Supplementary Material

Stress-Driven Discovery of New Angucycline-Type Antibiotics from a Marine *Streptomyces pratensis* NA-ZhouS1

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List of supporting information

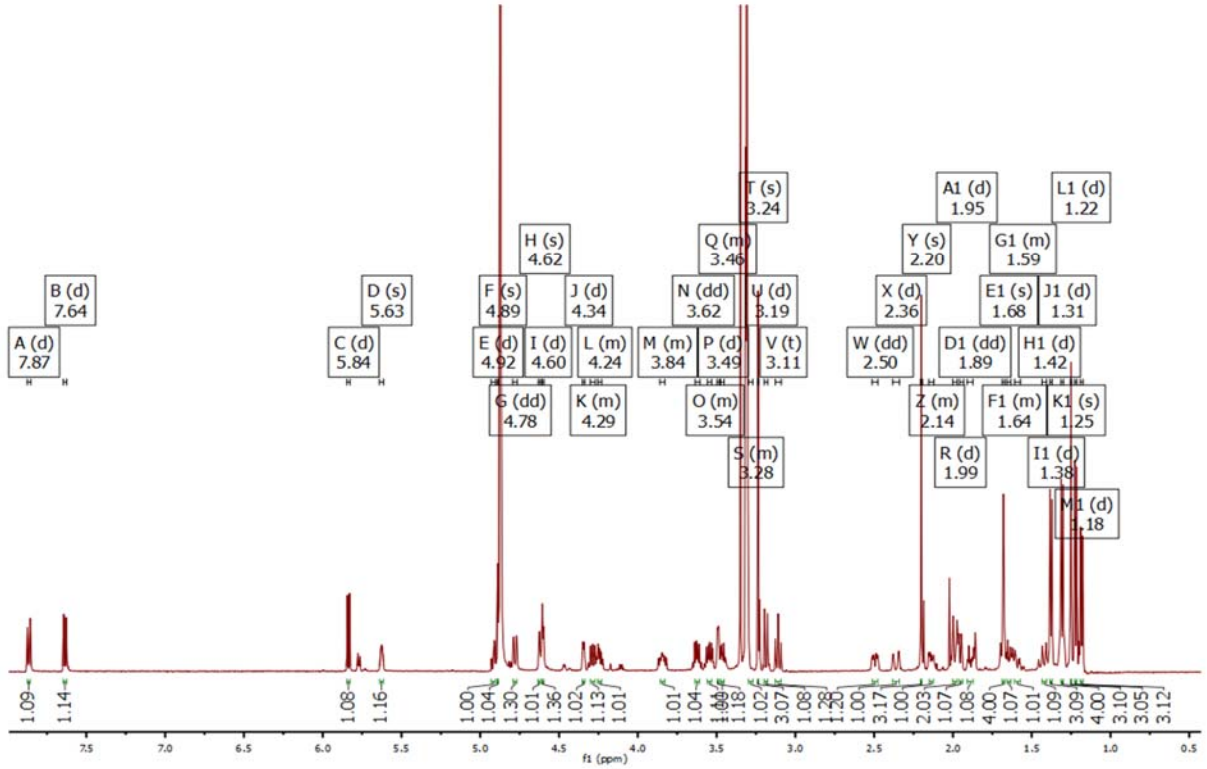

Figure S 1. [1]H NMR spectrum in MeOD for compound **1**.

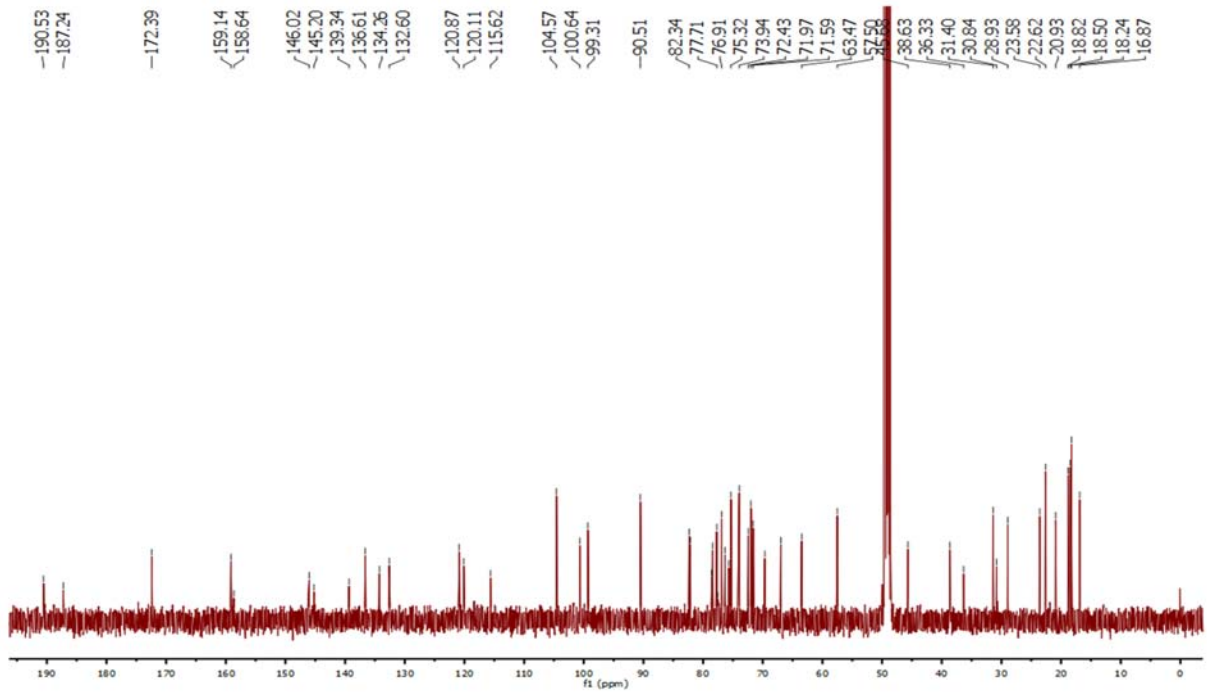

Figure S 2. [13]C NMR spectrum in MeOD for compound **1**.

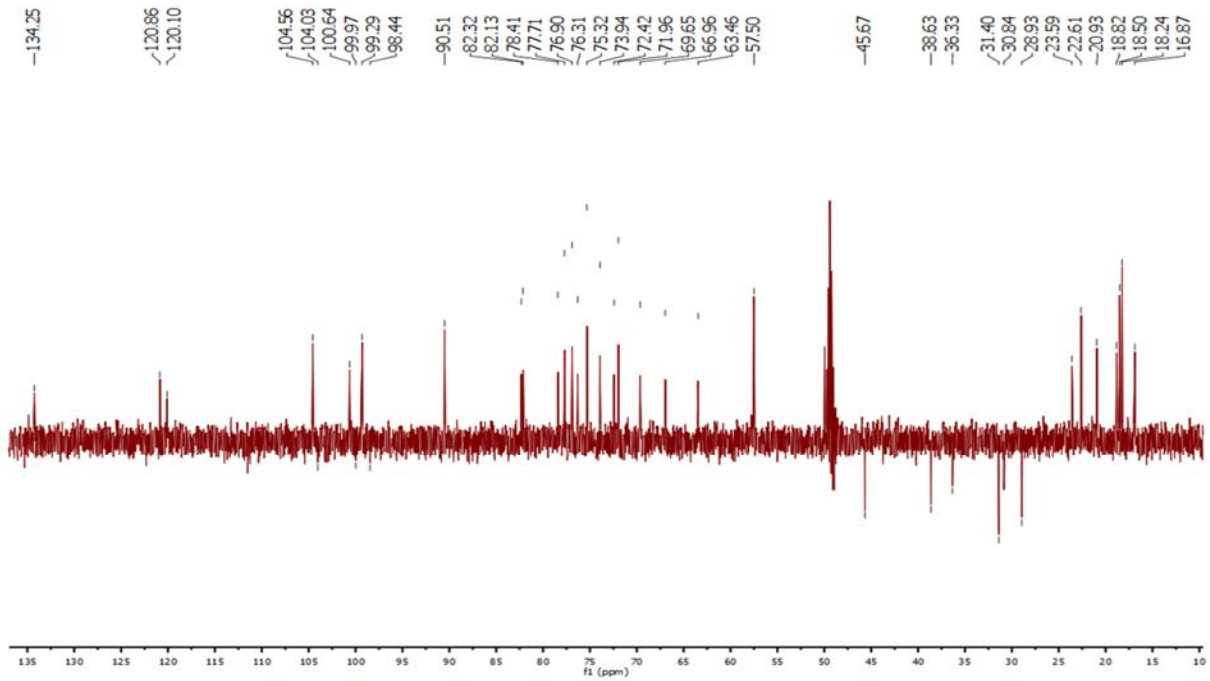

Figure S 3. DEPT-135 spectrum in MeOD for compound **1**.

