SUPPLEMENTAL MATERIAL

TABLE S1 Red soil sampling locations in this study.

TABLE S2 Compositions of media used in this study for isolation and fermentation of red soil actinomycetes.

TABLE S3 Distribution of the sequenced isolates at family and genus levels in different sampling locations.

TABLE S4 OTUs and isolates that share <99% 16S rRNA gene sequence similarity with the nearest type strain.

TABLE S5 Antimicrobial activities detected in representatives from different families and genera.

TABLE S6 Information of the 107 selected isolates for secondary metabolite analysis.

TABLE S7 Known secondary metabolites from the selected isolates.

FIG S1 Maximum-likelihood trees based on 16S rRNA gene sequences, showing the phylogenetic positions of 13 ‘ambiguous’ *Streptomyces* OTUs sharing > 99% 16S rRNA gene sequence similarity with the nearest type strain. Bootstrap proportions of NJ (NJ-BP) and ML (ML-BP) analyses are shown above internodes before and after the backslash, respectively; posterior probabilities (PP) of Bayesian analyses ($\geq$0.95) are shown below internodes; only values above 50% are given. Bar, 0.01 substitutions per site. OTU13 and OTU9 each may represent two new lineages. * indicated moderately acidophilic strains; ** indicated obligately acidophilic strains.

APPENDIX S1 Chemical data and detailed structure elucidation of the novel secondary metabolites.

TABLE S1 Red soil sampling locations in this study

Sampling location	GPS	pH value	Collection time	Soil sample ID
AU	28°45´N; 115°49´E	4.2-6.6	2007.08;	C1-C3;
			2009.09	D1-D3
LJZ	28°15´N; 116°55´E	4.9-5.2	2009.09	L1-L5
PYH	29°07´N; 115°55´E	4.8-6.2	2007.08	P1-P5
WS	29°44´N; 115°37´E	2.6-6.4	2007.08;	B1-B3;
			2009.09	W1-W3
XS	28°57´N; 115°58´E	4.7-5.0	2007.08	X1-X5
YL	29°30´N; 117°33´E	4.1-4.8	2007.08	A1-A5

TABLE S2 Composition of media used in this study for isolation and fermentation of red soil actinomycetes

Medium	Composition
M1	HV agar (Humic acid 1.0 g, NaH_2PO_4 0.5 g, $MgSO_4 \cdot 7H_2O$ 0.5 g, $CaCO_3$ 0.02 g, KCl 1.7 g, $FeSO_4 \cdot 7H_2O$ 0.018 g, B-vitamin solution 1 ml, agar 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M2	HVG (Humic acid 1.0 g, NaH_2PO_4 0.5 g, $MgSO_4 \cdot 7H_2O$ 0.5 g, $CaCO_3$ 0.02 g, KCl 1.7 g, $FeSO_4 \cdot 7H_2O$ 0.018 g, B-vitamin solution 1 ml, gellan gum 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M3	C agar (D-sucrose 10.0 g, L-glutamic acid 1.0 g, L-asparagines 1.0 g, $MgSO_4 \cdot 7H_2O$ 0.05 g, $FeSO_4 \cdot 7\ H_2O$ 0.01 g, $CaCO_3$ 0.02 g, K_2HPO_4 2.0 g, agar 20.0 g, distilled water 1000 ml, pH 5.0-5.5)
M4	Modified ISP9 (xylose 10.0 g, $FeSO_4 \cdot 7H_2O$ 0.001 g, $MnCl_2 \cdot 4H_2O$ 0.001 g, $ZnSO_4$ 0.001 g, agar 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M5	Minimal medium (L-asparagine 0.5 g, K_2HPO_4 0.5 g, $MgSO_4 \cdot 7H_2O$ 0.2 g, $FeSO_4 \cdot 7H_2O$ 0.01 g, glucose 10.0 g, agar 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M6	GTV (soil extract 500 ml, $CaCl_2$ 0.33 g, gellan gum 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M7	Modified starch casein agar (soluble starch 10.0 g, mannose 0.3 g, casein 0.3 g, KNO_3 2.0 g, $MgSO_4 \cdot 7H_2O$ 0.05 g, $FeSO_4 \cdot 7H_2O$ 0.01 g, K_2HPO_4 2.0 g, $CaCO_3$ 0.02 g, NaCl 2.0 g, agar 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M8	A+B mixed medium [(Solutions A: glucose 4.0 g, Difcoyeast extract 2.0 g and 18.0 g agar, distilled water 500 ml; Solution B: $(NH_4)_2SO_4$ 2.0 g, K_2HPO_4 0.5 g, $MgSO_4$.$7H_2O$ 0.5 g, KCl 0.1 g, distilled water 500 ml, pH 5.0-5.5]
M9	Modified mineral-medium (sorbitol 5.0 g, K_2HPO_4 1.0 g, KH_2PO_4 0.7 g, NH_4Cl 0.2 g, $MgSO_4 \cdot 7H_2O$ 0.03 g, $CaCl_2 \cdot H_2O$ 0.067 g, $NaHCO_3$ 0.3 g, $CuCl_2 \cdot H_2O$ 55 μg, $ZnCl_2$ 150 μg, $NiCl_2 \cdot 6\ H_2O$ 20 μg, $FeSO_4 \cdot 7\ H_2O$ 880 μg, $MnCl_2 \cdot 4\ H_2O$ 280 μg, $Al_2(SO_4)_3 \cdot 18\ H_2O$ 135 μg, $CoCl_2 \cdot 6\ H_2O$ 55 μg, $NaMoO_4 \cdot 2H_2O$ 30 μg, H_3BO_3 50 μg, agar 15.0 g, distilled water 1000 ml, pH 5.0-5.5)
M10	Chitin medium (KH_2PO_4 0.3 g, K_2HPO_4 0.7 g, $FeSO_4 \cdot 7H_2O$ 0.015 g, $MgSO_4 \cdot 7H_2O$ 0.5 g, $ZnSO_4 \cdot 7H_2O$ 0.002 g, 40 ml 5% colloidal chitin, agar 15.0 g, distilled water 960 ml, pH 5.0-5.5)
M11	GYM (yeast extract 4.0 g, malt extract 10.0 g, glucose 4.0 g, $CaCO_3$ 2.0 g, agar 15.0-20.0 g, distilled water 1000 ml, pH 5.0-5.5)
M12	MOSY (mannitol 10.0 g, oatmeal 5.0 g, soy peptone 5.0 g, yeast extract 2.0 g, NaCl 2.0 g, KH_2PO_4 0.5 g, $MgSO_4 \cdot 7H_2O$ 0.5 g, trace element solution 2.0 ml, agar 20.0 g, distilled water 1000 ml, pH 7.2, pH 5.0-5.5)
	Trace element solution: $ZnSO_4 \cdot 7H_2O$ 1.0 g, $FeSO_4 \cdot 7H_2O$ 1.0 g, $MnCl_2 \cdot 4H_2O$ 1.0 g, $CuSO_4 \cdot 5H_2O$ 1.0 g, $Na_2B_4O_7 \cdot 10H_2O$ 1.0 g, $(NH_4)_6Mo_7O_{24} \cdot 4H_2O$ 1.0 g, distilled water 1000 ml, pH 5.0-5.5)
M13	SGG (potato starch 10 g, glucose 10 g, glycerol 10 g, corn steep powder 2.5 g, peptone 5 g, yeast extract 2 g, NaCl 1 g, $CaCO_3$ 3 g, agar 20.0 g, tap water 1000 ml, pH 5.0-5.5)

TABLE S3 Distribution of the sequenced isolates at family and genus levels in different sampling locations

		No. of isolates						
Orders[a]	**Family/Genus**[a]	**AU**	**LJZ**	**PYH**	**WS**	**XS**	**YL**	**Total**
Catenulisporales	***Catenulisporaceae***							**5**
	Catenulispora		3		2			5
Corynebacteriales	***Mycobacteriaceae***							**2**
	Mycobacterium		2					2
	Nocardiaceae							**20**
	Nocardia	2	7				10	19
	Williamsia		1					1
	Tsukamurellaceae							**1**
	Tsukamurella		1					1
Micromonosporales	***Micromonosporaceae***							**27**
	Dactylosporangium		1			1		2
	Micromonospora	12	8		3	2		25
Propionibacteriales	***Nocardioidaceae***							**4**
	Kribella		1	2				3
	Marmoricola		1					1
Pseudonocardiales	***Pseudonocardiaceae***							**20**
	Actinomycetospora		1		2			3
	Actinosynnema		1					1
	Amycolatopsis		3	2	2		1	8
	Pseudonocardia		1		1			2
	Lentzea	1	1	1				3
	Saccharothrix		2		1			3
Streptomycetales	***Streptomycetaceae***							**213**

	Streptacidiphilus				4		1	5
	Streptomyces	46	77	28	29	7	21	208
Streptosporangiales	***Streptosporangiaceae***							**42**
	Microbispora	3	5		2			10
	Microtetraspora		1				1	1
	Nonomuraea	2	10		3			15
	Plantotraspora	1						1
	Sphaerisporangium		1					1
	Streptosporangium		12		1			13
	Thermomonosporaceae							**24**
	Actinoallomurus		13					13
	Actinocorallia		1					1
	Actinomadura		8		2			10
	Total	**67**	**162**	**33**	**52**	**10**	**34**	**358**

[a] The assignment of strains to orders and families is based on the hierarchical classification of the phylum *Actinobacteria* in the second edition of *Bergey's Manual of Systematic Bacteriology* (Ludwig *et al*., 2012).

TABLE S4 OTUs and isolates that share < 99% 16S rRNA gene sequence similarity with the nearest type strain

No.	OTU serial number	No. of lineages	No. of isolates	No. of antagonistic isolates	Representative isolate ID[a, b]	The most closely related species	16S rRNA gene sequence similarity
1	Singleton	1	1	0	FXJ1.1129*	*Actinomadura madurae*	96.20%
2	Singleton	1	1	0	FXJ1.556*	*Actinomycetospora lutea*	98.64%
3	Singleton	1	1	0	GTVL4-6*	*Actinosynnema pretiosum* subsp. *auranticum; Lechevalieria atacamensis*	97.52%
4	Singleton	1	1	0	FXJ1.244*	*Amycolatopsis bartoniae*	97.14%
5	Singleton	1	1	0	FXJ1.274*	*Amycolatopsis niigatensis*	98.37%
6	OTU53	1	2	0	FXJ1.974	*Dactylosporangium darangshiense*	98.89%
7	OTU57	1	2	1	FXJ1.034T*	*Lentzea kentuckyensis*	98.50%
8	OTU37	3	2	2	FXJ1.457*	*Microbispora hainanensis*	98.83%
			1	0	FXJ1.1062	*Microbispora amethystogenes*	98.83%
			4	1	FXJ1.541*	*Microbispora amethystogenes*	98.50%
9	OTU30	1	1	0	FXJ1.477*	*Microbispora rosea* subsp. *rosea*	98.84%
10	OTU11	1	2	1	FXJ1.347*	*Micromonospora eburnea*	98.90%
11	OTU24	1	3	0	FXJ1.353*	*Micromonospora rhizosphaerae*	98.88%
12	Singleton	1	1	0	FXJ1.1164*	*Mycobacterium duvalii*	98.75%
13	Singleton	1	1	0	FXJ1.077*	*Nocardia jiangxiensis*	98.17%
14	OTU25	1	2	0	FXJ1.258*	*Nocardia jiangxiensis*	98.81%
15	OTU66	1	3	1	FXJ1.011*	*Nocardia ninae*	98.41%
16	OTU27	1	2	1	FXJ1.242*	*Nocardia nova*	98.24%
17	Singleton	1	1	0	FXJ1.368*	*Nonomuraea candida*	98.86%
18	Singleton	1	1	0	FXJ1.102T*	*Nonomuraea candida*	98.86%
19	OTU26	2	1	0	FXJ1.958*	*Nonomuraea spiralis*	98.89%
			1	0	FXJ1.998*	*Nonomuraea candida*	98.90%

20	Singleton	1	1	0	FXJ1.482*	*Pseudonocardia alaniniphila*	98.68%
21	Singleton	1	1	0	FXJ1.271*	*Streptacidiphilus anmyonensis*	98.60%
22	OTU6	1	11	11	FXJ1.725*	*Streptomyces ferralitis*	98.90%
23	Singleton	1	1	0	FXJ1.042	*Streptomyces aureus*	98.84%
24	OTU16	1	5	1	FXJ1.238*	*Streptomyces caeruleatus*	98.75%
25	OTU15	1	3	1	FXJ1.451*	*Streptomyces caeruleatus*	98.78%
26	Singleton	1	1	0	FXJ1.197	*Streptomyces chromofuscus*	97.73%
27	Singleton	1	1	0	FXJ1.139*	*Streptomyces cocklensis*	97.65%
28	Singleton	1	1	0	FXJ1.124**	*Streptomyces cocklensis*	98.97%
29	Singleton	1	1	0	FXJ1.250	*Streptomyces muensis*	97.88%
30	OTU21	1	1	0	FXJ1.467*	*Streptomyces corchorusii*	98.83%
31	OTU63	1	2	2	FXJ1.978*	*Streptomyces cuspidosporu*	98.32%
32	OTU33	1	2	1	FXJ1.460*	*Streptomyces diastaticus* subsp. *ardesiacus*	98.16%
33	Singleton	1	1	1	FXJ1.194	*Streptomyces durhamensis*	98.09%
34	Singleton	1	1	0	FXJ1.038	*Streptomyces filipinensis*	98.38%
35	Singleton	1	1	0	FXJ1.257**	*Streptomyces griseorubiginosus*	98.62%
36	Singleton	1	1	0	FXJ1.255	*Streptomyces caeruleatus*	98.83%
37	Singleton	1	1	0	FXJ1.300**	*Streptomyces guanduensis*	98.67%
38	OTU50	1	6	1	FXJ1.1116	*Streptomyces malachitofuscus*	98.66%
39	OTU55	1	3	1	FXJ1.517*	*Streptomyces psammoticus*	98.53%
40	Singleton	1	1	0	FXJ1.1162*	*Streptomyces psammoticus*	98.69%
41	Singleton	1	1	0	FXJ1.056*	*Streptomyces psammoticus*	98.96%
42	Singleton	1	1	0	FXJ1.069*	*Streptomyces rubidus*	98.39%
43	Singleton	1	1	1	FXJ1.701	*Streptomyces sanglieri*	98.83%
44	OTU64	1	3	3	FXJ1.434*	*Streptomyces graminisoli*	98.97%
45	OTU31	1	4	1	FXJ1.470*	*Streptomyces somaliensis*	98.32%

46	Singleton	1	1	0	FXJ1.193*	*Streptomyces viridobrunneus*	98.46%
47	Singleton	1	1	0	FXJ1.461*	*Streptomyces yanglinensis*	98.74%
48	Singleton	1	1	0	GTVWS6G17*	*Streptomyces scopuliridis*	98.33%
49	OTU23	3	4	0	FXJ 1.973*	*Streptosporangium album*	98.60%
			2	1	FXJ1.1117*	*Streptosporangium pseudovulgare*	98.38%
			1	0	FXJ1.986*	*Streptosporangium carneum*	98.89%
Total	**49**	**54**	**101**	**32**			

[a] *, moderately acidophilic strains; **, obligately acidophilic strains.

[b] FXJ1.034[T] and FXJ1.102[T] have been proposed as type strains of *Lentzea jiangxiensis* sp. nov. and *Nonomuraea jiangxiensis* sp. nov., respectively (see Li *et al.*, 2012a,b).

TABLE S5 Antimicrobial activities detected in representatives from different families and genera

Family	**Genus**	**No. of isolates**	**No. of active isolates**	**Percentage of active isolates**
Catenulisporaceae	*Catenulispora*	5 [a]	1 [a]	20.0%
Mycobacteriaceae	*Mycobacterium*	2 [a]	0	0.0%
Nocardiaceae	*Nocardia*	19 [a]	2 [a]	10.5%
	Williamsia	1 [a]	0	0.0%
Tsukamurellaceae	*Tsukamurella*	1 [a]	0	0.0%
Micromonosporaceae	*Dactylosporangium*	2 [b]	0	0.0%
	Micromonospora	25 (23*a*+2*b*)	5 (4*a*+1*b*)	20.0%
Nocardioidaceae	*Kribella*	3 [a]	0	0.0%
	Marmoricola	1 [a]	0	0.0%
Pseudonocardiaceae	*Actinomycetospora*	3 [a]	0	0.0%
	Actinosynnema	1 [a]	0	0.0%
	Amycolatopsis	8 [a]	3 [a]	37.5%
	Pseudonocardia	2 [a]	0	0.0%
	Lentzea	3 (2*a*+1*b*)	1 [a]	33.3%
	Saccharothrix	3 [a]	1 [a]	33.3%
Streptomycetaceae	*Streptacidiphilus*	5 [a]	0	0.0%
	Streptomyces	208 (127*a*+81*b*)	112 (70*a*+42*b*)	53.8%
Streptosporangiaceae	*Microbispora*	10 (9*a*+1*b*)	3 [a]	30.0%
	Microtetraspora	2 [b]	0	0.0%
	Nonomuraea	15 (9*a*+6*b*)	2 (1*a*+1*b*)	13.3%
	Plantotraspora	1 [a]	0	0.0%
	Sphaerisporangium	1 [a]	0	0.0%
	Streptosporangium	13 [a]	7 [a]	53.8%
Thermomonosporaceae	*Actinoallomurus*	13 [a]	0	0.0%
	Actinocorallia	1 [b]	0	0.0%
	Actinomadura	10 (8*a*+2*b*)	4 (3*a*+1*b*)	40.0%
Total		**358**	**141**	**39.4%**

[a] Strains assigned to the acidophilic group.
[b] Strains assigned to the acidotolerant group.
[c] Figures indicate the number of strains.

TABLE S6 Information of the 107 selected isolates for secondary metabolite analysis

Family	**Strain**[a, b]	**Location**	**Bioactivity**[c]
Catenulisporaceae	*Catenulispora* sp. AL4G16[a]	LJZ	*Vc*
	Catenulispora sp. SCAWS2A[a]	WS	N
Micromonosporaceae	*Dactylosporangium* sp. FXJ1.262[†]	XS	N
	Micromonospora sp. FXJ1.144[a]	AU	N
	Micromonospora sp. FXJ1.347[a, †]	AU	*Af, Kp*
	Micromonospora sp. FXJ1.351[a, †]	AU	N
	Micromonospora sp. FXJ1.361[a]	AU	*Pa*
	Micromonospora sp. FXJ1.507[a]	LJZ	N
Nocardiaceae	*Nocardia* sp. FXJ1.009[a]	YL	N
	Nocardia sp. FXJ1.010[a, †]	YL	N
	Nocardia sp. FXJ1.016[a, †]	YL	N
	Nocardia sp. FXJ1.516[a]	LJZ	N
	Williamsia sp. FXJ1.547[a]	LJZ	N
Pseudonocardiaceae	*Actinosynnema* sp. GTVL4-6[a, †]	LJZ	N
	Amycolatopsis sp. FXJ1.244[a, †]	YL	N
	Amycolatopsis sp. FXJ1.274[a, †]	PYH	*Kp*
	Amycolatopsis sp. FXJ1.406[a]	LJZ	*Sa*
	Amycolatopsis sp. FXJ1.428[a]	WS	N
	Amycolatopsis sp. FXJ1.444[a]	WS	N
	Amycolatopsis sp. GTVL4-7[a]	LJZ	N
	Actinomycetospora sp. FXJ1.479[a]	WS	N
	Actinomycetospora sp. FXJ1.484[a]	WS	N
	Lentzea jiangxiensis FXJ1.034[Ta, †]	AU	*Ca, Kp*
	Pseudonocardia sp. FXJ1.453[a]	WS	N
	Saccharothrix sp. FXJ1.021[a]	WS	*Ca, Kp, Sa*
	Saccharothrix sp. FXJ1.486[a]	LJZ	N
Streptomycetaceae	*Streptomyces* sp. FXJ1.008[a]	YL	N
	Streptomyces sp. FXJ1.013[†]	YL	N
	Streptomyces sp. FXJ1.019	YL	N
	Streptomyces sp. FXJ1.020	YL	*Pa, Sa*
	Streptomyces sp. FXJ1.029[a]	AU	N
	Streptomyces sp. FXJ1.030	AU	*Pa*
	Streptomyces sp. FXJ1.031[a]	AU	N
	Streptomyces sp. FXJ1.032[†]	AU	*Ca, Ec, Fo, Sa,*
	Streptomyces sp. FXJ1.033	AU	N
	Streptomyces sp. FXJ1.040[a]	AU	N
	Streptomyces sp. FXJ1.042[†]	AU	N
	Streptomyces sp. FXJ1.044	YL	*Pa*
	Streptomyces sp. FXJ1.050[a]	AU	*Cp*
	Streptomyces sp. FXJ1.054[†]	AU	N
	Streptomyces sp. FXJ1.055[a]	AU	*Kp, Sa*

Streptomyces sp. FXJ1.060[a]	AU	*Sa*
Streptomyces sp. FXJ1.066	AU	N
Streptomyces sp. FXJ1.068	AU	*Af, Ca, Sa, Vc*
Streptomyces sp. FXJ1.069[a, †]	AU	N
Streptomyces sp. FXJ1.075[a]	AU	*Af, Ca, Fo, Sa*
Streptomyces sp. FXJ1.076[a]	AU	*Af, Ca, Ec, Fo, Sa*
Streptomyces sp. FXJ1.079[a, †]	AU	*Sa*
Streptomyces sp. FXJ1.092[a]	AU	*Kp, Sa*
Streptomyces sp. FXJ1.093[†]	AU	*Ec, Kp, Sa*
Streptomyces sp. FXJ1.172[a]	XS	*Af, Ec, Sa*
Streptomyces sp. FXJ1.234	PYH	*Af, Ca*
Streptomyces sp. FXJ1.235[†]	PYH	*Ec*
Streptomyces sp. FXJ1.238[a, †]	PYH	*Pa*
Streptomyces sp. FXJ1.249	YL	*Ca, Ec, Sa*
Streptomyces sp. FXJ1.250[†]	YL	*Fo*
Streptomyces sp. FXJ1.253[a]	AU	*Af, Ca, Ec, Fo, Sa, Vc*
Streptomyces sp. FXJ1.264	YL	*Ec, Kp, Pa, Sa, Vc*
Streptomyces sp. FXJ1.272	PYH	N
Streptomyces sp. FXJ1.275	PYH	N
Streptomyces sp. FXJ1.297[a, †]	PYH	N
Streptomyces sp. FXJ1.309	XS	*Ca, Ec, Sa, Vc*
Streptomyces sp. FXJ1.310	XS	*Ca, Ec, Sa*
Streptomyces sp. GA60	AU	*Ca, Kp, Pa, Vc*
Streptomyces sp. FXJ1.401[a]	LJZ	*Sa*
Streptomyces sp. FXJ1.407[a]	LJZ	*Af, Ca, Sa*
Streptomyces sp. FXJ1.408[a, †]	LJZ	*Af, Ca, Fo*
Streptomyces sp. FXJ1.409[a]	LJZ	*Ca, Cp, Sa*
Streptomyces sp. FXJ1.414[a,†]	WS	*Ca, Fo*
Streptomyces sp. FXJ1.417[a]	WS	*Af, Fo, Sa*
Streptomyces sp. FXJ1.429[a]	WS	*Ca, Cp, Ec, Fo, Kp, Pa, Sa, Vc*
Streptomyces sp. FXJ1.430[a]	LJZ	*Af, Ca, Cp, Sa*
Streptomyces sp. FXJ1.433	LJZ	*Ca, Cp, Sa*
Streptomyces sp. FXJ1.434[a, †]	LJZ	*Ca, Cp*
Streptomyces sp. FXJ1.437[a]	LJZ	*Ca, Cp*
Streptomyces sp. FXJ1.439[a, †]	LJZ	*Cp, Kp*
Streptomyces sp. FXJ1.442[a]	WS	*Af, Ca, Cp, Ec, Fo, Kp, Pa, Sa, Vc*
Streptomyces sp. FXJ1.447[a]	LJZ	*Ca, Cp, Fo, Sa*
Streptomyces sp. FXJ1.450[a]	WS	*Ca, Cp, Fo, Ec, Kp, Pa, Sa, Vc*
Streptomyces sp. FXJ1.470[a, †]	WS	N
Streptomyces sp. FXJ1.474[a, †]	LJZ	*Ca*
Streptomyces sp. FXJ1.475[a]	LJZ	*Ca, Cp, Sa*
Streptomyces sp. FXJ1.502[a]	LJZ	*Af, Ca, Sa*
Streptomyces sp. FXJ1.512[a]	LJZ	*Af, Ca*
Streptomyces sp. FXJ1.532[a, †]	LJZ	*Af, Ca, Cp, Fo*

	Streptomyces sp. FXJ1.535[a,†]	LJZ	*Sa*
	Streptomyces sp. FXJ1.701[†]	YL	*Af, Cp, Fo*
	Streptomyces sp. FXJ1.907[a,†]	LJZ	*Cp, Sa*
	Streptomyces sp. FXJ1.1116[†]	LJZ	*Af*
	Streptomyces sp. GTVL2G15[†]	LJZ	*Sa, Vc*
	Streptomyces sp. FXJ23y[a,†]	LJZ	*Af, Ca*
Streptosporangiaceae	*Nonomuraea jiangxiensis* FXJ1.102^{T} [a,†]	AU	N
	Nonomuraea sp. FXJ1.368[a,†]	AU	N
	Microbispora sp. FXJ1.457[a,†]	WS	*Sa*
	Microbispora sp. FXJ1.769[a,†]	AU	N
	Microbispora sp. FXJ1.1062[†]	LJZ	N
	Microtetraspora sp. FXJ1.1037	YL	N
	Sphaerisporangium sp. FXJ1.452[a]	LJZ	N
	Streptosporangium sp. FXJ1.481[a]	WS	N
	Streptosporangium sp. FXJ1.1111[a]	LJZ	*Af, Ca*
	Streptosporangium sp. FXJ1.1117[a,†]	LJZ	*Af, Cp*
Thermomonosporaceae	*Actinoallomurus* sp. FXJ1.503[a]	LJZ	N
	Actinocorallia sp. FXJ1.544	LJZ	N
	Actinomadura sp. FXJ1.340[a]	WS	*Ca, Sa, Vc*
	Actinomadura sp. FXJ1.344[a]	WS	N
	Actinomadura sp. FXJ1.848[a]	LJZ	N
	Actinomadura sp. FXJ1.1129[a,†]	LJZ	N

[a] Strains assigned to the acidophilic group.

