

Supporting Information

Neoantimycins A and B, two unusual benzamido nine-membered dilactones from marine-derived *Streptomyces antibioticus* H12-15

Chen Hu¹, Shi-Wen Zhou¹, Fang Chen¹, Xin-Heng Zheng¹, Hui-Fang Shen², Bi-Run Lin² and
Guang-Xiong Zhou^{1,*}

¹ College of Pharmacy, Jinan University, Guangzhou 510632, China; kitten_hc@163.com (C.H.);
1240097288@qq.com (S.-W. Z.); 1415010302@qq.com (F. C.); 916648282@qq.com (X.-H. Z.)

² Institute of Plant Protection, Guangdong Academy of Agricultural Sciences, Guangzhou 510632, China;
shenhf@gdppri.com (H.-F.S.); linbr@126.com (B.-R.L.)

* Correspondence: guangxzh@sina.com; Tel.: +86-20-8522-1469; Fax: +86-20-8522-1559

Contents

Table S1. 1D and 2D NMR data of 1 (δ in ppm) in CDCl_3	4
Table S2. 1D and 2D NMR data of 2 (δ in ppm) in CDCl_3	5
Table S3. B3LYP-Calculated relative energies (kcal mol^{-1}) and conformational population (%) for the most stable conformers of $(3R,4S,7R,8R,9S,2''S)$ - 1	6
Table S4. Coordinates of computations ($(3R,4S,7R,8R,9S,2''S)$ - 1)	6
Table S5. B3LYP-Calculated relative energies (kcal mol^{-1}) and conformational population (%) for the most stable conformers of $(3R,4S,7R,8R,9S,2''R)$ - 1	10
Table S6. Coordinates of computations ($(3R,4S,7R,8R,9S,2''R)$ - 1)	10
Table S7. 2D Structure of compound 1	12
Figure S1. B3LYP/6-31 G optimized lowest energy 3D conformer of 1	14
Figure S2. Experimental ECD spectra of 1 and calculated ECD spectra for $(3R,4S,7R,8R,9S,2''S)$ - 1 and $(3R,4S,7R,8R,9S,2''R)$ - 1	14
The spectra of neoantimycin A (1)	15
Figure S3. IR spectrum of compound 1	15
Figure S4. CD spectrum and UV spectrum of compound 1 in MeOH.	16
Figure S5. HR-TOF-MS of compound 1	17
Figure S6. The ^1H -NMR spectrum of compound 1	17
Figure S7. The ^1H -NMR spectrum of compound 1	18
Figure S8. The ^{13}C -NMR spectrum of compound 1	18
Figure S9. The ^{13}C -NMR and DEPT spectra of compound 1	19
Figure S10. The ^1H - ^1H COSY spectrum of compound 1	19
Figure S11. The HSQC spectrum of compound 1	20
Figure S12. The HMBC spectrum of compound 1	20
The spectra of neoantimycin B (2)	21
Figure S15. CD spectrum and UV spectrum of compound 2 in MeOH.	22
Figure S16. HR-TOF-MS of compound 2	22
Figure S17. The ^1H -NMR spectrum of compound 2	23
Figure S19. The ^{13}C -NMR spectrum of compound 2	24
Figure S20. The ^{13}C -NMR and DEPT spectra of compound 2	24
Figure S21. The ^1H - ^1H COSY spectrum of compound 2	25

Figure S22. The HSQC spectrum of compound 2	25
Figure S23. The HMBC spectrum of compound 2	26
Figure S24. The NOESY spectrum of compound 2	26
Figure S25. Phylogenetic tree of H12-15.	28
Figure S26. 16S rDNA gene sequence of H12-15.	29
Figure S27. Scanning electron micrographs of strain H12-15 on Gauze No.1 medium	29

Table S1. 1D and 2D NMR data of **1** (δ in ppm) in CDCl₃.

No.	δ_c	δ_H (J in Hz)	¹ H- ¹ H COSY	HMBC	NOE
2	170.8	-	-	-	-
3	54.2	5.34, t, 7.8	H-4, 7'-NH	C-2, 4, 11	H-4, H-8
4	71.5	5.75, p, 6.7	H-3, H-11	C-2, 3, 6, 11	H-3, H-8
6	173.2	-	-	-	-
7	50.3	2.50, m	H-8, H-1'''	C-6, 8, 1'', 2''	H-9
8	75.6	5.09, t, 9.9	H-7, H-9	C-7, 9, 10, 1'', 1'''	H-3, H-4
9	74.6	4.99, m	H-8, H-10	C-7, 8, 11	H-7
10	18.0	1.28, d, 6.1	H-9	C-2, 8, 9	-
11	15.2	1.32, d, 6.7	H-4	2-2, 3	-
1'	133.4	-	-	-	-
2'	127.3	7.82, d, 7.7	H-3'	C-1', 3', 4', 7'	-
3'	128.9	7.47, t, 7.7	H-2', H-4'	C-1', 2', 4', 5'	-
4'	132.3	7.55, t, 7.4	H-3', H-5'	C-2', 3', 5', 6'	-
5'	128.9	7.47, t, 7.7	H-4', H-6'	C-1', 3', 4', 6'	-
6'	127.3	7.82, d, 7.7	H-5'	C-1', 4', 5', 7'	-
7'	167.0	-	-	-	-
		1.67, m			-
1''	28.6	1.25, m	H-7, H-2''	C-6, 8	-
2''	22.6	1.25, m	H-1'', H-3''	-	-
3''	27.1	1.25, m	H-2'', H-4''	-	-
4''	31.6	1.25, m	H-3'', H-5''	-	-
5''	29.1	1.25, m	H-4'', H-6''	-	-
6''	14.2	0.85, t, 6.6	H-5''	C-4'', 5''	-
1'''	175.4	-	-	-	-
2'''	41.4	2.41, dt, 10.6, 5.3	H-3''', H-5'''	C-1''', 3''', 4''', 5'''	-
		1.71, m			-
3'''	26.6	1.49, m	H-2''', H-4'''	C-1''', 2''', 4''', 5'''	-
4'''	11.9	0.94, t, 7.4	H-3'''	C-2''', 3'''	-
5'''	16.9	1.18, d, 7.0	H-2'''	C-1''', 2''', 3'''	-
7'-NH	-	6.86, d, 7.8	H-2	C-2, 7'	-

Table S2. 1D and 2D NMR data of **2** (δ in ppm) in CDCl₃.

No.	δ_c	δ_H (J in Hz)	¹ H- ¹ H COSY	HMBC	NOE
2	170.8	-	-	-	-
3	54.2	5.34, t, 7.8	H-4, 7'-NH	C-2, 4, 11	H-4, H-8
4	71.5	5.75, p, 6.8	H-3, H-11	C-2, 3, 6, 11	H-3, H-8
6	173.2	-	-	-	-
7	50.3	2.52, m	H-8, H-1'''	C-6, 8, 1'', 2''	H-9
8	75.6	5.08, t, 9.9	H-7, H-9	C-7, 9, 10, 1'', 1'''	H-3, H-4
9	74.6	5.00, m	H-8, H-10	C-7, 8, 11	H-7
10	18.0	1.28, d, 6.5	H-9	C-2, 8, 9	-
11	15.2	1.32, d, 6.7	H-4	C-2, 3	-
1'	133.4	-	-	-	-
2'	127.3	7.82, d, 7.4	H-3'	C-1', 3', 4', 7'	-
3'	128.9	7.47, t, 7.7	H-2', H-4'	C-1', 2', 4', 5'	-
4'	132.3	7.55, t, 7.4	H-3', H-5'	C-2', 3', 5', 6'	-
5'	128.9	7.47, t, 7.7	H-4', H-6'	C-1', 3', 4', 6'	-
6'	127.3	7.82, d, 7.4	H-5'	C-1', 4', 5', 7'	-
7'	167.0	-	-	-	-
		1.66, m			-
1''	28.6	1.25, m	H-7, H-2''	C-6, 8	-
2''	22.6	1.25, m	H-1'', H-3''	-	-
3''	27.1	1.25, m	H-2'', H-4''	-	-
4''	31.6	1.25, m	H-3'', H-5''	-	-
5''	29.1	1.25, m	H-4'', H-6''	-	-
6''	14.2	0.86, t, 6.8	H-5''	C-4'', 5''	-
1'''	175.7	-	-	-	-
2'''	34.3	2.61, t, 7.0	H-3''', H-5'''	C-1''', 3''', 4'''	-
3'''	19.1	1.22, d, 2.5	H-2''', H-4'''	C-1''', 2''', 4'''	-
4'''	19.1	1.21, d, 2.5	H-2''', H-3'''	C-2''', 3'''	-
7'-NH	-	6.86, d, 7.8	H-2	C-2, 7'	-

Table S3. B3LYP-Calculated relative energies (kcal mol⁻¹) and conformational population (%) for the most stable conformers of (3*R*,4*S*,7*R*,8*R*,9*S*,2''*S*)-1.

Conformers	Rel. E	Percent (%)
1-a	0	58.46%
1-b	0.239705	39.00%
1-c	2.579025	0.75%
1-d	2.582163	0.75%
1-e	2.756607	0.56%
1-f	2.826260	0.49%
1-g	3.123695	0.30%
1-h	3.177660	0.27%
1-i	3.202760	0.26%
1-j	3.371557	0.20%
1-k	3.384735	0.19%
1-l	3.519020	0.15%
1-m	3.567965	0.14%
1-n	3.763745	0.10%
1-o	3.935052	0.08%

Table S4. Coordinates of computations ((3*R*,4*S*,7*R*,8*R*,9*S*,2''*S*)-1)

Conformer 1-a

Standard orientation:					
Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	6	0	-6.366453	0.356599	-0.229171
2	6	0	-7.379725	0.693531	-1.139236
3	6	0	-8.721485	0.531648	-0.795832
4	6	0	-9.068459	0.041184	0.467093
5	6	0	-8.066109	-0.284736	1.384750
6	6	0	-6.721988	-0.129672	1.038944
7	6	0	-4.946535	0.562165	-0.679845
8	7	0	-3.964676	-0.042257	0.054049
9	8	0	-4.671567	1.248826	-1.665850
10	6	0	-2.572343	0.033430	-0.337409
11	6	0	-1.849128	1.377274	0.106034
12	8	0	-0.503679	1.046848	0.550592
13	6	0	0.460416	0.856082	-0.389945

14	6	0	1.664009	0.124689	0.203588
15	6	0	1.627526	-1.370666	-0.224370
16	8	0	0.365988	1.215382	-1.542361
17	6	0	0.361662	-2.145820	0.206875
18	8	0	-0.737481	-1.438186	-0.433480
19	6	0	-1.840059	-1.152499	0.279639
20	8	0	-2.184760	-1.722162	1.295026
21	6	0	0.336632	-3.603030	-0.233804
22	8	0	2.742846	-2.018335	0.433449
23	6	0	3.641880	-2.715499	-0.320999
24	6	0	4.724487	-3.335167	0.552423
25	6	0	6.089963	-3.322094	-0.158377
26	8	0	3.552435	-2.843397	-1.523007
27	6	0	6.652362	-1.918646	-0.411713
28	6	0	4.295189	-4.770804	0.927521
29	6	0	2.970388	0.814963	-0.237727
30	6	0	3.105311	2.252443	0.286055
31	6	0	4.432976	2.912484	-0.112663
32	6	0	4.562888	4.360934	0.377414
33	6	0	5.890560	5.025619	-0.012203
34	6	0	6.005811	6.476299	0.470837
35	6	0	-2.512580	2.094122	1.269112
36	1	0	-7.092083	1.082583	-2.110697
37	1	0	-9.496909	0.790331	-1.512152
38	1	0	-10.114198	-0.081625	0.737140
39	1	0	-8.328437	-0.654885	2.372341
40	1	0	-5.964640	-0.369655	1.780817
41	1	0	-4.181996	-0.670296	0.817542
42	1	0	-2.504526	-0.030959	-1.426257
43	1	0	-1.775691	2.026800	-0.767178
44	1	0	1.579068	0.160367	1.296525
45	1	0	1.757323	-1.452875	-1.306896
46	1	0	0.227082	-2.069041	1.290149
47	1	0	0.442551	-3.684429	-1.320509
48	1	0	-0.610654	-4.060139	0.067784
49	1	0	1.148873	-4.162675	0.238744
50	1	0	4.784939	-2.742549	1.473688
51	1	0	5.998843	-3.863029	-1.108144
52	1	0	6.793265	-3.889900	0.465428
53	1	0	6.003560	-1.340259	-1.079505
54	1	0	7.640132	-1.975939	-0.883480
55	1	0	6.764462	-1.357873	0.525439
56	1	0	4.195667	-5.394360	0.031700
57	1	0	3.340744	-4.780053	1.465434