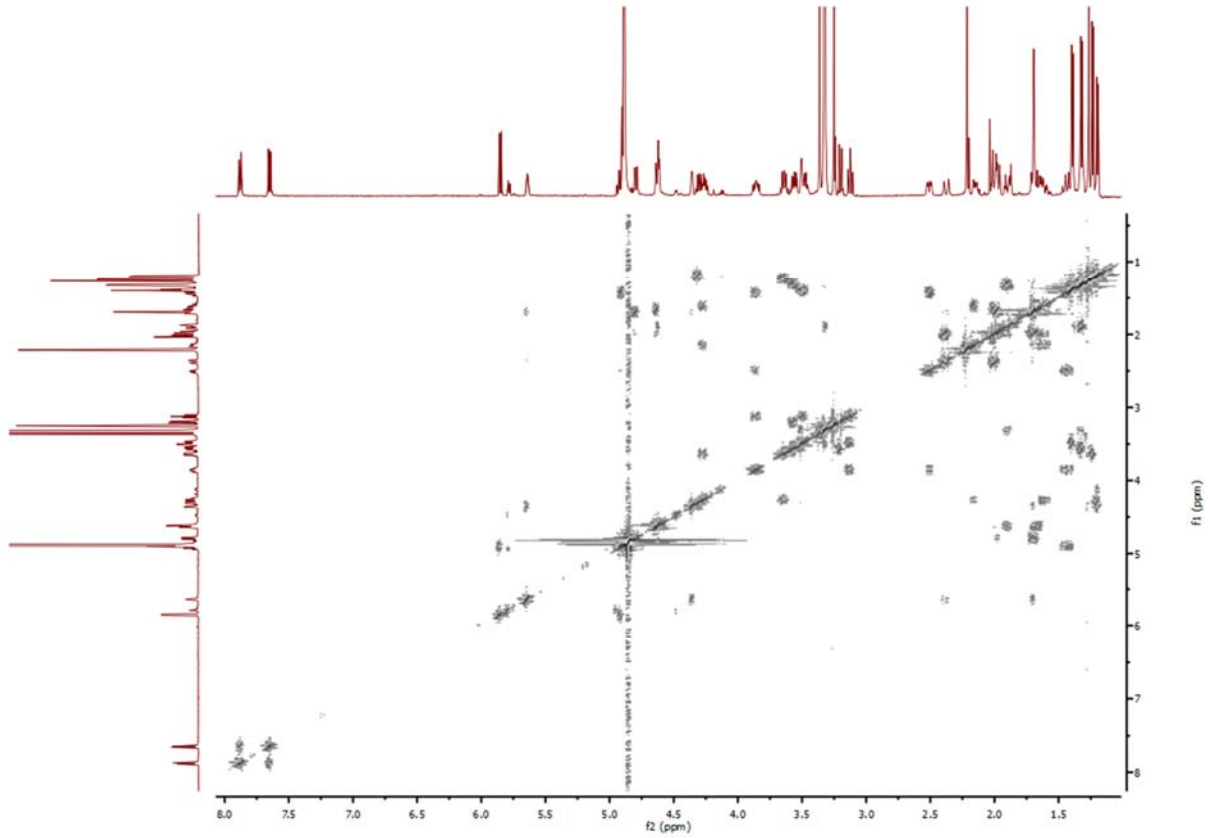

Figure S 4. COSY spectrum in MeOD for compound **1.**

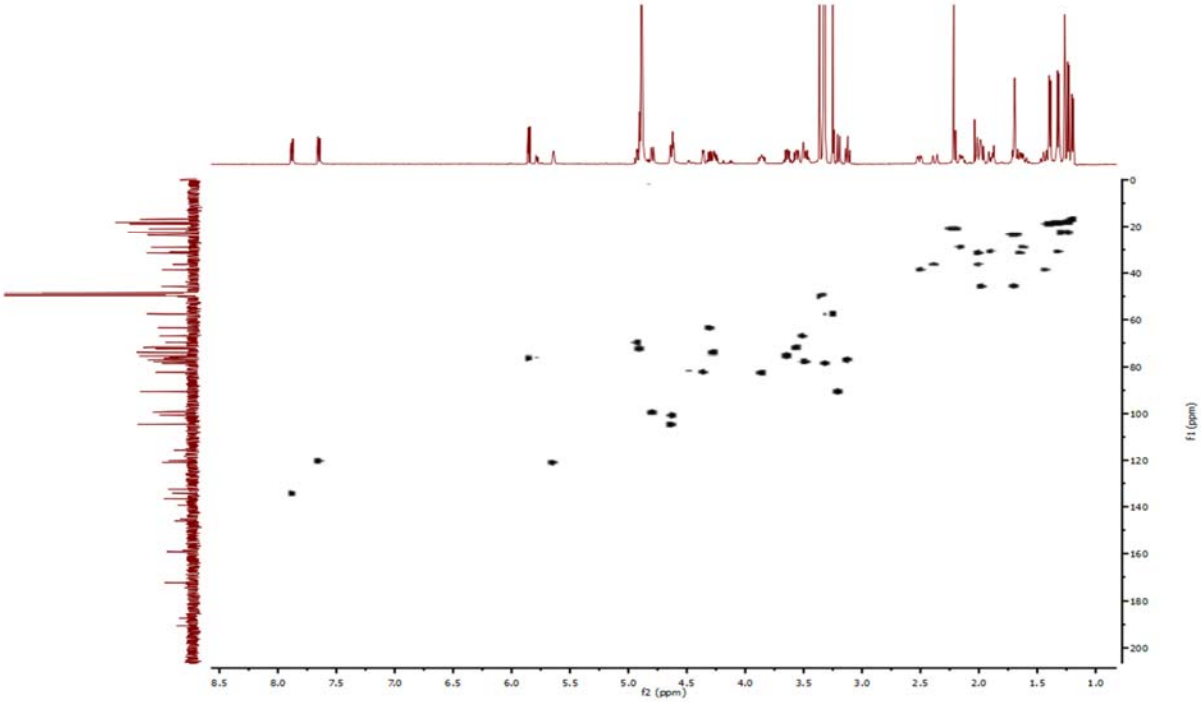

Figure S 5. HSQC spectrum in MeOD for compound **1**.

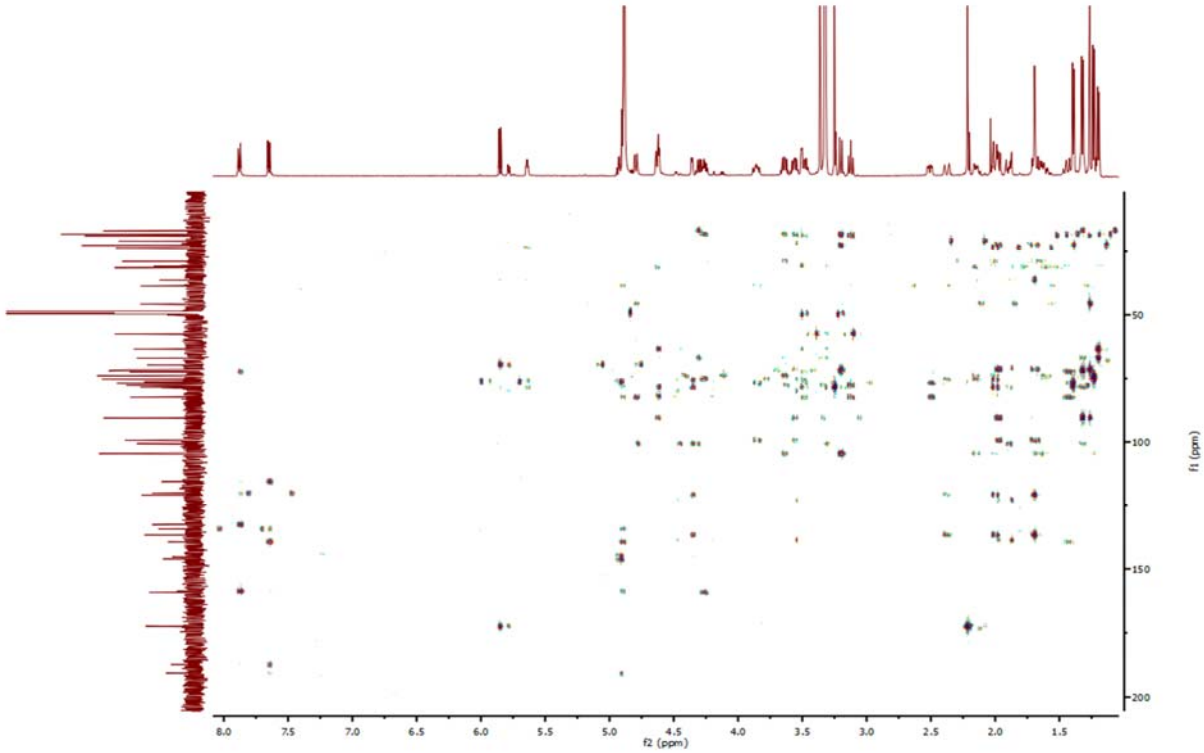

Figure S 6. HMBC spectrum in MeOD for compound **1**.

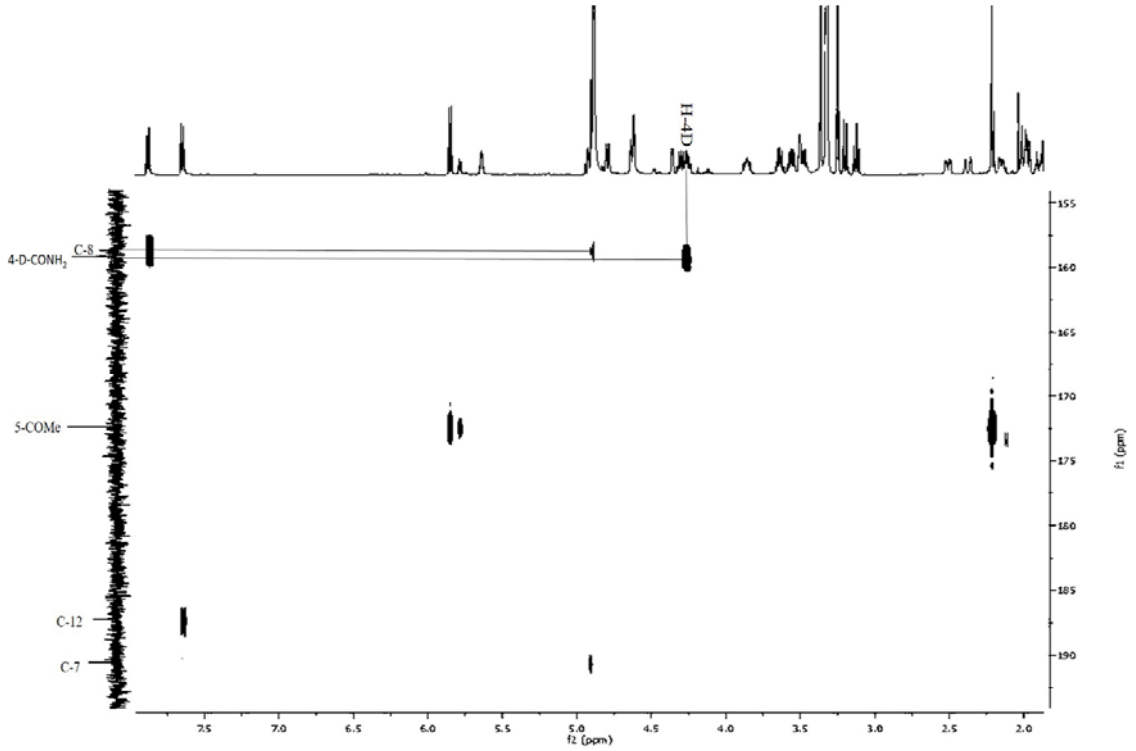

Figure S 7. HMBC-2 spectrum in MeOD for compound **1**. Enlarged view of the spectrum to clarify the cross peaks of H-4D to carbamoyl carbon resonated at δc 159.6.