[b] Stains marked with ([†]) share < 99% 16S rRNA gene sequence similarity with the nearest type strain.

[c] Strains are antagonistic to the following indicators: *Af, Aspergillus fumigatus; Fo, Fusarium oxysporum; Ca, Candidia albicans; Cp, Candida pseudorugosa; Ec, Escherichia Coli; Kp, Klebsiella pneumonia; Pa, Pseudomonas aeruginosa; Sa, Staphylococcus aureus; Vc, Vibrio cholera*. N, no antimicrobial activity shown.

TABLE S7 Known secondary metabolites from the selected isolates

No.	Strain	Producing medium	Compound(s)[c]	Structural class	Chemical data: UV (MeOH)	Chemical data: MS (*m/z*)[d]
Streptomycetes						
1	*Streptomyces* sp. FXJ1.050[a]	GYM	Nigericin[†]	Polyether	None	$[M-H]^-$=723.6
			Niphimycin	Macrolide	231	$[M+H]^+$=1142.7343
2	*Streptomyces* sp. FXJ1.055[a]	GYM	3 albonoursin type compounds	Diketopiperazine	317	Not measured
3	*Streptomyces* sp. FXJ1.066	GYM	Lobophorins A&B[†]	Macrolide	240, 266, 282(sh)	$[M+H]^+$=1157.5, 1185.7
		SGG	Spoxazomicins A&B Spoxazomicin C	Siderophore	243, 303 241, 248, 260(sh), 300	$[M+H]^+$=336.1384, 336.1382 $[M+H]^+$=194.0821
4	*Streptomyces* sp. FXJ1.068	GYM	5 milbemycins	Macrolide	241/237/243/237/243	$[2M+Na]^+$=1111.4; $[M+H_2O]^+$=644.3, 646.2, 658.2, 660.2
			4 nanchangmycins[*]	Polyether	234 236/234/238	$[M+Na]^+$=889.9 $[M+Na]^+$=889.8, 889.8, 889.8
5	*Streptomyces* sp. FXJ1.069[a, b]	SGG	Desferrioxamines E&G, ferrioxamine E	Siderophore	End abs.	$[M+H]^+$=601.3565, 654.2683, 619.3657
6	*Streptomyces* sp. FXJ1.076[a]	GYM/MOSY	6 elaiophylin-type compounds	Macrolide	249	$[M+Na]^+$=1019.5, 1033.8, 1047.6, 1047.8, 1061.5, 729.4
		GYM	Nigericin[†]	Polyether	None	$[M-H]^-$=723.6
7	*Streptomyces* sp. FXJ1.092[a]	GYM	3 Albonoursin type diketopiperazines	Diketopiperazine	231, 315	Not measured
8	*Streptomyces* sp. FXJ1.093[b]	SGG	6 Albonoursin type diketopiperazines	Diketopiperazine	233, 317	$[M+H]^+$=271.3, others not measured
9	*Streptomyces* sp. FXJ1.172[a]	MOSY	Thienodolin[†]	Indole derivative	236, 289, 329	$[M-H]^-$=248.9889
		GYM	Lasalocid A-E[*]	Polyether	243, 302 243, 302	$[M-H]^-$=589.4 $[M-H]^-$=603.4, 603.4, 603.4, 603.4
		GYM	Desferrioxamine E	Siderophore	End abs.	$[M+H]^+$=601.4
10	*Streptomyces* sp. FXJ1.235[b]	MOSY/SGG	Antibiotic PI 220 or Furaquinocins	Quinone derivative	221, 268, 294, 414	$[M-H]^-$=385.1650
11	*Streptomyces* sp. FXJ1.249	MOSY	β-rubromycin and 3’-OH-β-rubromycin[#]	Related to anthracycline	228, 312, 348, 487/512	$[M+H]^+$=553.0988, 537.1050
12	*Streptomyces* sp. FXJ1.253[a]	GYM/MOSY	6 elaiophylins	Macrolide	249	Same as those of FXJ1.076
		GYM	Nigericin	Polyether	None	$[M-H]^-$=723.6

13	*Streptomyces* sp. FXJ1.264	GYM/MOSY	Antibiotic BE 24566B[†,#]	Antharcycline	273, 364	[2M-H]$^-$=723.6
		GYM	Desferrioxamine E	Siderophore	End abs.	[M+H]$^+$=601.4
		GYM	Etheromycin[†]	Polyether	None	[M-H]$^-$=913.3
14	*Streptomyces* sp. FXJ1.297[a, b]	GYM	6, 8-dihydroxy-3-methyl-1H-isochromen-1-one[†]	Isocoumarin	236, 243, 277, 326	[2M-H]$^-$=382.8
15	*Streptomyces* sp. FXJ1.408[a, b]	GYM/MOSY/SGG	Brunefungin or flavopentin	Polyene macrolide	264, 363	[M+H]$^+$=721.2
16	*Streptomyces* sp. FXJ1.409	MOSY	5-(3-Indolyl)oxazole Antibiotic SF 2583A	Indole-oxazole Chlorinated indole-oxazole	221, 265, 300(sh) 220, 271, 287	[M+H]$^+$=185.0717 [M+H]$^+$=219.0334
17	*Streptomyces* sp. FXJ1.414[a, b]	GYM/MOSY/SGG	Brunefungin or flavopentin	Polyene macrolide	264, 363	[M+H]$^+$=721.2
18	*Streptomyces* sp. FXJ1.417[a]	MOSY	Cyclothiazomycin	Thiopeptide	221, 270(sh)	[M-H]$^-$=1471.4
19	*Streptomyces* sp. FXJ1.437[a]	MOSY	1 micropeptin type compound	Peptide	220, 280	[M+H]$^+$=1003.6
20	*Streptomyces* sp. FXJ1.450[a]	MOSY	Borrelidin	PKS type macrolide	254	[M-H]$^-$=488.5
21	*Streptomyces* sp. FXJ1.502[a]	MOSY	Cyclothiazomycin	Thiopeptide	221, 270(sh)	[M-H]$^-$=1471.6
22	*Streptomyces* sp. FXJ1.535[a, b]	SGG	Ochromycinone	Angucycline	265, 400	[M+H]$^+$=307.0977
23	*Streptomyces* sp. FXJ1.701[b]	SGG	Anisomycin C	Benzylpyrrolidine	230(sh), 276	[M+H]$^+$=292.1055
24	*Streptomyces* sp. FXJ1.907[a, b]	GYM	4-5 milbemycins β series compounds	Macrolide	237-241	Similar to those of FXJ1.068
			2 nanchangmycins	Polyether	234/236	Similar to those of FXJ1.068
25	*Streptomyces* sp. GTVL2G15[b]	SGG	Oxachelin	Siderophore	242, 250, 260(sh), 303	[M+H]$^+$=636.2
Non-streptomycete actinomycetes						
1	*Nocardia* sp. FXJ1.010[a, b]	GYM/MOSY	Guanidylfungin A&B	Macrolide	End abs.	[M-H]$^-$=1114.5, 1128.5
2	*Amycolatopsis* sp. FXJ1.274[a, b]	SGG	Apoptolidin A, isoapoptolidin and 8 related derivatives	Macrolide	230, 323 233, 313 232, 322 234, 305 234, 304	[M+Na]$^+$=1251.5 [M+Na]$^+$=1251.5 [M+Na]$^+$=1151.9 [M+Na]$^+$=1151.7 Others not measured
3	*Actinomadura* sp. FXJ1.344[a]	SGG	Homoprejadomycin	Angucycline	265, 400	[M+H]$^+$=339.3

[a] Strains assigned to the acidophilic group.

[b] Stains represented putative new species.

[c] The compounds marked with (†), (*) and (#) were also subjected to NMR, tandem-MS and CD analyses, respectively. Niphimycin was produced at pH 7.2.

[d] Figures accurate to one decimal place were generated by regular MS, and figures accurate to four decimal places were generated by HR-MS.

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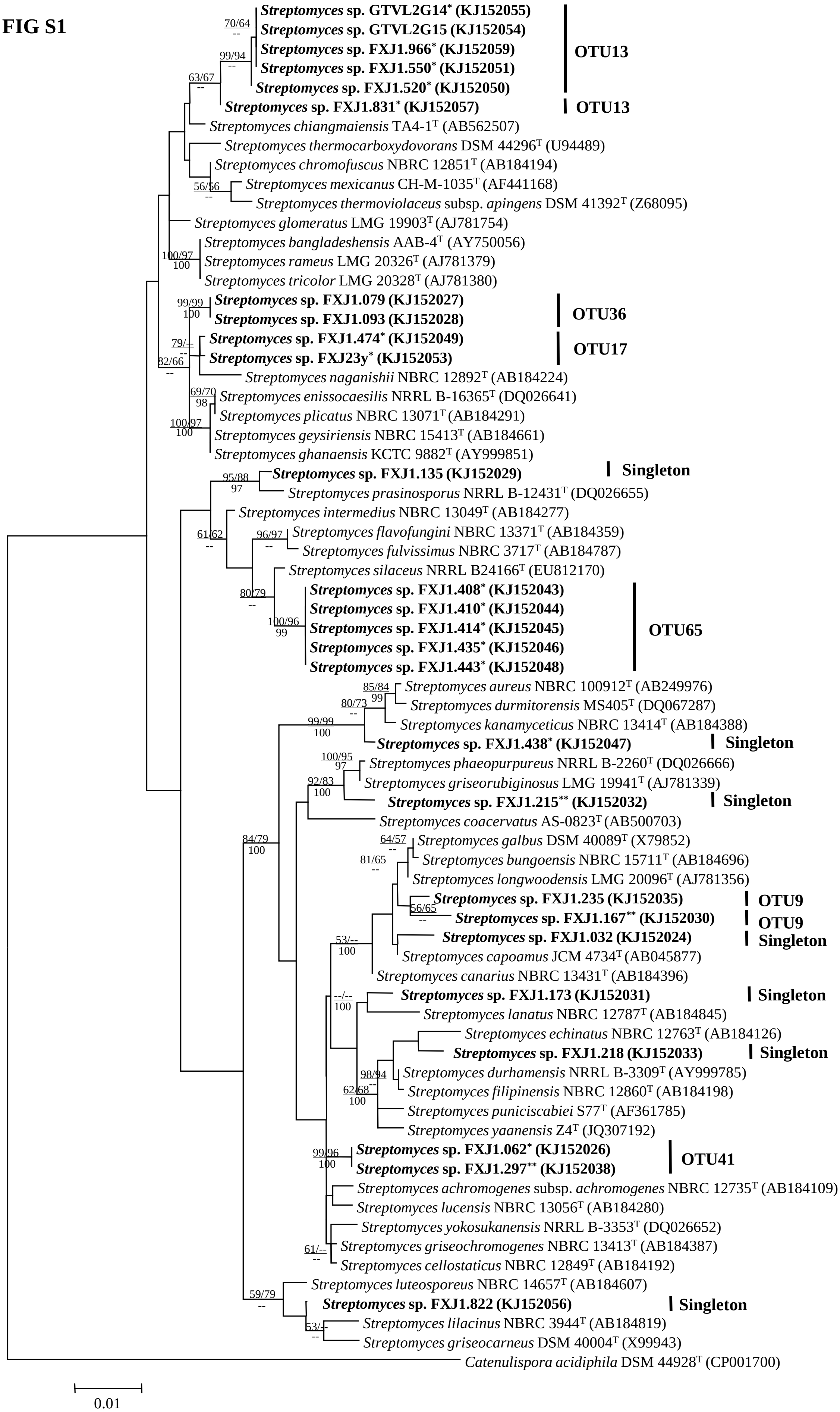
Ludwig W, Euzéby J, Schumann P, Busse HJ, Trujillo ME, Kämpfer P, Whitman WB. 2012. Road map of the phylum *Actinobacteria*, p 1–28. *In* Goodfellow M, Kämpfer P, Busse HJ, Trujillo ME, Suzuki K, Ludwig W, Whitman WB (ed) Bergey's manual of systematic bacteriology, 2nd ed, vol 5. Springer, New York, NY.

FIG S1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Streptomyces sp. GTVL2G15 (KJ152054)
Streptomyces sp. FXJ1.966* (KJ152059)
Streptomyces sp. FXJ1.550* (KJ152051)
Streptomyces sp. FXJ1.520* (KJ152050)
OTU13
Streptomyces sp. FXJ1.831* (KJ152057)
OTU13
Streptomyces chiangmaiensis TA4-1T (AB562507)
Streptomyces thermocarboxydovorans DSM 44296T (U94489)
Streptomyces chromofuscus NBRC 12851T (AB184194)
Streptomyces mexicanus CH-M-1035T (AF441168)
Streptomyces thermoviolaceus subsp. apingens DSM 41392T (Z68095)
Streptomyces glomeratus LMG 19903T (AJ781754)
Streptomyces bangladeshensis AAB-4T (AY750056)
Streptomyces rameus LMG 20326T (AJ781379)
Streptomyces tricolor LMG 20328T (AJ781380)
Streptomyces sp. FXJ1.079 (KJ152027)
Streptomyces sp. FXJ1.093 (KJ152028)
OTU36
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Streptomyces sp. FXJ23y* (KJ152053)
OTU17
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Streptomyces enissocaesilis NRRL B-16365T (DQ026641)
Streptomyces plicatus NBRC 13071T (AB184291)
Streptomyces geysiriensis NBRC 15413T (AB184661)
Streptomyces ghanaensis KCTC 9882T (AY999851)
Streptomyces sp. FXJ1.135 (KJ152029)
Singleton
Streptomyces prasinosporus NRRL B-12431T (DQ026655)
Streptomyces intermedius NBRC 13049T (AB184277)
Streptomyces flavofungini NBRC 13371T (AB184359)
Streptomyces fulvissimus NBRC 3717T (AB184787)
Streptomyces silaceus NRRL B24166T (EU812170)
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Streptomyces sp. FXJ1.443* (KJ152048)
OTU65
Streptomyces aureus NBRC 100912T (AB249976)
Streptomyces durmitorensis MS405T (DQ067287)
Streptomyces kanamyceticus NBRC 13414T (AB184388)
Streptomyces sp. FXJ1.438* (KJ152047)
Singleton
Streptomyces phaeopurpureus NRRL B-2260T (DQ026666)
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Streptomyces sp. FXJ1.215** (KJ152032)
Singleton
Streptomyces coacervatus AS-0823T (AB500703)
Streptomyces galbus DSM 40089T (X79852)
Streptomyces bungoensis NBRC 15711T (AB184696)
Streptomyces longwoodensis LMG 20096T (AJ781356)
Streptomyces sp. FXJ1.235 (KJ152035)
OTU9
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OTU9
Streptomyces sp. FXJ1.032 (KJ152024)
Singleton
Streptomyces capoamus JCM 4734T (AB045877)
Streptomyces canarius NBRC 13431T (AB184396)
Streptomyces sp. FXJ1.173 (KJ152031)
Singleton
Streptomyces lanatus NBRC 12787T (AB184845)
Streptomyces echinatus NBRC 12763T (AB184126)
Streptomyces sp. FXJ1.218 (KJ152033)
Singleton
Streptomyces durhamensis NRRL B-3309T (AY999785)
Streptomyces filipinensis NBRC 12860T (AB184198)
Streptomyces puniciscabiei S77T (AF361785)
Streptomyces yaanensis Z4T (JQ307192)
Streptomyces sp. FXJ1.062* (KJ152026)
Streptomyces sp. FXJ1.297** (KJ152038)
OTU41
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Streptomyces lucensis NBRC 13056T (AB184280)
Streptomyces yokosukanensis NRRL B-3353T (DQ026652)
Streptomyces griseochromogenes NBRC 13413T (AB184387)
Streptomyces cellostaticus NBRC 12849T (AB184192)
Streptomyces luteosporeus NBRC 14657T (AB184607)
Streptomyces sp. FXJ1.822 (KJ152056)
Singleton
Streptomyces lilacinus NBRC 3944T (AB184819)
Streptomyces griseocarneus DSM 40004T (X99943)
Catenulispora acidiphila DSM 44928T (CP001700)
0.01

APPENDIX S1 Chemical data and detailed structure elucidation of the novel secondary metabolites

New compounds from Streptomyces sp. *FXJ1.532*

After isolation and purification, two pure compounds [**FXJ15321** (30 mg) and **FXJ15322** (18 mg)] were obtained.

FXJ15321 was obtained as pale yellow solid. Its molecular formula was established as $C_{41}H_{66}O_{13}$ according to the $[M+Na]^+$ at m/z 789.4402 (calcd. 789.4401) (see supplemental Fig. AS1) combined with the ^{13}C-NMR data and corresponding to nine degrees of unsaturation. The ^{1}H-NMR, ^{13}C-NMR, DEPT 135 and 2D-HSQC spectra (supplemental Figs. AS2-AS5) revealed the presences of three cabonyl groups, one ester or amide group, two olefinic groups, six methylene groups, 17 non-olefinic methine groups, nine methyl groups and one methoxy group (Table A1).

TABLE A1 NMR data of **FXJ15321 and FXJ15322** in *$CDCl_3$* [[1]H- (600 MHz) and [13]C-NMR (150 MHz), *δ* in ppm, *J* in Hz]

FXJ15321						**FXJ15322**				
No.	**δ_C**	**δ_H**	**COSY**	**HMBC(H→C)**	**ROESY**	**δ_C**	**δ_H**	**COSY**	**HMBC(H→C)**	**ROESY**
1	172.8, C	—		2, 3, 24		172.7, C	—		2, 3, 24	
2	39.6, CH2	2.43(dd; 10.8, 15.0) a	3	3		39.8, CH2	2.42(dd; 11.4, 15.0) a	3	3, 4	
		2.67(dd; 2.4, 15.0) b			3		2.70(dd; 2.4, 15.0) b			3
3	70.7, CH	4.27(m)	2, 4	2, 4, 28	2b	70.9, CH	4.28(ddd, 2.4, 9.9, 9.9)	2, 4	2, 4, 28	2b
4	44.8, CH	3.49(m)	3, 28	2, 28	7, 28	44.8, CH	3.47(m)	3, 28	2, 3, 28	7, 28
5	204.9, C	—		3, 4, 7, 28, 29		205, C	—		3, 4, 7, 28, 29	
6	138.8, C	—		8, 30		136.6, C	—		8, 29	
7	140.9, CH	6.47(d; 9.6)	29	8, 29, 30	4	142.6, CH	6.66(d; 9.6)	29	8, 29, 30	4
8	48.2, CH	3.85(m)	7, 30	7, 30	29, 30	44.5, CH	4.01(dq, 6.6, 9.6)	7, 30	7, 30	7, 29, 30
9	208.8, C	—		7, 8, 10, 30		210.9, C	—		7, 8, 10, 11, 30	
10	40.8, CH2	2.35(dd; 2.4, 16.2) a	11		11, 31	47.2, CH2	2.33(dd; 9.6, 13.8) a	11	11, 12	11
		2.92(dd; 10.8, 16.2) b			31		3.03(dd; 3.6, 13.8) b			11, 31
11	73.8, CH	4.34(ddd, 2.4, 3.6-4.2, 10.8)	10, 12	10, 12, 13, 15, 31	10a, 12, 15b, 31	78.2, CH	3.52(ddd, 3.6, 9.6, 9.6)	10, 12	10, 12, 13, 15, 31	10,
12	38.4, CH	1.92(m)	11, 13, 31	10, 31	11, 31	43.9, CH	1.53(ddq; 9.6, 9.6, 6.6,)	11, 13, 31	10, 31	10, 31
13	80.1, CH	3.43(m)	12, 14	12, 14, 15, 31	31, a	83.9, CH	3.07(dd; 10.2, 10.2)	12, 14	11, 12, 14, 15, 16, 31, a	11, 16, 31, a
14	38.1, CH	1.58(m)	13, 15, 16	13, 15, 16	15b	39.8, CH	1.39(m)	13, 15, 16	13, 15, 16, 17	15b, 16b
15	66.1, CH2	3.26(m) a	14	13, 16	16b	70.1, CH	2.82(dd, 12.0, 12.0) a	14	13, 16	11

		3.71(dd; 3.6-4.2; 12.0) b			11, 14		3.75(dd; 4.8; 12.0) b			14
16	34.1, CH2	1.26(m), a	14, 17	13, 15, 32		32.3, CH2	0.88(m) a	14, 17	13, 15, 32	13, 14, 17
		2.15(m), b			15a		2.54(m) b			13, 14
17	38, CH	3.16(m)	16, 32	16, 19	19, 32	37.79, CH	3.08(m)	16, 32	16, 19, 20, 32	15b, 16a, 20, 32
18	205.9, C	—		16, 17, 19, 20, 32		206, C	—		16, 17, 19, 20, 32	
19	131.6, CH	6.16(d; 16.2)	20	21	17, 20	131.4, CH	6.12(d; 16.2)	20	20, 21	20, 21
20	146.3, CH	6.97(ddd; 16.2, 6.6, 6.6)	19, 21	21, 22	17, 19,	146.8, CH	6.95(ddd; 16.2, 6.6, 6.6)	19, 21	19, 21, 22	19, 17
21	37.9, CH2	2.29(m) a	20, 22	19, 20		37.85, CH2	2.27(m) a	20, 22	19, 20, 22	22, 23
		2.50(m) b			33		2.49(m) b			33
22	68.6, CH	3.89(m)	21, 23	20, 21, 24, 33	23	68.4, CH	3.85(m)	21, 23	20, 21, 24, 33	24, 23, 21a
23	39.5, CH	1.90(m)	22, 24, 33	21, 24, 33	22	39.6, CH	1.92(m)	22, 24, 33	21, 24, 33	21a, 22, 24, 33
24	78.6, CH	5.06(dd; 4.2, 8.4)	23, 25	22, 23, 26, 33, 34	22	78.5, CH	5.07(dd; 3.6, 9.0)	23, 25	22, 23, 26, 33, 34	22, 23, 25
25	40, CH	1.85(m)	24, 26, 34	24, 27, 34	26	39.9, CH	1.86(m)	24, 26, 34	24, 27, 34	
26	65.6, CH	4.03(dq; 2.4, 6.0)	25, 27	24, 27, 34	25, 27	65.6, CH	4.07(dq; 6.6; 2.4-3.0)	25, 27	24, 27, 34	25, 27
27	20.7, CH3	1.23(d; 6.6)	26	26	26	20.7, CH3	1.22(d; 6.6)	26	26	26
28	13.6, CH3	1.03(d; 7.2)	4	4	4	14, CH3	1.01(d; 7.2)	4	3, 4	4
29	10.9, CH3	1.96(s)	7	7	8	10.6, CH3	1.87(s)	7	7	8
30	14.2, CH3	1.22(d; 6.6)	8	7, 8	8	16, CH3	1.21(d; 6.6)	8	7, 8	8
31	12.5, CH3	1.03(d; 7.2)	12	11, 12, 13	10, 11, 13, a	12.1, CH3	1.07(d; 6.6)	12	11, 12, 13	10b, 13, a
32	16.6, CH3	1.05(d; 7.2)	17	16, 17	17	18.6, CH3	1.01(d; 7.2)	17	16, 17	17
33	8.9, CH3	0.93(d; 7.2)	23	22, 23, 24	21b	8.8, CH3	0.92(d; 7.2)	23	22, 23, 24	21b, 23

34	9.8, CH3	0.97(d; 7.2)	25	25, 26		9.9, CH3	0.98(d; 7.2)	25	24, 25, 26	25
a	102.9, CH	4.26(d; 7.8)	b	13, b, e	13, 31, b, e	102.9, CH	4.33(d; 7.2)	b	13, b, e	13, 31, b, cb, e
b	74.3, CH	3.17(ddd; 0, 7.2, 7.2)	a, c	c, d	a, ca	74.7, CH	3.20(ddd; 0, 7.2, 7.2)	a, c	a, c, d	a
c	37.2, CH2	1.17(m) ca	b, d		b	37.2, CH2	1.18(m) ca	b, d	b, d	
		2.12(m) cb			d, e		2.13(ddd, 1.8, 5.4, 12.6) cb			d, e
d	80.2, CH	3.24(m)	c, e	b, c, f, g	cb	80.3, CH	3.27(m)	c, e	b, c, e, g	a, cb
e	67.4, CH	3.56(dq, 6.6, 1.8)	d, f	c, f	a, cb	67.3, CH	3.55(dq, 6.0, 1.8)	d, f	c, f	a, cb
f	20, CH3	1.21(d; 6.6)		e		19.9, CH3	1.23(d; 6.6)		e	e
g	56, CH3	3.43(s)		d		55.9, CH3	3.44(s)		d	

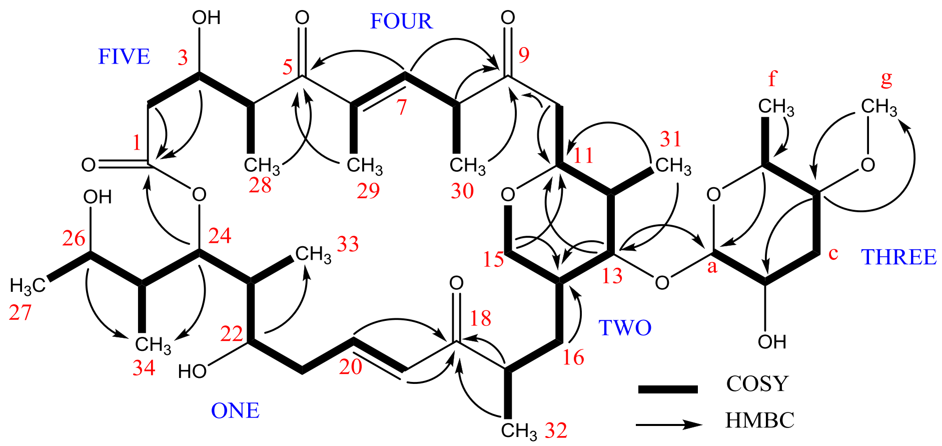


FIG A1 Key ^{1}H-^{1}H COSY and HMBC correlations of **FXJ15321**

Detailed analysis of 2D-NMR spectra (supplemental Figs. AS5-AS7) revealed that **FXJ15321** was comprised of five partial structures (Fig. A1). Partial structure **one** was featured by the connections from H-19 to H-27, established by the COSY signals among these hydrogen atoms, and could be further sustained by the key HMBC correlations from H-22 to C-33, and from H-24, H-26 to C-34. Partial structure **two** was featured by the connections from H-10 to H-17, established by the COSY signals, and could be further sustained by the key HMBC correlations from H-31, H-15, H-13 and H-10 to C-11, from H-31 to C-13, and from H-16, H-15 and H-13 to C-14; and according to these correlations, an hexatomic ring system consisting C-11, C-12, C-13, C-14, C-15 and an oxygen atom could be established. Partial structure **three** was featured by the COSY connections with H-a/H-b/H-c/H-d/H-e/H-f, and was further sustained by the key HMBC correlations from H-f to C-e, from H-e to C-a, from H-d to C-b, C-g and from H-g to C-d; and according to these signals, a sugar ring composed of C-a, C-b, C-c, C-d, C-e, C-f and C-g was established. Partial structures **four** and **five** were elucidated by the connectivities among H-30/H-8/H-9/H-7/H-6/H-29 and H-2/H-3/H-4/H-28, and confirmed by their key HMBC correlations, respectively. The connectivities among these partial structures were mainly established by the HMBC correlations. For example, the connection between partial structures **one** and **five** could be recognized by the HMBC signals of H-24, H-2 and H-3 to C-1.

