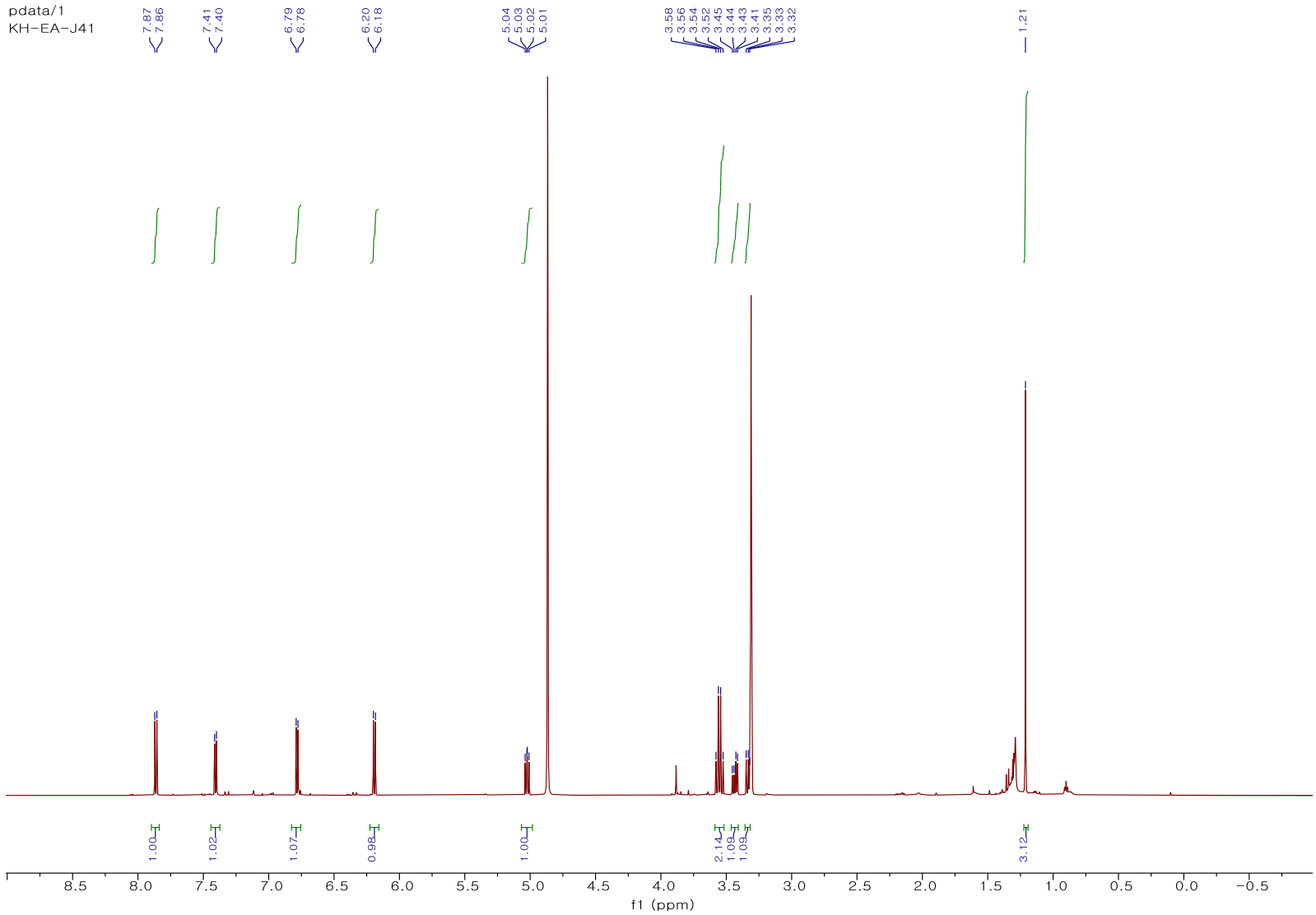
S14. HRESIMS spectrum of the new compound **3**.