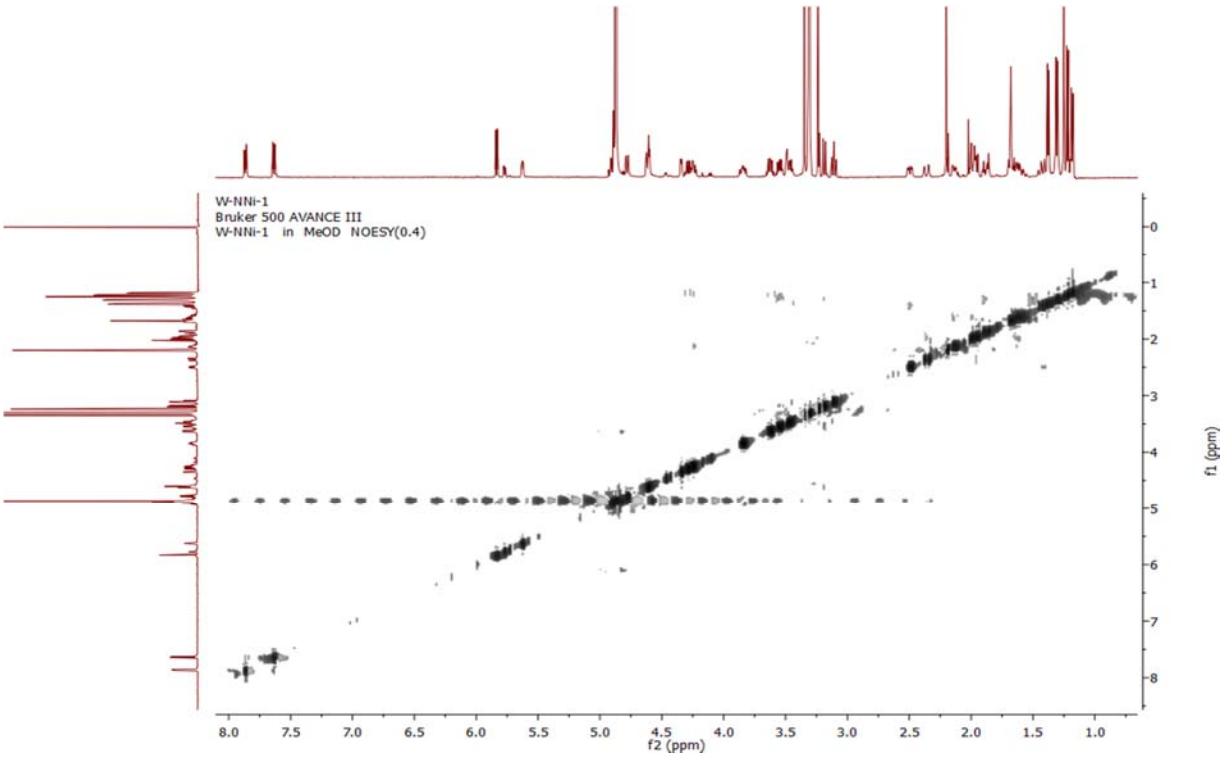

Figure S 8. NOESY spectrum in MeOD for compound **1**.

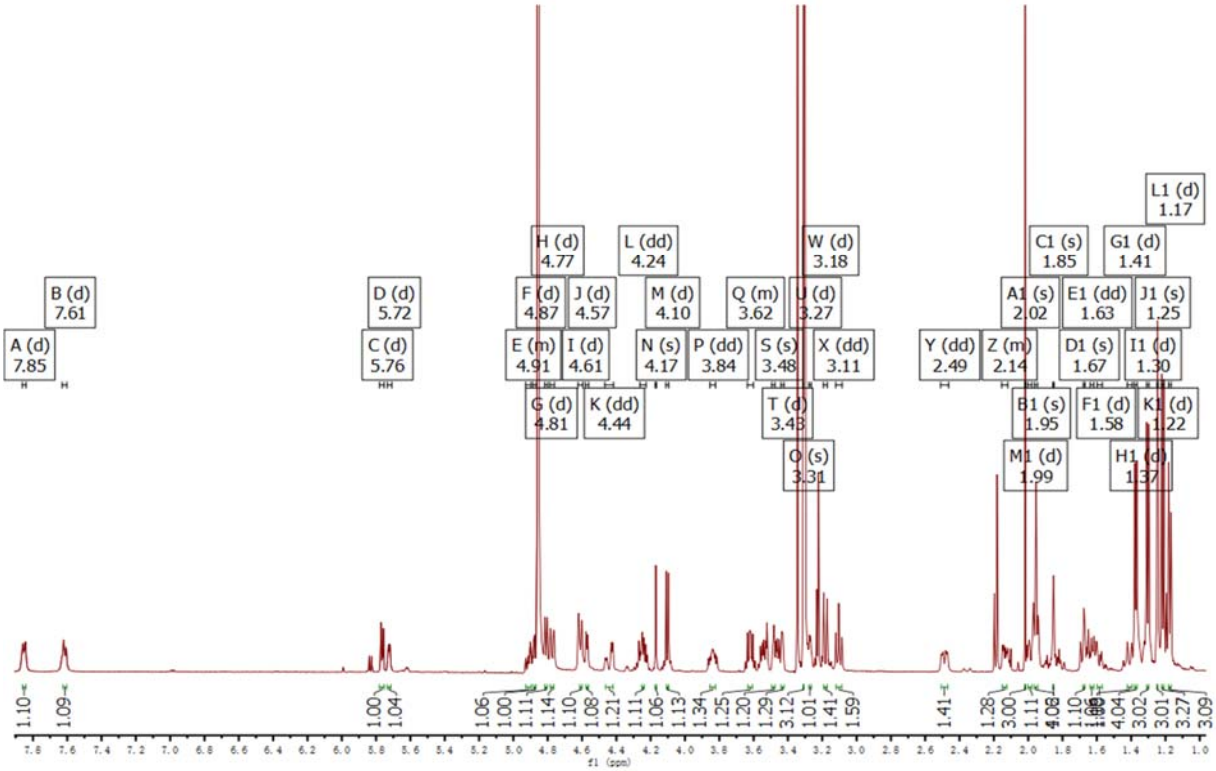

Figure S 9. [1]H NMR spectrum in MeOD for compound **2**.

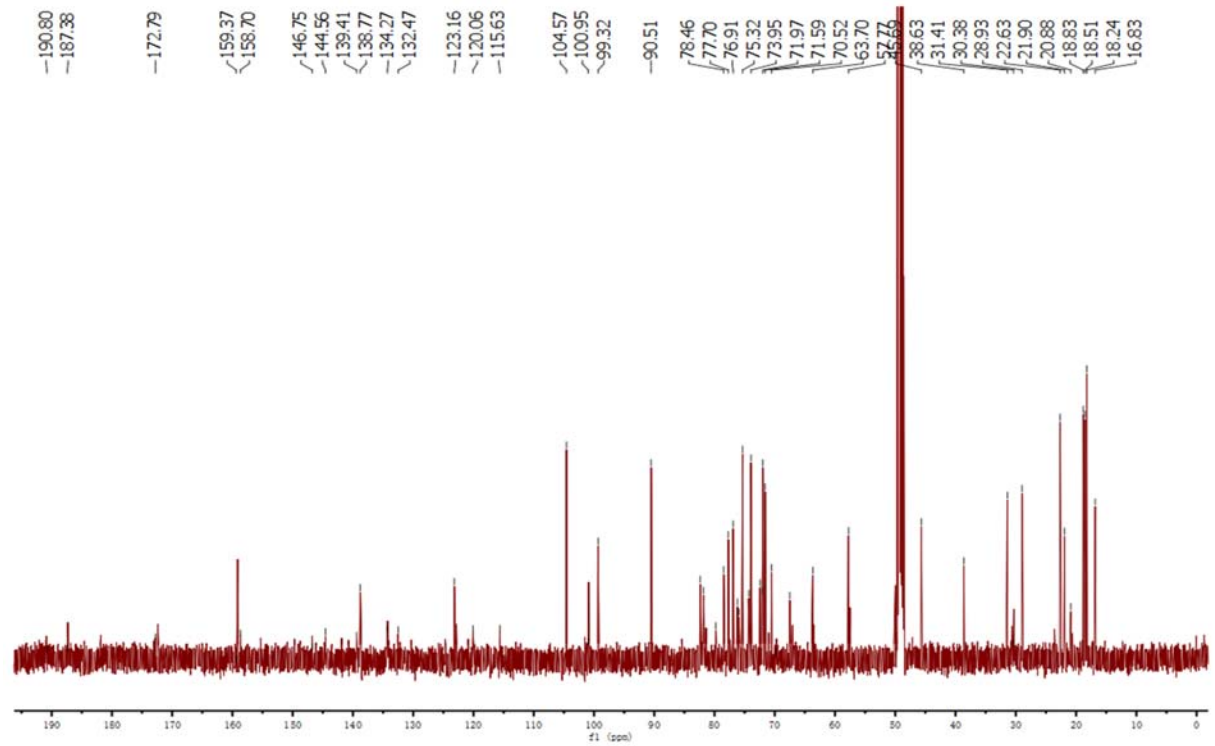

Figure S 10. [13]C NMR spectrum in MeOD for compound **2**.