58	1	0	5.050947	-5.225344	1.577814
59	1	0	3.816162	0.220997	0.126267
60	1	0	3.017872	0.814667	-1.333854
61	1	0	2.275394	2.864223	-0.094048
62	1	0	3.015414	2.251908	1.383027
63	1	0	5.269853	2.317480	0.283773
64	1	0	4.532880	2.890126	-1.208122
65	1	0	4.453610	4.386361	1.472698
66	1	0	3.728995	4.955215	-0.026108
67	1	0	6.002795	4.994769	-1.105817
68	1	0	6.724463	4.436422	0.396928
69	1	0	5.931379	6.537948	1.564381
70	1	0	5.206168	7.098876	0.049177
71	1	0	6.964136	6.921129	0.176735
72	1	0	-2.600786	1.443056	2.145473
73	1	0	-1.908386	2.965285	1.542709
74	1	0	-3.508972	2.442327	0.985815

Conformer 1-b

Standard orientation:

Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	6	0	-6.332634	0.362910	-0.313724
2	6	0	-6.781908	-0.824866	0.281115
3	6	0	-8.136128	-1.000456	0.565103
4	6	0	-9.051982	0.007742	0.258702
5	6	0	-8.611827	1.188890	-0.344174
6	6	0	-7.260815	1.362820	-0.633834
7	6	0	-4.894653	0.627521	-0.655049
8	7	0	-3.961128	-0.135941	-0.009694
9	8	0	-4.561963	1.491540	-1.464828
10	6	0	-2.551019	-0.009506	-0.304815
11	6	0	-1.877928	1.310183	0.260158
12	8	0	-0.521434	0.988855	0.673125
13	6	0	0.425564	0.855908	-0.292925
14	6	0	1.661709	0.144755	0.257106
15	6	0	1.637683	-1.351369	-0.165886
16	8	0	0.295790	1.241464	-1.431820
17	6	0	0.388880	-2.139294	0.287836
18	8	0	-0.713144	-1.476740	-0.389663
19	6	0	-1.832753	-1.205628	0.305564
20	8	0	-2.194017	-1.785306	1.307201

21	6	0	0.398903	-3.613317	-0.092177
22	8	0	2.782054	-1.973324	0.461181
23	6	0	3.640793	-2.688310	-0.323152
24	6	0	4.789976	-3.246465	0.505729
25	6	0	6.064542	-3.384728	-0.343360
26	8	0	3.475290	-2.872673	-1.507925
27	6	0	6.637312	-2.049207	-0.828563
28	6	0	4.352548	-4.598593	1.108316
29	6	0	2.937389	0.854506	-0.235503
30	6	0	3.083199	2.282886	0.306938
31	6	0	4.378904	2.968255	-0.146683
32	6	0	4.526927	4.398207	0.388055
33	6	0	5.820773	5.090855	-0.059074
34	6	0	5.958468	6.518517	0.479408
35	6	0	-2.560017	1.879574	1.492120
36	1	0	-6.088173	-1.633449	0.495367
37	1	0	-8.476066	-1.927529	1.018401
38	1	0	-10.106516	-0.129939	0.482256
39	1	0	-9.323092	1.972514	-0.590544
40	1	0	-6.897937	2.266253	-1.112719
41	1	0	-4.202664	-0.715530	0.783125
42	1	0	-2.407523	-0.013650	-1.387125
43	1	0	-1.836391	2.041830	-0.547054
44	1	0	1.616229	0.179908	1.351958
45	1	0	1.739490	-1.434521	-1.251083
46	1	0	0.241517	-2.025326	1.366119
47	1	0	0.531749	-3.738773	-1.170989
48	1	0	-0.548269	-4.070251	0.208196
49	1	0	1.208479	-4.137685	0.422863
50	1	0	4.969793	-2.546522	1.331082
51	1	0	5.842689	-4.026064	-1.204293
52	1	0	6.815753	-3.909768	0.260917
53	1	0	5.927507	-1.526889	-1.478883
54	1	0	7.557048	-2.205543	-1.402745
55	1	0	6.880167	-1.388627	0.013274
56	1	0	4.122047	-5.320568	0.316869
57	1	0	3.467848	-4.485597	1.743558
58	1	0	5.159231	-5.012958	1.722276
59	1	0	3.806628	0.262202	0.071059
60	1	0	2.924087	0.874970	-1.331947
61	1	0	2.226024	2.888674	-0.017269
62	1	0	3.050011	2.260821	1.406433
63	1	0	5.241944	2.367128	0.176587
64	1	0	4.414050	2.985193	-1.245691

65	1	0	4.486814	4.381506	1.487665
66	1	0	3.664006	4.997965	0.062551
67	1	0	5.860516	5.108437	-1.157457
68	1	0	6.683350	4.491733	0.266230
69	1	0	5.957636	6.530585	1.576454
70	1	0	5.128060	7.150953	0.142005
71	1	0	6.890822	6.985581	0.142114
72	1	0	-2.639636	1.129155	2.285659
73	1	0	-1.972195	2.721762	1.869586
74	1	0	-3.559199	2.242340	1.241516

Table S5. B3LYP-Calculated relative energies (kcal mol⁻¹) and conformational population (%) for the most stable conformers of (3*R*,4*S*,7*R*,8*R*,9*S*,2''*R*)-1.

Conformers	Rel. E	Percent (%)
1-a	0	81.17
1-b	1.714957	4.48
1-c	1.736292	4.32
1-d	1.787747	3.96
1-e	1.910110	3.22
1-f	1.986665	2.83
1-g	1.988547	2.82
1-h	2.262137	1.78
1-i	2.423405	1.35
1-j	2.956152	0.55

Table S6. Coordinates of computations ((3*R*,4*S*,7*R*,8*R*,9*S*,2''*R*)-1)

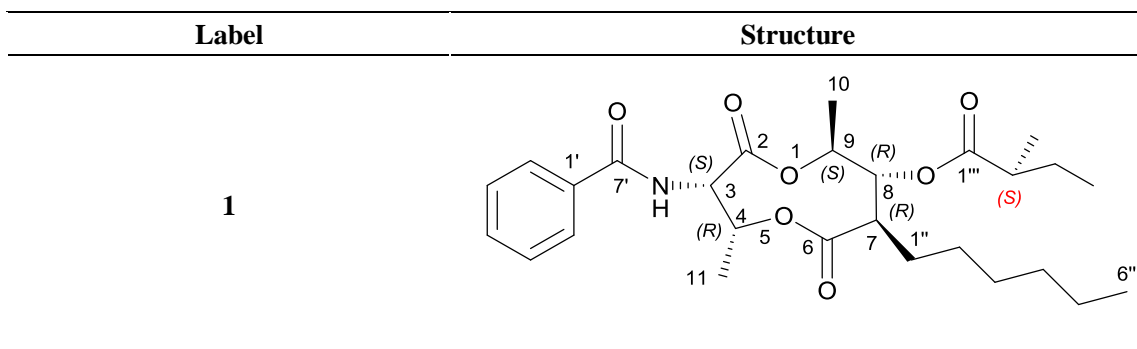
Conformer 2-a

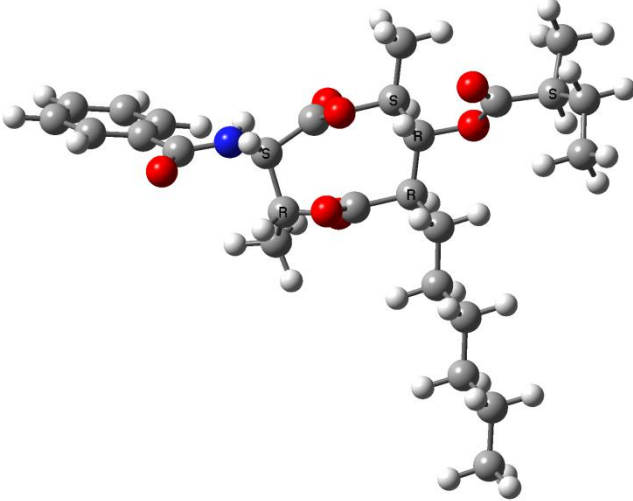
Standard orientation:					
Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	6	0	-6.146977	-0.128755	-0.310721
2	6	0	-7.160333	0.800115	-0.583149
3	6	0	-8.494287	0.477633	-0.346802
4	6	0	-8.831407	-0.782142	0.154678
5	6	0	-7.829282	-1.719272	0.413043
6	6	0	-6.492486	-1.395497	0.181791
7	6	0	-4.734579	0.297492	-0.590297
8	7	0	-3.744004	-0.429124	0.011583
9	8	0	-4.471475	1.255606	-1.315166

10	6	0	-2.347304	-0.145348	-0.233631
11	6	0	-1.815572	1.171510	0.470002
12	8	0	-0.426302	0.960964	0.845573
13	6	0	0.512391	1.011564	-0.136172
14	6	0	1.830985	0.401166	0.340309
15	6	0	1.946327	-1.068072	-0.157711
16	8	0	0.318762	1.470805	-1.238226
17	6	0	0.783098	-1.997800	0.252108
18	8	0	-0.377005	-1.420158	-0.405069
19	6	0	-1.526286	-1.316338	0.287111
20	8	0	-1.840005	-2.007383	1.232669
21	6	0	0.950589	-3.445014	-0.188632
22	8	0	3.140514	-1.624135	0.438384
23	6	0	4.099277	-2.136046	-0.388426
24	6	0	5.301965	-2.621641	0.409495
25	6	0	5.930083	-3.863669	-0.245847
26	8	0	4.004033	-2.164585	-1.594650
27	6	0	5.019531	-5.095510	-0.251269
28	6	0	6.318541	-1.465461	0.521356
29	6	0	3.010577	1.257273	-0.157737
30	6	0	3.054580	2.659712	0.464993
31	6	0	4.240355	3.491278	-0.044040
32	6	0	4.389681	4.867493	0.628278
33	6	0	3.223182	5.849633	0.418336
34	6	0	2.982446	6.242759	-1.043993
35	6	0	-2.540949	1.523031	1.757224
36	1	0	-6.875710	1.767625	-0.983256
37	1	0	-9.272282	1.206822	-0.555751
38	1	0	-9.872335	-1.035766	0.336680
39	1	0	-8.087925	-2.706000	0.787190
40	1	0	-5.729261	-2.149196	0.356283
41	1	0	-3.943605	-1.095415	0.745754
42	1	0	-2.184227	-0.033065	-1.307109
43	1	0	-1.865760	1.985347	-0.253822
44	1	0	1.819217	0.377445	1.436374
45	1	0	2.052606	-1.084325	-1.245516
46	1	0	0.620334	-1.946849	1.333031
47	1	0	0.057151	-4.012833	0.085625
48	1	0	1.811226	-3.899323	0.310057
49	1	0	1.096124	-3.509804	-1.271624
50	1	0	4.951530	-2.872388	1.418068
51	1	0	6.857861	-4.094600	0.293429
52	1	0	6.213501	-3.608980	-1.273721
53	1	0	4.112587	-4.915152	-0.838707

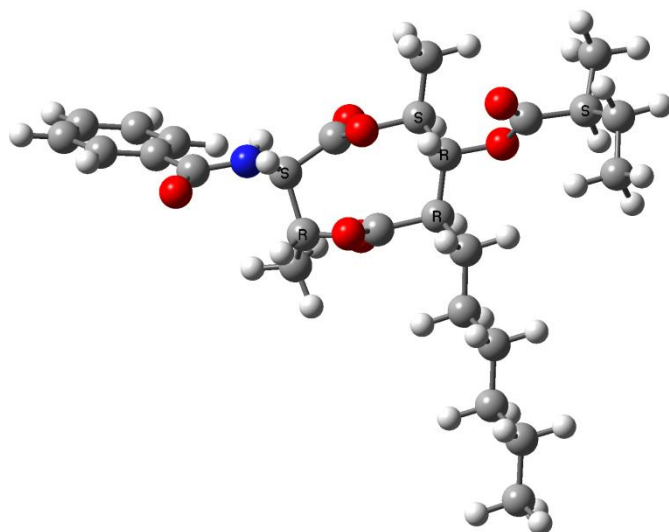
54	1	0	4.718442	-5.375476	0.766124
55	1	0	5.531406	-5.956991	-0.693834
56	1	0	6.660447	-1.153809	-0.471617
57	1	0	5.885097	-0.596039	1.026562
58	1	0	7.191639	-1.790777	1.097155
59	1	0	3.945735	0.734408	0.070728
60	1	0	2.942400	1.339536	-1.249020
61	1	0	2.115504	3.183339	0.245659
62	1	0	3.114417	2.572111	1.560423
63	1	0	5.167937	2.924314	0.120463
64	1	0	4.153720	3.613605	-1.132255
65	1	0	5.313326	5.336229	0.259566
66	1	0	4.534916	4.718404	1.708102
67	1	0	3.431118	6.756306	1.002473
68	1	0	2.300269	5.429043	0.839724
69	1	0	3.889838	6.665252	-1.494031
70	1	0	2.190476	6.996153	-1.122984
71	1	0	2.678569	5.384934	-1.654255
72	1	0	-2.049230	2.381474	2.224795
73	1	0	-3.578646	1.792575	1.548927
74	1	0	-2.523419	0.686251	2.463336

Table S7. 2D Structure of compound **1**.