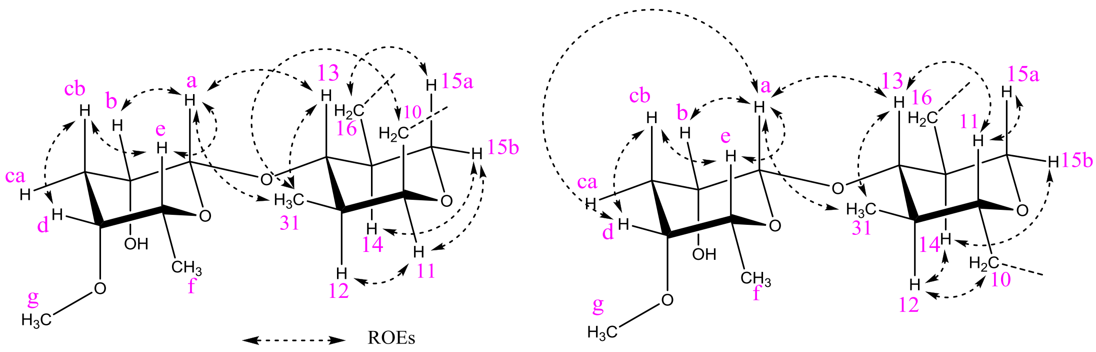


FIG A2 Key NOE correlations of **FXJ15321** (left) and **FXJ15322** (right)

The possible relative configurations within partial structures **two** and **three** could be suggested according the ROESY experiment (Fig. A2, supplemental Fig. AS8). The NOE correlations between H-12 and H-11, H-11 and H-15b, H15b and H14, H-13 and H-31, H16 and H15a, and between H-31 and H-10 suggested that H-12, H-14, H-15 and H-11 were on one face of the ring, and H-31, H-13 and H-10 on the other face of the ring. However, a certain deduction could not be made owing to a lack of coupling constants and direct ROE correlations between H12 and H14, H13 and H10, H13 and H15a, and between H15a and H10. The NOE correlations between H-a and H-e, H-a and H-b, H-e and H-cb, and between H-cb and H-d revealed that H-a, H-b, H-cb, H-d and H-e were on the same side of sugar ring. The strong NOE signals between H-a and H-13 and between H-a and H-31 stabilized the relative positions of the two rings. The very low J_{bca} (=0) and the strong NOE correlations observed between Ha and Hb supported the equatorial bond of Hb, although the coupling constants of J_{ab} and J_{bcb} were not small enough (7.2 Hz). Therefore, the relative configuration could be suggested as 11*S**, 12*R**, 13*R**, 14*S**, a*R**, b*S**, d*R** and e*R**. The C-19/C-20 olefin was assigned *E*-geometry based on their large coupling constant (16.2 Hz); the C-6/C-7 olefin was proposed as *E*-geometry based on the NOE correlation between H-29 and H-8 observed in both the ROESY and NOE difference experiments (supplemental Figs. AS8 and AS9).

FXJ15322 was obtained as pale yellow solid. It's molecular formula was established as $C_{41}H_{66}O_{13}$ according to the $[M+Na]^+$ at m/z 789.4408 (calcd. 789.4401) (supplemental Fig. AS10) combined with the ^{13}C-NMR data and corresponding to nine degrees of unsaturation, too. Careful analysis of its 1D/2D-NMR data (supplemental Figs. AS11-AS17) revealed that the planar structure and most of the NOE correlations were identical with those of FXJ15321, with difference lying in the C-11 position. According to the ROESY experiment (supplemental Fig. AS17), NOE correlations between H-10 and H-12, H-14 and H-12, H-14 and H-15b, H-11 and H-13, and between H-11 and H-15a revealed that the relative configuration of C-11 position was changed (Fig. A2), and an *R** configuration was therefore proposed.

After isolation and purification, three pure compounds [**FXJ10761** (8.2 mg, efomycin M), **FXJ10762** (7.4 mg, new compound) and **FXJ10763** (4.0 mg, new natural product)] were obtained. **FXJ10761** was obtained as white solid. It's molecular formula was established as $C_{42}H_{64}O_{10}$ according to the $[M+H]^+$ at m/z 729.4 and $^1H/^{13}C$/DEPT 135-NMR data (Table A2, supplemental Figs. AS18-AS21). After careful analyses of its ^1H-, ^{13}C-NMR, ^3J coupling constant and 2D-NMR data, including COSY, HSQC, HMBC and ROESY spectra (supplemental Figs. AS22-AS25), coupled with the optical rotation value $[\alpha]_D^{25}$= +103° (c=0.4, MeOH), this compound was identified to be efomycin M (Antonicek *et al.*, 1996; Roland & Johann, 2007) (Fig. A3).

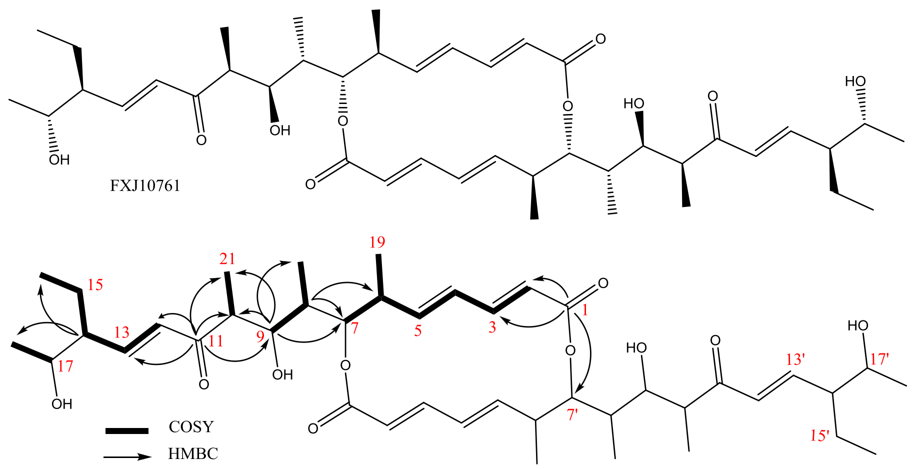


FIG A3 Structure and Key ^1H-^1H COSY, HMBC correlations of **FXJ10761**

TABLE A2 NMR data of **FXJ10761** in *$CDCl_3$* [^{1}H- (600 MHz) and ^{13}C-NMR (150 MHz), δ in ppm, *J* in Hz]. The COSY, HMBC and ROESY spectra were shown for half structure

No.	δ_C	δ_H	COSY	HMBC(H→C)	ROESY
1 and 1'	168.38, C	—		2, 3, 7'	
2 and 2'	121.14, CH	5.61(d, 15.6)	3	3, 4	
3 and 3'	145.25, CH	6.96(dd, 15.0, 11.4)	2, 4	4, 5	
4 and 4'	131.35, CH	6.05(dd, 15.0, 11.4)	3, 5	2, 3, 6	
5 and 5'	144.50, CH	5.64(m)	4, 6	3, 6, 7, 19	
6 and 6'	41.51, CH	2.49(m)	5, 7, 19	4, 5, 7, 19	
7 and 7'	76.63, CH	5.09(dd, 9.6, 0)	6	5, 9, 6, 8, 19, 20	8
8 and 8'	35.98, CH	1.94(m)	9, 20	6, 9, 10, 20	7
9 and 9'	71.54, CH	3.73(dd, 7.2, 0)	8	7, 8, 10, 20, 21	20
10 and 10'	45.47, CH	2.90(m)	21	21	20
11 and 11'	203.17, C	—		9, 10, 12, 13, 21	
12 and 12'	131.00, CH	6.23(d, 16.2)	13	13, 14	
13 and 13'	147.61, CH	6.72(dd; 9.6, 16.2)	12, 14	14, 15, 17	
14 and 14'	52.38, CH	2.04(m)	13, 15	12, 13, 15, 16, 17, 18	
15 and 15'	23.54, CH2	1.43(m), 1.61(m)	14, 16	13, 14, 16, 17	
16 and 16'	11.92, CH3	0.86(d; 7.2)	15	14, 15	15a (0.86ppm)
17 and 17'	69.55, CH	3.82(m)	18	13, 14, 15, 18	
18 and 18'	21.34, CH3	1.17(d; 6.6)	17	14, 17	
19 and 19'	15.32, CH3	1.03(d; 6.6)	6	5, 6, 7	21
20 and 20'	9.25, CH3	0.92(d; 6.6)	8	7, 8, 9	6, 9, 10, 18, 21
21 and 21'	9.21， CH3	1.17(d; 6.6)	10	9, 10	19

FXJ10762 was obtained as white solid. It's molecular formula was established as $C_{41}H_{62}O_{10}$ according to the $[M+HCOO]^-$ at m/z 759.4320 (calcd. 759.4320) and $^{1}H/^{13}C$/DEPT 135-NMR data (Table A3, supplemental Figs. AS26-AS29). The planar structure was deduced mainly according to comparison of ^{1}H and ^{13}C-NMR data with those of **FXJ10761**. The 2D-COSY/HSQC/HMBC spectra (supplemental Figs. AS30-AS32) demonstrated that the compound lacked the C-16' group, and thus the planar structure was established (Fig. A4). Because the correlation signals of 2D-NOESY spectrum (supplemental Fig. AS33) were not strong enough, the stereo-structure was proposed to be identical with that of **FXJ10761** mainly owing to the high similarity in ^{1}H and ^{13}C NMR data.

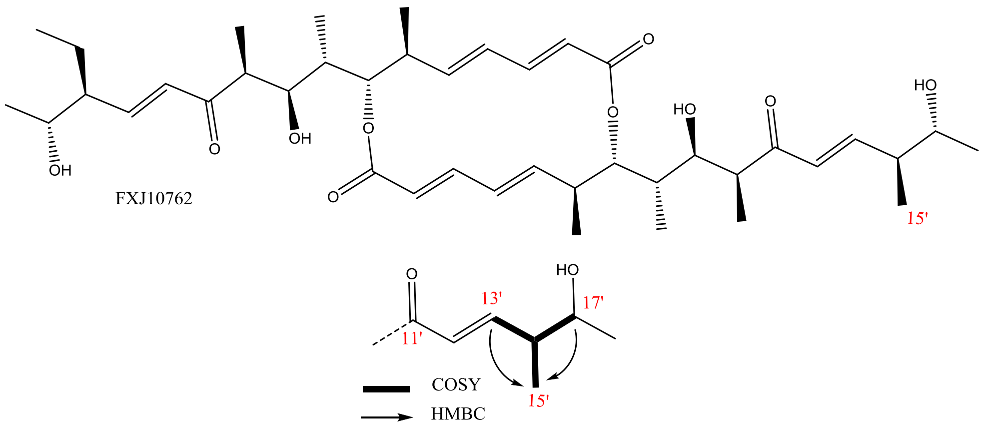


FIG A4 Structure and key ^{1}H-^{1}H COSY and HMBC correlations of **FXJ10762**

TABLE A3 NMR data of **FXJ10762** in *$CDCl_3$* [^{1}H- (600 MHz) and ^{13}C-NMR (150 MHz), δ in ppm, J in Hz]

No.	δ_C	δ_H	COSY	HMBC(C→H)	ROESY	No.	δ_C	δ_H	COSY	HMBC(C→H)	ROESY
1	168.38, C	—		2, 3, 7'		1'	168.38, C	—		2', 3', 7	
2	121.15, CH	5.61(m)	3	3, 4		2'	121.11, CH	5.61(m)	3'	3', 4'	
3	145.24, CH	6.96(m)	2, 4	4, 5		3'	145.31, CH	6.96(m)	2', 4'	4', 5'	
4	131.34, CH	6.05(m)	5, 3	2, 3, 6	6	4'	131.34, CH	6.05(m)	5', 4'	2', 3', 6'	6'
5	144.47, CH	5.62(m)	4, 6	3, 6, 7, 19		5'	144.56, CH	5.62(m)	4', 6'	3', 6', 7', 19'	
6	41.53, CH	2.49(m)	5, 7, 19	4, 5, 7, 19	4	6'	41.53, CH	2.49(m)	5', 7', 19'	4', 5', 7', 19'	4'
7	76.63, CH	5.09(m)	6, 8	5, 6, 9, 19, 20	8	7'	77.20, CH	5.09(m)	6', 8'	5', 6', 9', 19', 20'	8'
8	35.97, CH	1.94(m)	7, 9, 20	6, 9, 10, 20	7	8'	35.89, CH	1.94(m)	7', 9', 20'	6', 9', 10', 20'	7'
9	71.54, CH	3.74(m)	8, 10	7, 8, 10, 20, 21	10, 12	9'	71.64, CH	3.74(m)	8', 10'	7', 8', 10', 20', 21'	10', 12'
10	45.47, CH	2.89(m)	9, 21	8, 21	9, 21	10'	45.65, CH	2.89(m)	9', 21'	8', 21'	9', 21'
11	203.17, C	—		9, 10, 12, 13, 21		11'	203.49, C	—		9', 10', 12', 13', 21'	
12	131.00, CH	6.25(m)	13	13, 14	9	12'	129.03, CH	6.25(m)	13'	13', 14'	9'
13	147.60,CH	6.74(m)	12, 14	14, 15, 17		13'	149.14,CH	6.87(m)	12', 14'	14', 15', 17'	
14	52.38, CH	2.04(m)	13, 15, 17	12, 13, 15, 16, 17, 18		14'	44.37, CH	2.34(m)	13', 15', 17'	12', 13', 15', 17', 18'	
15	23.55, CH2	1.43(m), 1.61(m)	14, 16	13, 14, 16, 17		15'	15.60, CH3	1.07(m)	14'	13', 14', 16', 17'	
16	11.92, CH3	0.87(m)	15	14, 15		16'	none	none			
17	69.56, CH	3.82(m)	14, 18	13, 14, 15, 18		17'	70.85, CH	3.74(m)	14', 18'	13', 14', 15', 18'	
18	21.35, CH3	1.17(m)	17	14, 17		18'	20.82, CH3	1.17(m)	17'	14', 17'	
19	15.32, CH3	1.04(m)	6	5, 6, 7		19'	15.32, CH3	1.04(m)	6'	5', 6', 7'	
20	9.28, CH3	0.93(m)	8	7, 8, 9		20'	9.28, CH3	0.93(m)	8'	7', 8', 9'	
21	9.21，CH3	1.17(m)	10	9, 10		21'	9.40，CH3	1.17(m)	10'	9', 10'	

FXJ10763 was obtained as white solid. It's molecular formula was established as $C_{48}H_{76}O_{14}$ according to the $[M+HCOO]^-$ at m/z 921.5228 (calcd. 921.5212) and $^{1}H/^{13}C$/DEPT 135-NMR data (Table A4, supplemental Figs. AS34-AS37). Careful comparison with the NMR data of **FXJ10761** revealed that half structure of the compound was in accordance with **FXJ10761**, with differences lying in another half structure. To deduce the differences, the 2D-COSY/HSQC/HMBC spectra (supplemental Figs. AS38-AS40) were made and key H-H and C-H correlation signals relevant to the different positions were analyzed (Fig. A5). From the COSY and HMBC spectra, we could establish two ring systems from C-11' to C-18' and from C-a to C-f, which was further verified by the comparison of ^{13}C-NMR data with the ring system of compound elaiophylin. The planar structure was thus established (Fig. A5). The chemical shifts from C-1 to C-21 and corresponding H were in accordance with those of FXJ10761, meanwhile, the chemical shifts from C-1' to C-21', and from C-a to C-f and corresponding H were in accordance with those of elaiophylin (Cui *et al*., 2001), thus, the stereo-structure of FXJ10763 was proposed (Fig. A5). The optical rotation value of $[\alpha]_D^{25}$= +10 ° (c=0.21, MeOH) indicated that it might be identical with compound 38 ($[\alpha]_D^{25}$= +13 °) synthesized by Hammann *et al*. (1990).

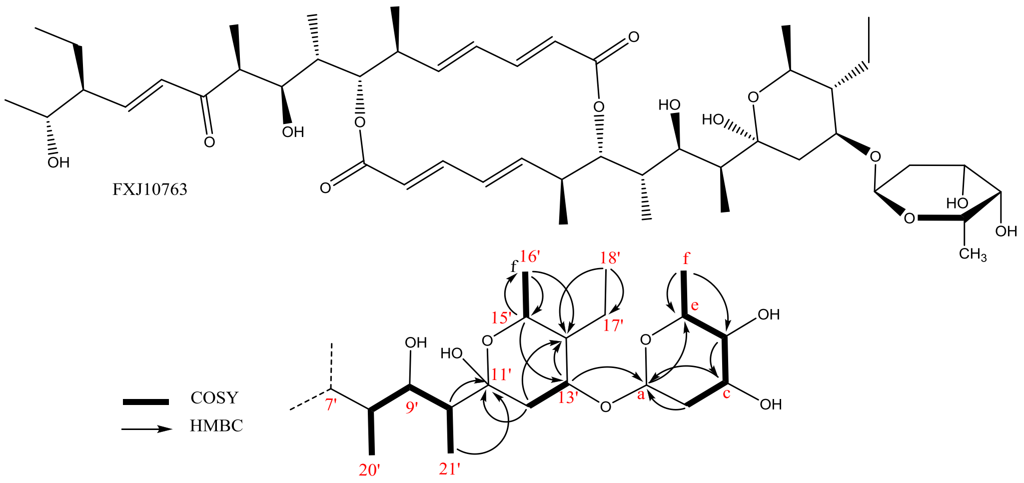


FIG A5 Structure and key ^{1}H-^{1}H COSY and HMBC correlations of **FXJ10763**

TABLE A4 NMR data of **FXJ10763** in *$CDCl_3$* [^{1}H- (600 MHz) and ^{13}C-NMR (150 MHz), δ in ppm, J in Hz]

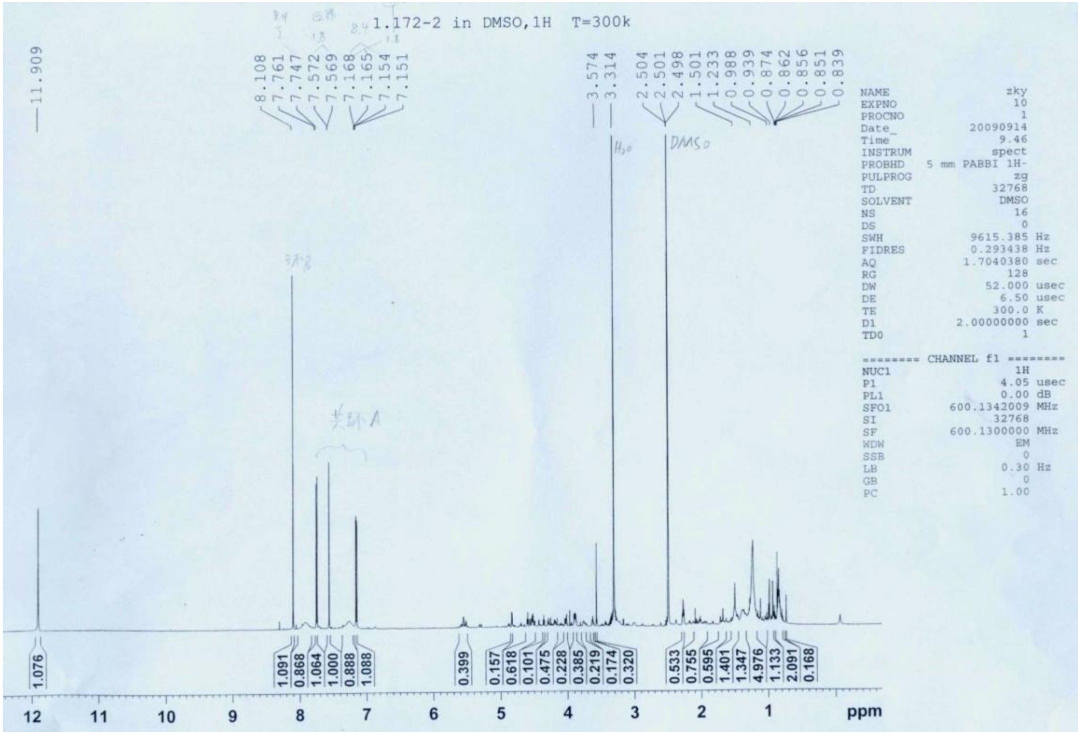
No.	δ_C	δ_H	COSY	HMBC(H→C)	No.	δ_C	δ_H	COSY	HMBC(H→C)
1	170.05, C	—		2, 3, 7'	1'	168.36, C	—		2', 3', 7
2	121.14, CH	5.62(d, 15.0)	3	3, 4	2'	120.99, CH	5.61(d, 15.0)	3'	3', 4'
3	145.18, CH	6.97(m)	2, 4	4, 5	3'	145.02, CH	6.97(m)	2', 4'	4', 5'
4	131.50, CH	6.07(dd, 15.0, 15.0)	5, 3	2, 3, 6	4'	131.92, CH	6.07(dd, 15.0, 15.0)	5', 3'	2', 3', 6'
5	144.64, CH	5.67(dd, 15.0, 7.8)	4, 6	3, 6, 7, 19	5'	144.18, CH	5.66(dd, 15.0, 7.8)	4', 6'	3', 6', 7', 19'
6	41.34, CH	2.52(m)	5, 7, 19	4, 5, 7, 19	6'	40.95, CH	2.52(m)	5', 7', 19'	4', 5', 7', 19'
7	76.75, CH	5.05(m)	6, 8	5, 6, 9, 19, 20	7'	77.81, CH	4.75(dd, 10.2, 10.2)	6', 8'	5', 6', 9', 19', 20'
8	36.10, CH	1.95(m)	7, 9, 20	7, 9, 20	8'	35.84, CH	1.95(m)	7', 9', 20'	7', 9', 20'
9	71.47, CH	3.74(dd, 8.4, 8.4)	8, 10	7, 8, 10, 20, 21	9'	70.66, CH	4.11(dd, 9.6, 9.6)	8', 10'	7', 8', 11', 20', 21'
10	45.54, CH	2.89(m)	9, 21	21	10'	41.61, CH	1.71(m)	9', 21'	21'
11	203.03, C	—		9, 10, 12, 13, 21	11'	99.04, C	—		10', 12', 21'
12	130.96, CH	6.24(d, 15.6)	13	14	12'	38.89, CH2	1.02(m), 2.37(dd, 10.8, 3.0)	13'	none
13	147.53,CH	6.72(dd, 15.0, 9.6)	12, 14	14, 15, 17	13'	70.20, CH	3.98(m)	12'	12', 15'
14	52.37, CH	2.03(m)	13, 15, 17	12, 13, 15, 16, 17, 18	14'	48.42, CH	1.17(m)	none	12', 13', 16', 18'
15	23.55, CH2	1.42(m), 1.61(m)	14, 16	13, 14, 16, 17	15'	66.54, CH	3.90(dt, 9.6, 5.4)	16'	16'
16	11.91, CH3	0.86(m)	15	14, 15	16'	19.14, CH3	1.10(d, 5.4)	15'	15'
17	69.55, CH	3.81(td, 5.4, 5.4)	14, 18	13, 14, 15, 18	17'	19.37, CH2	0.84(m), 1.00(m)	none	18'
18	21.34, CH3	1.17(m)	17	14, 17	18'	9.07, CH3	0.86(m)	none	none
19	15.27, CH3	1.04(d, 6.6)	6	5, 6, 7	19'	14.91, CH3	1.03(d, 6.0)	6'	5', 6'
20	9.19, CH3	0.92(d, 6.6)	8	7, 8, 9	20'	8.75, CH3	0.81(d, 6.0)	8'	7', 8'
21	9.07, CH3	1.17(m)	10	9, 10	21'	7.04, CH3	1.00(m)	10'	9', 10'
					a	93.24, CH	5.05(s)	b	13', b, c
					b	33.54, CH2	1.79(m)	a, c	d
					c	66.06, CH	3.98(m)	b, d	b, d
					d	71.47, CH	3.62(m)	c, e	b, f, c or e
					e	65.90, CH	3.98(m)	d, f	a, f
					f	16.79, CH3	1.24(d, 6.6)	e	e

New compound from Streptomyces *sp. FXJ1.172*

After isolation and purification, one pure compound--**thienodolin** (>50 mg, from 12 L fermentation mixture) was obtained. A hydroxyl derivative was also discovered but very unstable, and could rapidly degrade to thienodolin after the crude extract was isolated either by silica-gel, LH-20 gel, RP-18 gel or by HPLC with natural pH water, 0.05% acetic acid or 0.05% ammonia water. Therefore, the structure of this new compound was deduced mainly according to the comparison of HR-MS/MS and ^{1}H-NMR spectra with thienodolin. The ^{1}H-NMR spectrum was obtain according to the procedure below: the crude extract was redissolved using methanol in which the new compound was relatively stable (it was very unstable in DMSO), and subjected to HPLC directly (according to our experiment, this compound could exist for about one day after HPLC preparation at natural pH) for 20 injections with 30 µl per injection; the collected liquid was concentrated to dryness in vacuum as soon as possible, follow by the redissolving with *methanol-d_4*, and the ^{1}H-NMR spectrum was made immediately.