Single Mass Analysis
Tolerance = 50.0 PPM / DBE: min = -1.5, max = 50.0
Element prediction: Off
Number of isotope peaks used for i-FIT = 3
Monoisotopic Mass, Even Electron Ions
47 formula(e) evaluated with 3 results within limits (up to 20 closest results for each mass)
Elements Used:

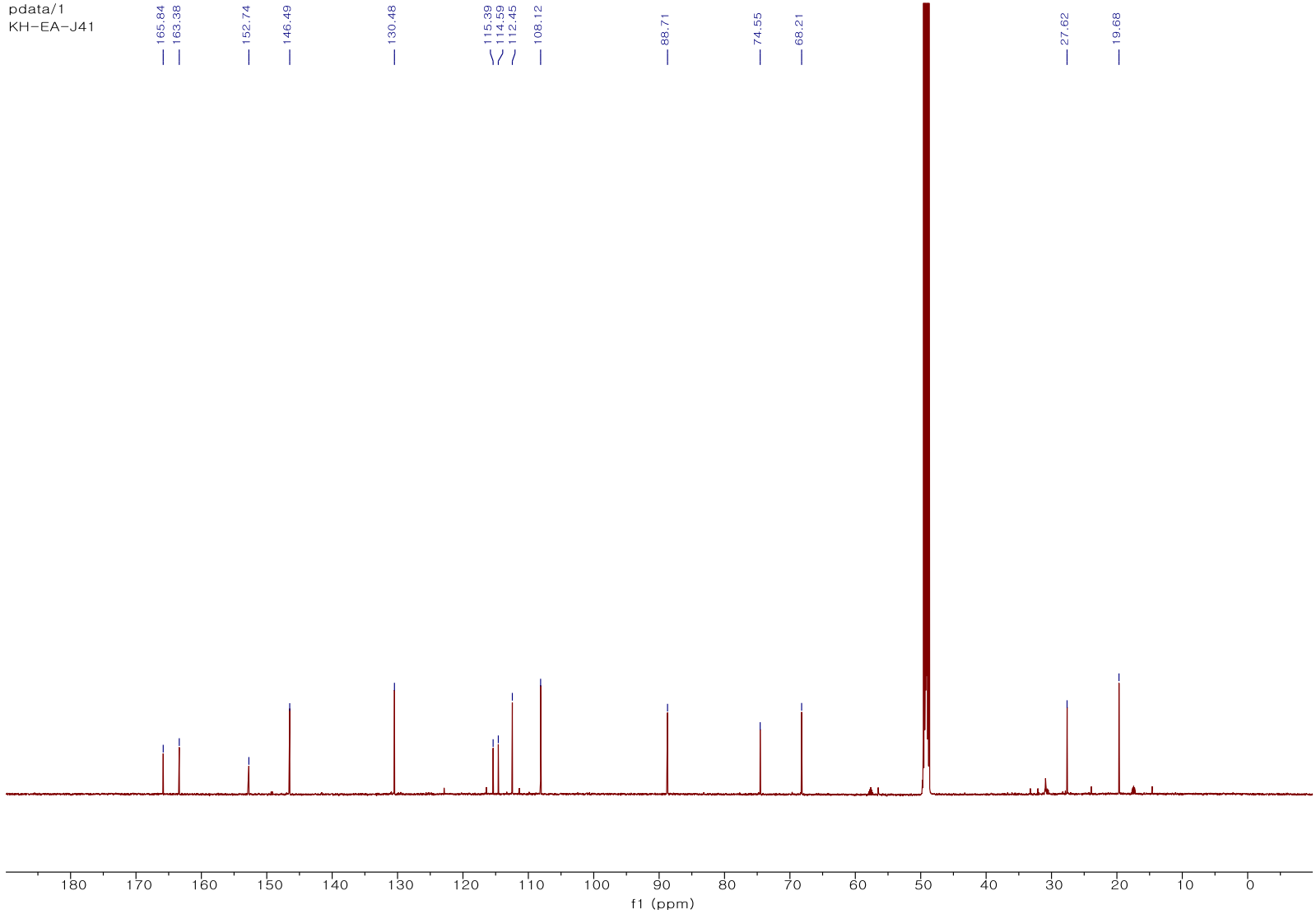