Label	Conformer	Boltzmann weighting factors
1-a	 A 3D ball-and-stick model of a complex organic molecule. The structure features a central sulfur atom (S) bonded to a nitrogen atom (N) and two oxygen atoms (O). The nitrogen atom is further bonded to a carbon chain. The oxygen atoms are part of a cyclic or chain-like structure. The molecule is shown in a perspective view, with atoms represented by spheres of different colors: carbon (grey), hydrogen (white), sulfur (yellow), nitrogen (blue), and oxygen (red).	58.46%

1-b



39.00%

Figure S1. B3LYP/6-31 G optimized lowest energy 3D conformer of **1**.

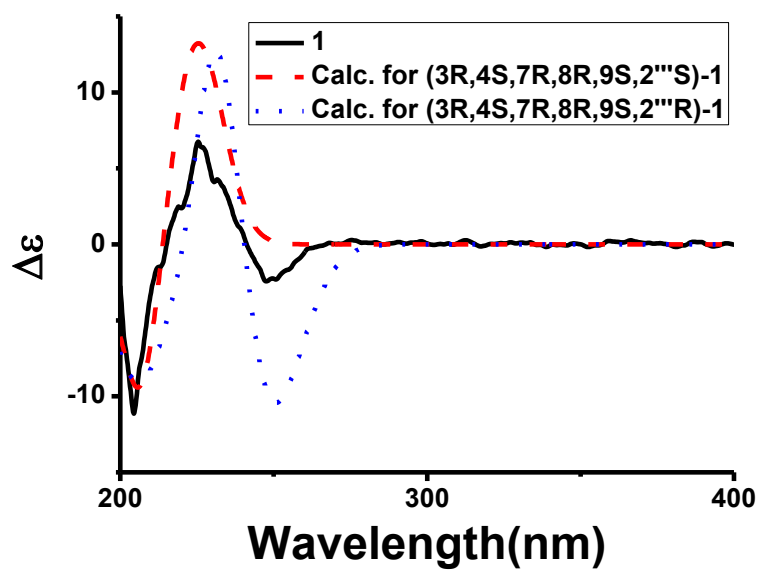


Figure S2. Experimental ECD spectra of **1** and calculated ECD spectra for $(3R,4S,7R,8R,9S,2'''S)$ -**1** and $(3R,4S,7R,8R,9S,2'''R)$ -**1**.

The spectra of neoantimycin A (1)

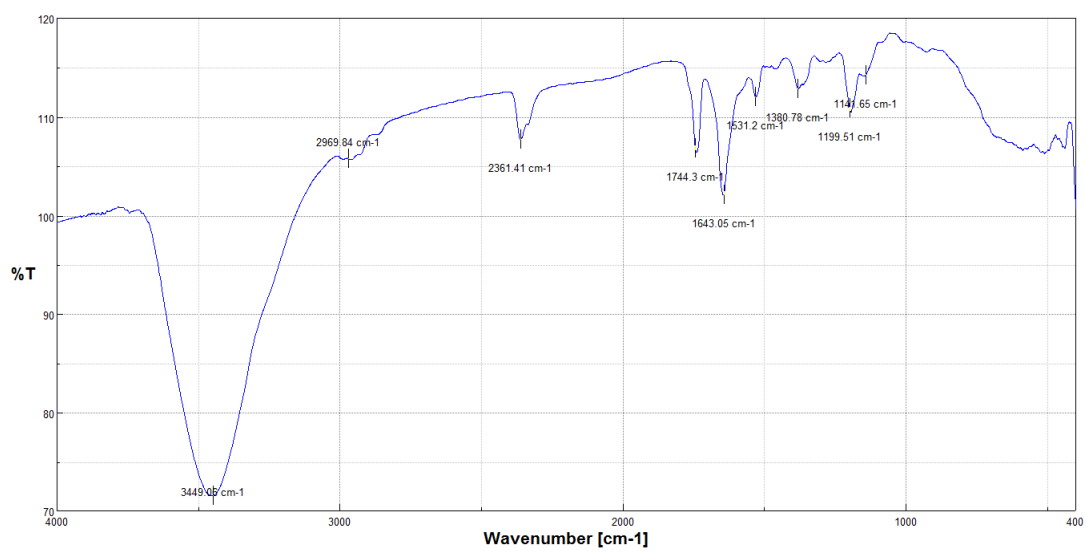


Figure S3. IR spectrum of compound 1.

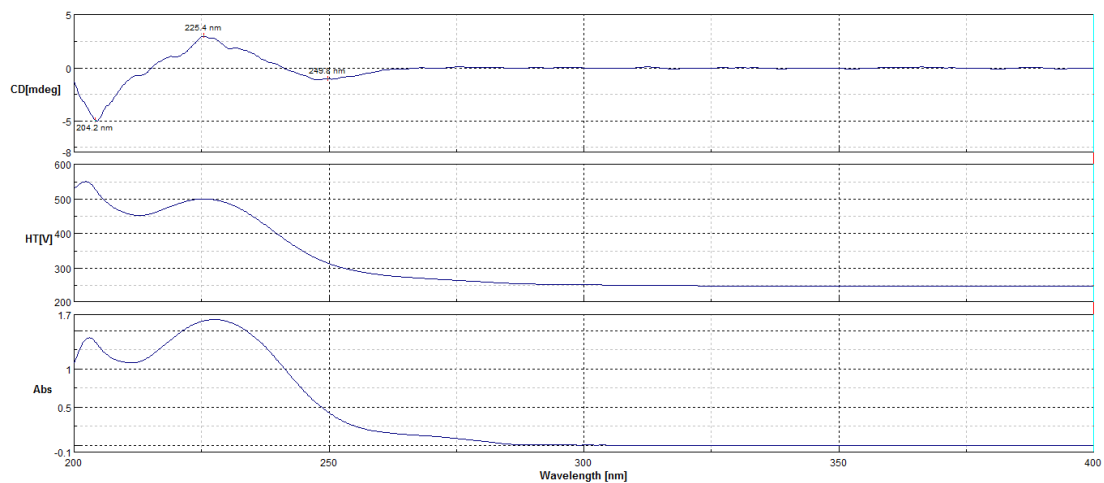


Figure S4. CD spectrum and UV spectrum of compound **1** in MeOH.

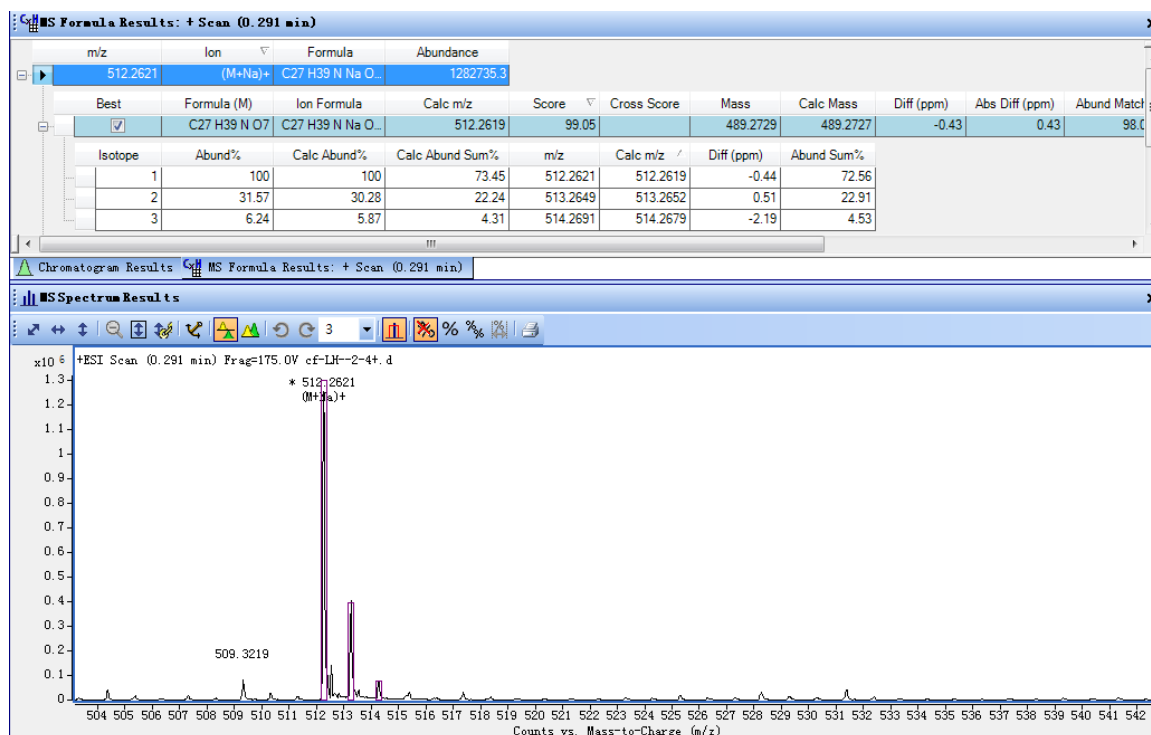


Figure S5. HR-TOF-MS of compound 1.

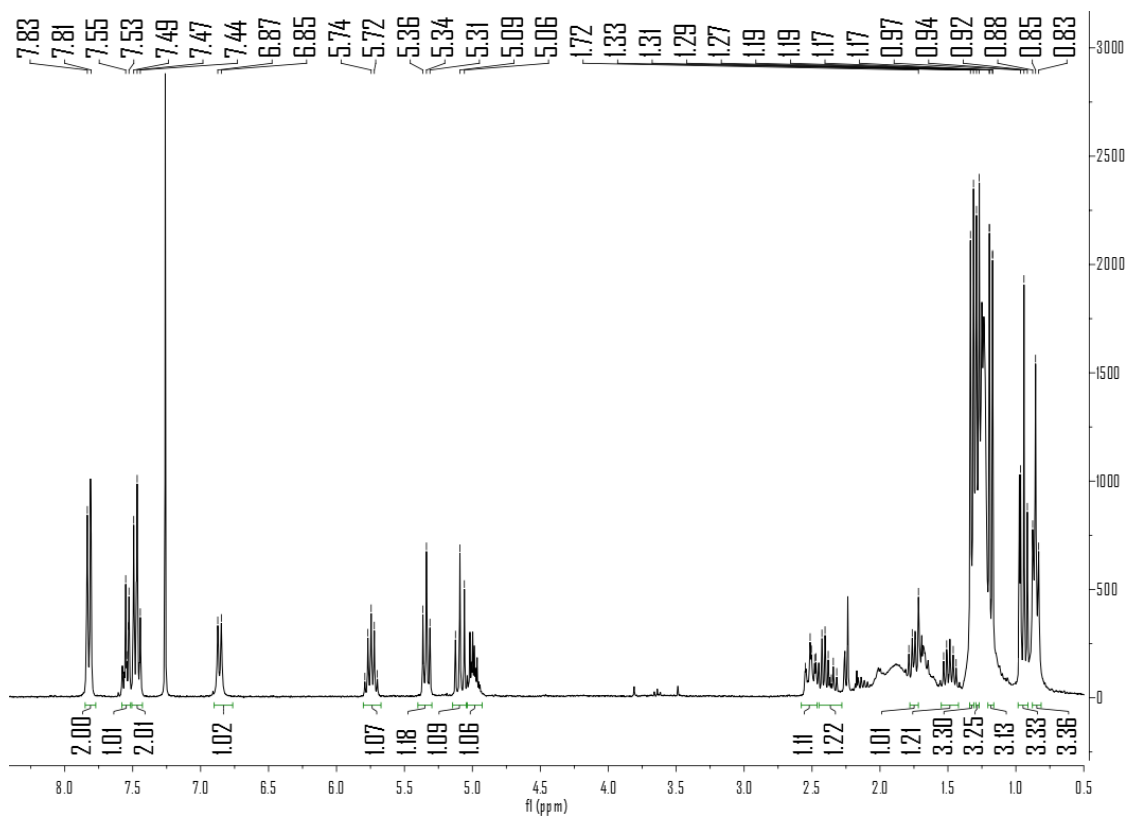


Figure S6. The ¹H-NMR spectrum of compound 1.