The molecular formula of the new compound was established as $C_{11}H_7ClN_2O_2S$ according to the $[M-H]^-$ at m/z 264.9878 (calcd. 264.9839). Thiendolion was obtain as $C_{11}H_7ClN_2OS$ according to the $[M-H]^-$ at m/z 248.9889 (calcd. 248.9890).

By comparing the ^{1}H-NMR spectra of thienodolin and the new compound (Fig. A6), we found their signals between 7.0-8.2 ppm, which were attributed to the hydrogen signals of aromatic and thiophene rings, were nearly identical, indicating that the hydroxylation was occurred neither on the aromatic ring nor on the thiophene ring. Further MS2 fragment ions of the two compounds (Figs. A7 and A8) indicated that the hydroxylation was not on the NH_2-C=O group. Therefore, the hydroxylation should be occurred on the nitrogen atom of the indole ring, and the new compound was identified as **N-hydroxythienodolin**.



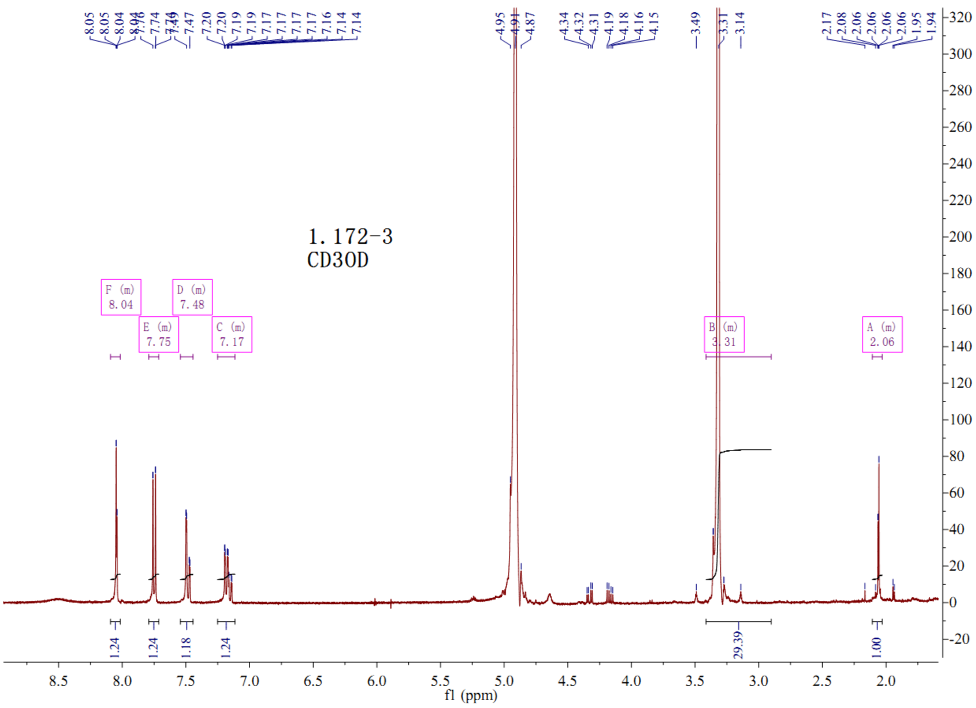
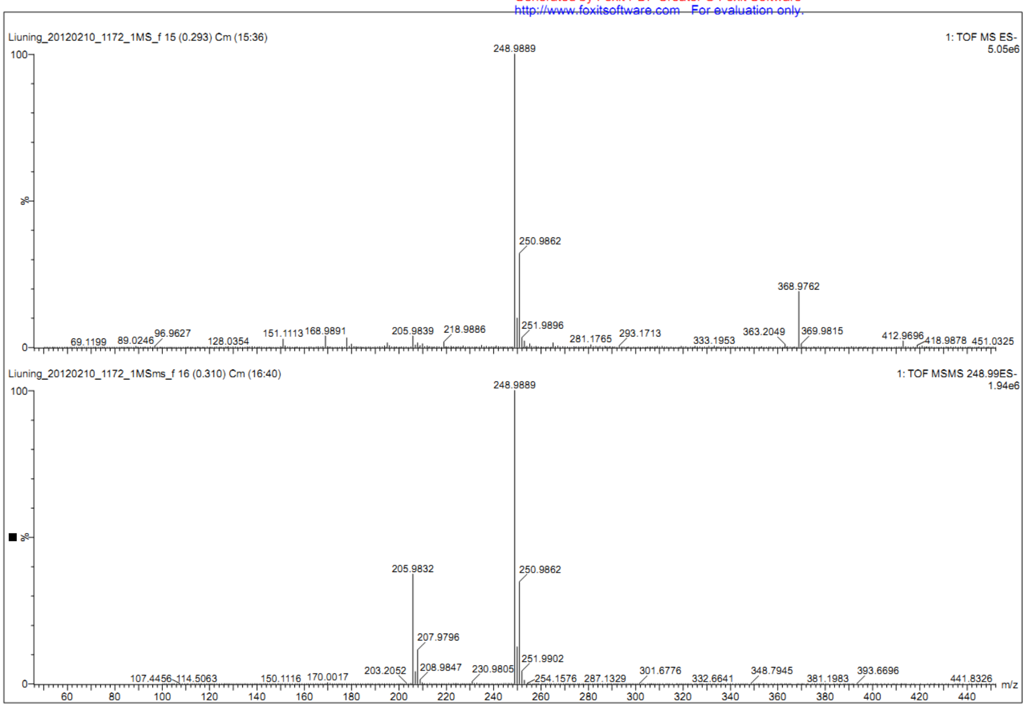


FIG A6 ^{1}H-NMR of thienodolin (upper) and N-hydroxytheinodolin (lower)



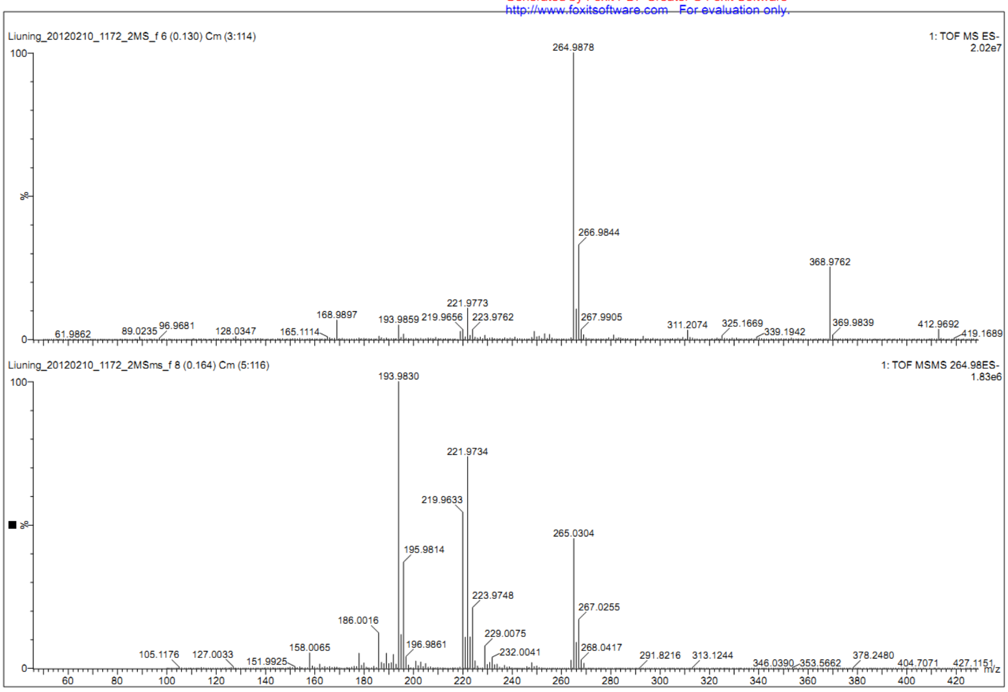


FIG A7 MS/MS fragments of thienodolin (upper) and N-hydroxytheinodolin (lower)

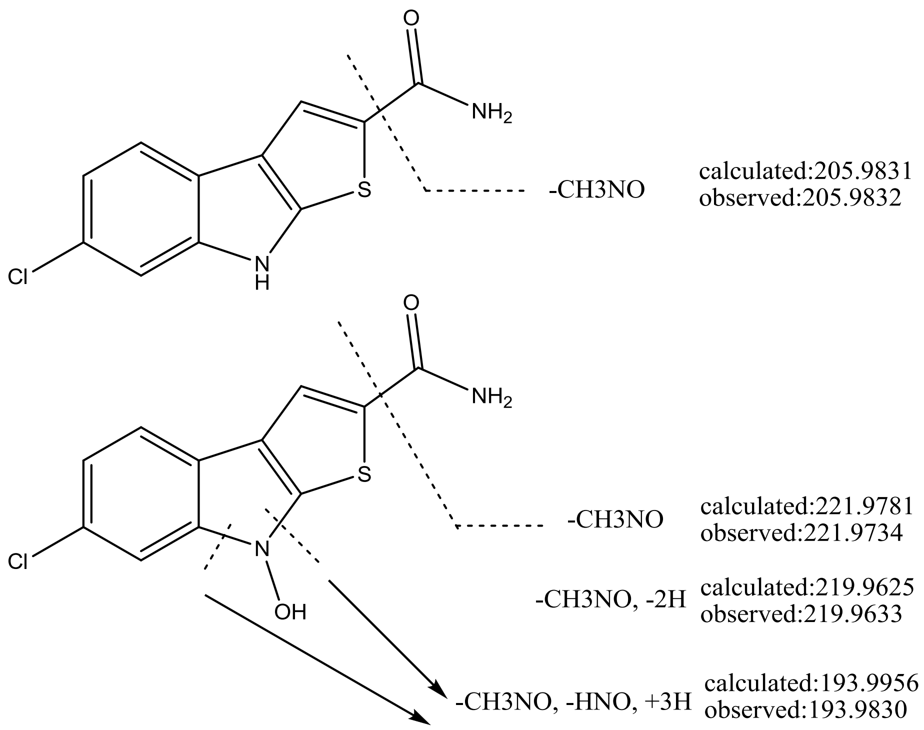


FIG A8 MS/MS fracture patterns of thienodolin (upper) and N-hydroxytheinodolin (lower)

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Supplemental Figures

FIG. AS1 HR-ESI-MS spectrum of **FXJ15321**.
FIG. AS2 ^{1}H-NMR spectrum (600 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS3 ^{13}C-NMR spectrum (150 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS4 DEPT 135 spectrum (150 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS5 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS6 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS7 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS8 ^{1}H-^{1}H-ROESY spectrum (600 × 600 MHz, *CD$_3$OD*) of **FXJ15321**.
FIG. AS9 NOE difference spectrum (H-29 irradiated) (600 MHz, *CD$_3$OD*) of **FXJ15321**
FIG. AS10 HR-ESI-MS spectrum of **FXJ15322**.
FIG. AS11 ^{1}H-NMR spectrum (600 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS12 ^{13}C-NMR spectrum (150 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS13 DEPT 135 spectrum (150 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS14 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS15 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS16 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS17 ^{1}H-^{1}H-ROESY spectrum (600 × 600 MHz, *CD$_3$OD*) of **FXJ15322**.
FIG. AS18 ESI-MS spectrum of **FXJ10761**.
FIG. AS19 ^{1}H-NMR spectrum (600 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS20 ^{13}C-NMR spectrum (150 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS21 DEPT 135 spectrum (150 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS22 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS23 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS24 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS25 ^{1}H-^{1}H-ROESY spectrum (600 × 600 MHz, *CDCl$_3$*) of **FXJ10761**.
FIG. AS26 HR-ESI-MS spectrum of **FXJ10762**.
FIG. AS27 ^{1}H-NMR spectrum (600 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS28 ^{13}C-NMR spectrum (150 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS29 DEPT 135 spectrum (150 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG AS30 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS31 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS32 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS33 ^{1}H-^{1}H-ROESY spectrum (600 × 600 MHz, *CDCl$_3$*) of **FXJ10762**.
FIG. AS34 HR-ESI-MS spectrum of **FXJ10763**.
FIG. AS35 ^{1}H-NMR spectrum (600 MHz, *CDCl$_3$*) of **FXJ10763**.
FIG. AS36 ^{13}C-NMR spectrum (150 MHz, *CDCl$_3$*) of **FXJ10763**.
FIG. AS37 DEPT 135 spectrum (150 MHz, *CDCl$_3$*) of **FXJ10763**.
FIG. AS38 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CDCl$_3$*) of **FXJ10763**.
FIG. AS39 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10763**.
FIG. AS40 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10763**.