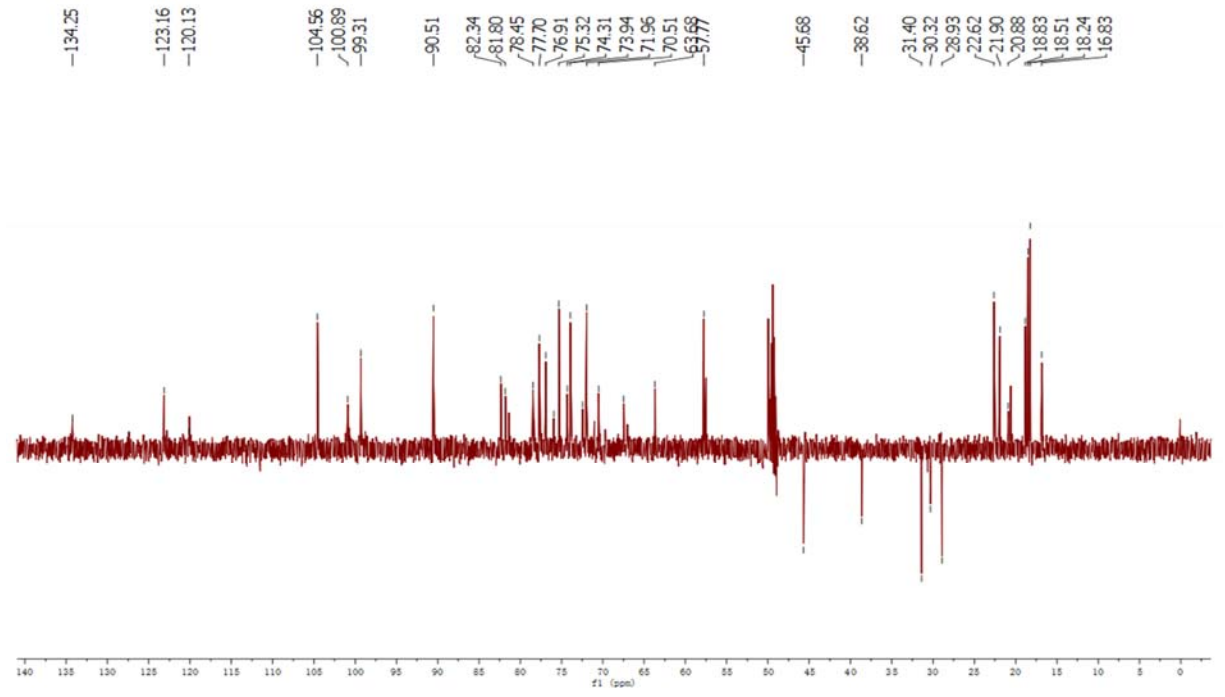

Figure S 11. DEPT-135 spectrum in MeOD for compound **2.**

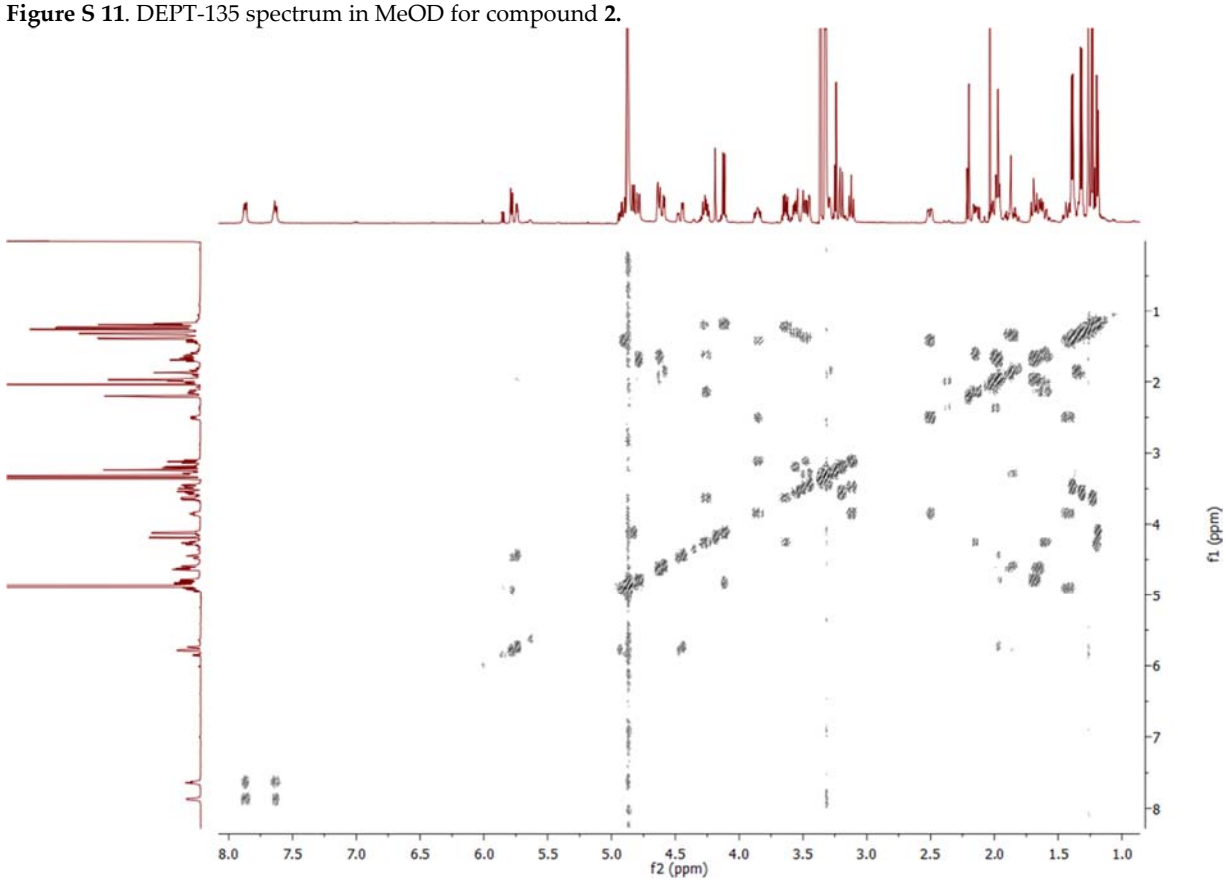

Figure S 12. COSY spectrum in MeOD for compound **2**.

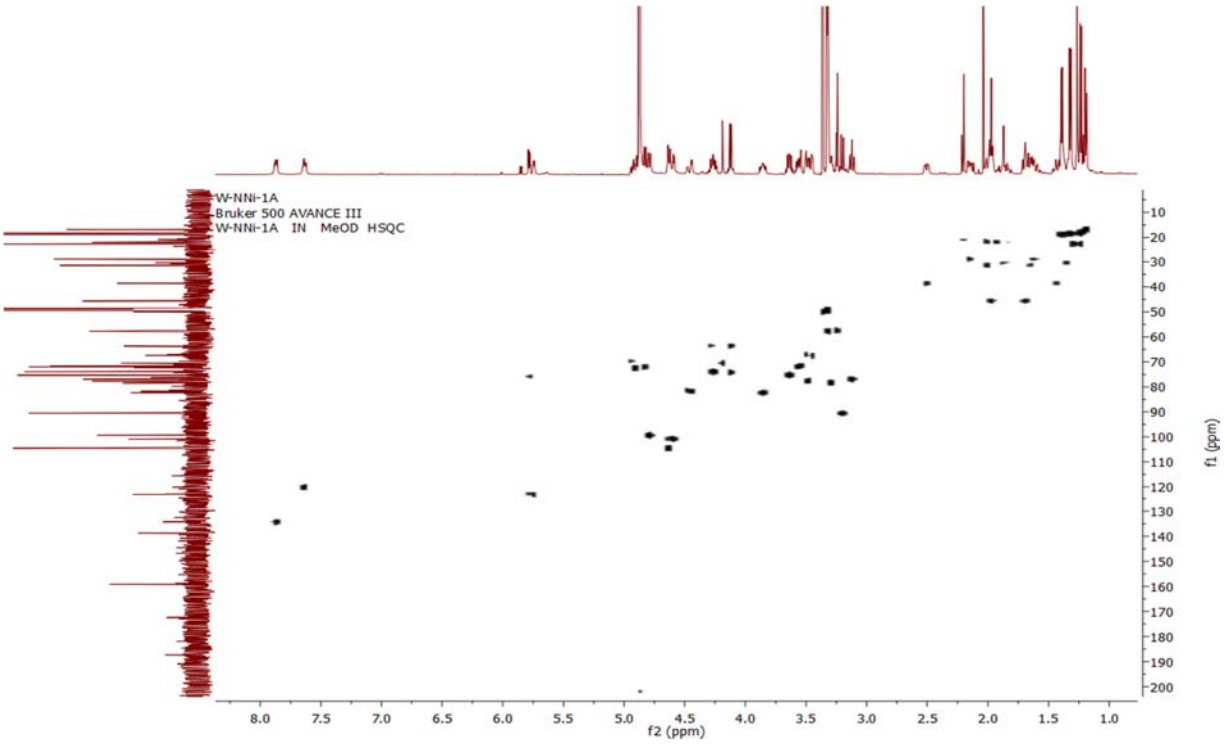

Figure S 13. HSQC spectrum in MeOD for compound **2**.

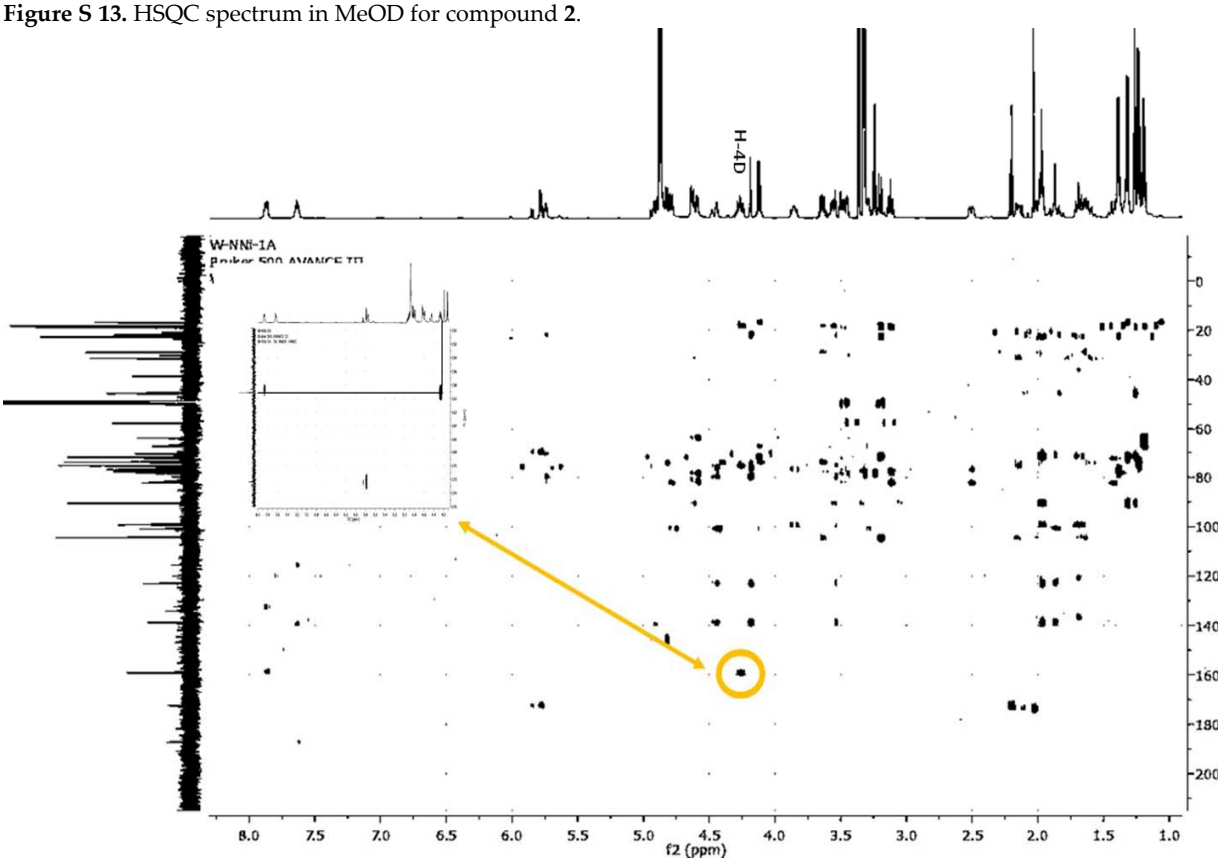

Figure S 14. HMBC spectrum in MeOD for compound **2**.