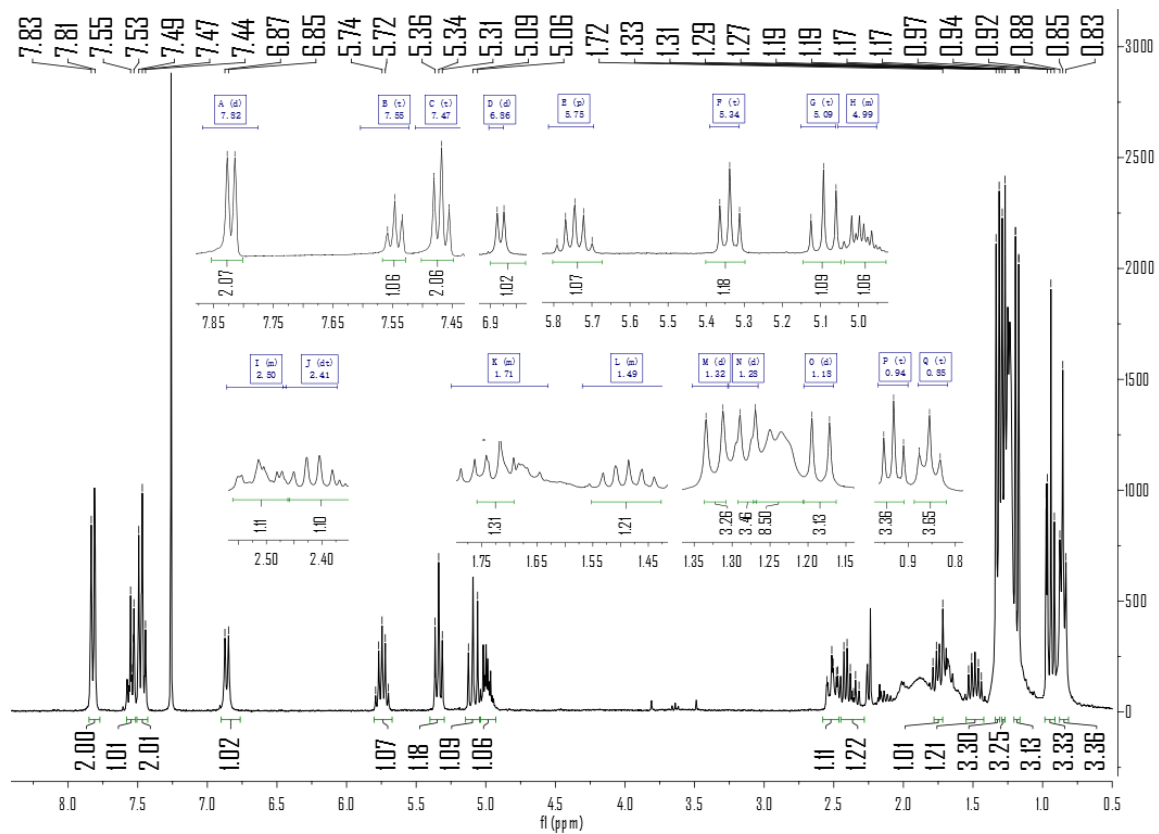


Figure S7. The ^1H -NMR spectrum of compound **1**.

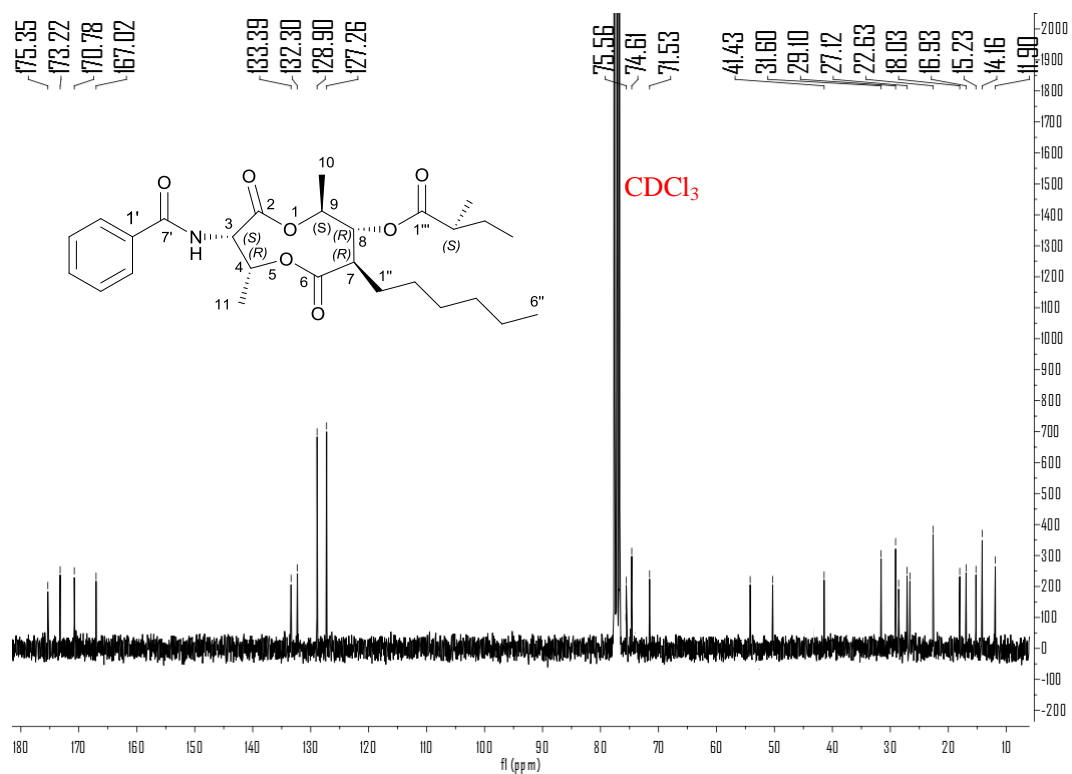


Figure S8. The ^{13}C -NMR spectrum of compound **1**.

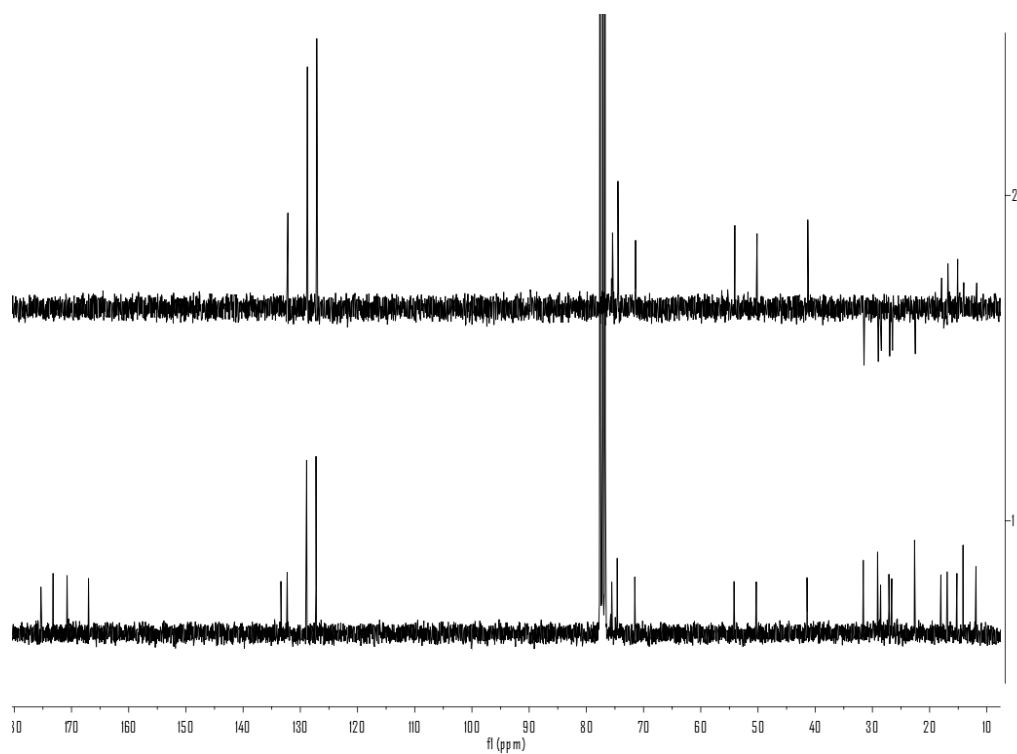


Figure S9. The ¹³C-NMR and DEPT spectra of compound **1**.

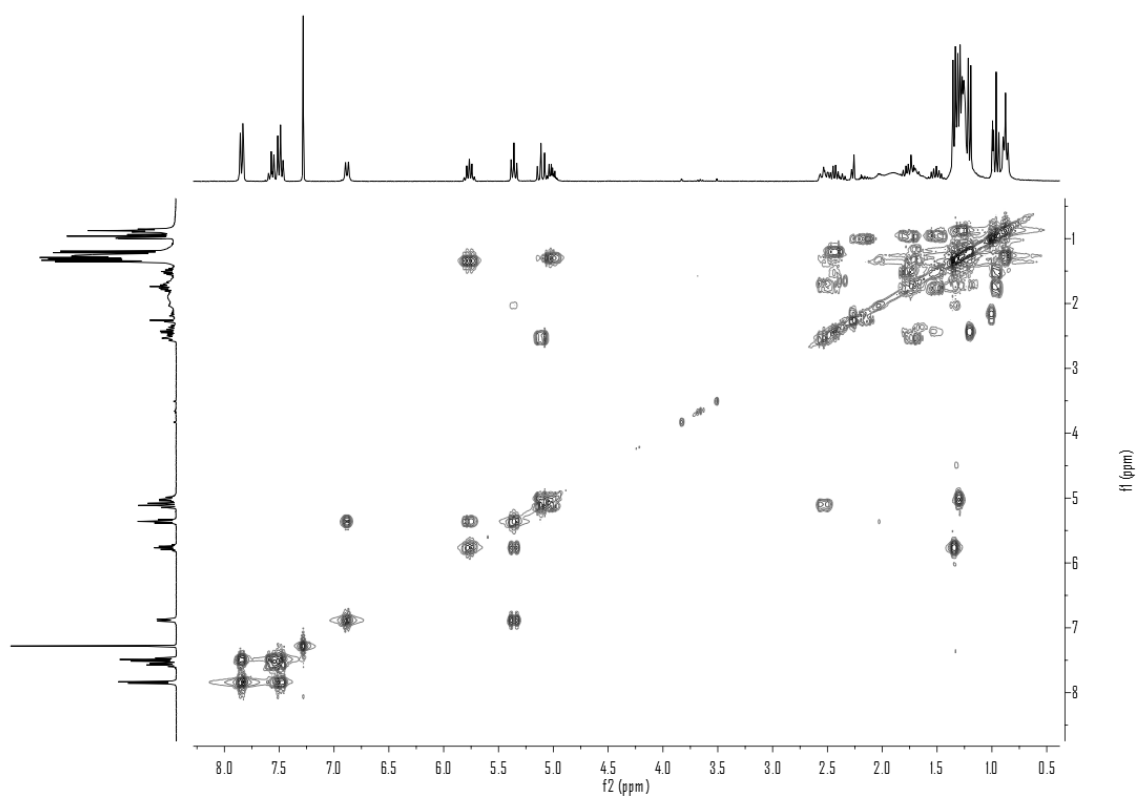


Figure S10. The ¹H-¹H COSY spectrum of compound **1**.