FIG AS1 HR-ESI-MS spectrum of **FXJ15321**

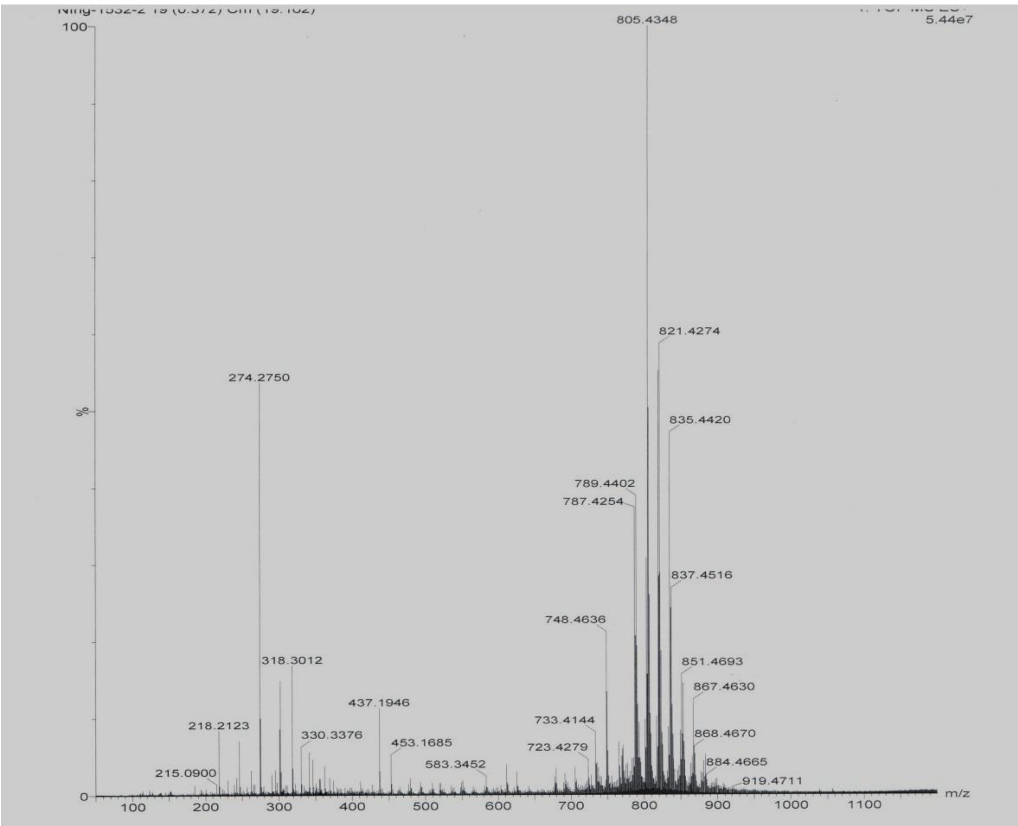

FIG AS2 [1]H-NMR spectrum (600 MHz, *CD_3OD*) of **FXJ15321**

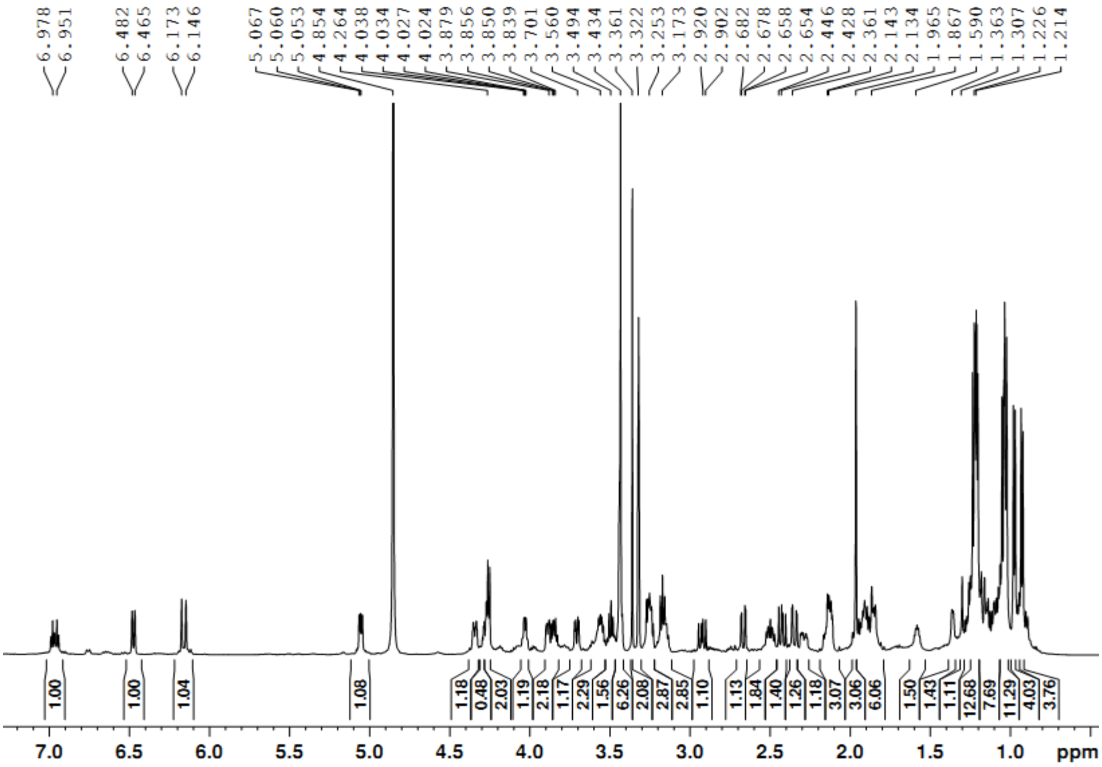

FIG AS3 ^{13}C-NMR spectrum (150 MHz, *CD_3OD*) of **FXJ15321**

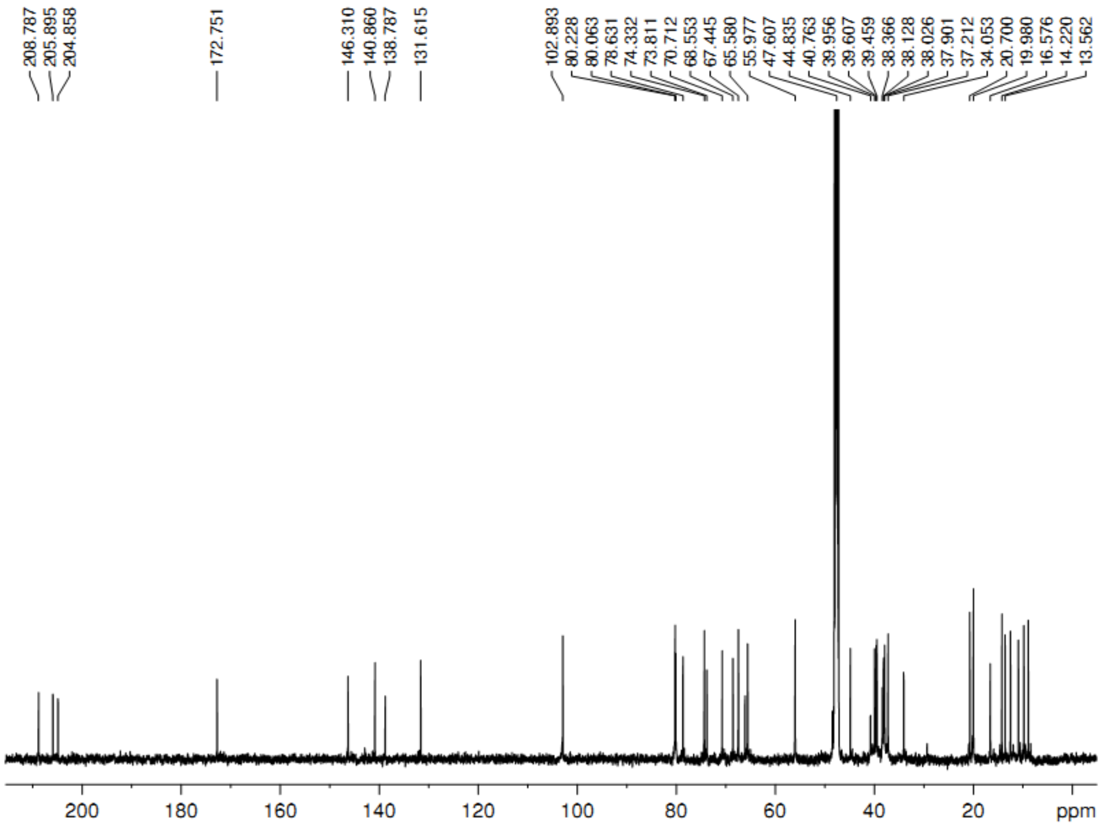

FIG AS4 DEPT135 spectrum (150 MHz, *CD_3OD*) of **FXJ15321**

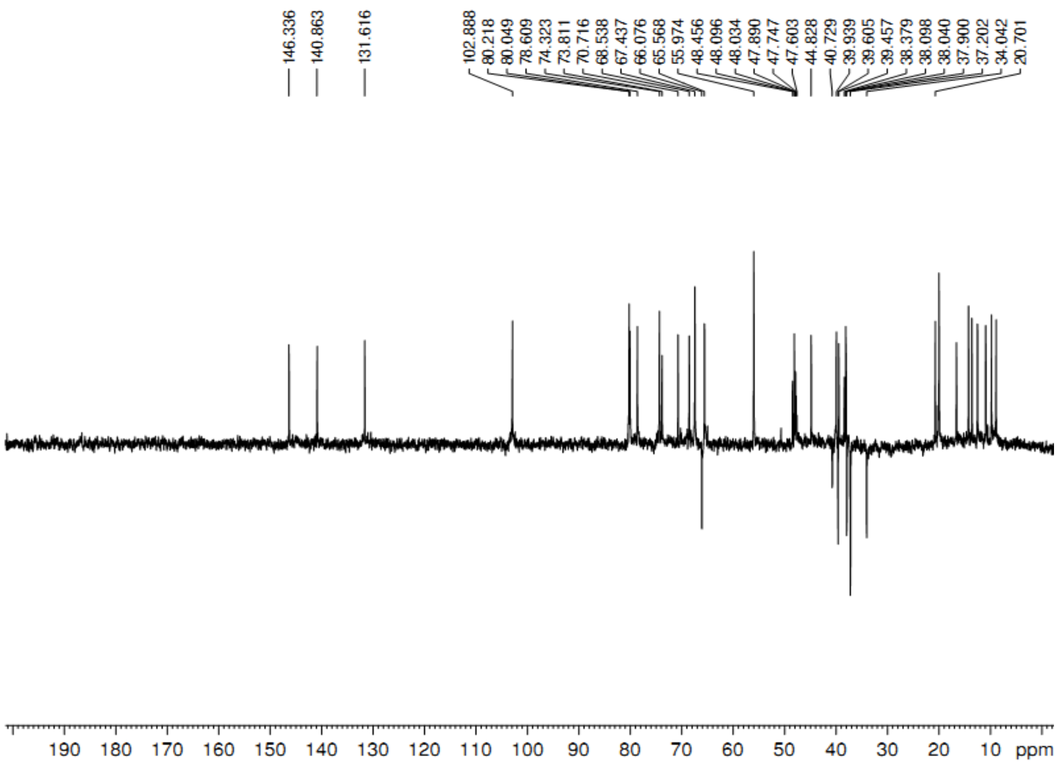

FIG AS5 ^{1}H–^{13}C-HSQC spectrum (600 × 150 MHz, *CD_3OD*) of **FXJ15321**

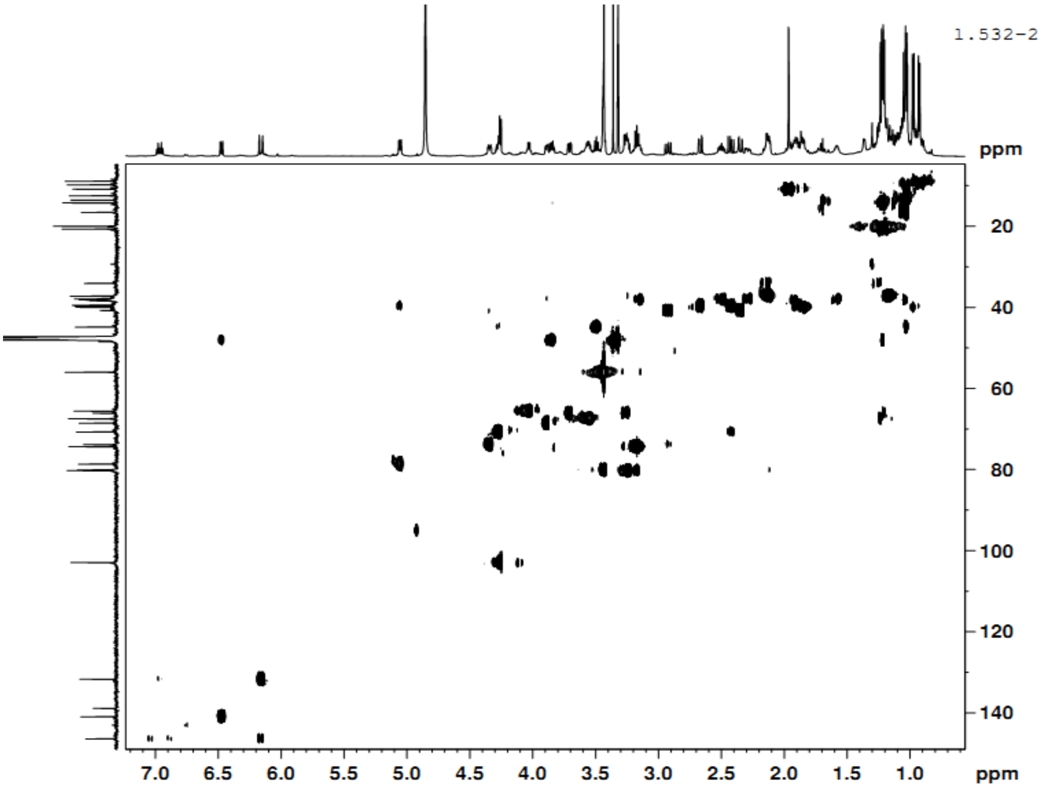

FIG AS6 ^{1}H–^{1}H-COSY spectrum (600 × 600 MHz, *CD_3OD*) of **FXJ15321**

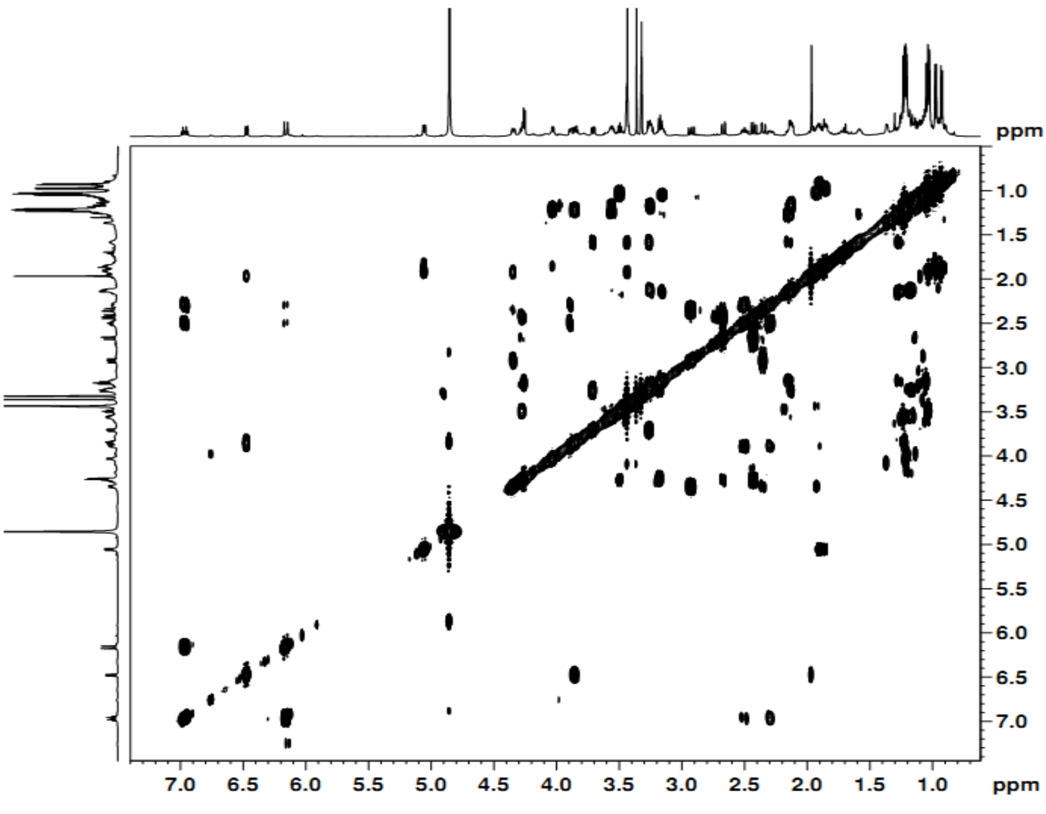

FIG AS7 ^{1}H–^{13}C-HMBC spectrum (600 × 150 MHz, *CD_3OD*) of **FXJ15321**

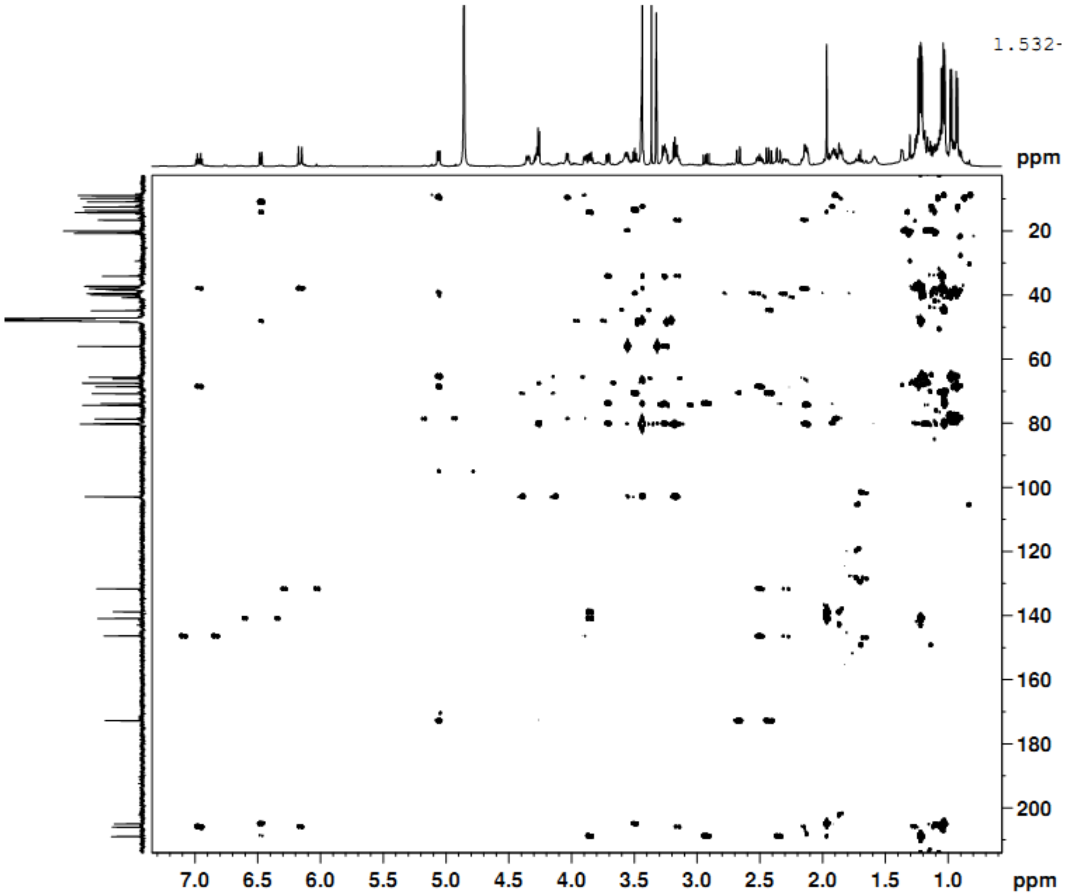

FIG AS8 ^{1}H–^{1}H-ROESY spectrum (600 × 600 MHz, *CD_3OD*) of **FXJ15321**

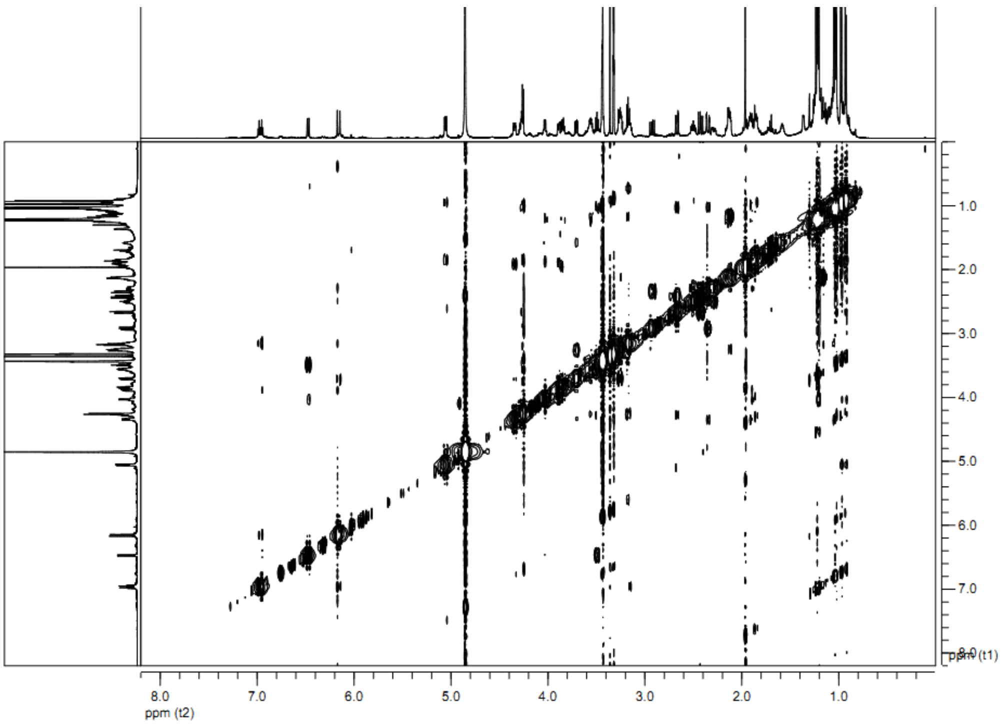

FIG AS9 NOE difference spectrum (H-29 irradiated) (600 MHz, CD_3OD) of **FXJ15321**