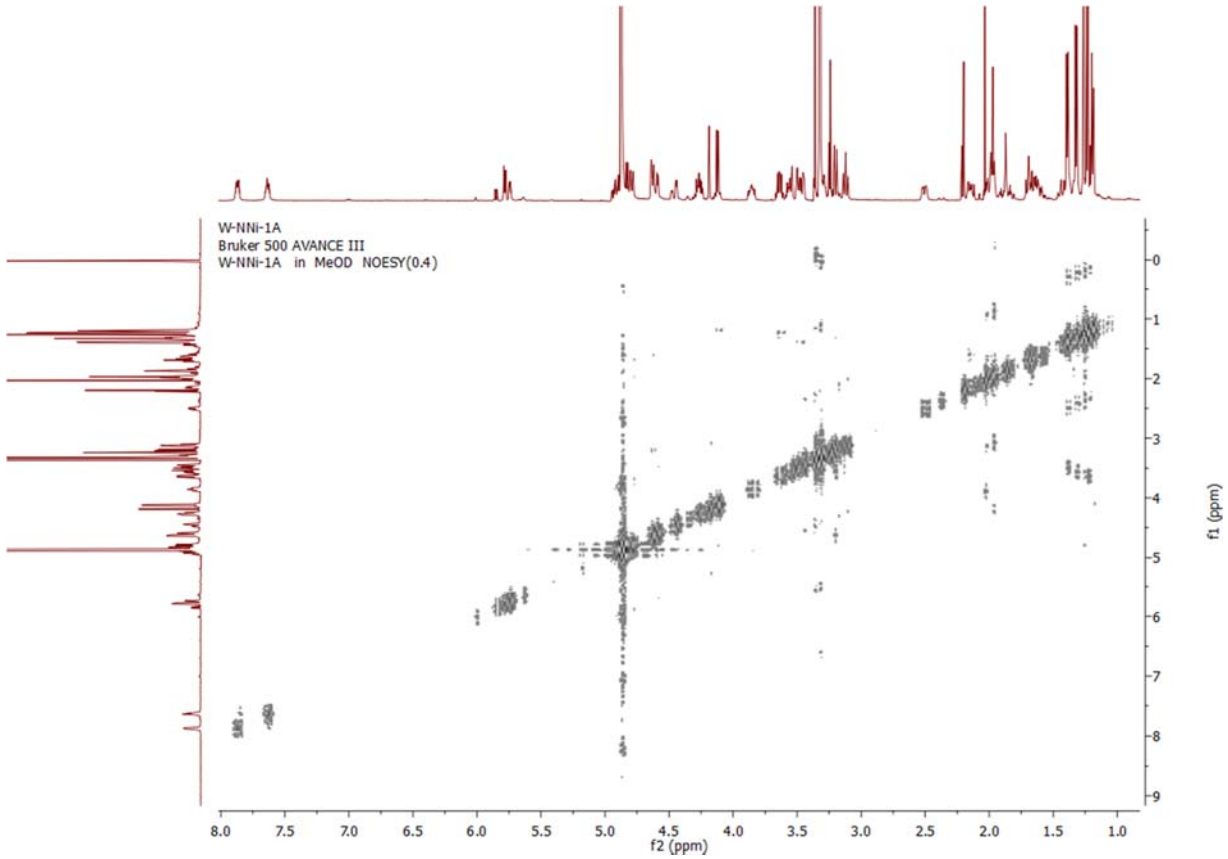

Figure S 15. NOESY spectrum in MeOD for compound **2**.

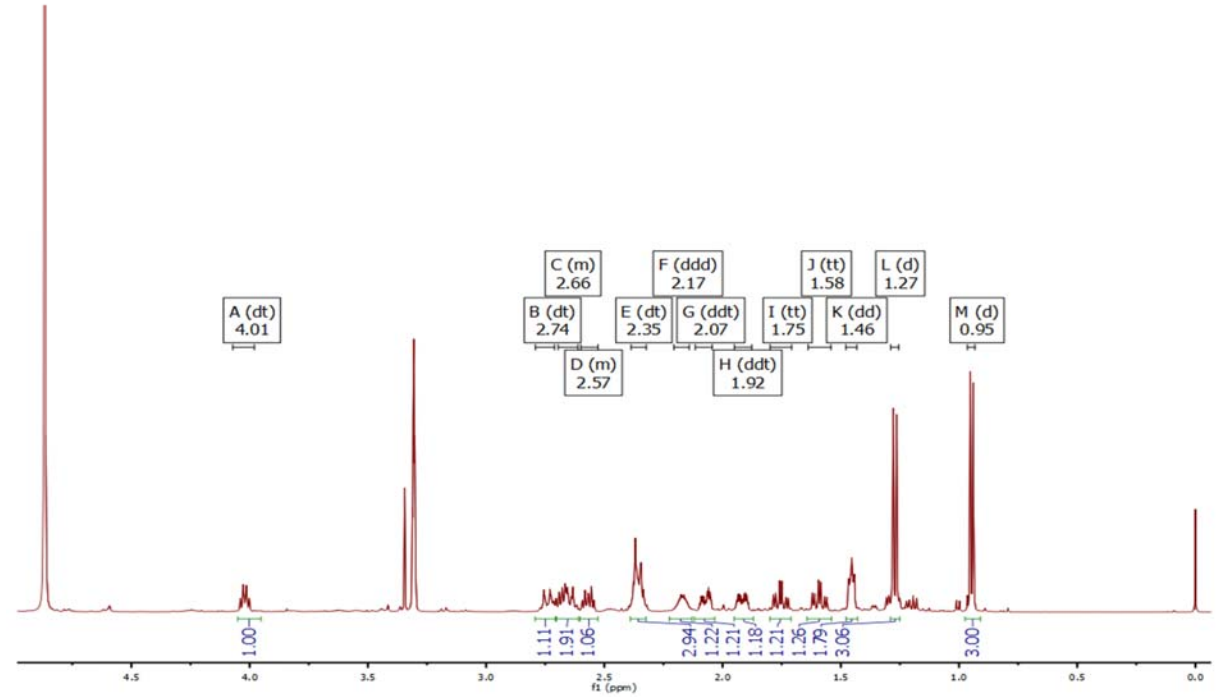

Figure S 16. ^{1}H NMR spectrum in MeOD for compound **3**.