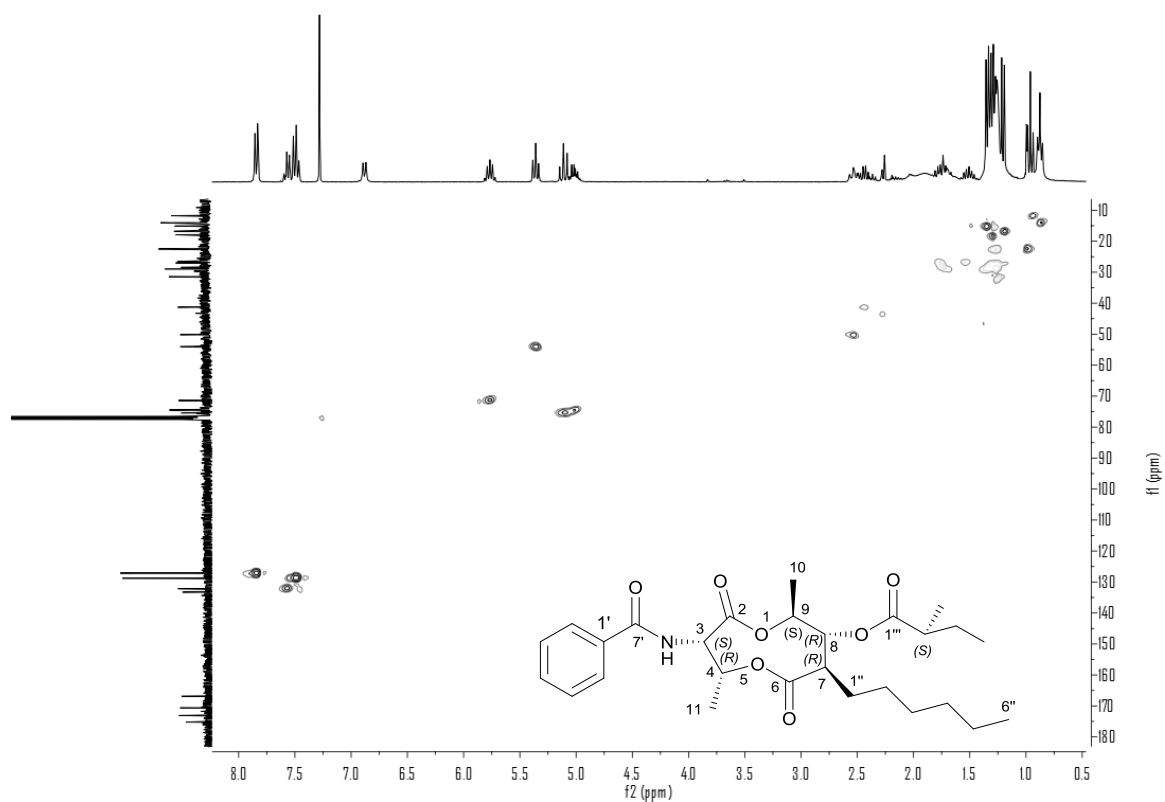


Figure S11. The HSQC spectrum of compound **1**.

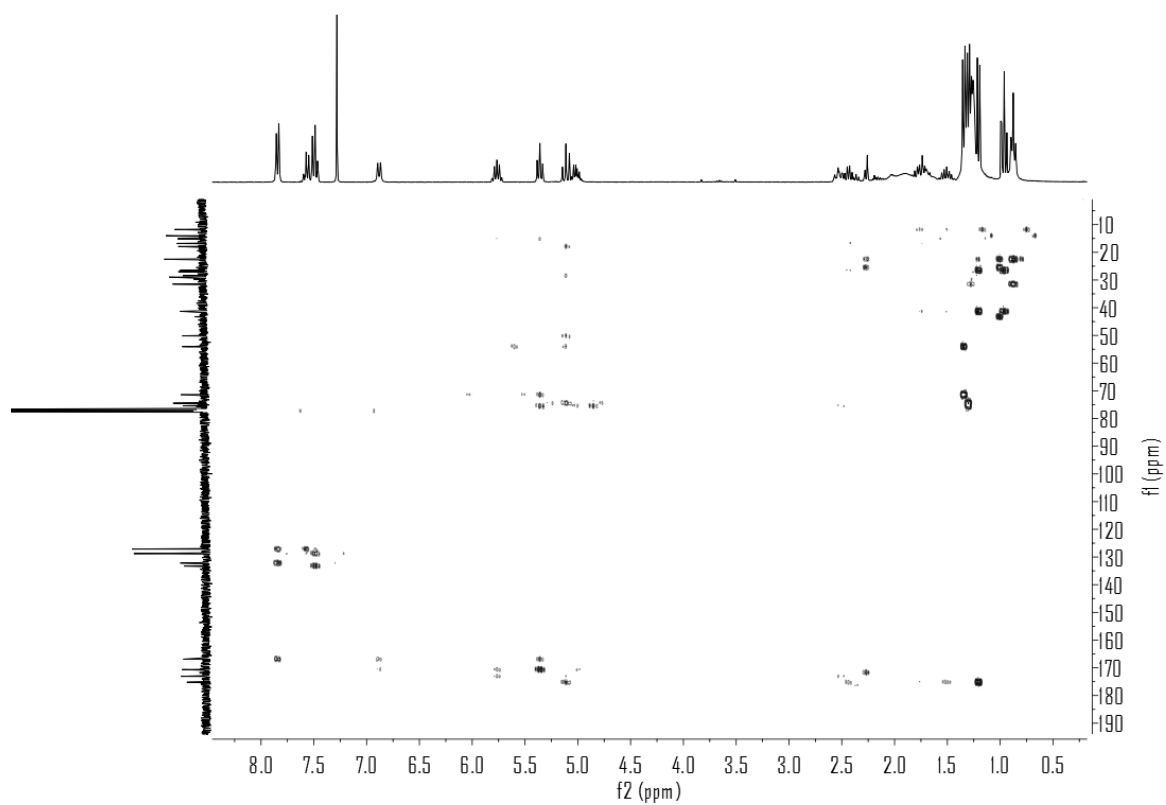


Figure S12. The HMBC spectrum of compound **1**.

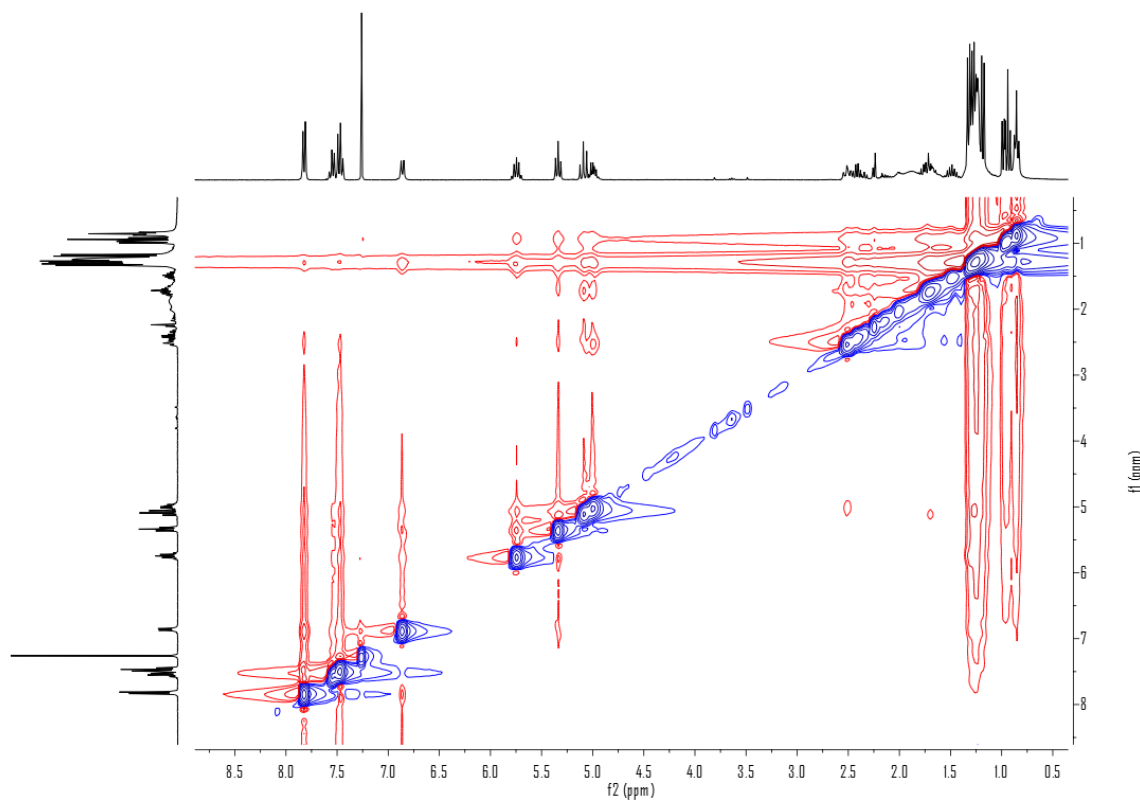


Figure S13. The NOESY spectrum of compound **1**.

The spectra of neoantimycin B (2)

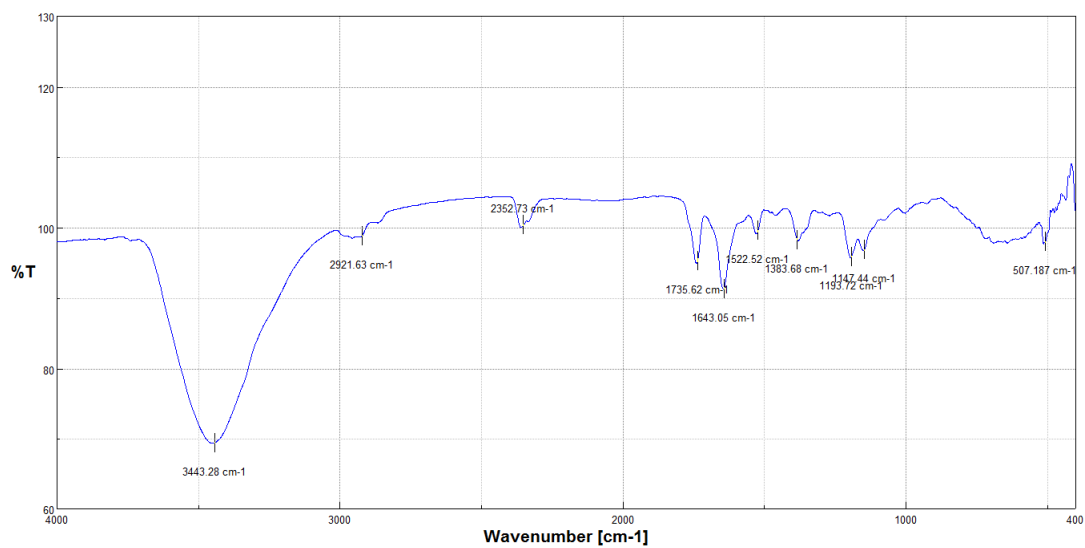


Figure S14. IR spectrum of compound **2**.

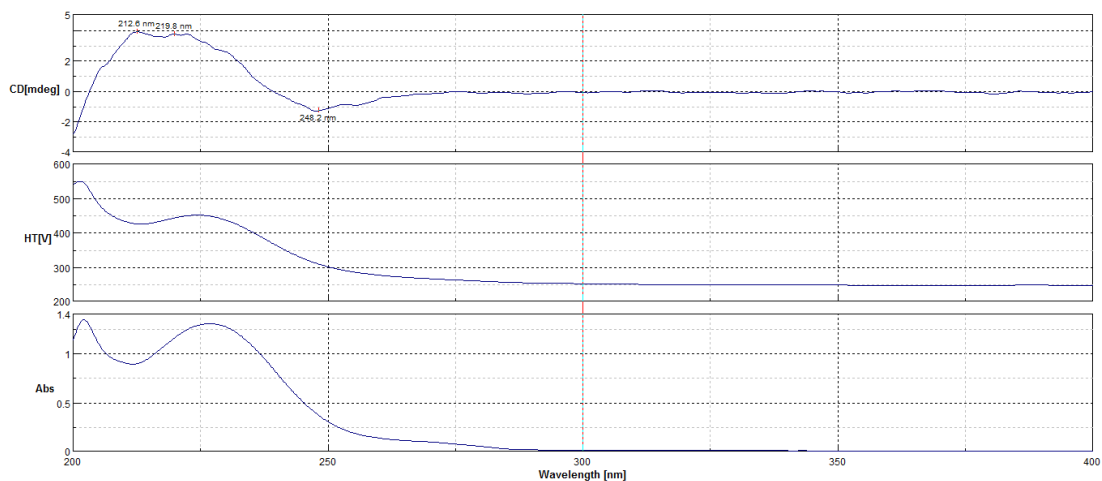


Figure S15. CD spectrum and UV spectrum of compound 2 in MeOH.