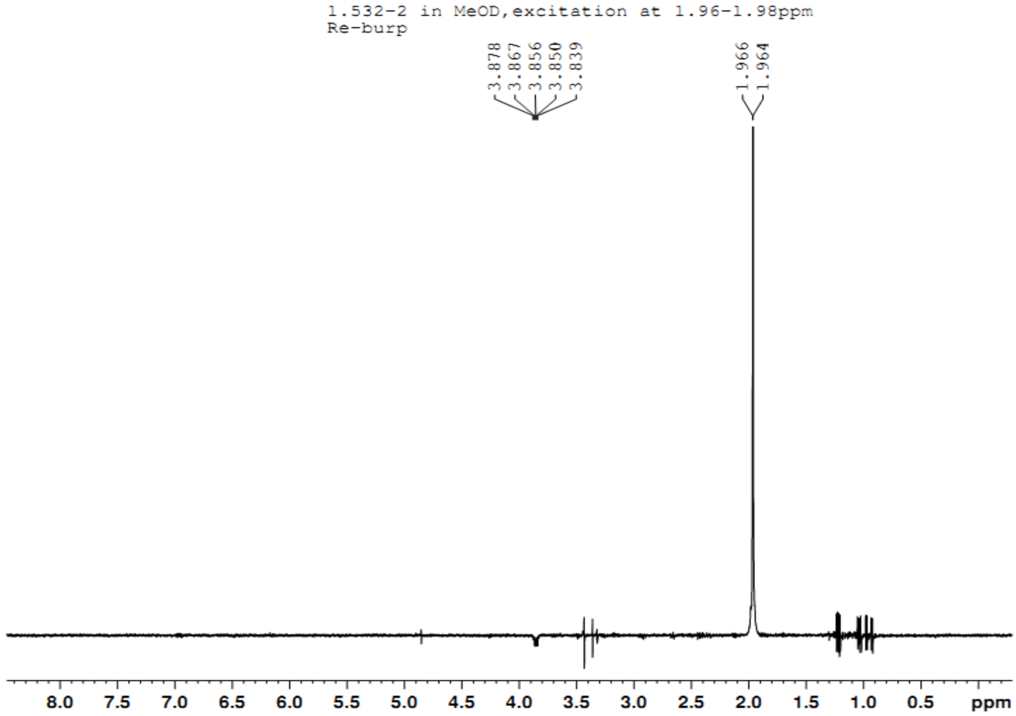

FIG AS10 HR-ESI-MS spectrum of **FXJ15322**

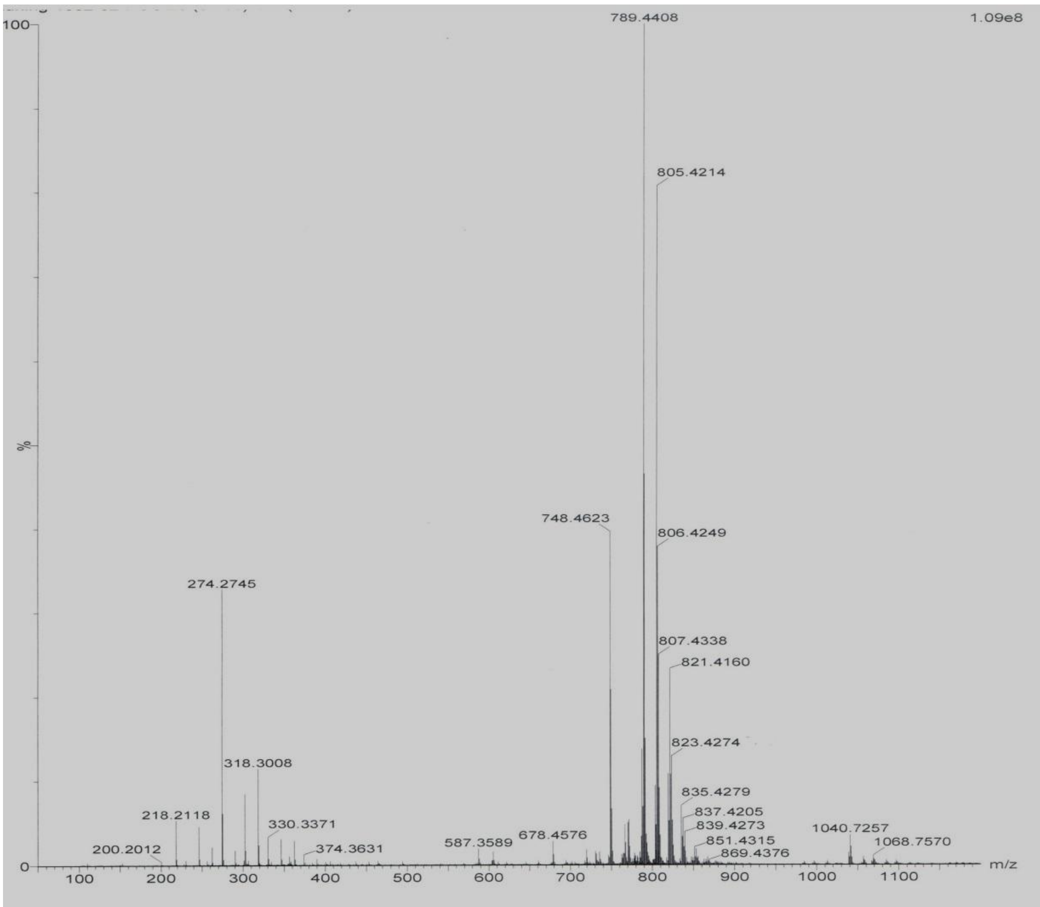

FIG AS11 [1]H-NMR spectrum (600 MHz, *CD_3OD*) of **FXJ15322**

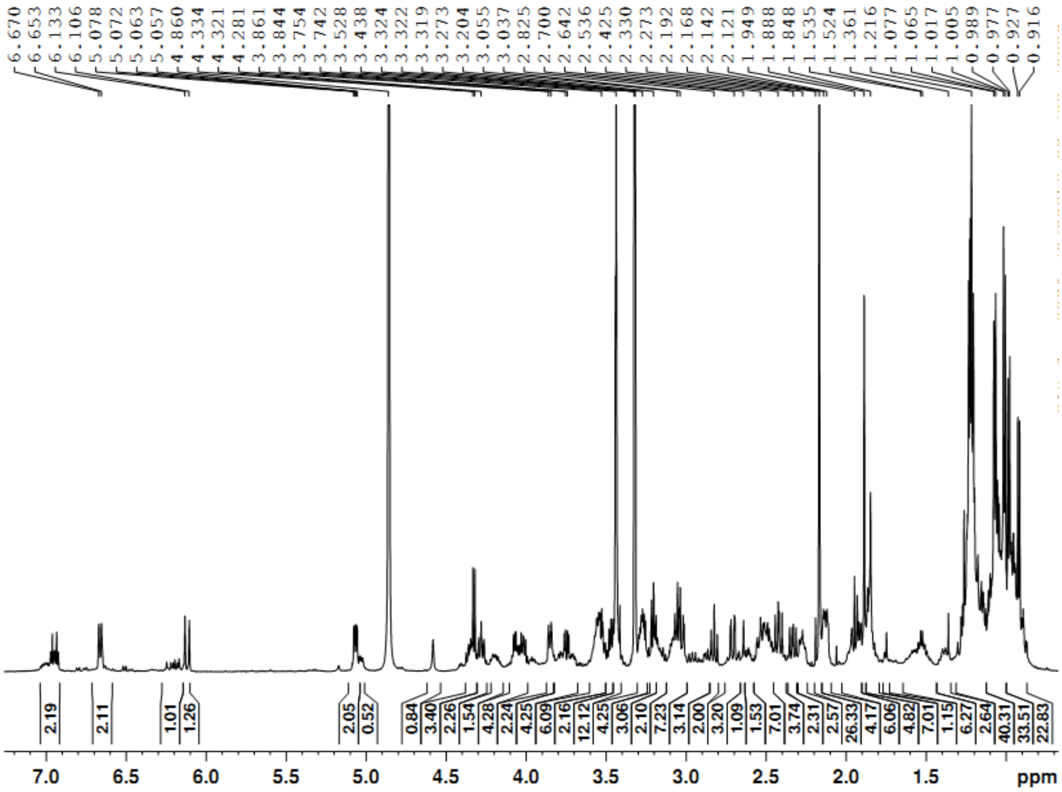

FIG AS12 [13]C-NMR spectrum (150 MHz, *CD_3OD*) of **FXJ15322**

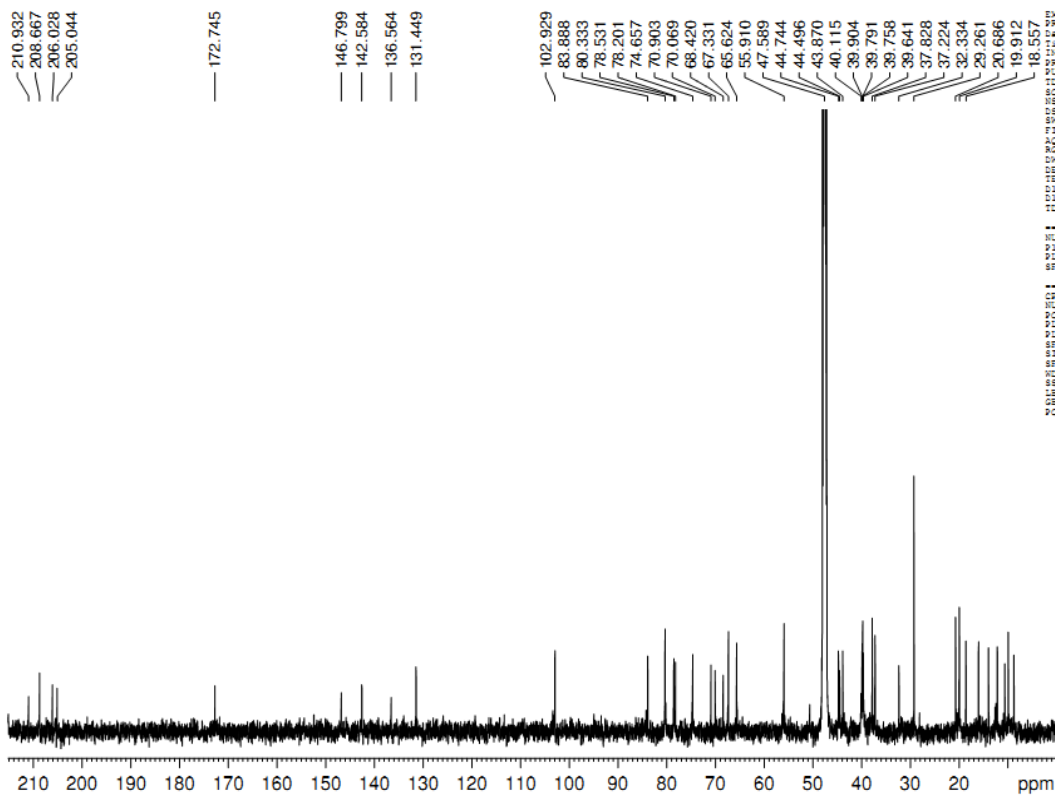

FIG AS13 DEPT135 spectrum (150 MHz, *CD_3OD*) of **FXJ15322**

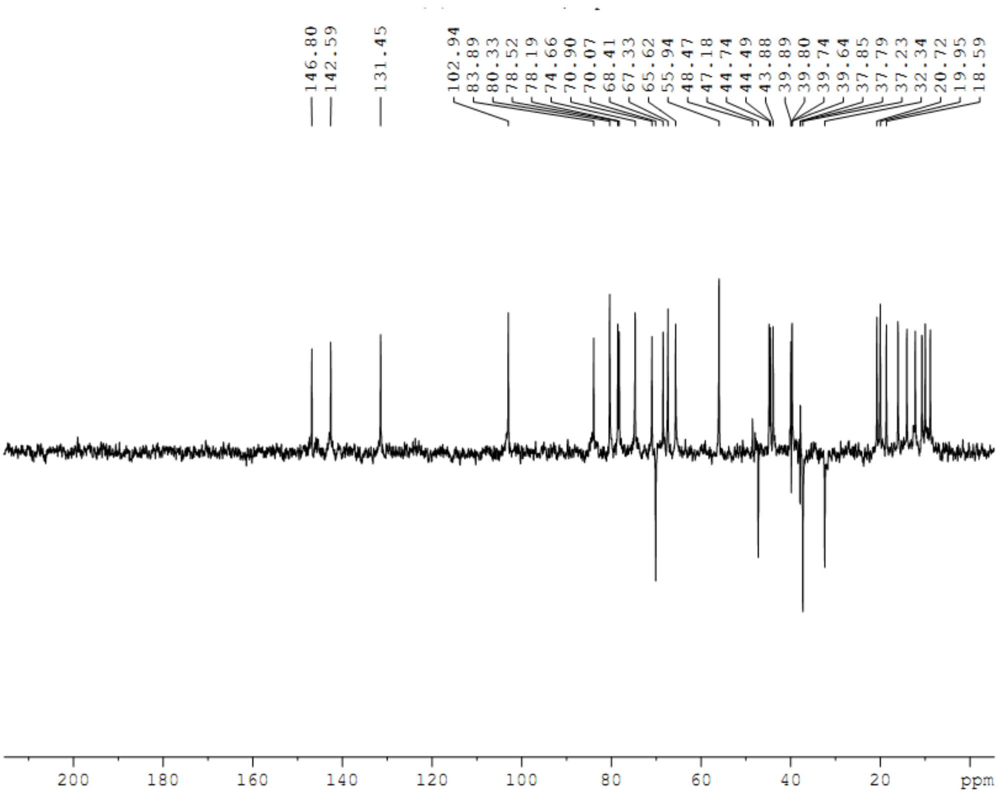

FIG AS14 ^{1}H–^{1}H-COSY spectrum (600 × 600 MHz, *CD_3OD*) of **FXJ15322**

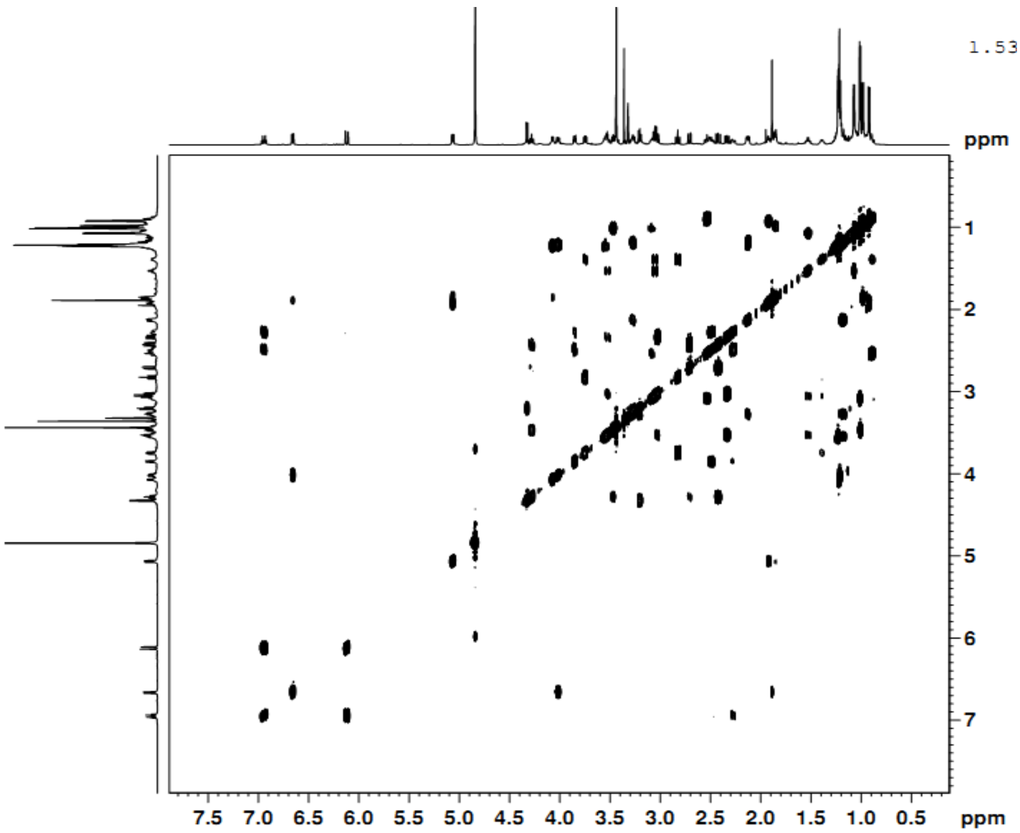

FIG AS15 ^{1}H–^{13}C-HSQC spectrum (600 × 150 MHz, *CD_3OD*) of **FXJ15322**

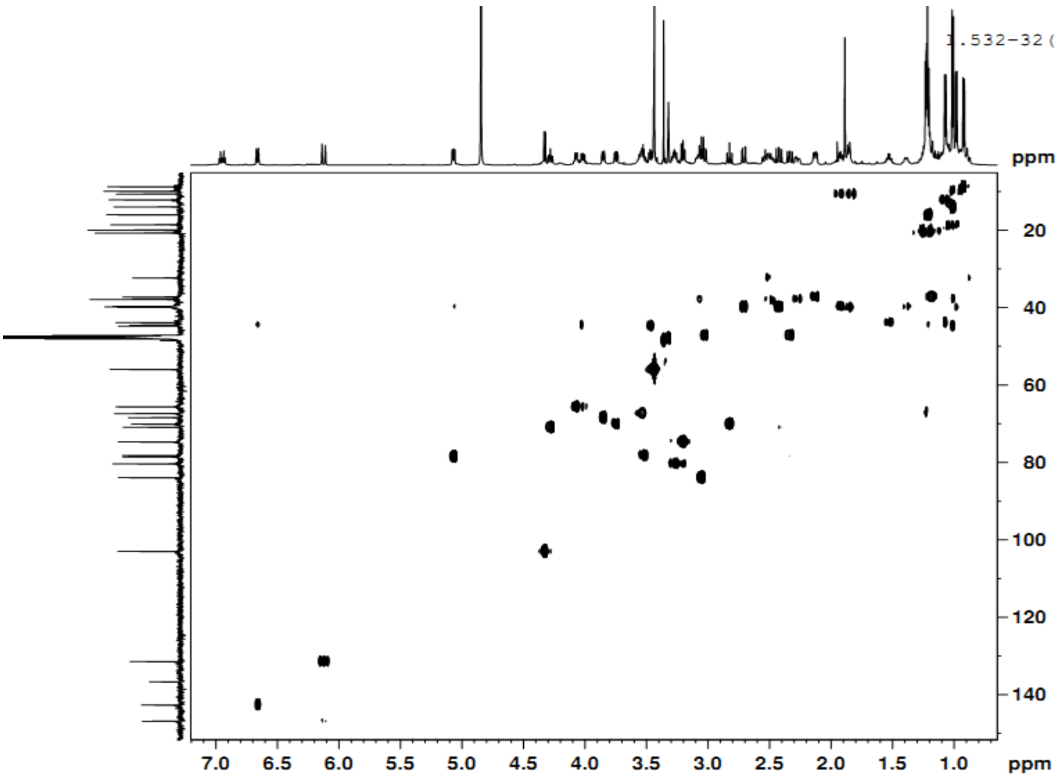

FIG AS16 ^{1}H–^{13}C-HMBC spectrum (600 × 150 MHz, *CD_3OD*) of **FXJ15322**

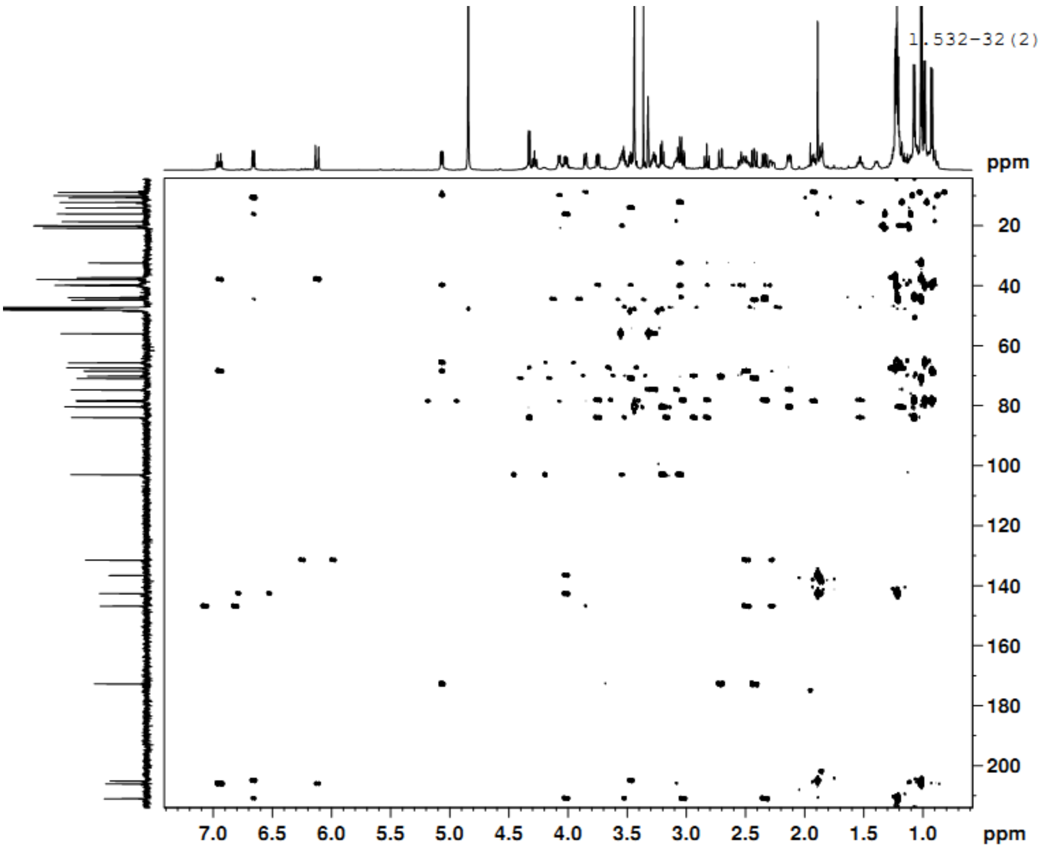

FIG AS17 [1]H–[1]H-ROESY spectrum (600 × 600 MHz, *CD_3OD*) of **FXJ15322**

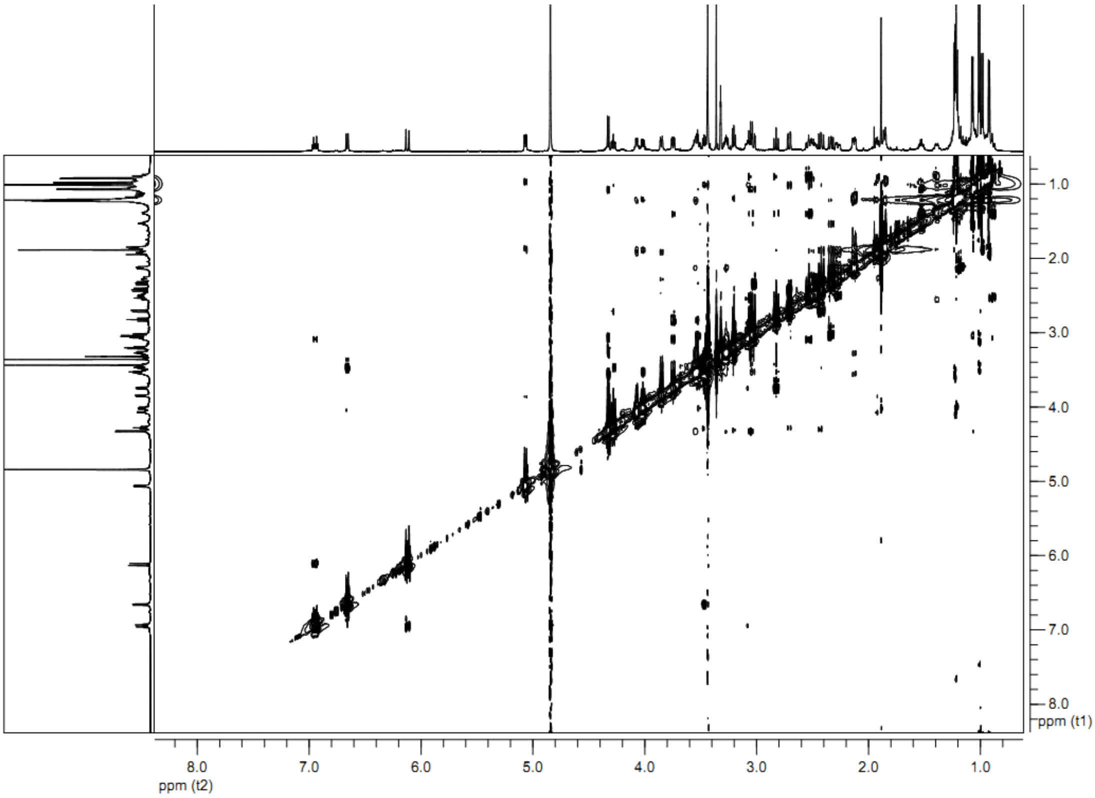

FIG AS18 ESI-MS spectrum of **FXJ10761**

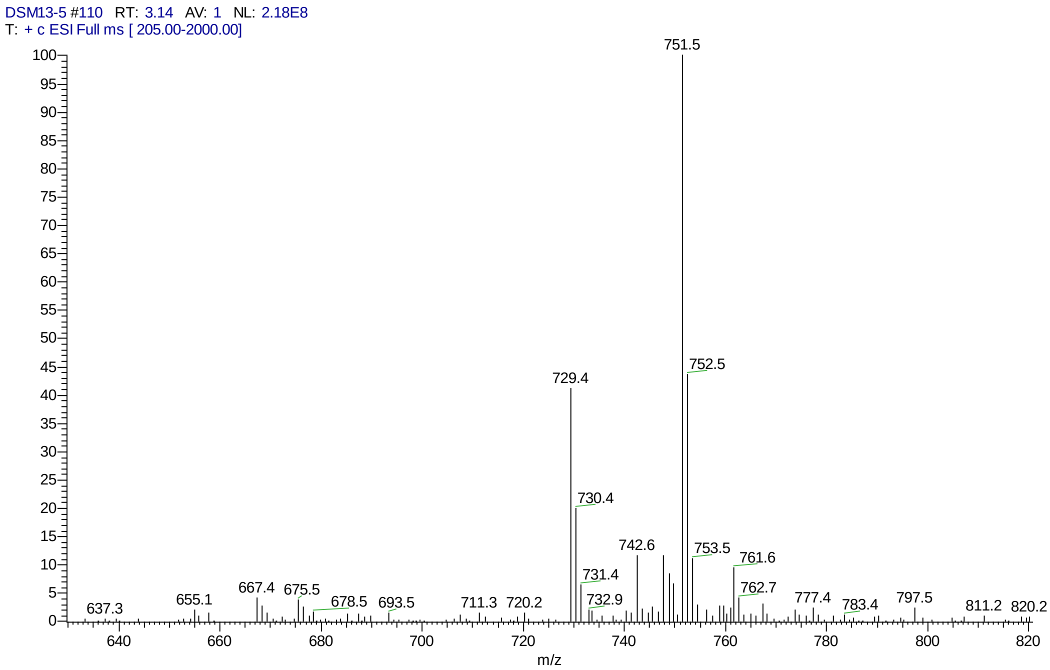

FIG AS19 ^{1}H-NMR spectrum (600 MHz, *$CDCl_3$*) of **FXJ10761**

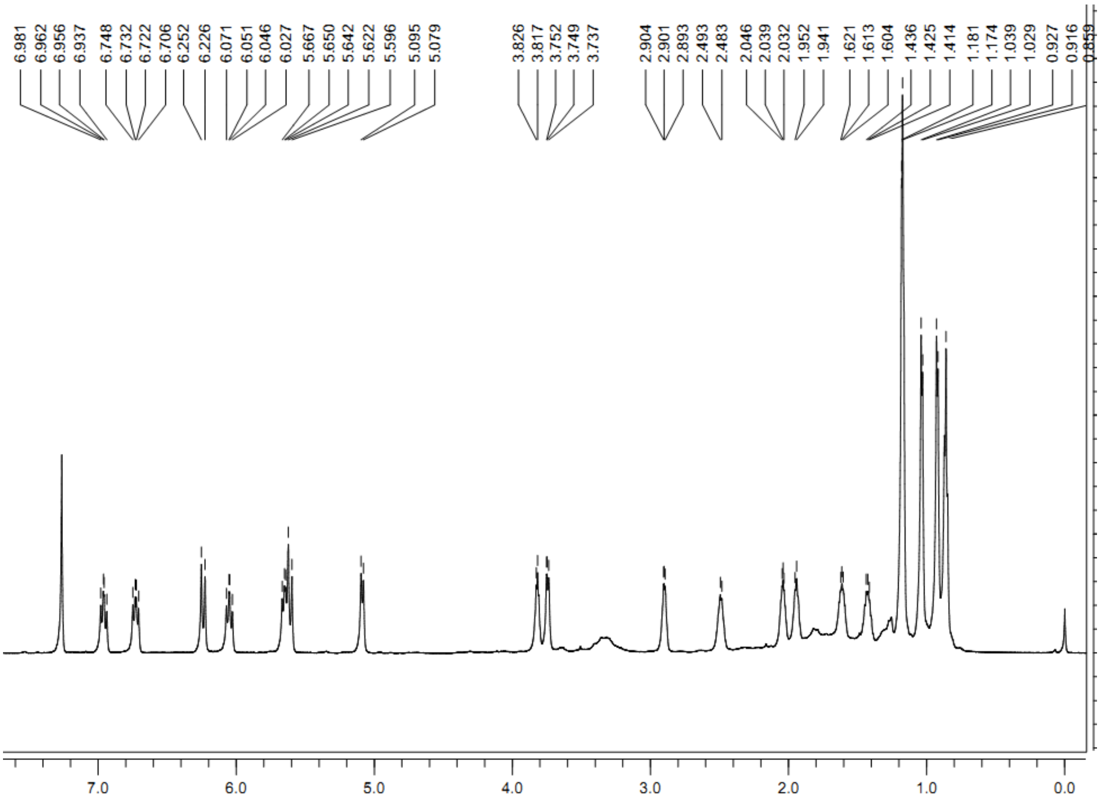

FIG AS20 ^{13}C-NMR spectrum (150 MHz, *$CDCl_3$*) of **FXJ10761**

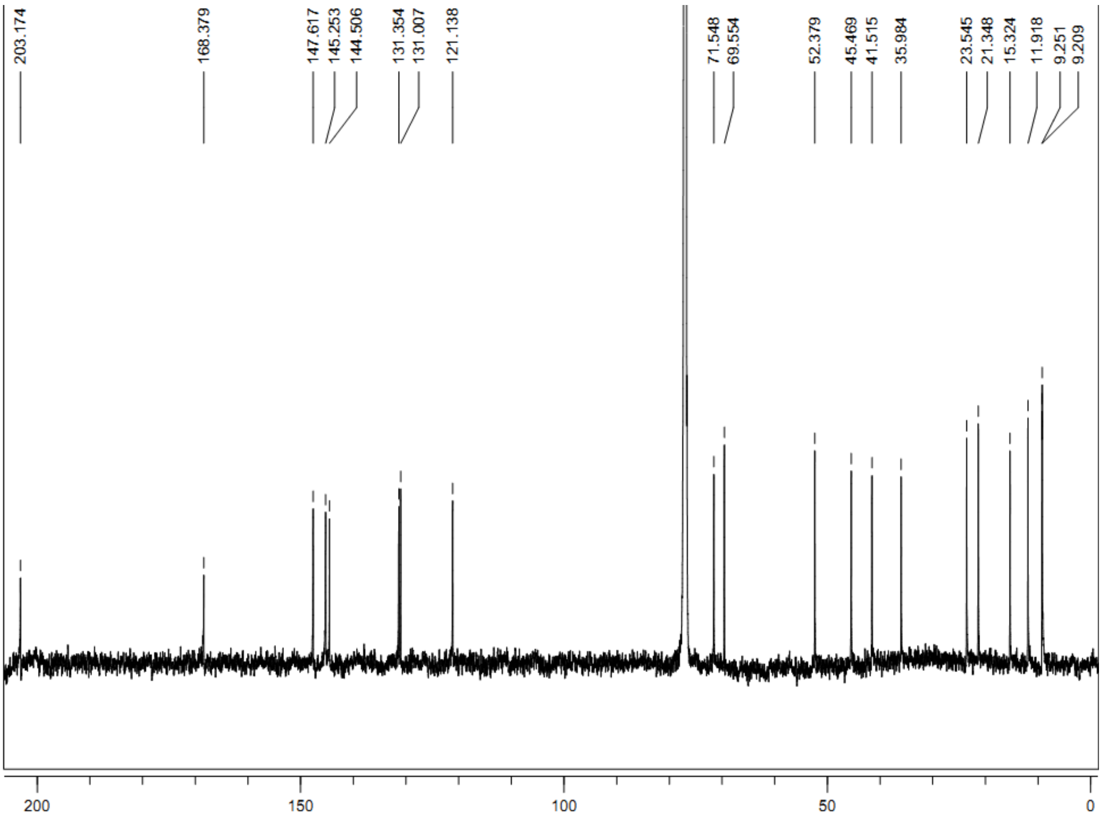

FIG AS21 DEPT 135 spectrum (150 MHz, *$CDCl_3$*) of **FXJ10761**

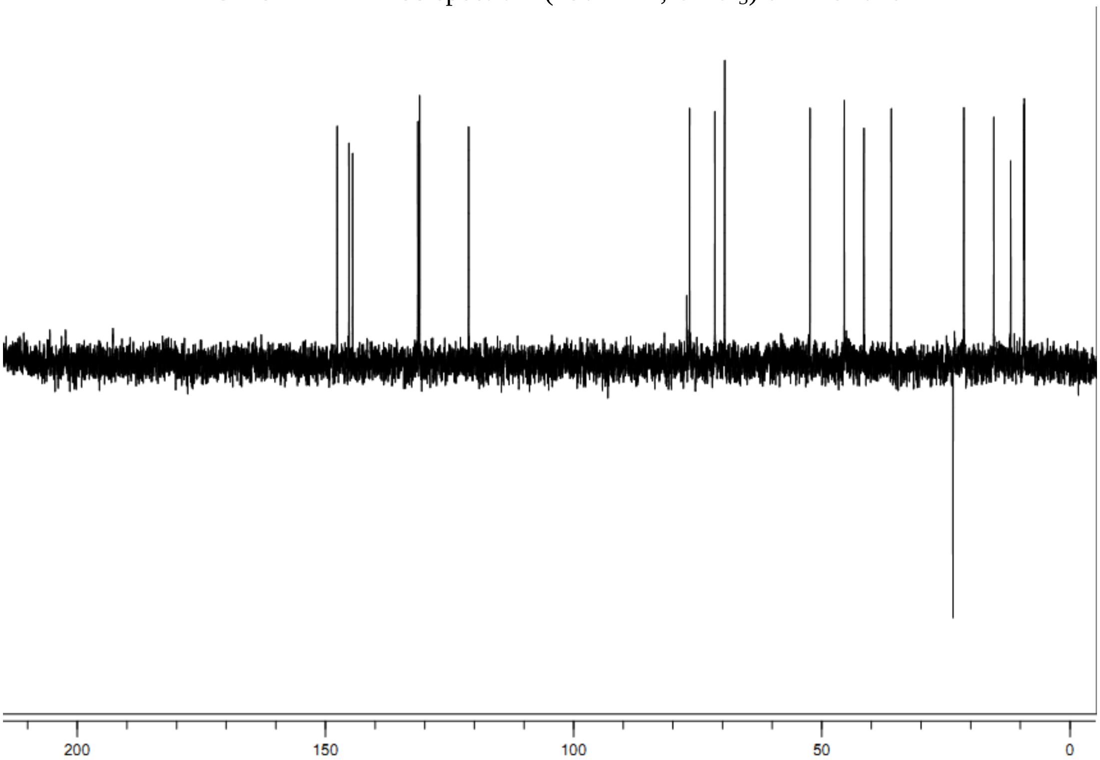

FIG AS22 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *$CDCl_3$*) of **FXJ10761**