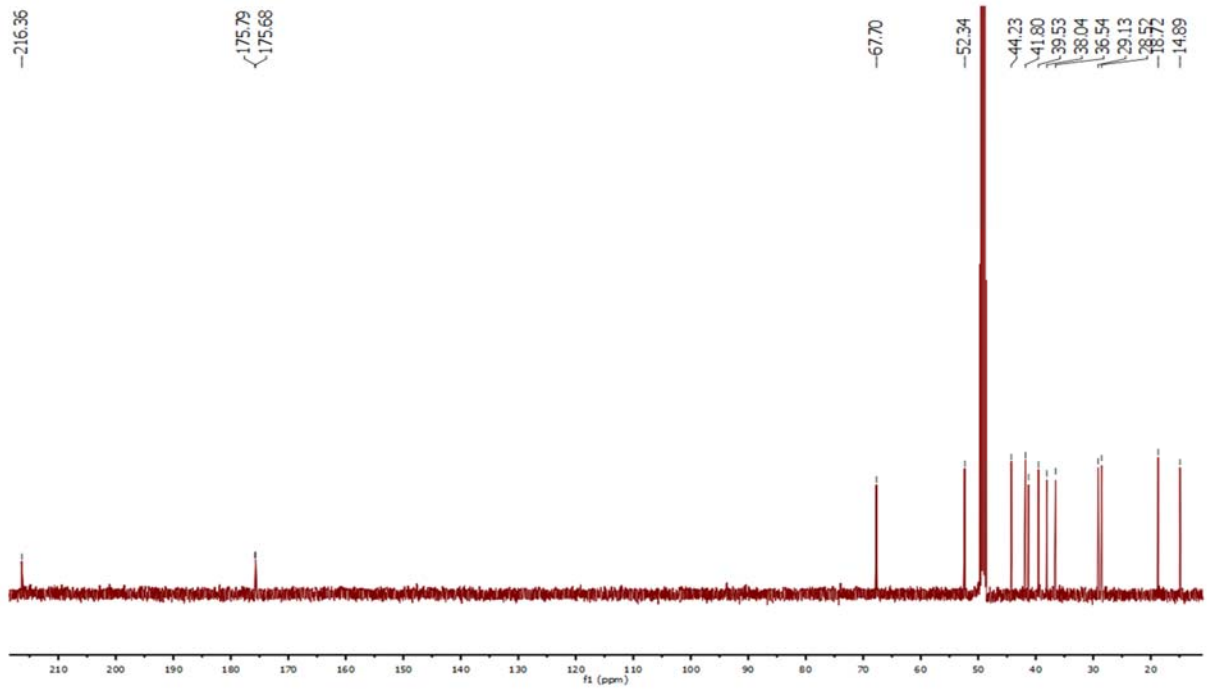

Figure S 17. ^{13}C NMR spectrum in MeOD for compound **3.**

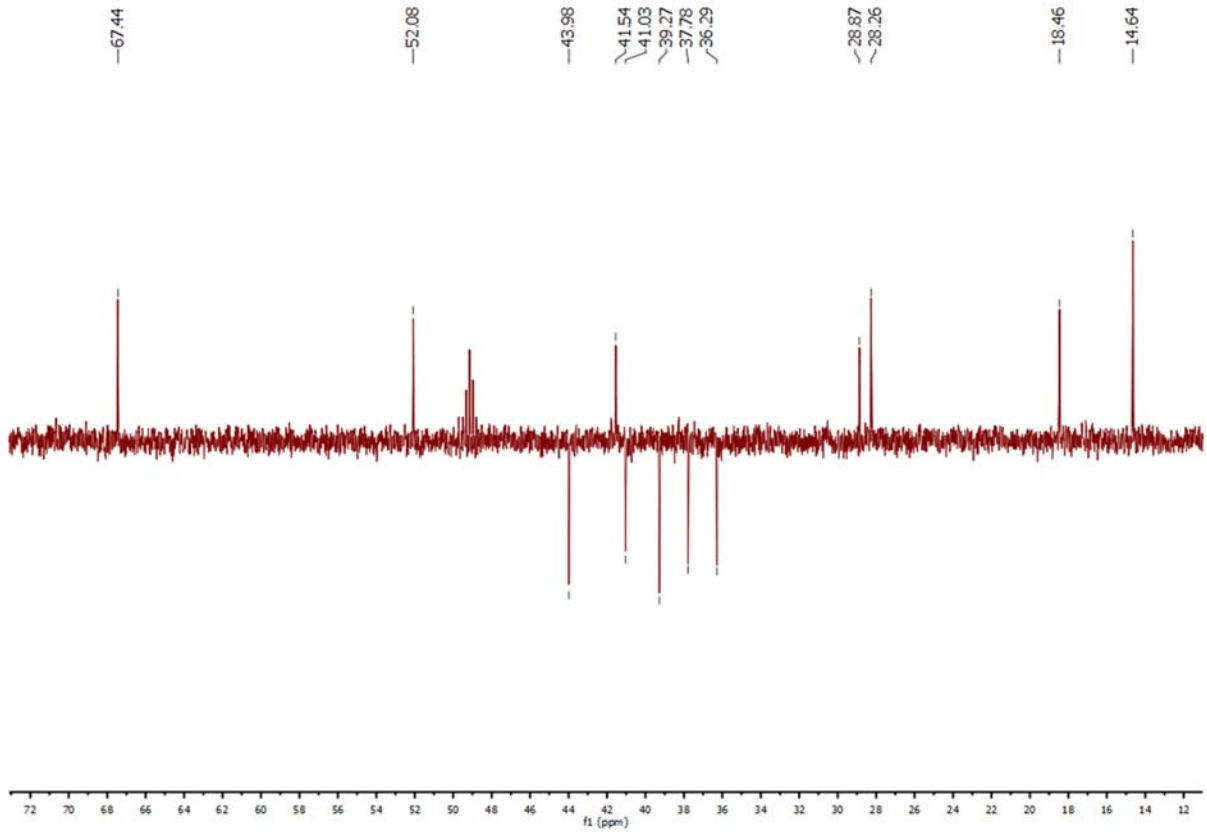

Figure S 18. DEPT-135 spectrum in MeOD for compound **3**.

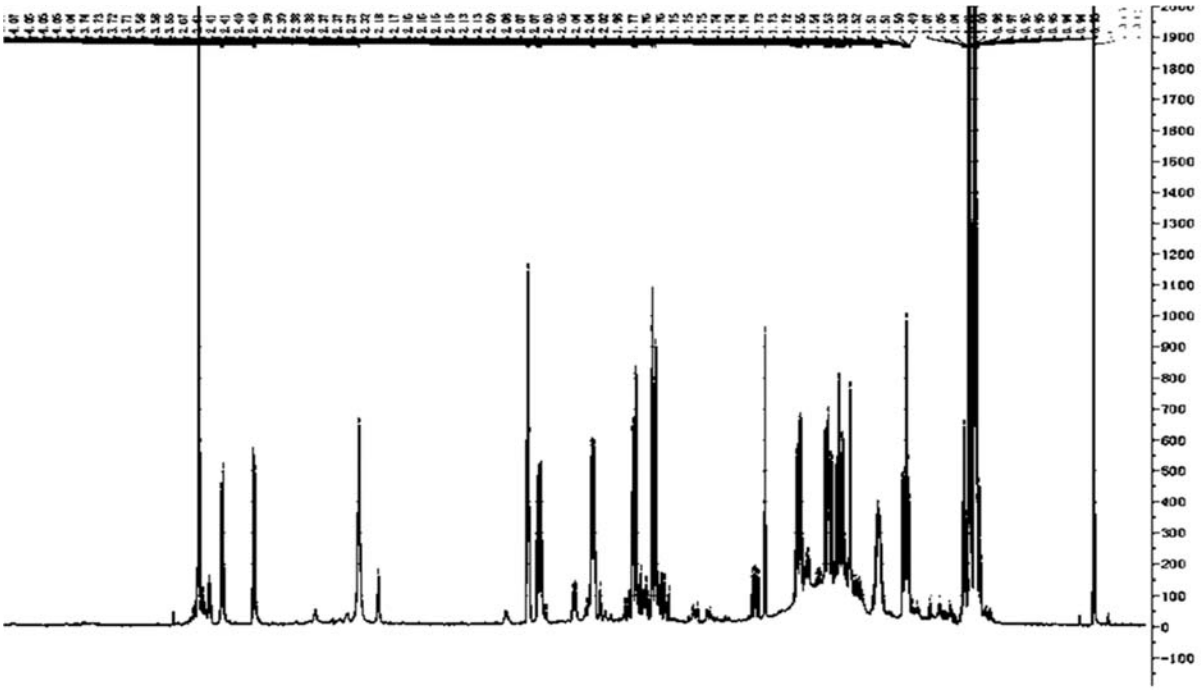

Figure S 19. ^{1}H NMR spectrum in $CDCl_3$ for compound **4**.

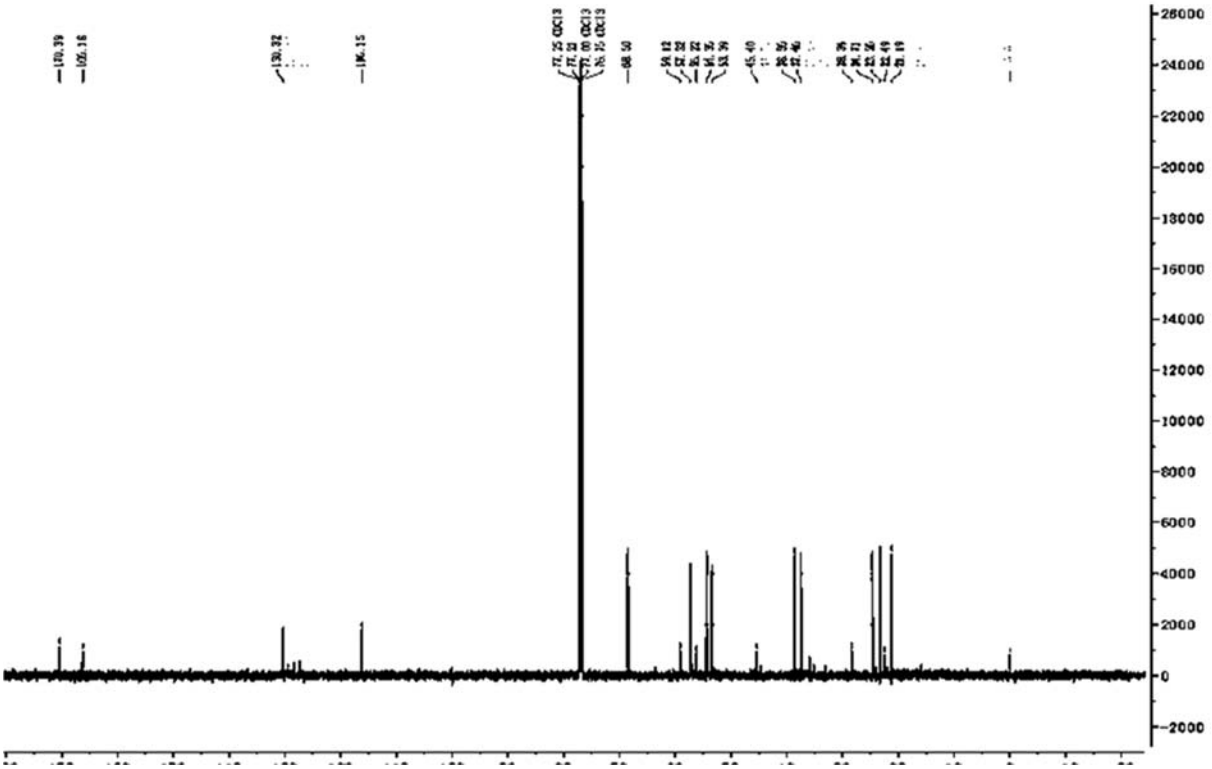

Figure S 20. ^{13}C NMR spectrum in $CDCl_3$ for compound **4**.

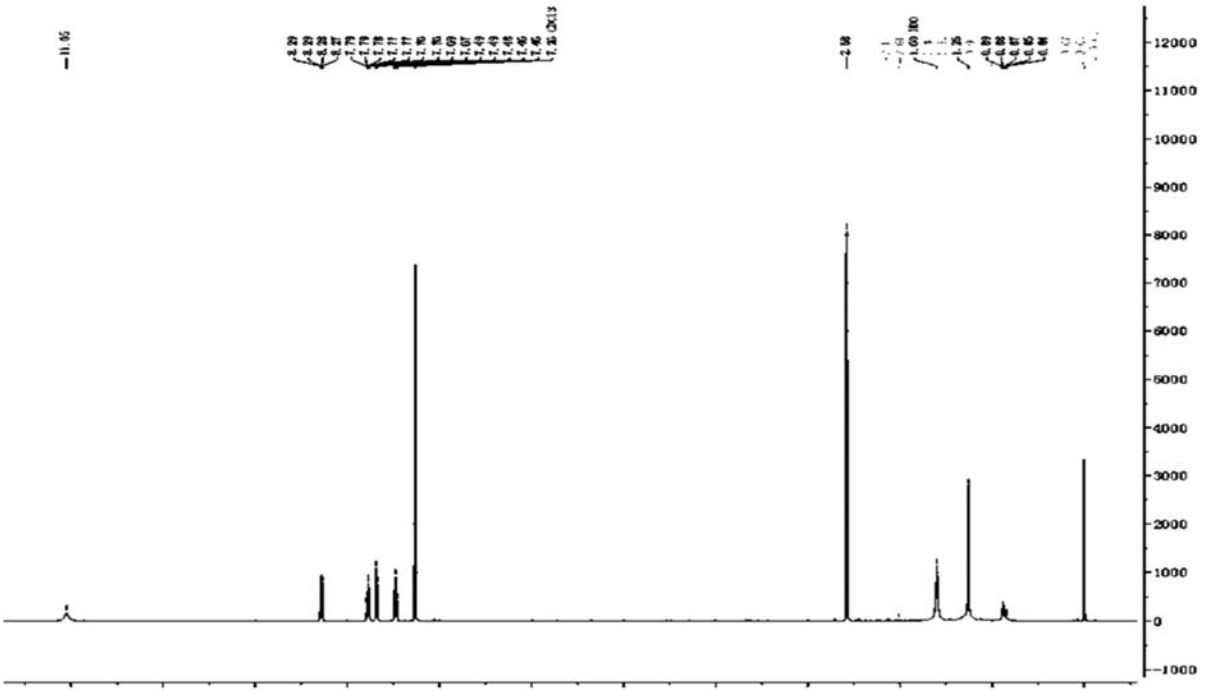

Figure S 21. ^{1}H NMR spectrum in $CDCl_3$ for compound **5**.