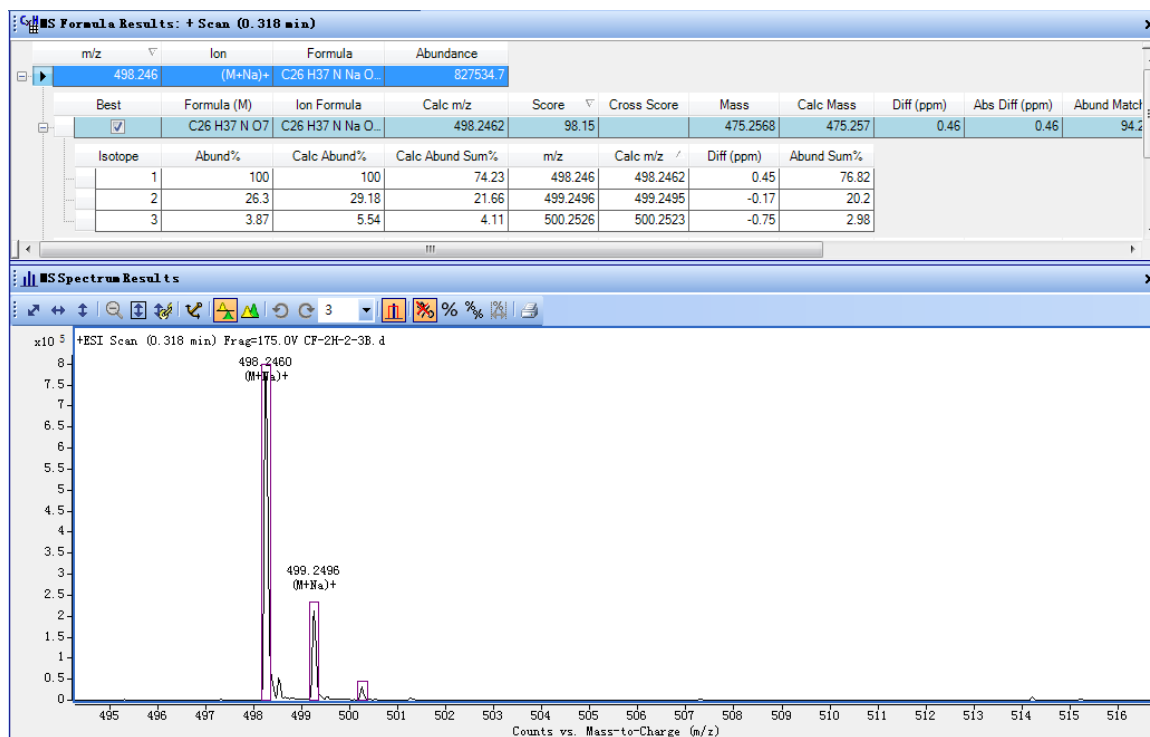


Figure S16. HR-TOF-MS of compound 2.

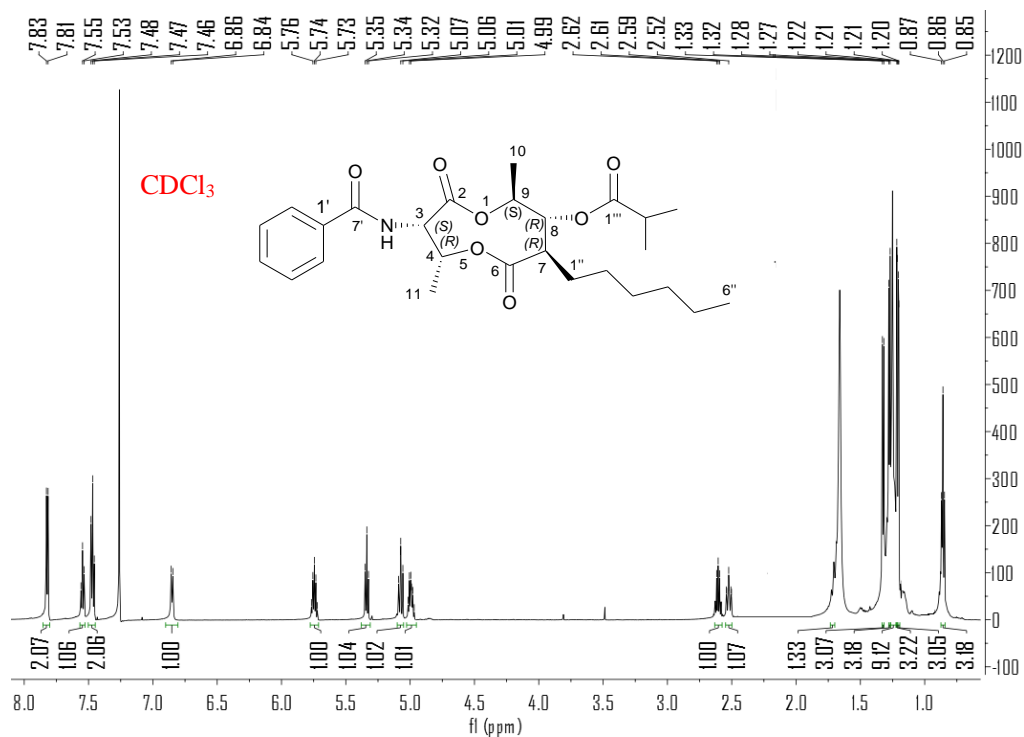


Figure S17. The $^1\text{H-NMR}$ spectrum of compound 2.

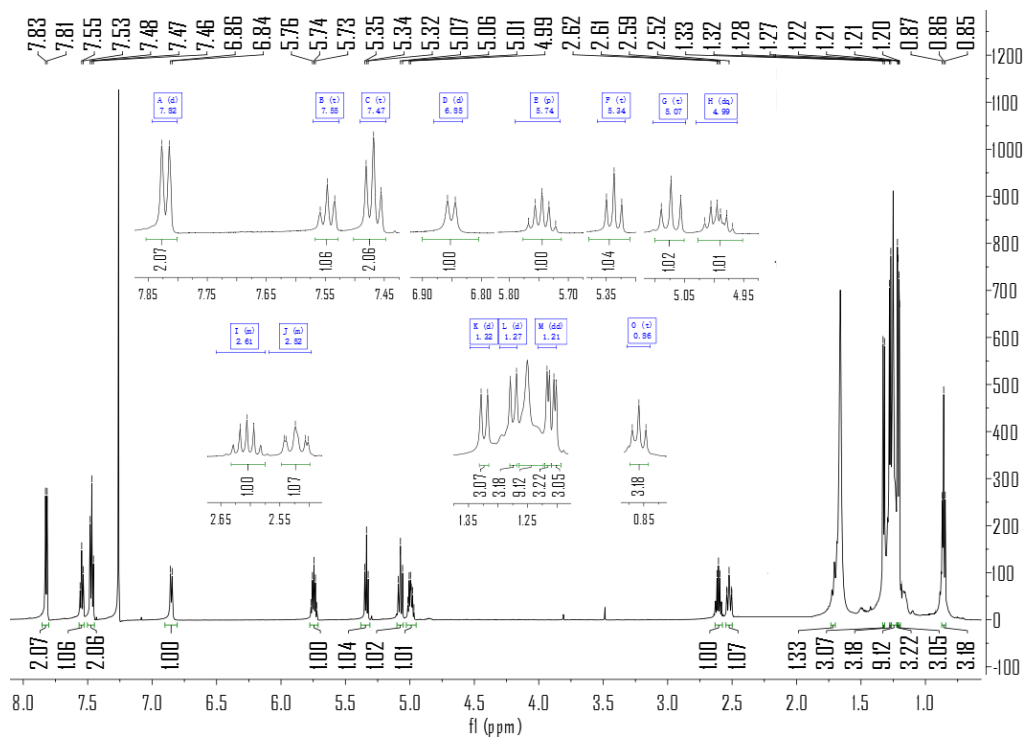


Figure S18. The $^1\text{H-NMR}$ spectrum of compound 2.

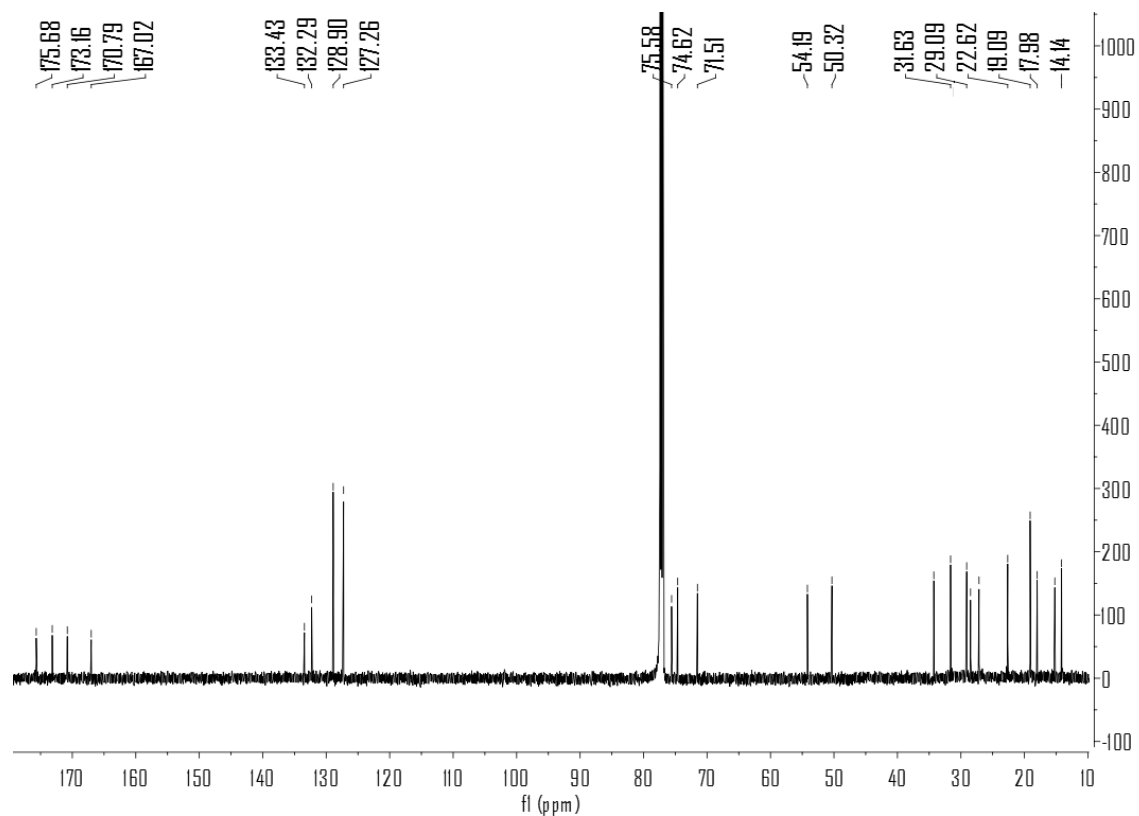


Figure S19. The ^{13}C -NMR spectrum of compound **2**.