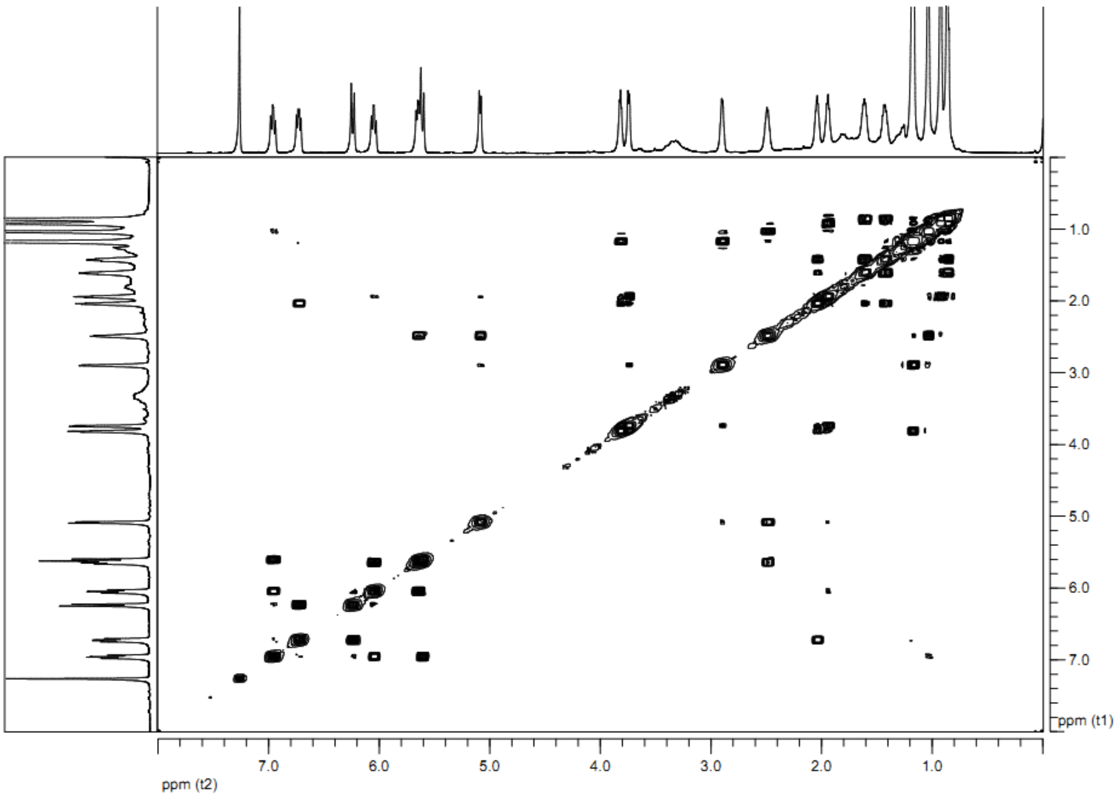

FIG AS23 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *$CDCl_3$*) of **FXJ10761**

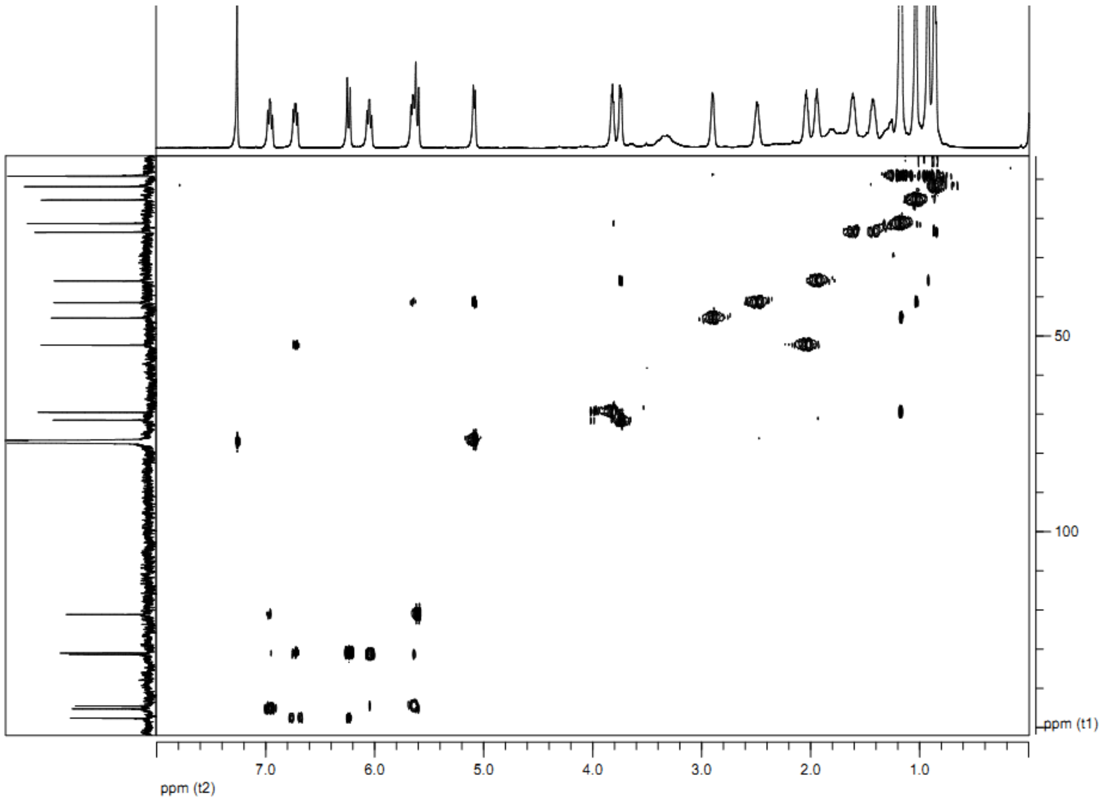

FIG AS24 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *$CDCl_3$*) of **FXJ10761**

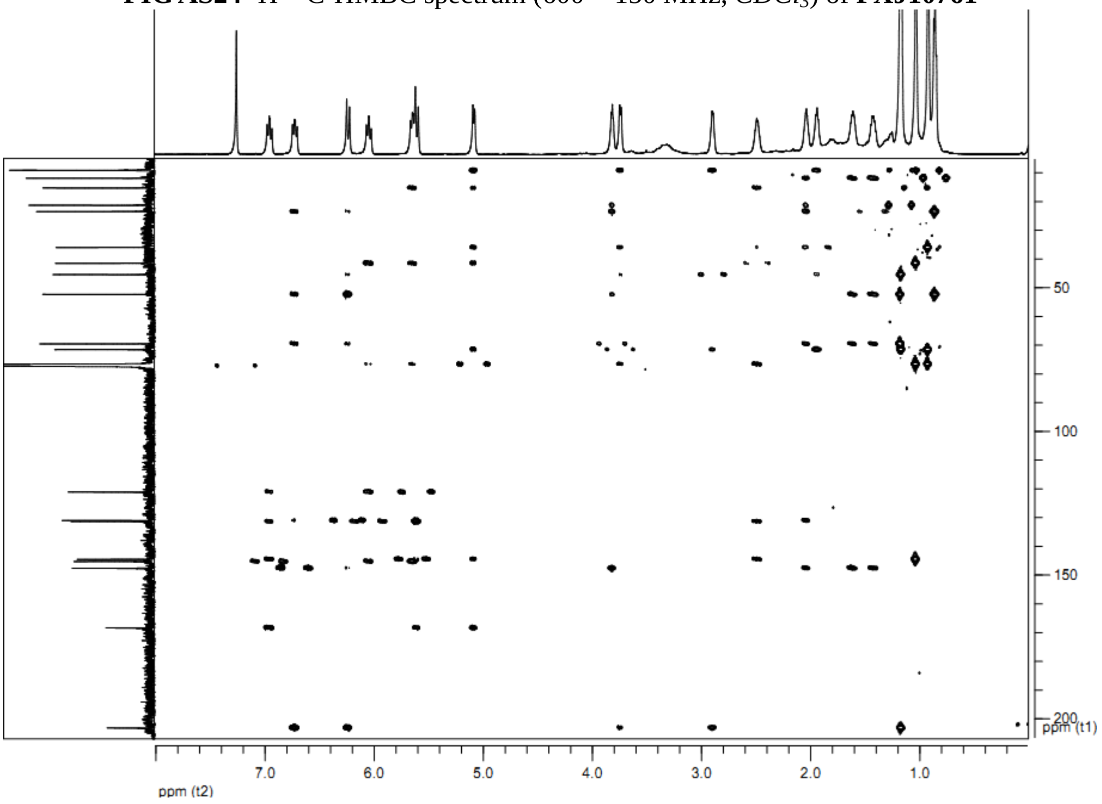

FIG AS25 ^1H-^1H-ROESY spectrum (600 × 600 MHz, *$CDCl_3$*) of **FXJ10761**

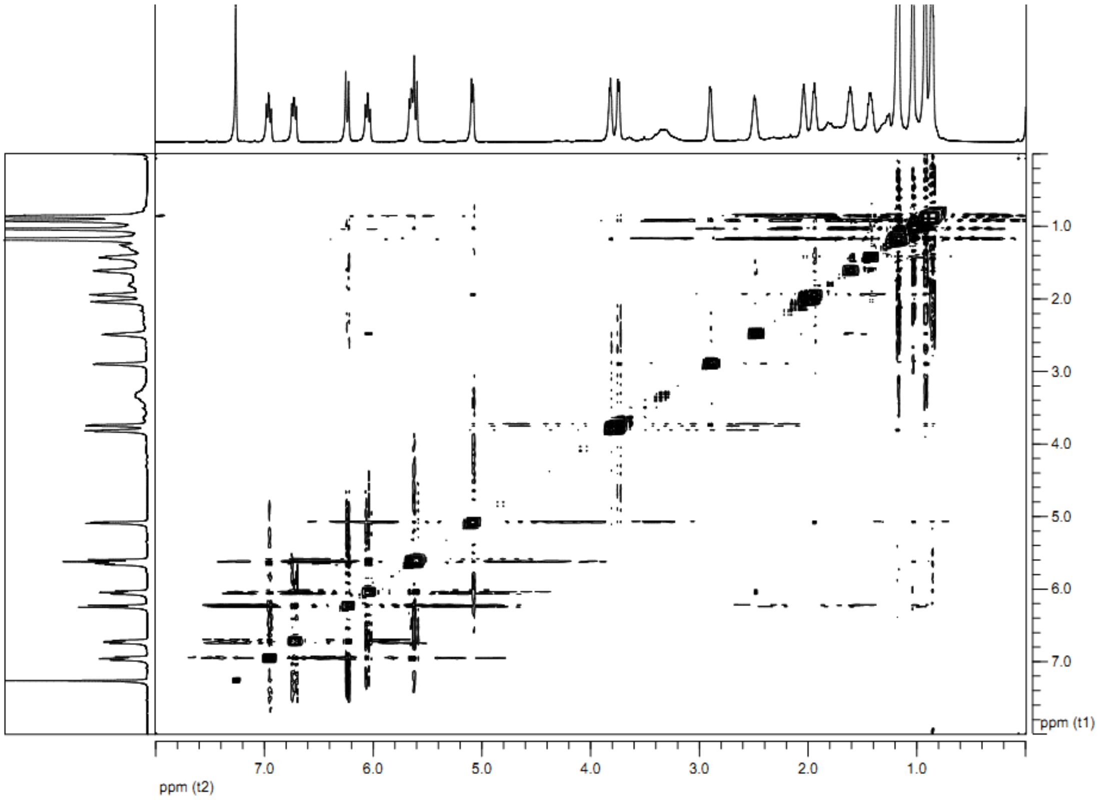

FIG AS26 HR-ESI-MS spectrum of **FXJ10762**

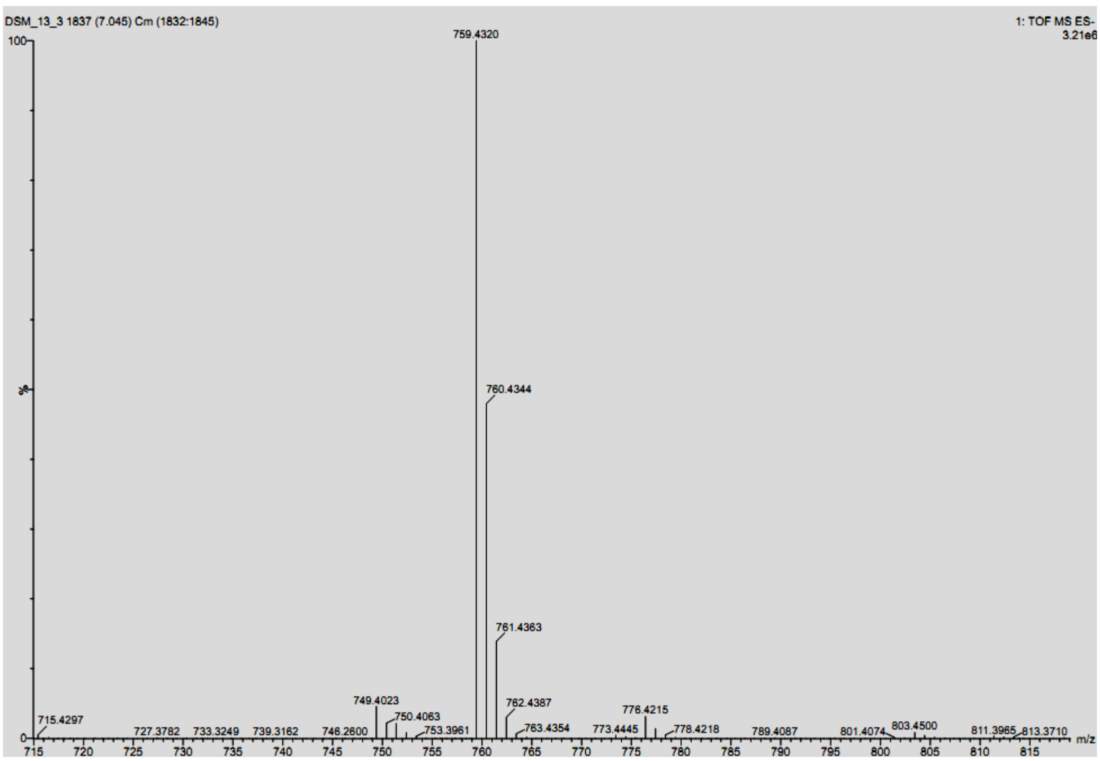

FIG AS27 ^{1}H-NMR spectrum (600 MHz, *$CDCl_3$*) of **FXJ10762**

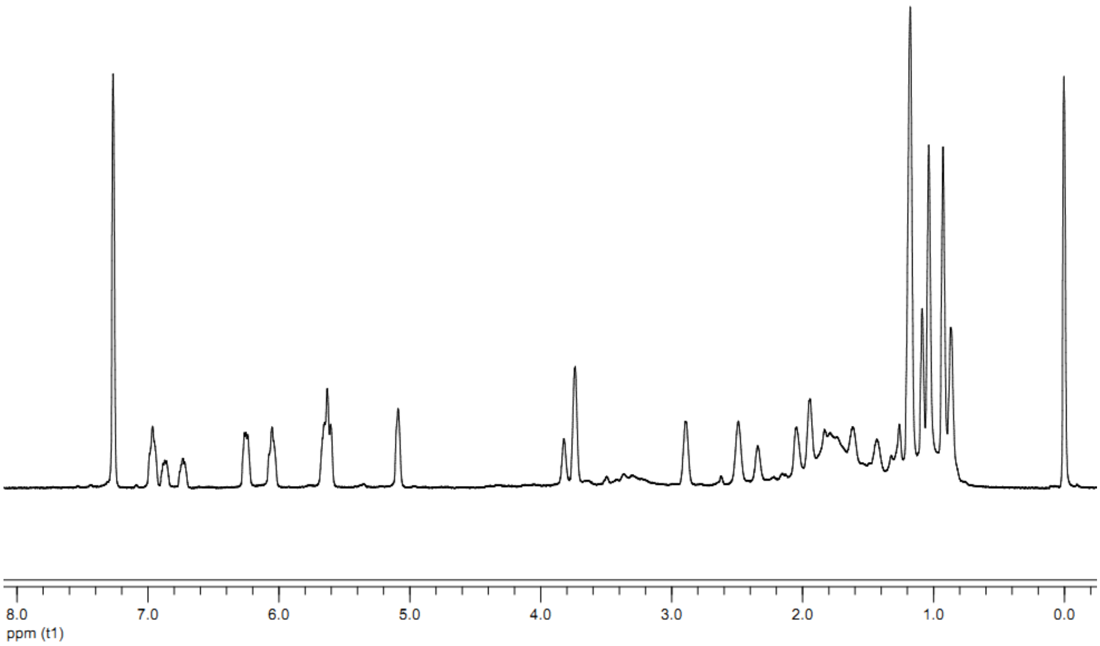

FIG AS28 ^{13}C-NMR spectrum (150 MHz, *$CDCl_3$*) of **FXJ10762**

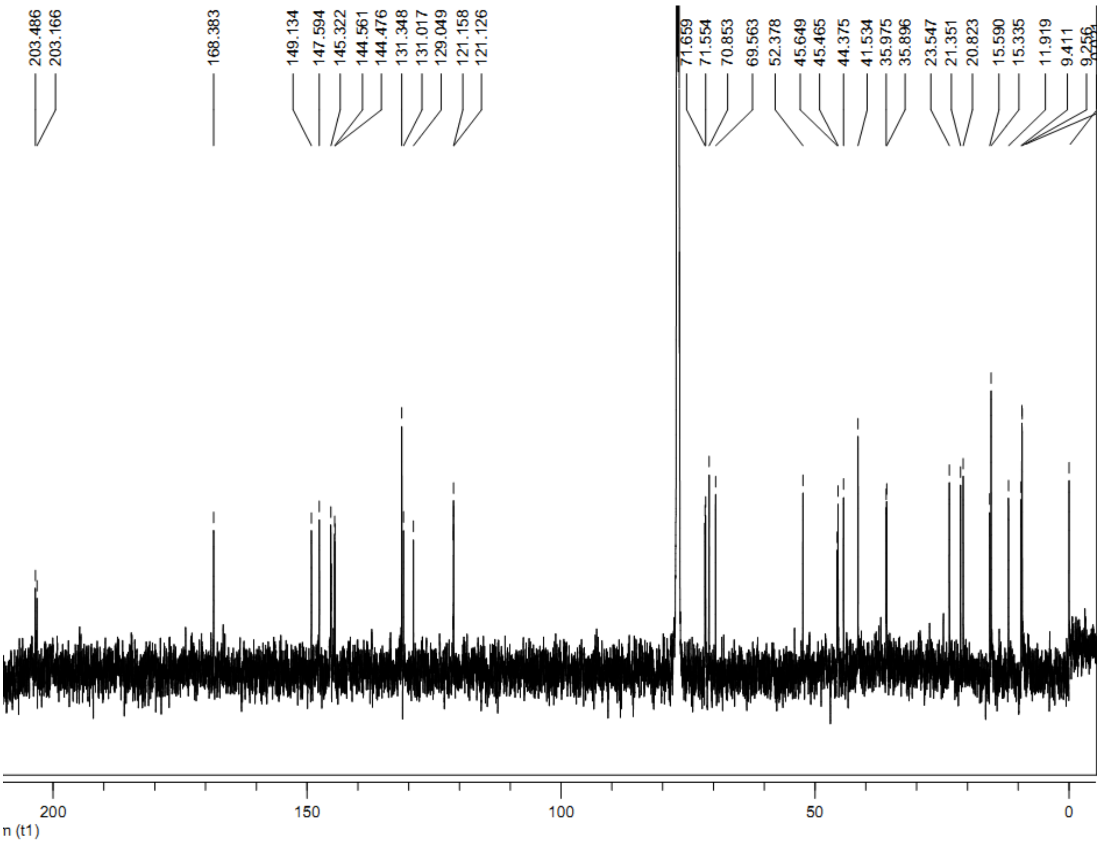

FIG AS29 DEPT 135 spectrum (150 MHz, *CDCl₃*) of **FXJ10762**

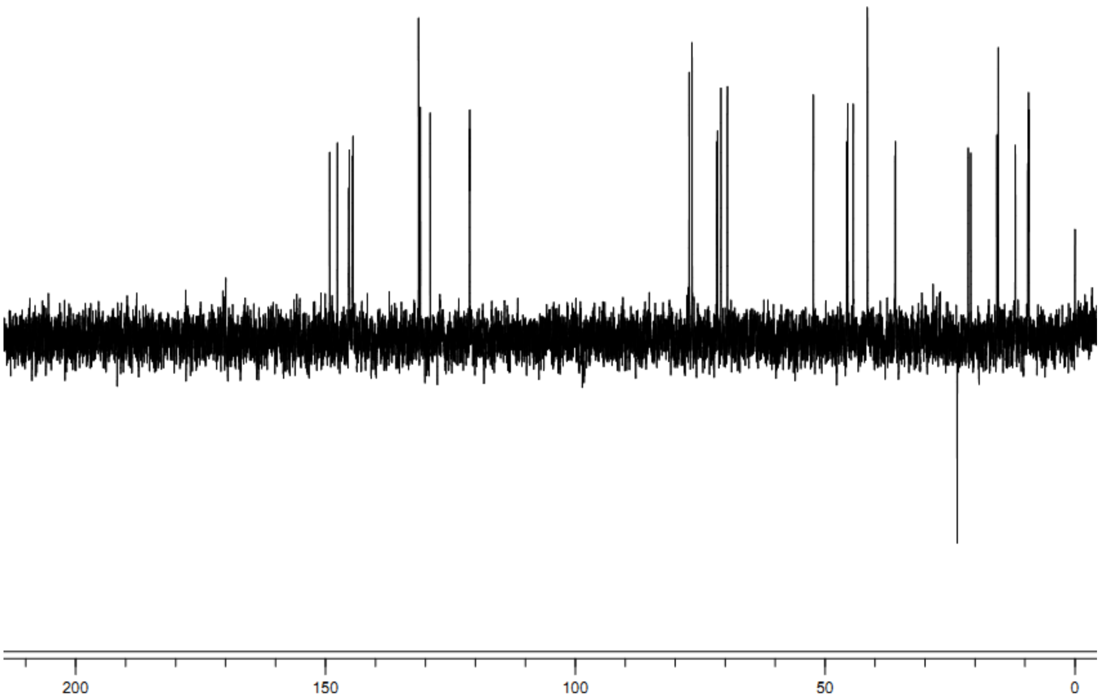

FIG AS30 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CDCl₃*) of **FXJ10762**