Mass	Calc. Mass	mDa	PPM	DBE	Formula	i-FIT	i-FIT Norm	Fit Conf %	C	H	O
263.0905	263.0919	-1.4	-5.3	7.5	C14 H15 O5	1188.2	0.012	98.82	14	15	5
	263.0861	4.4	16.7	16.5	C21 H11	1192.7	4.451	1.17	21	11	
	263.0978	-7.3	-27.7	-1.5	C7 H19 O10	1197.1	8.887	0.01	7	19	10



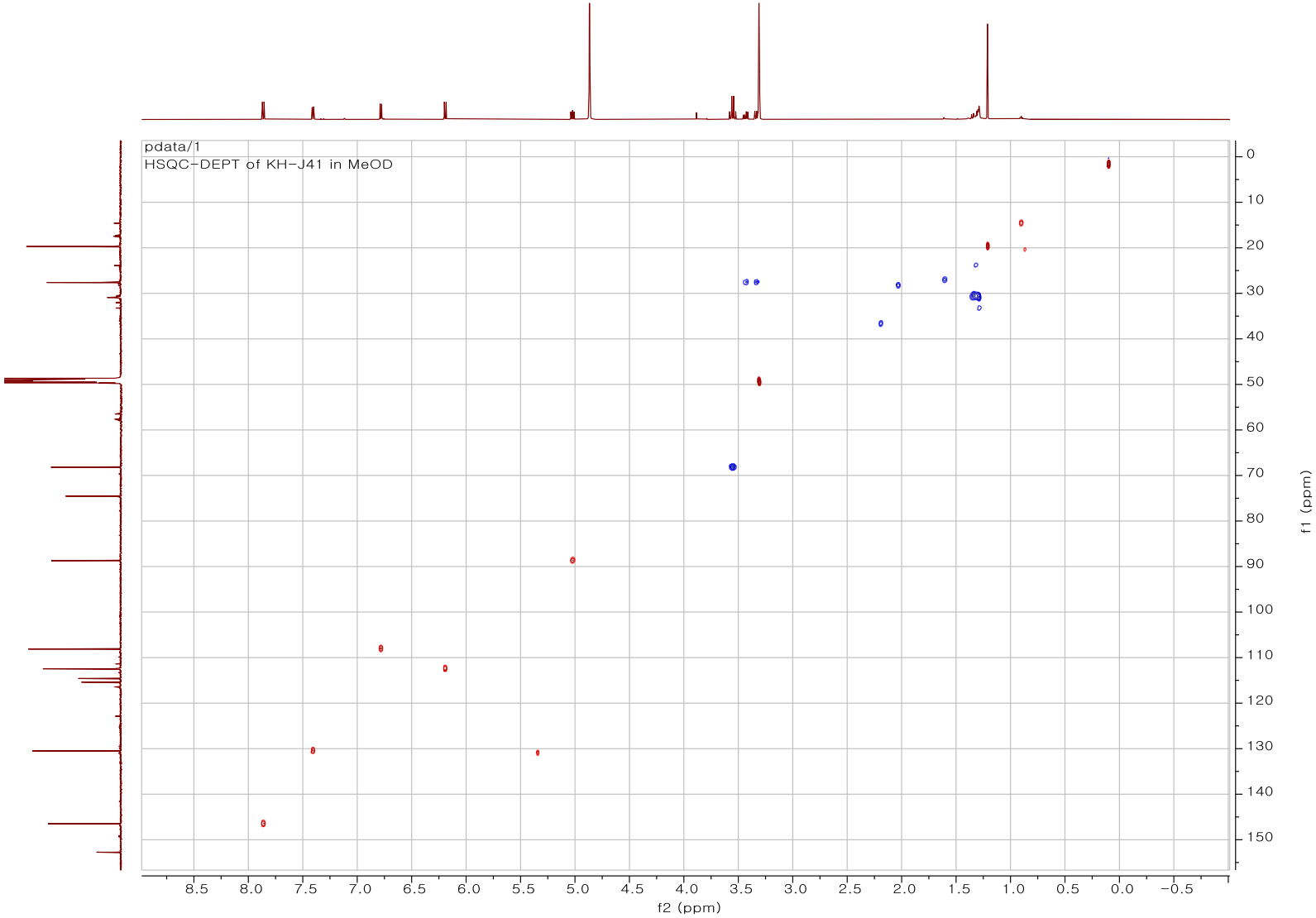
S15. ^{1}H NMR spectrum (600 MHz, methanol-d_4) of the new compound **3**.