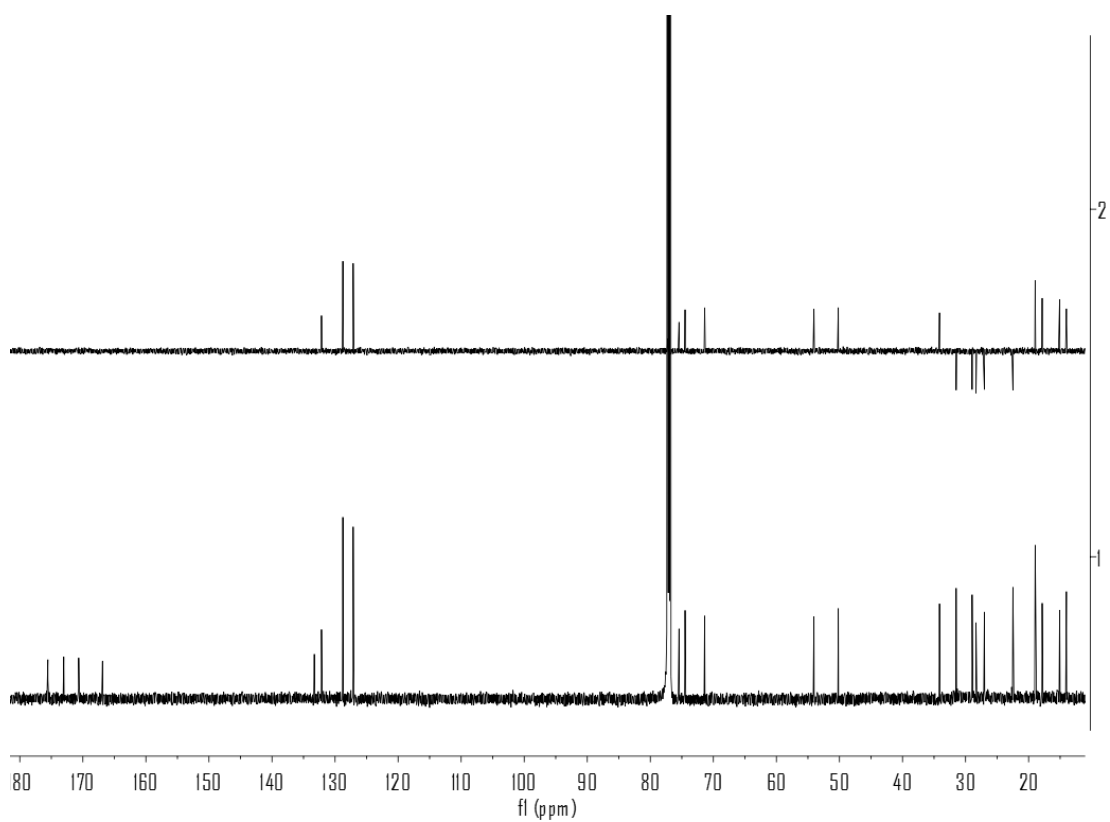


Figure S20. The ^{13}C -NMR and DEPT spectra of compound **2**.

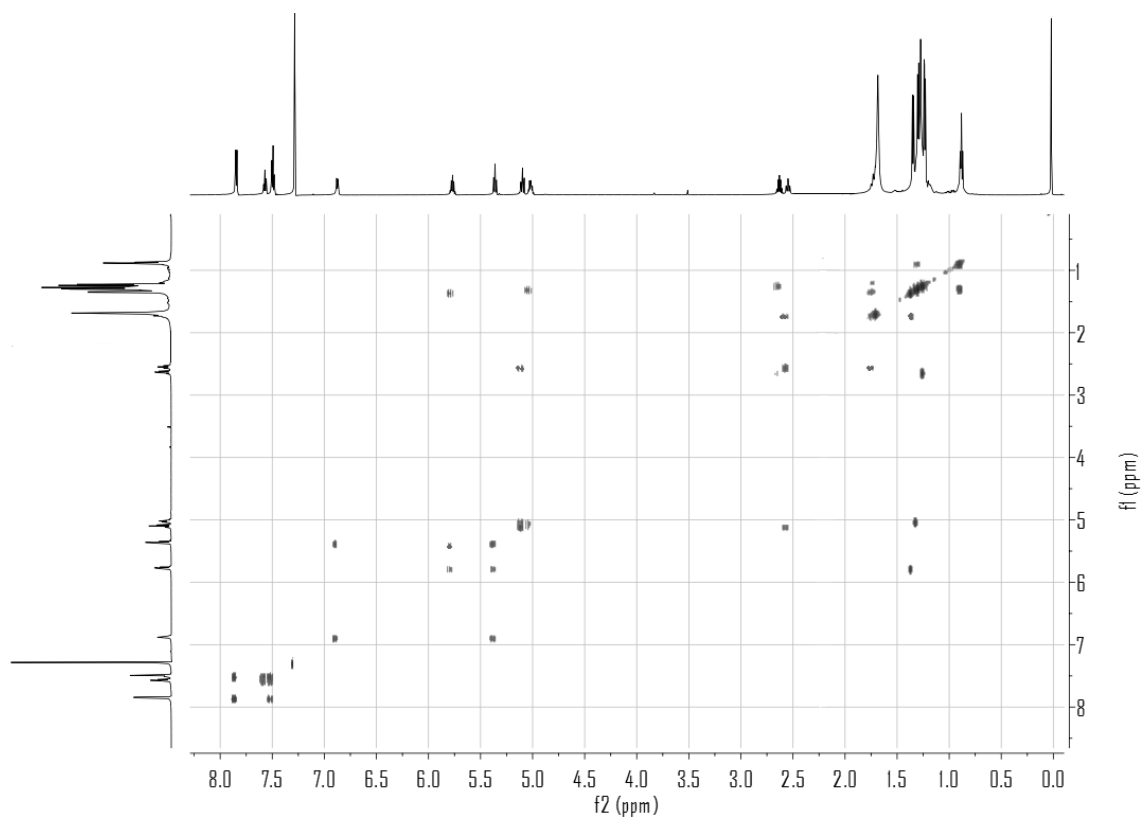


Figure S21. The ^1H - ^1H COSY spectrum of compound **2**.

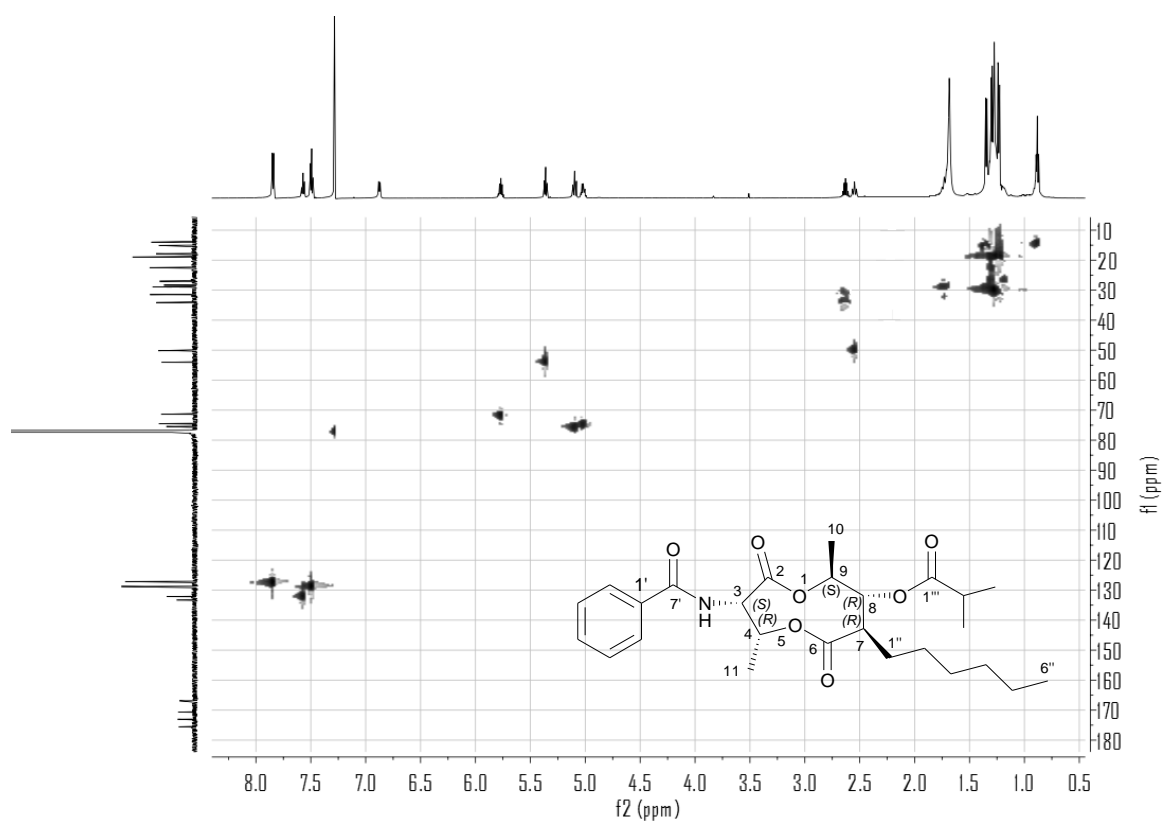


Figure S22. The HSQC spectrum of compound **2**.

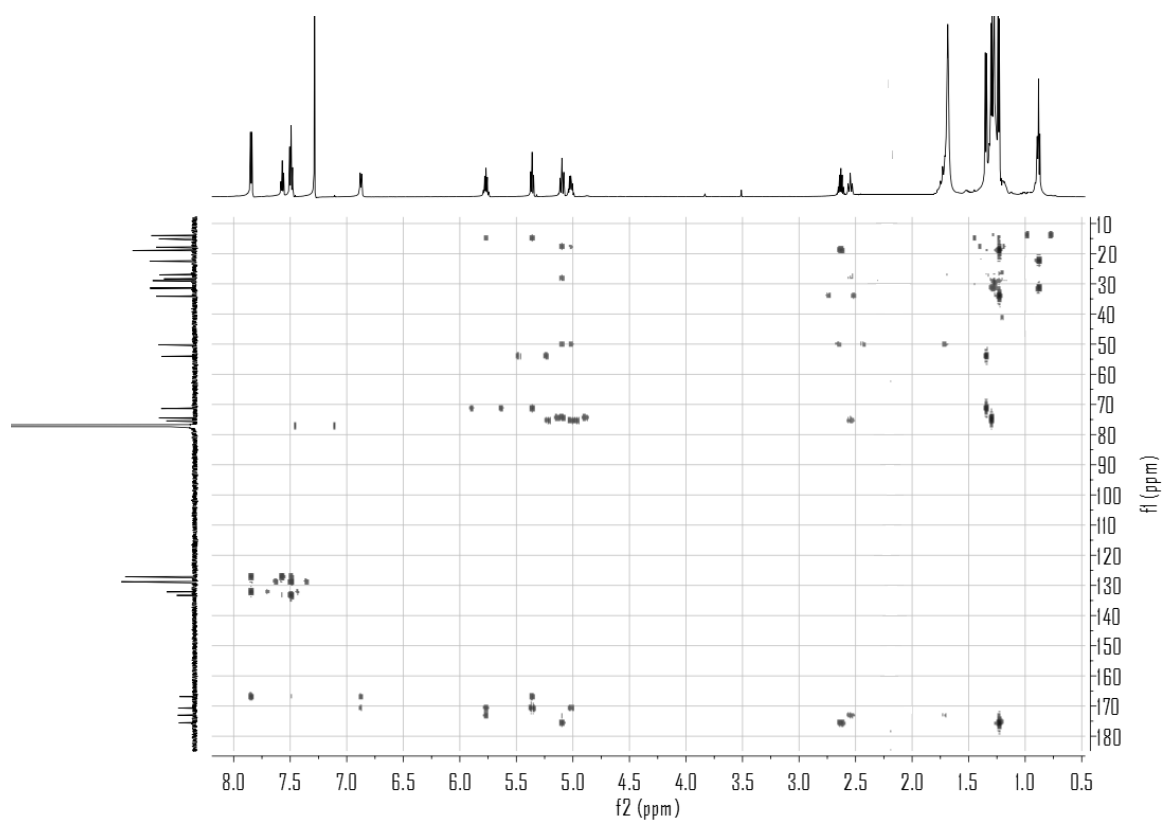


Figure S23. The HMBC spectrum of compound **2**.