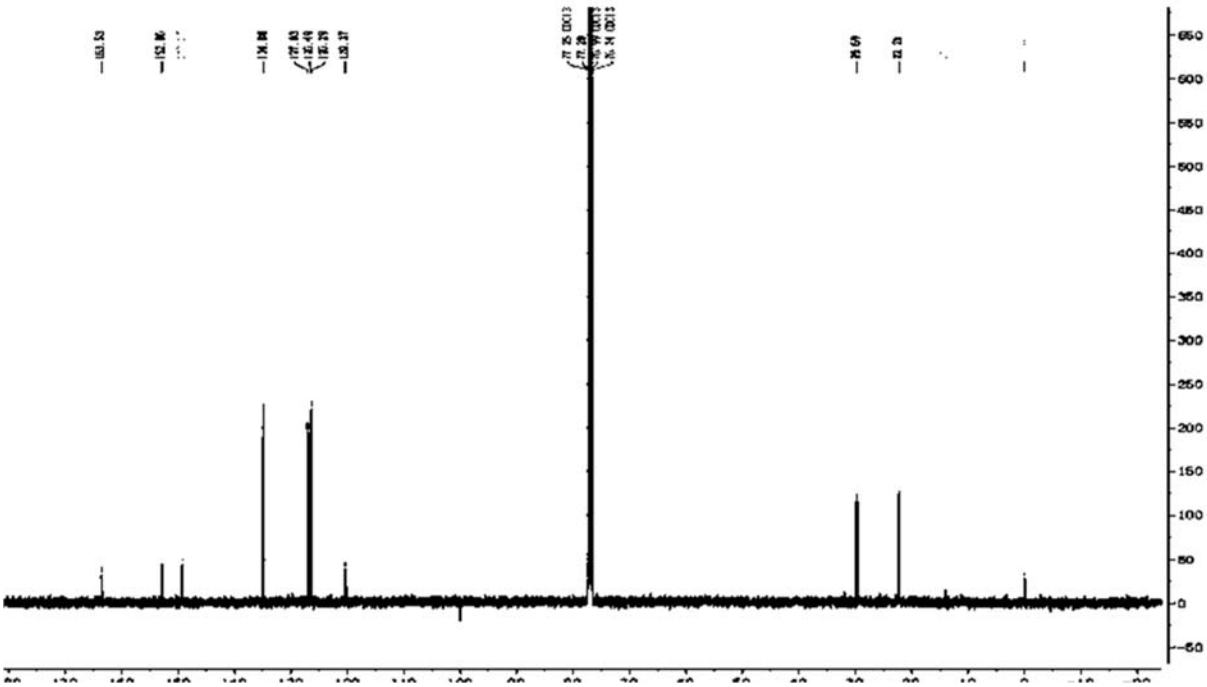

Figure S 22. ^{13}C NMR spectrum in $CDCl_3$ for compound **5**.

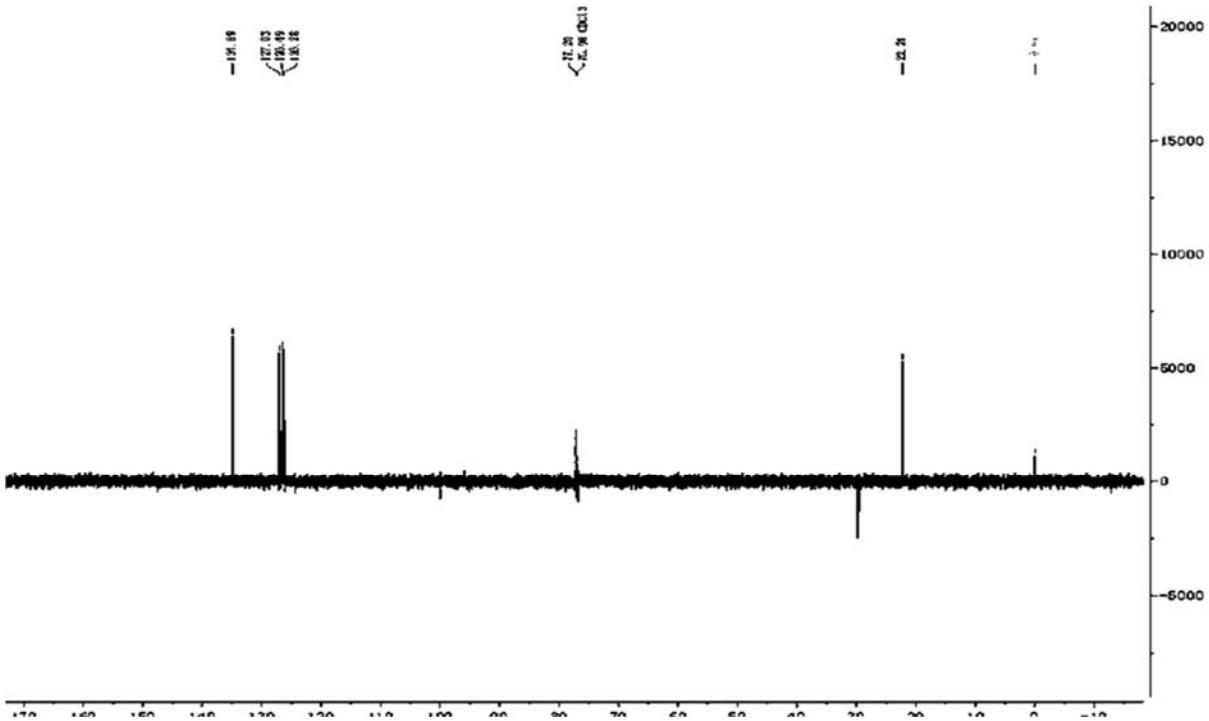

Figure S 23. DEPT spectrum in $CDCl_3$ for compound **5**.

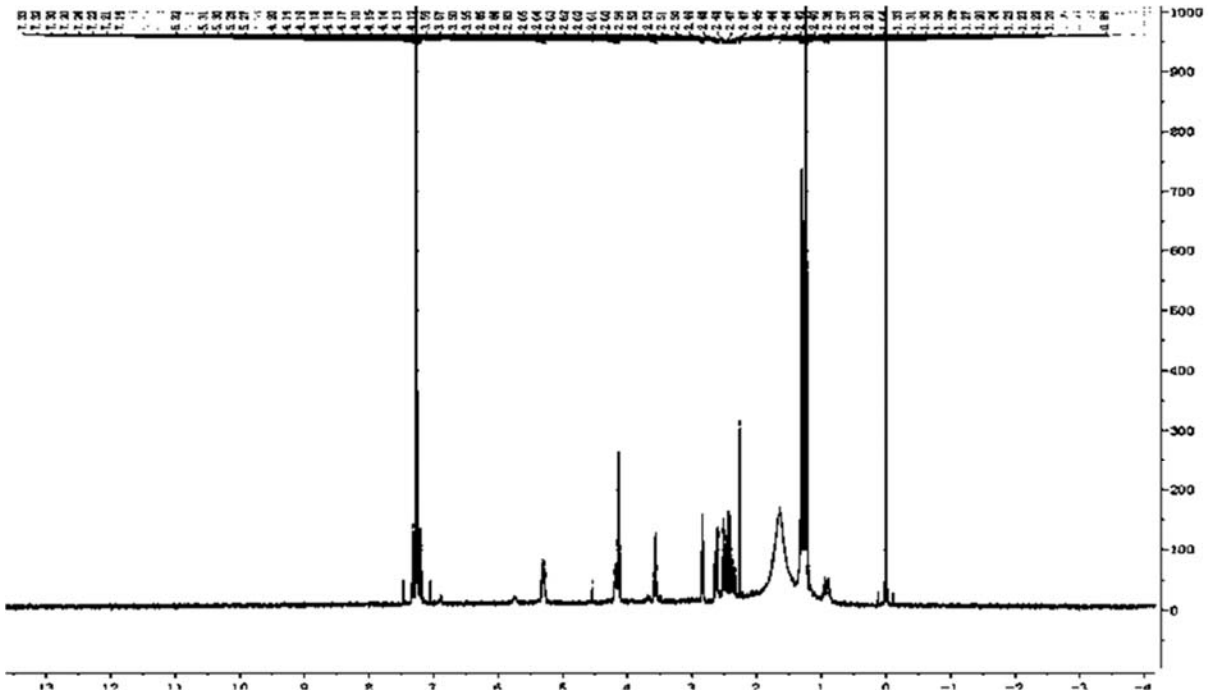

Figure S 24. ^1H NMR spectrum in $CDCl_3$ for compound **6**.