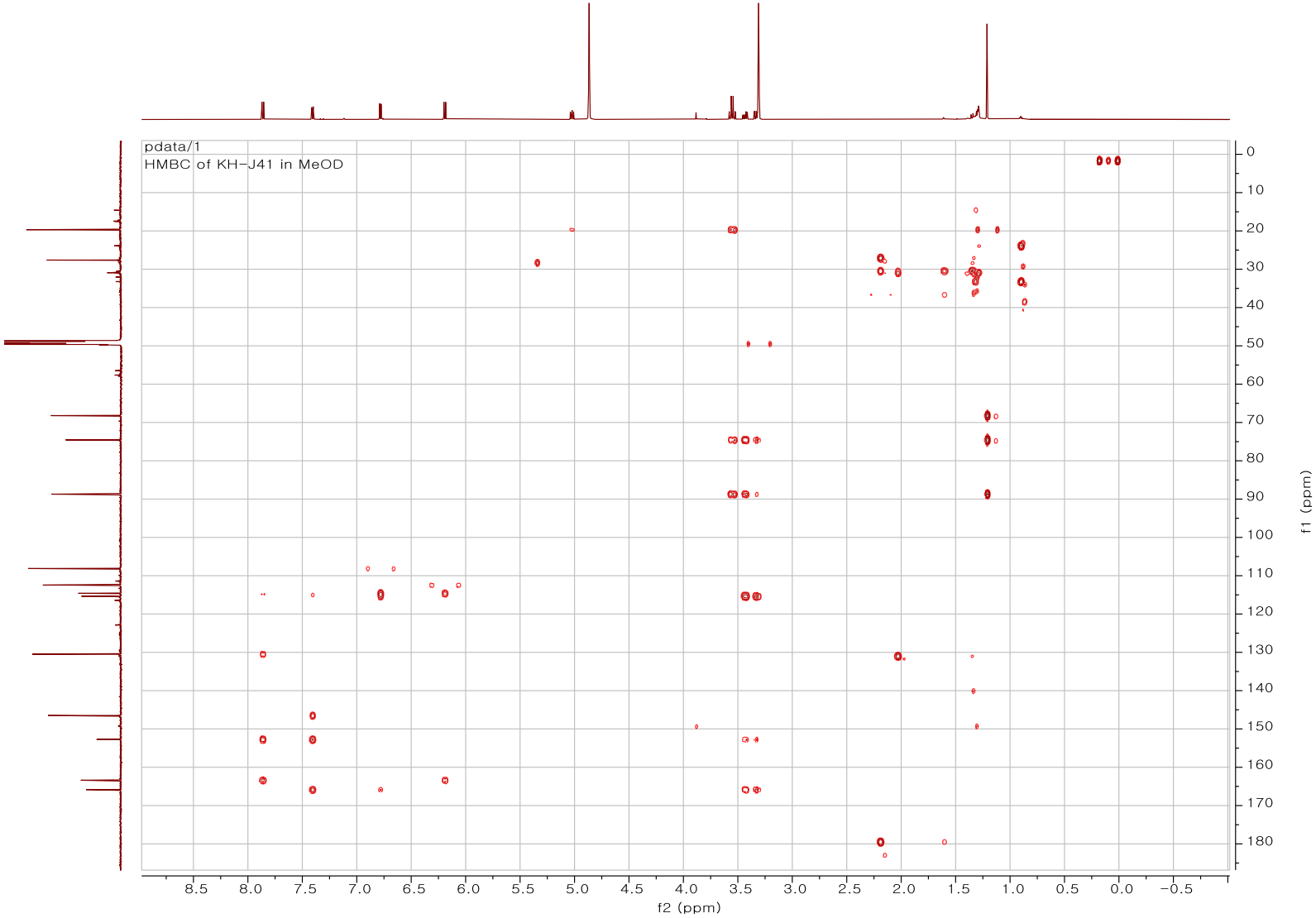
S16. ^{13}C NMR spectrum (150 MHz, methanol-d_4) of the new compound **3**.