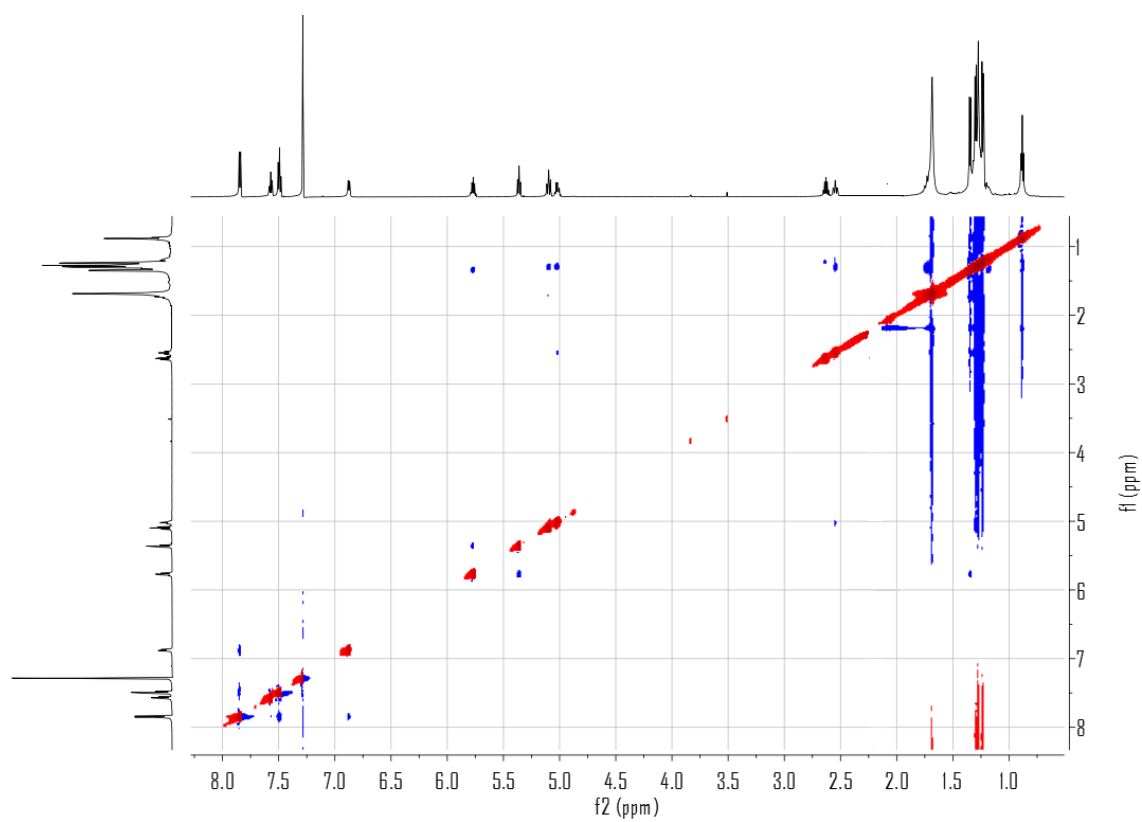


Figure S24. The NOESY spectrum of compound **2**.

Table S5. ^1H (300 MHz) and ^{13}C (75 MHz) NMR data of **3-5** (δ in ppm J in Hz).

No.	3		4		5	
	δ_{C}	δ_{H}	δ_{C}	δ_{H}	δ_{C}	δ_{H}
2	170.1		170.1		170.1	
3	53.7	5.32 (1H, t, 7.7)	53.6	5.32 (1H, t, 7.7)	53.6	5.32 (1H, t, 7.7)
4	70.9	5.75 (1H, p, 7.0)	70.9	5.75 (1H, p, 7.0)	70.9	5.75 (1H, p, 7.0)
6	172.9		172.9		172.9	
7	50.2	2.52 (1H, m)	50.1	2.52 (1H, m)	50.1	2.52 (1H, m)
8	75.4	5.11 (1H, t, 9.9)	75.4	5.11 (1H, t, 9.9)	75.4	5.11 (1H, t, 9.9)
9	74.7	4.97 (1H, m)	74.9	4.97 (1H, m)	74.9	4.97 (1H, m)
10	17.8	1.28 (3H, d, 6.3)	17.8	1.28 (3H, d, 6.3)	17.8	1.28 (3H, d, 6.3)
11	14.9	1.30 (3H, d, 6.7)	15	1.30 (3H, d, 6.7)	15	1.30 (3H, d, 6.7)
1'	112.6		112.5		112.5	
2'	150.6		150.6		150.6	
3'	127.5		127.4		127.4	
4'	124.8	8.54 (1H, d, 8.1)	124.8	8.54 (1H, d, 8.1)	124.8	8.54 (1H, d, 8.1)
5'	118.9	6.89 (1H, t, 8.1)	119	6.89 (1H, t, 8.1)	119	6.89 (1H, t, 8.1)
6'	120.1	7.23 (1H, d, 8.3)	120.1	7.23 (1H, d, 8.3)	120.1	7.23 (1H, d, 8.3)
7'	169.4		169.3		169.3	
8'	159.1	8.50 (1H, d, 1.7)	159.1	8.50 (1H, d, 1.7)	159.1	8.50 (1H, d, 1.7)
1''	28.6	1.68 (1H, m)	28.3	1.68 (1H, m)	28.3	1.68 (1H, m)
2''	22.6	1.23 (2H, m)	22.5	1.23 (2H, m)	22.5	1.23 (2H, m)
3''	27.2	1.23 (2H, m)	27	1.23 (2H, m)	27	1.23 (2H, m)
4''	31.4	1.23 (2H, m)	31.5	1.23 (2H, m)	31.5	1.23 (2H, m)
5''	29.2	1.23 (2H, m)	28.9	1.23 (2H, m)	28.9	1.23 (2H, m)
6''	14.2	0.85 (3H, t, 7.1)	14	0.85 (3H, t, 7.1)	14	0.85 (3H, t, 7.1)
7'-NH		8.43 (1H, d, 8.1)		8.43 (1H, d, 8.1)		8.43 (1H, d, 8.1)
8'-NH		9.20 (1H, br.s)		9.20 (1H, br.s)		9.20 (1H, br.s)
a						
1'''	175.2		175.6		175.6	
2'''	41.3	2.41 (1H, m)	34.1	2.61 (1H, t, 7.0)	34.1	2.61 (1H, t, 7.0)
3'''	26.5	1.74 (1H, m), 1.50 (1H, m)	18.9	1.22 (3H, d, 2.5)	18.9	1.22 (3H, d, 2.5)
4'''	11.7	0.94 (3H, t, 7.4)	18.9	1.21, (3H, d, 2.5)	18.9	1.21, (3H, d, 2.5)
5'''	16.7	1.18 (3H, d, 7.0)				
b						
1'''	171.7					
2'''	43.2	2.24 (2H, d, 6.8)				
3'''	25.5	2.13 (1H, m)				
4'''	22.4	0.98 (3H, d, 6.6)				
5'''	22.4	0.98 (3H, d, 6.6)				

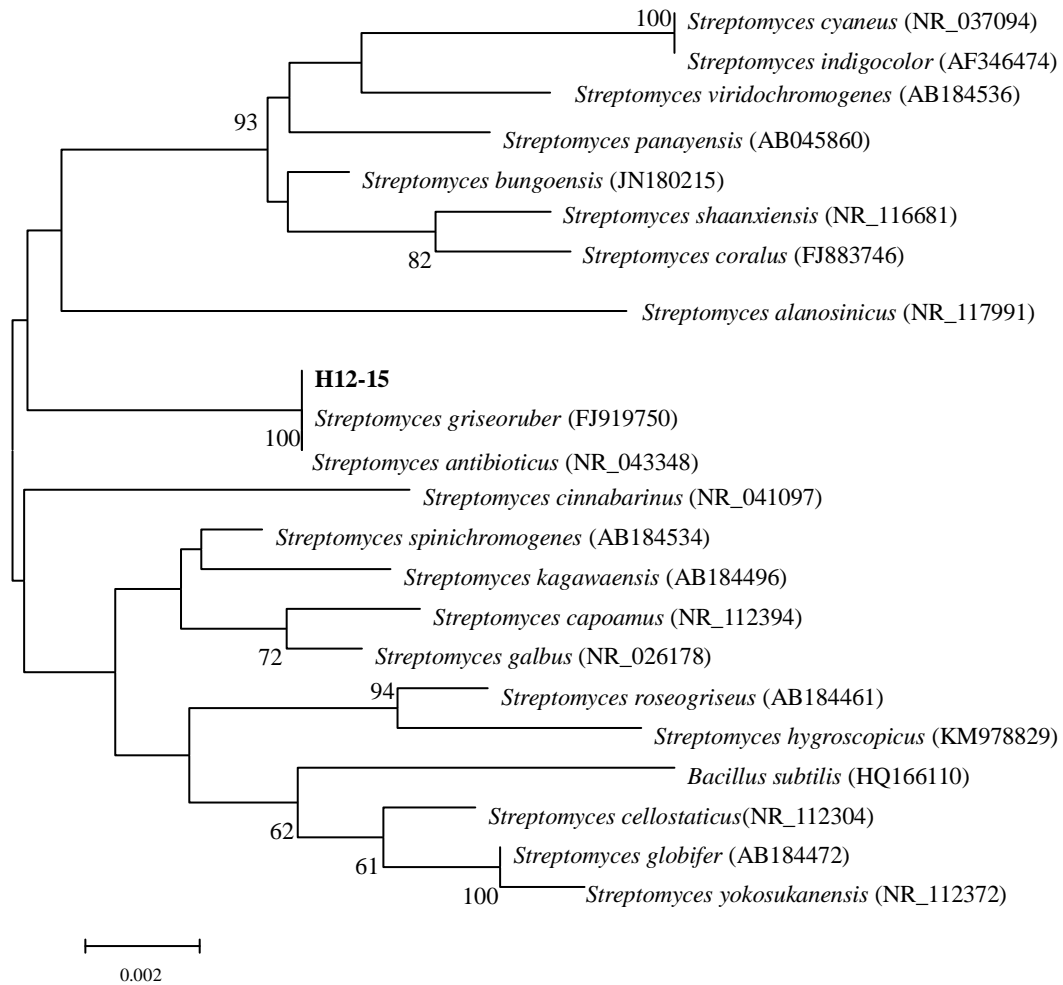


Figure S25. Phylogenetic tree of H12-15.

1CGGCTTGCCGCGTGCTACCATGCAAGTCGAACGATGAAGCCCTTCGGGGTGGATTAG
 58TGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACTCTGGGACAAGCCCT
 114GGAAACGGGGTCTAATACCGGATATCACTCTTGACAGGCATCTGTGAGGGTTCGAAAG
 170CTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAAGTAATGGCT
 226ACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGAC
 280TGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGG
 335GCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTA
 390CCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGG
 444CTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGAATT
 500ATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTTCGGGTGTGAAAGCCCGGGG
 555CTTAACCCCGGGTCTGCATTTCGATACGGGCTAGCTAGAGTGTGGTAGGGGAGATCG
 621GAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGA
 676AGGCGGATCTCTGGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAAC
 731AGGATTAGATACCCTGGTAGTCCACGCCGTAACGGTGGGAAGTAGGTGTTGGCGA
 787CATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAAGTTCCTCCCGCCTGGGGAGTAC
 843GGCCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCAGCGGAG

897CATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATACACCG
953GAAACGGCCAGAGATGGTCGCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCT
1008GTCGTCAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT
1063TGTTCTGTGTTGCCAGCATGTCCTTCGGGATGATGGGGACTCACAGGAGACCGCC
1118GGGGTCAACTCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCTTATGTC
1173TTGGGCTGCACACGTGCTACAATGGCCGGTACAAAGAGCAGCGATACCGTGAGGT
1228GGAGCGAATCTCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCC
1283CATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCTGCGGTGAATACGTTT
1349CCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTCGGTAACACCCGAAGC
1403CGGTGGCCCAACCCCTTGTGGGAGGGAGCTTCGAAGTGAACCGAACTT

Figure S26. 16S rDNA gene sequence of H12-15.

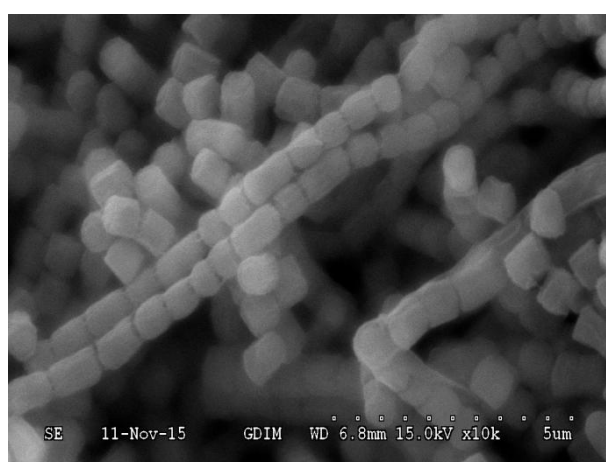


Figure S27. Scanning electron micrographs of strain H12-15 on Gauze No.1 medium