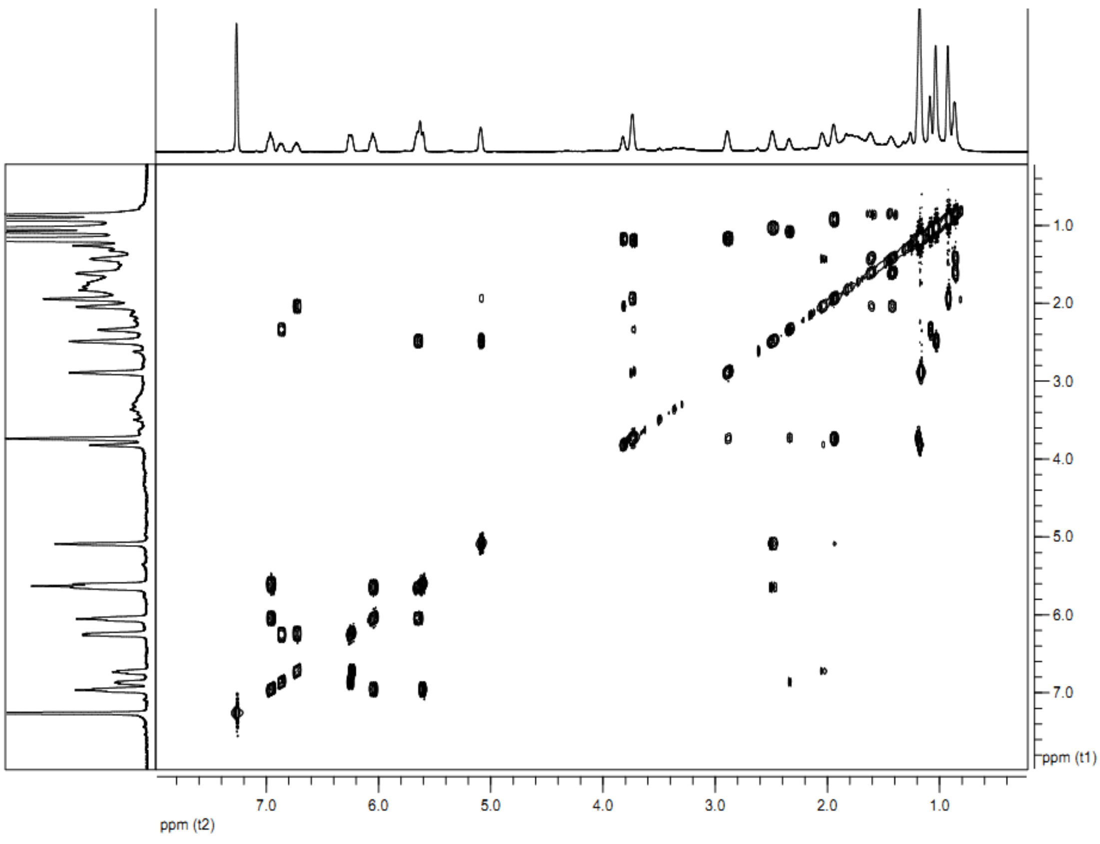

FIG AS31 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10762**

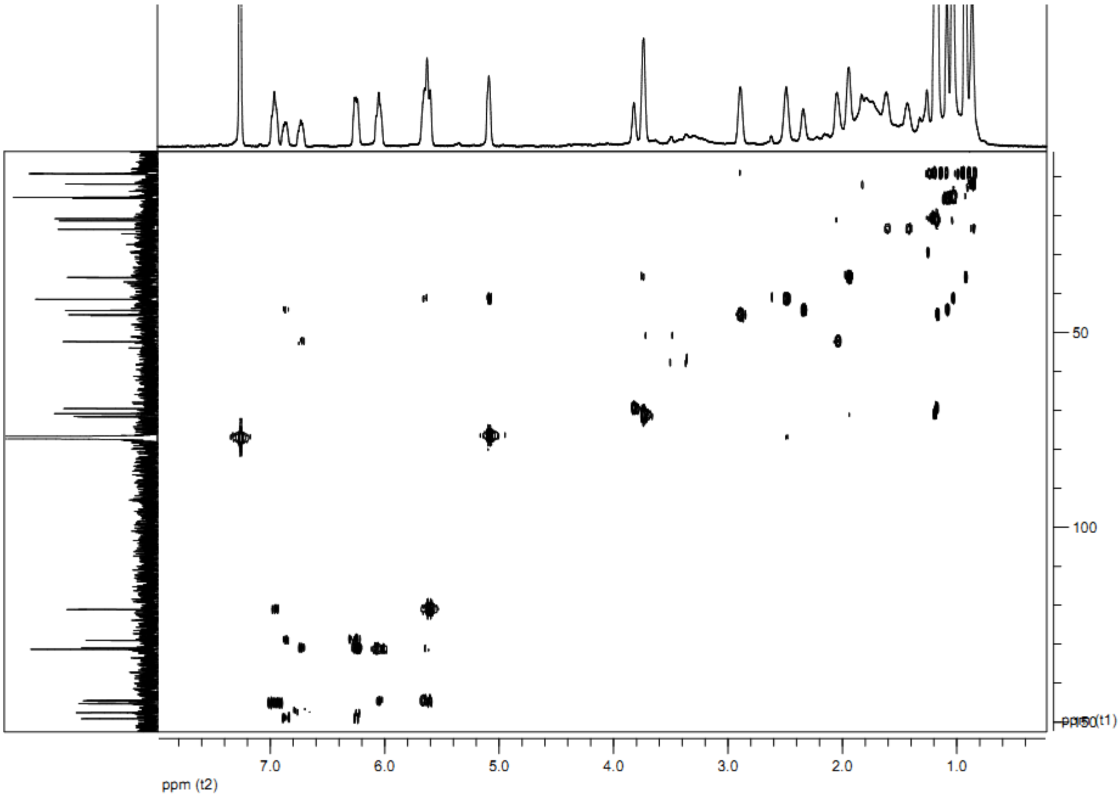

FIG AS32 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10762**

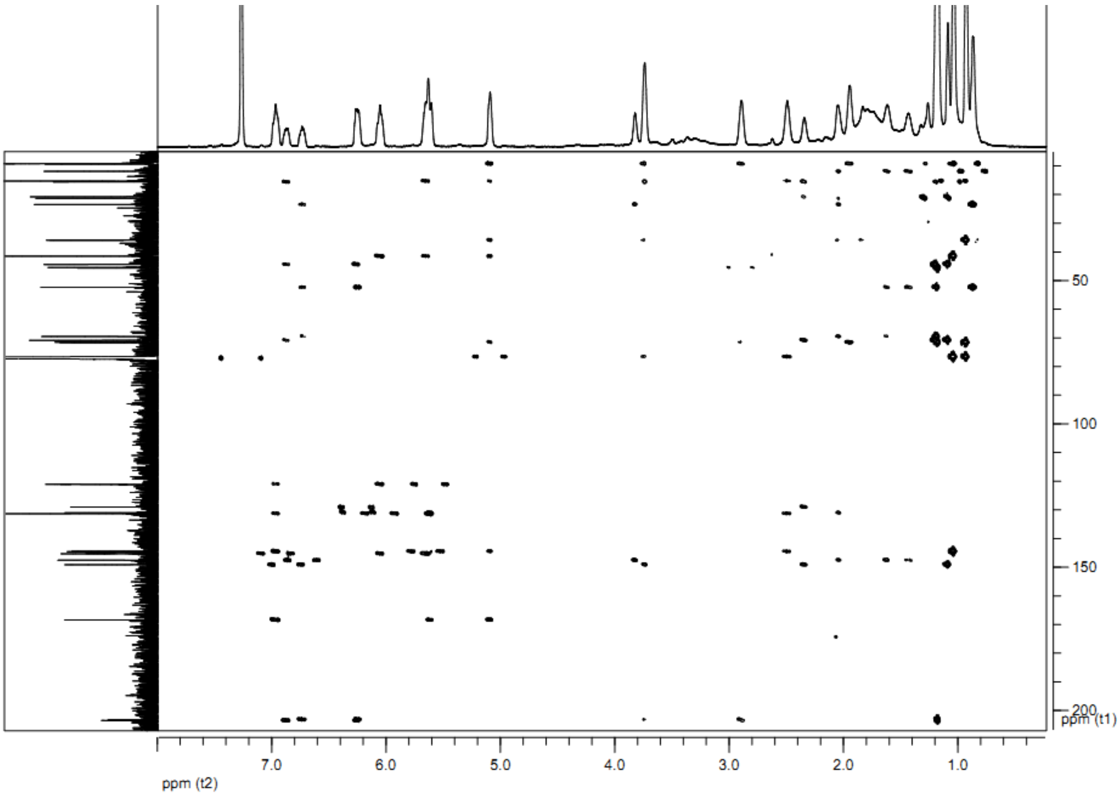

FIG AS33 ^{1}H-^{1}H-ROESY spectrum (600 × 600 MHz, *$CDCl_3$*) of **FXJ10762**

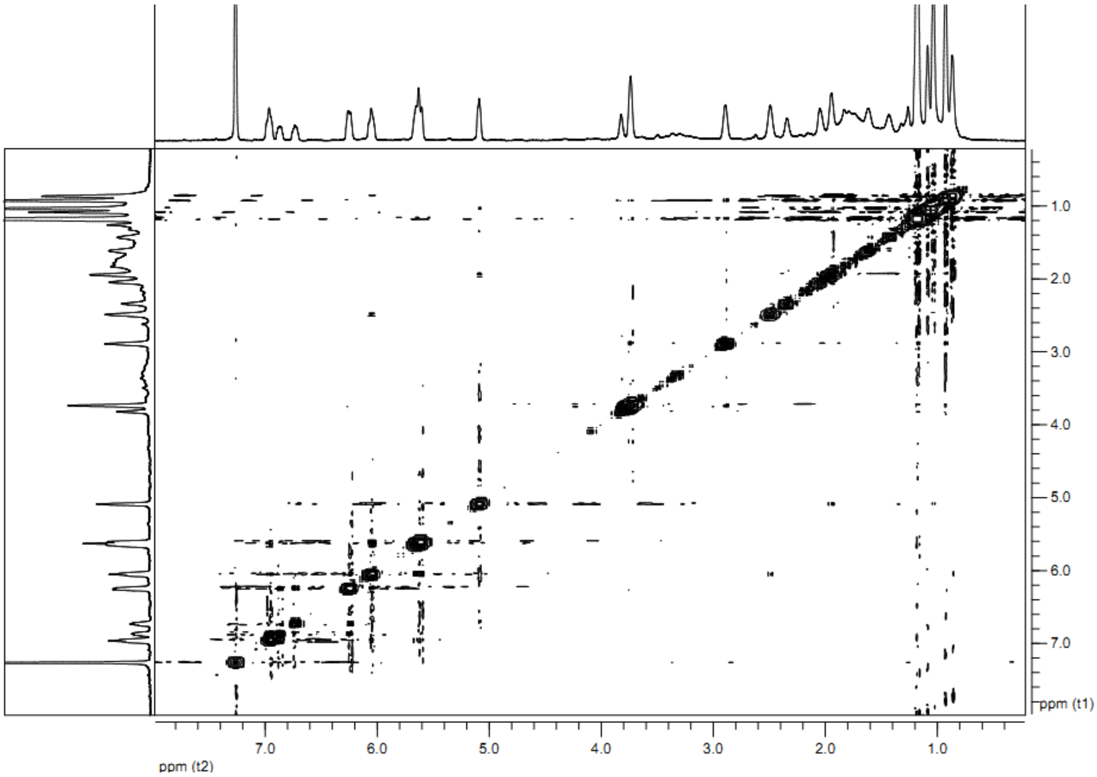

FIG AS34 HR-ESI-MS spectrum of **FXJ10763**

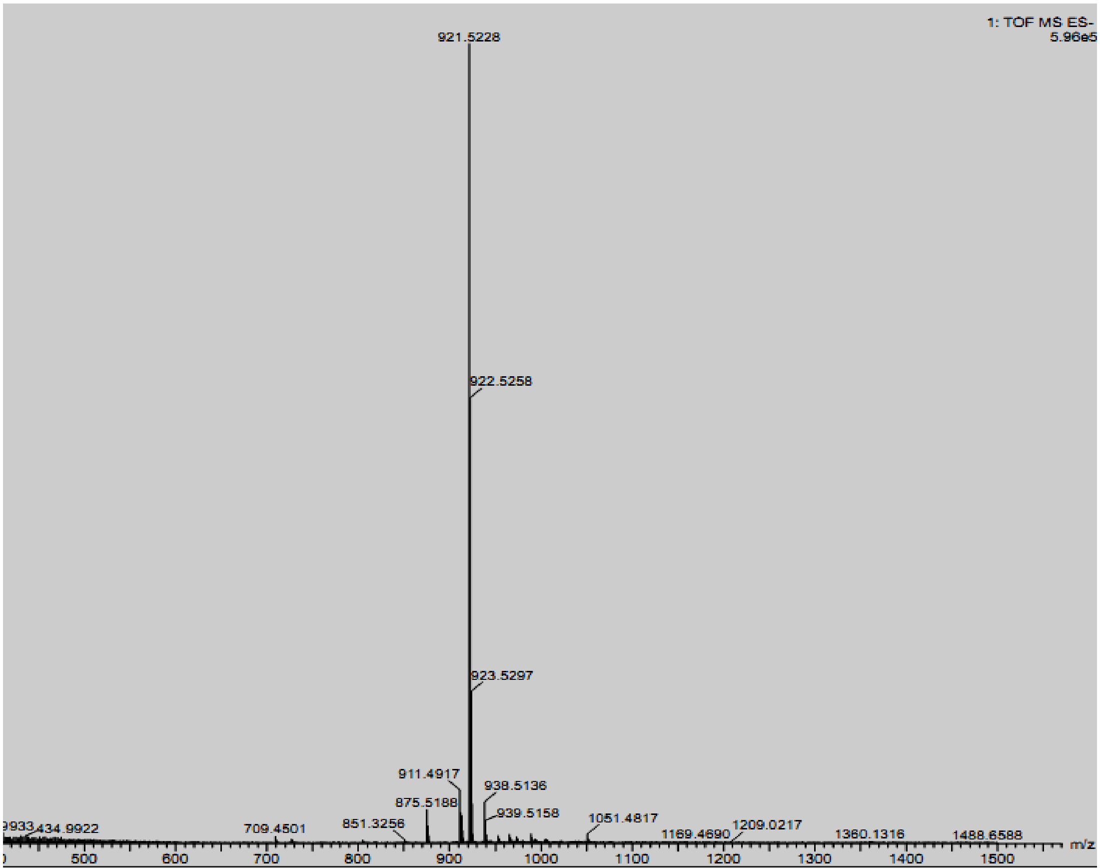

FIG AS35 [1]H-NMR spectrum (600 MHz, *$CDCl_3$*) of **FXJ10763**

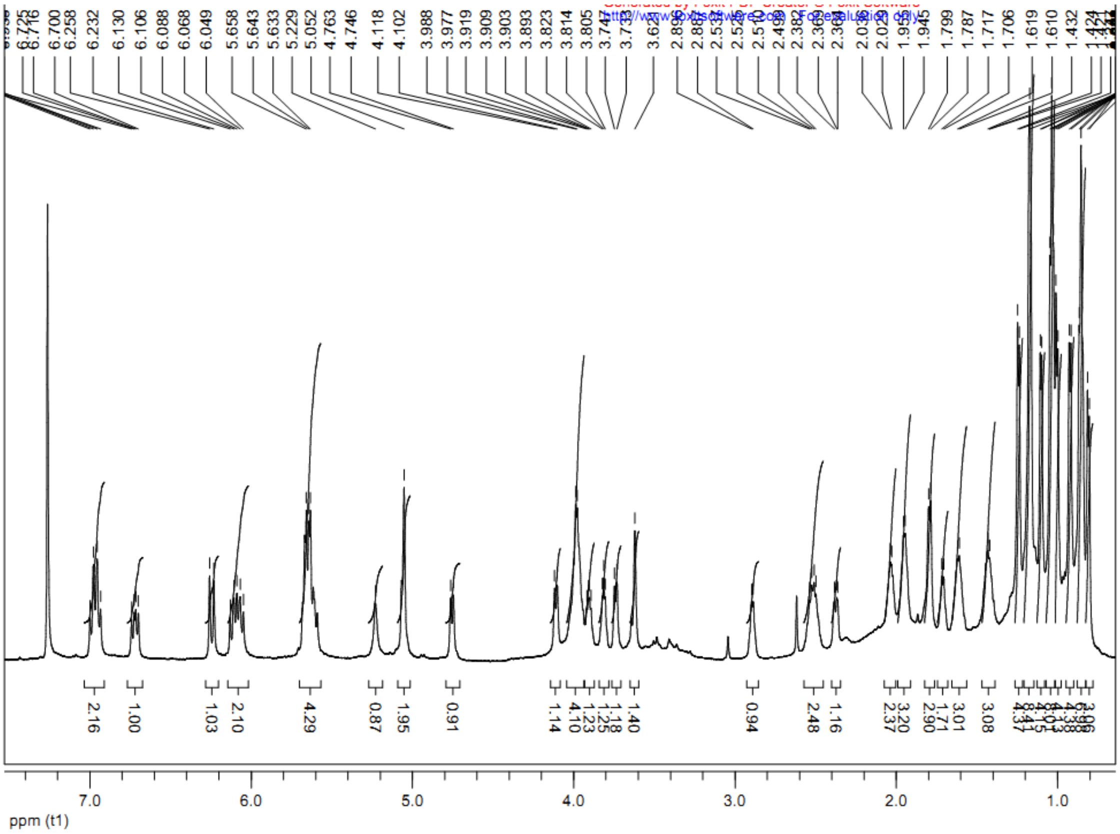

FIG AS36 [13]C-NMR spectrum (150 MHz, *$CDCl_3$*) of **FXJ10763**

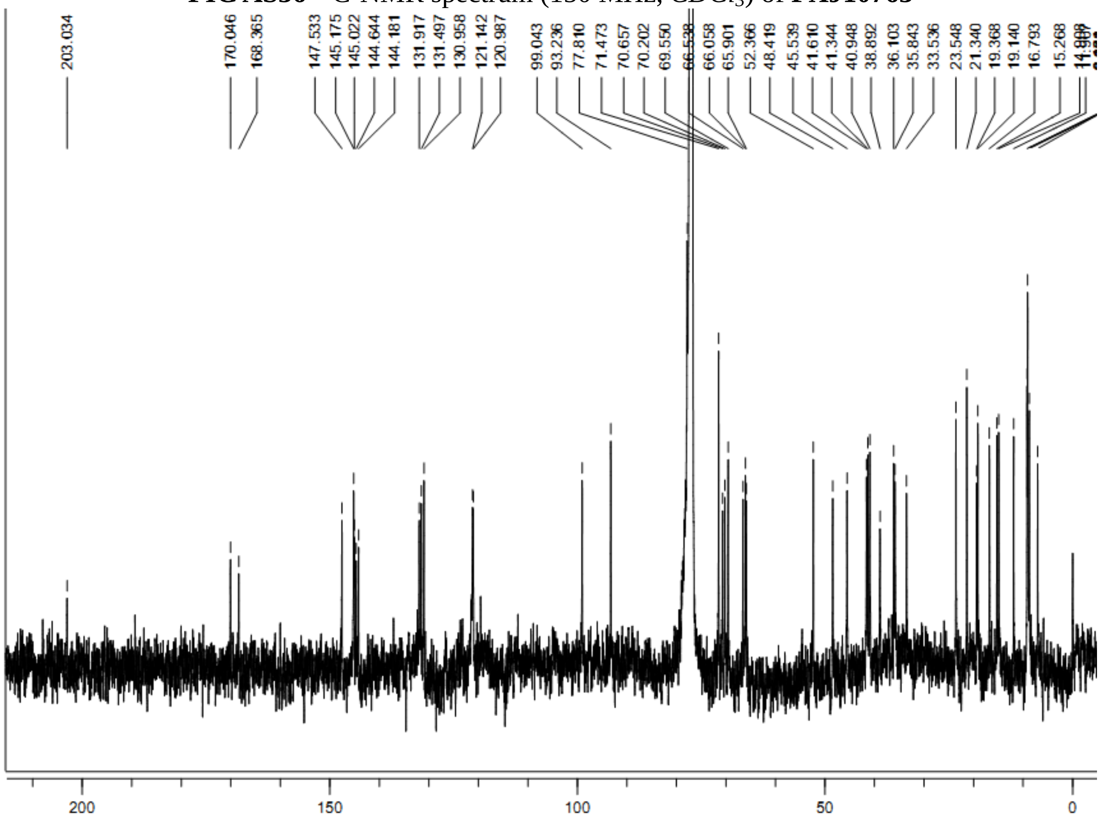

FIG AS37 DEPT 135 spectrum (150 MHz, *CDCl₃*) of **FXJ10763**

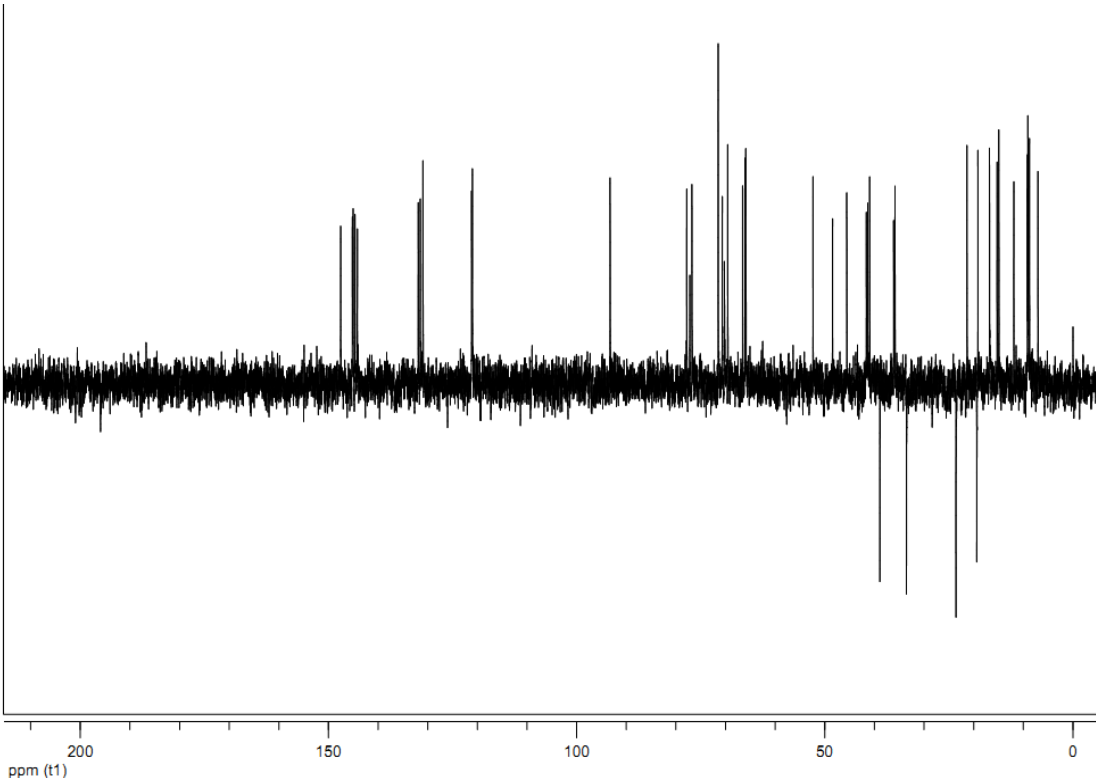

FIG AS38 ^{1}H-^{1}H-COSY spectrum (600 × 600 MHz, *CDCl₃*) of **FXJ10763**

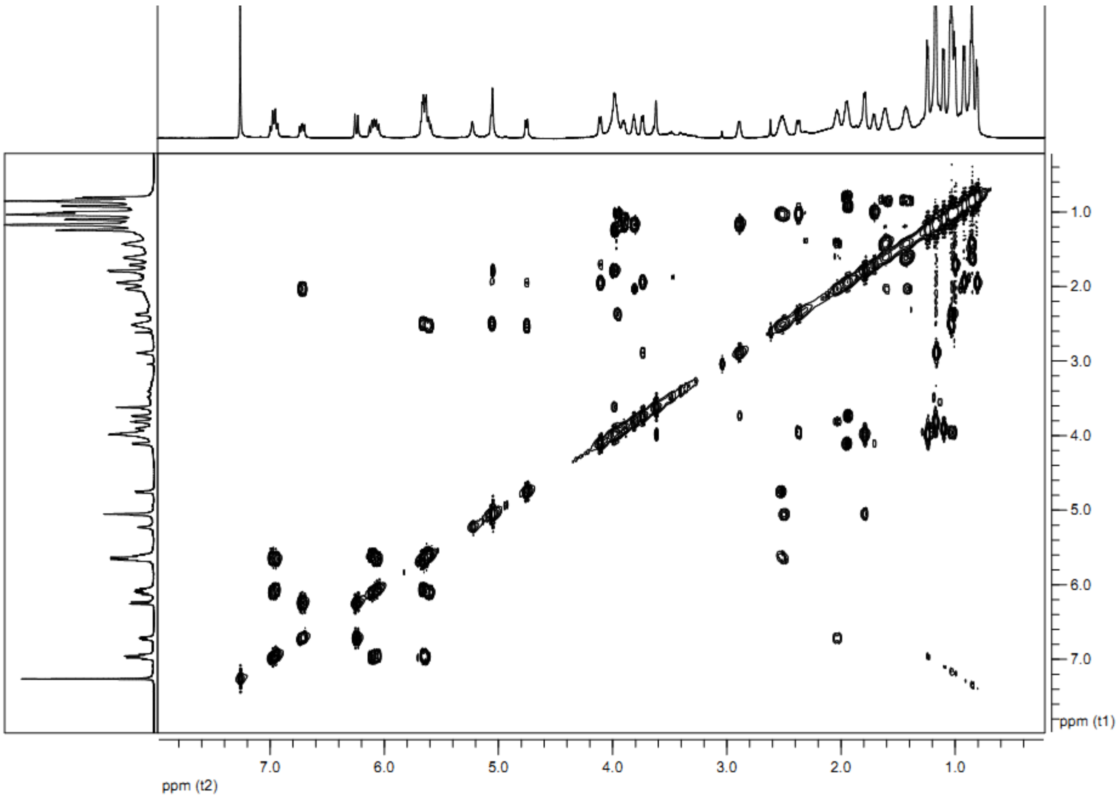

FIG AS39 ^{1}H-^{13}C-HSQC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10763**

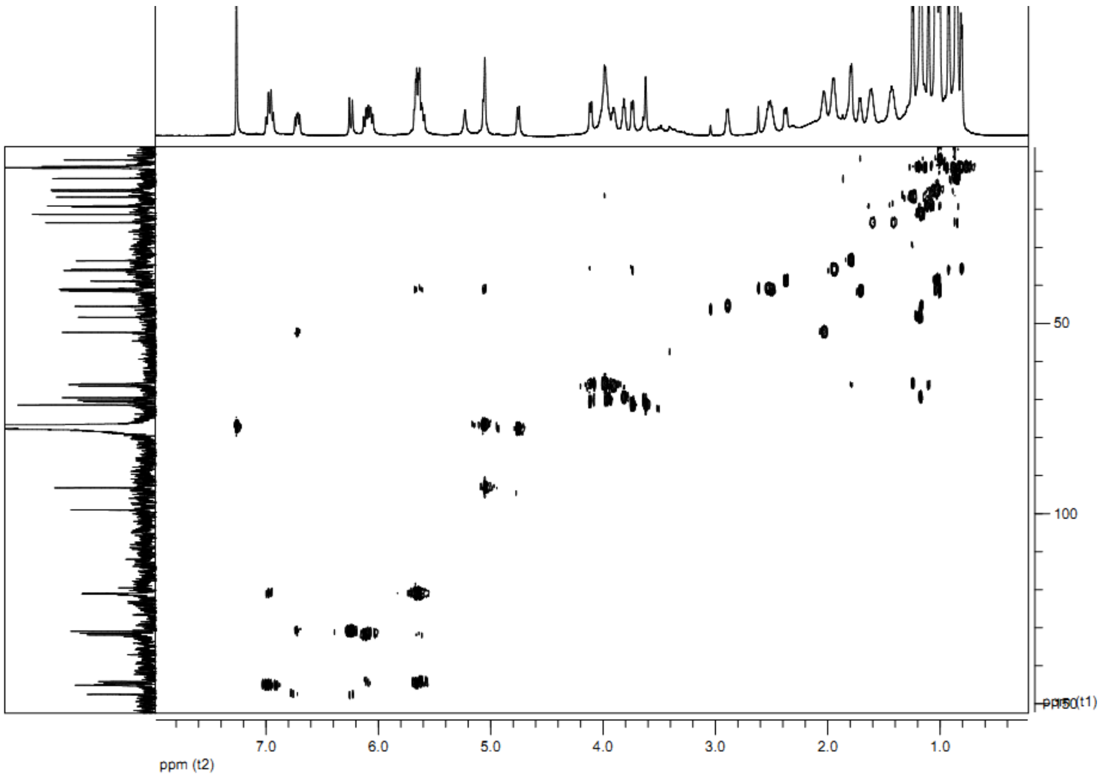

FIG AS40 ^{1}H-^{13}C-HMBC spectrum (600 × 150 MHz, *CDCl$_3$*) of **FXJ10763**