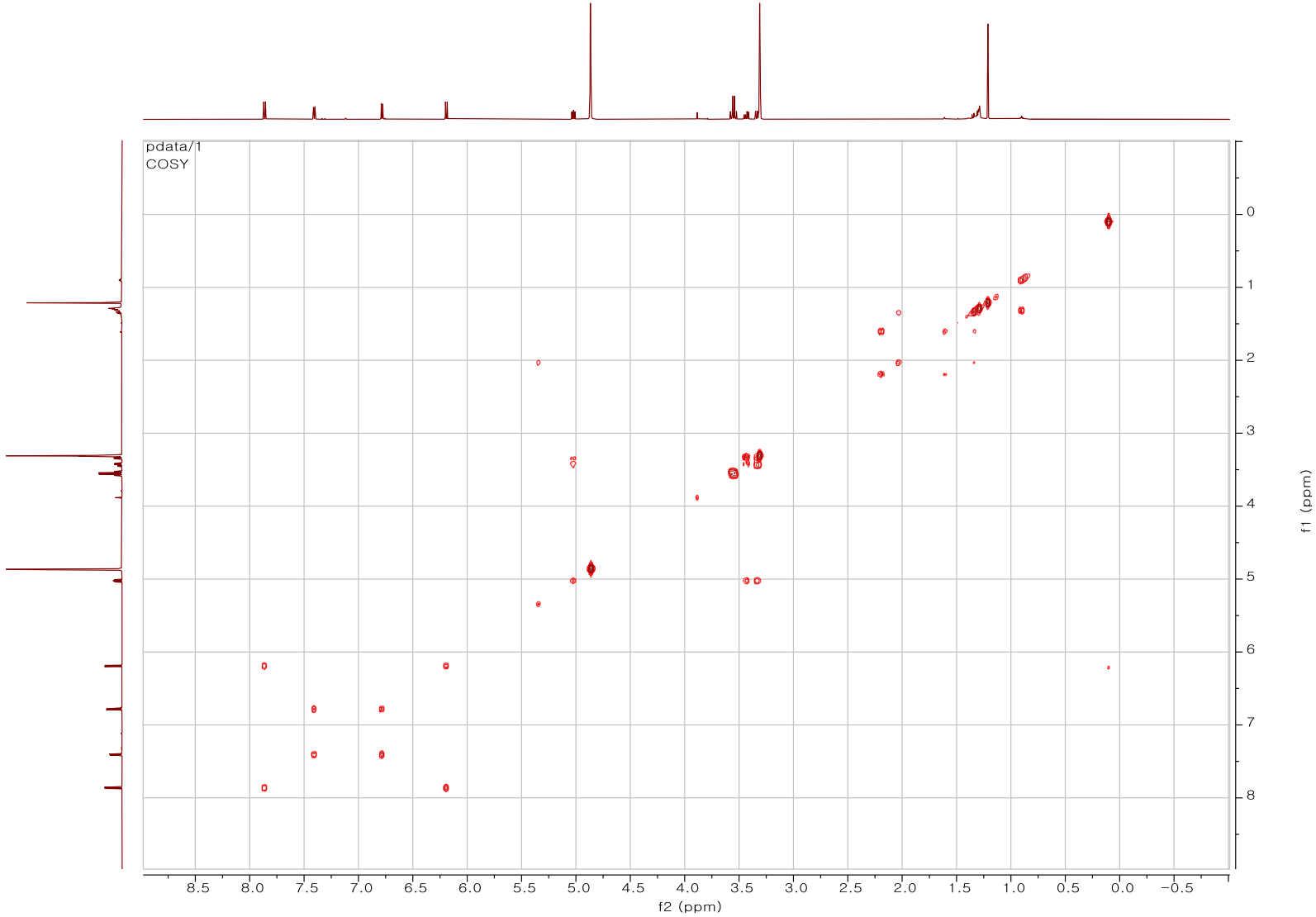
S17. HSQC spectrum of the new compound **3**.



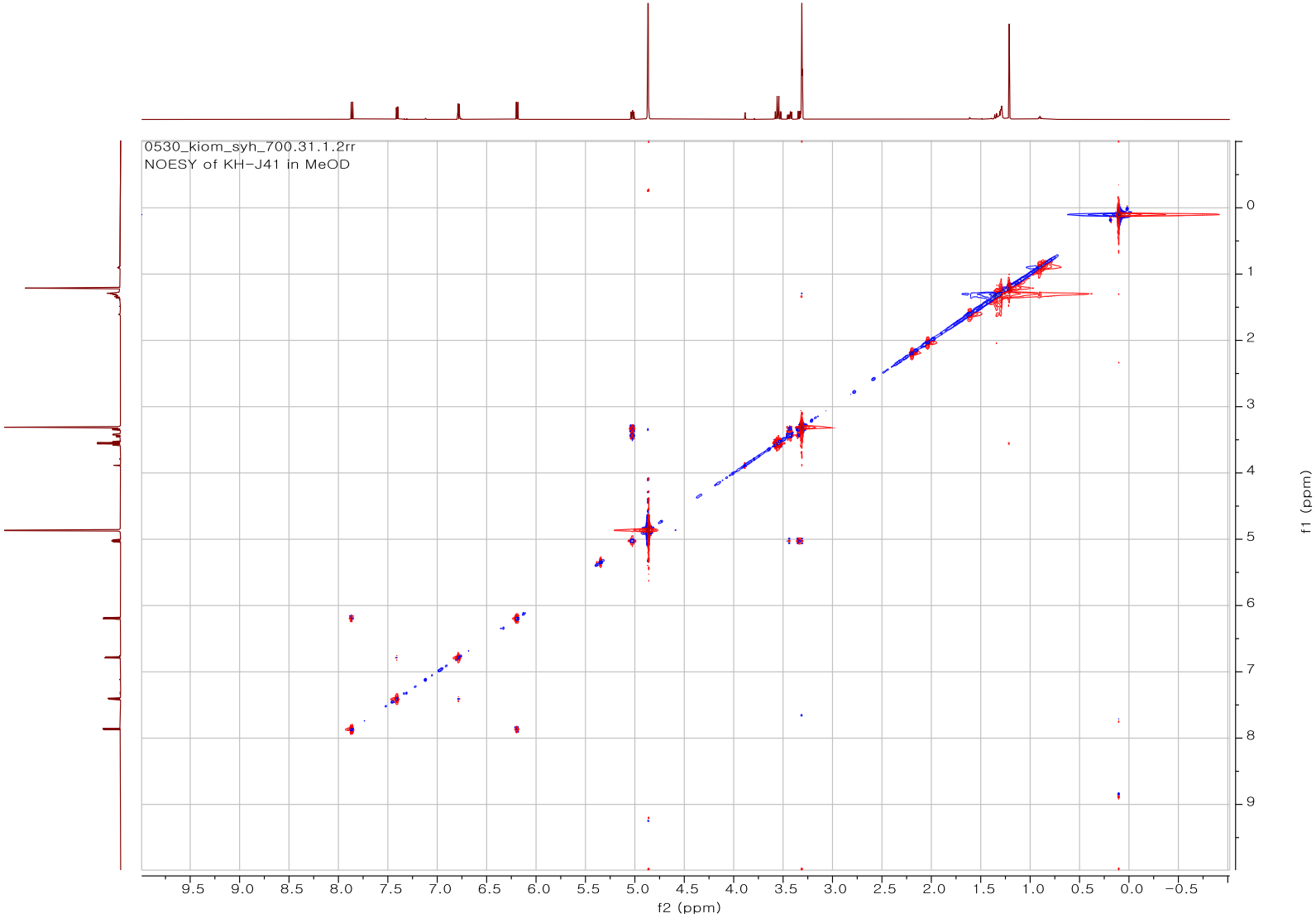
S18. HMBC spectrum of the new compound **3**.



S19. COSY spectrum of the new compound **3**.



S20. NOESY spectrum of the new compound **3**.



S21. ClustalW multiple ITS sequence alignment of four plant species (*A. reflexa*, *O. grosseserratum*, *N. forbesii*, and *N. incisum*) and herbal materials used in this work*.

*ITS sequences of seven plant samples (KIOM200801001479, KIOM2014-KR1-05, KIOM2007-KR1-15, KIOM2014-KR2-10, KIOM200901002595, KIOM201101004294, and KIOM200701000583) and two herbal materials were obtained by the PCR amplification and sequencing for this work. The other thirteen ITS sequences were used registered in the GenBank database (OK041326, OK041325, MW433729, MT735398, and GU390409 for *O. grosseserratum*; JQ936556, GU390407, MH807979, and KX674898 for *N. forbesii*; AB558252, DQ278168, KX674900, and GQ379335 for *N. incisum*). Green box indicates the aligned ITS sequences of *A. reflexa* and two plant samples used in this study. Dots(·) indicate the identical sequences with KIOM200801001479 of *A. reflexa*, and dash(-) represents gaps introduced to maximize alignment.