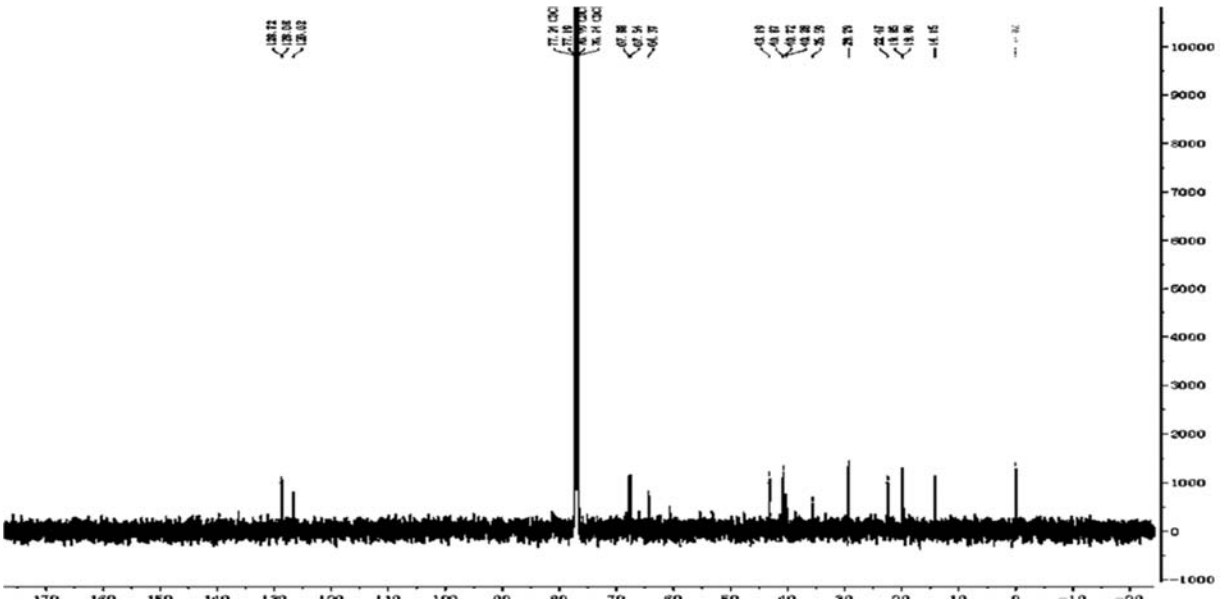

Figure S 25. ^{1}H NMR spectrum in $CDCl_3$ for compound **6**.

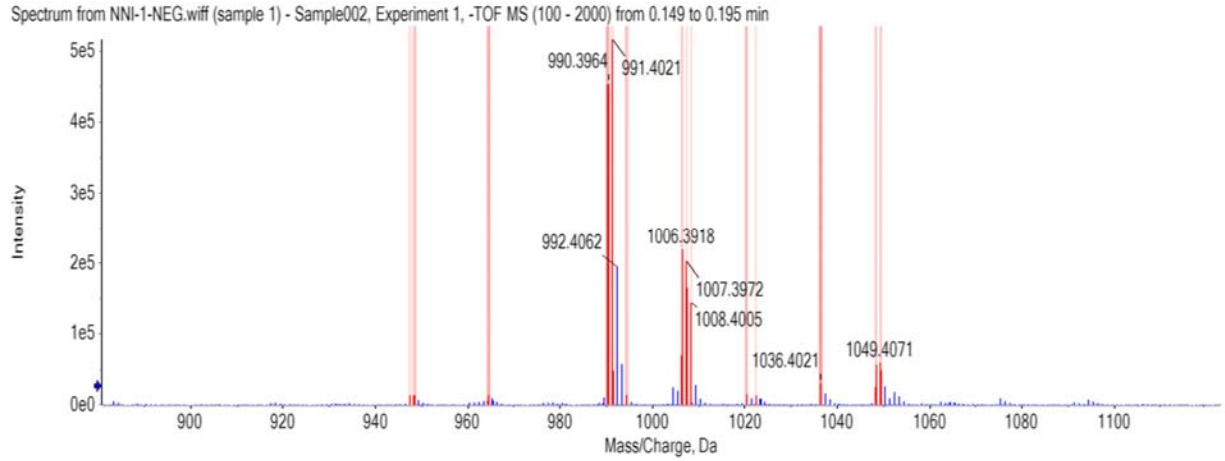

Figure S 26. HR-TOF-MS spectrum in negative mode for compound **1.**

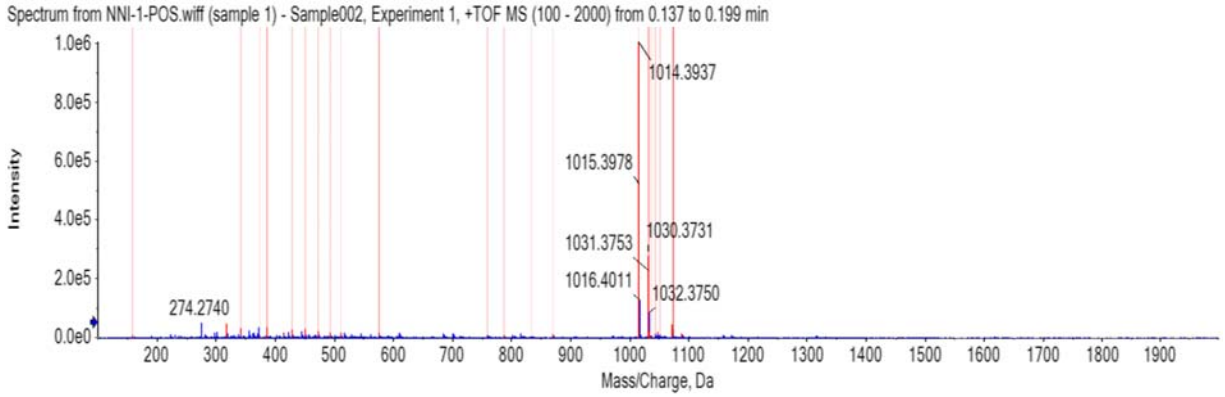

Figure S 27. HR-TOF-MS spectrum in positive mode for compound **1.**

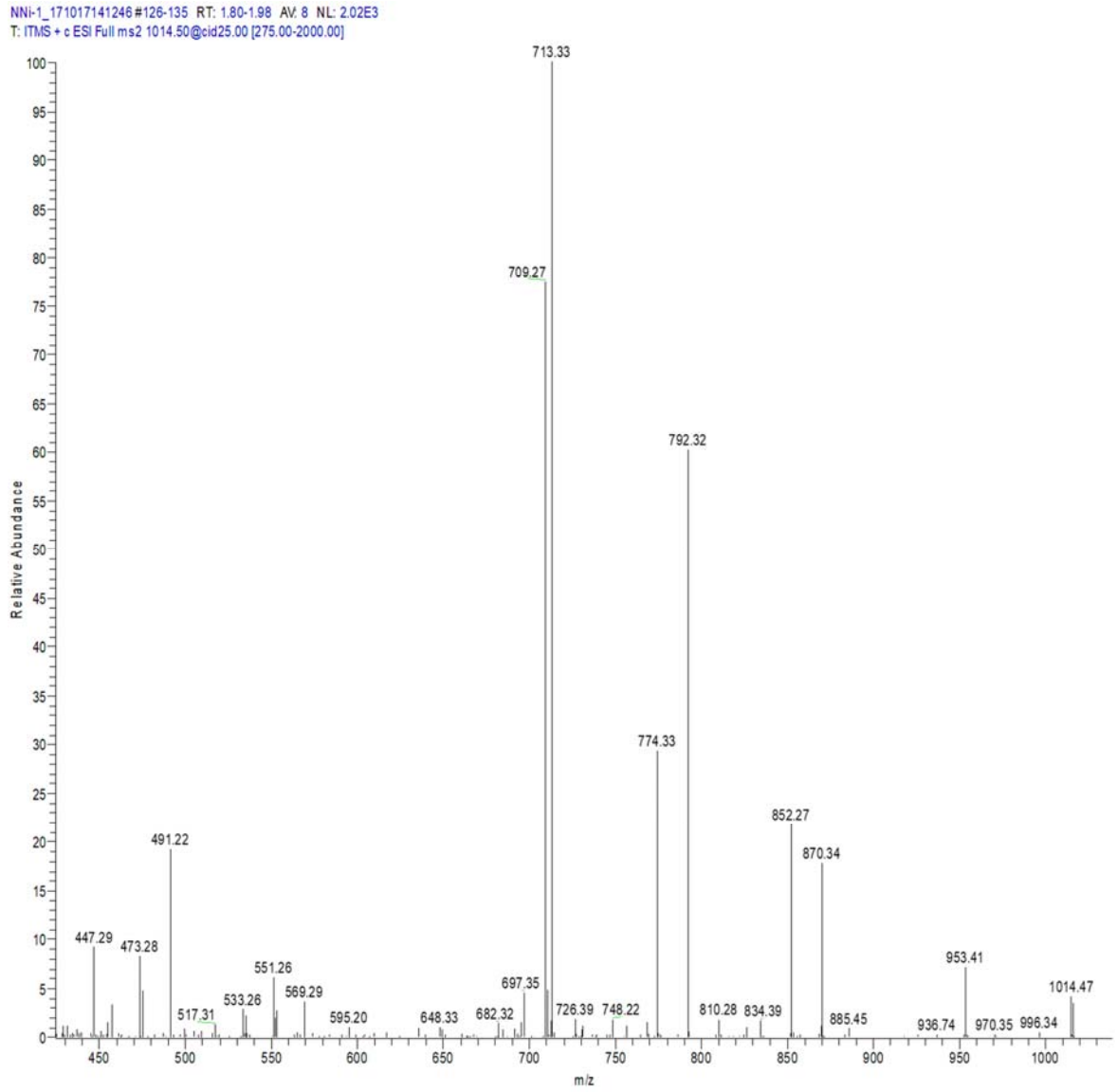

Figure S 28. MS^n Spectrum for compound **1**.

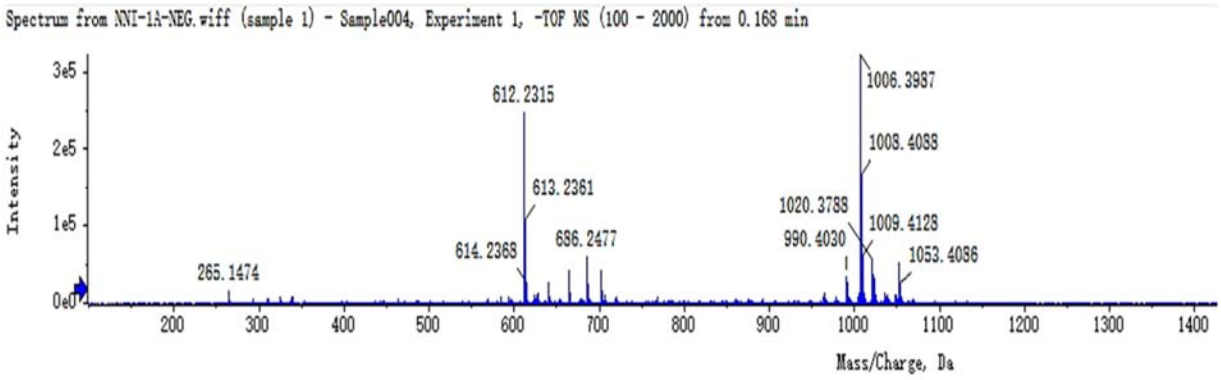

Figure S 29. HR-TOF-MS spectrum in negative mode for compound **2.**

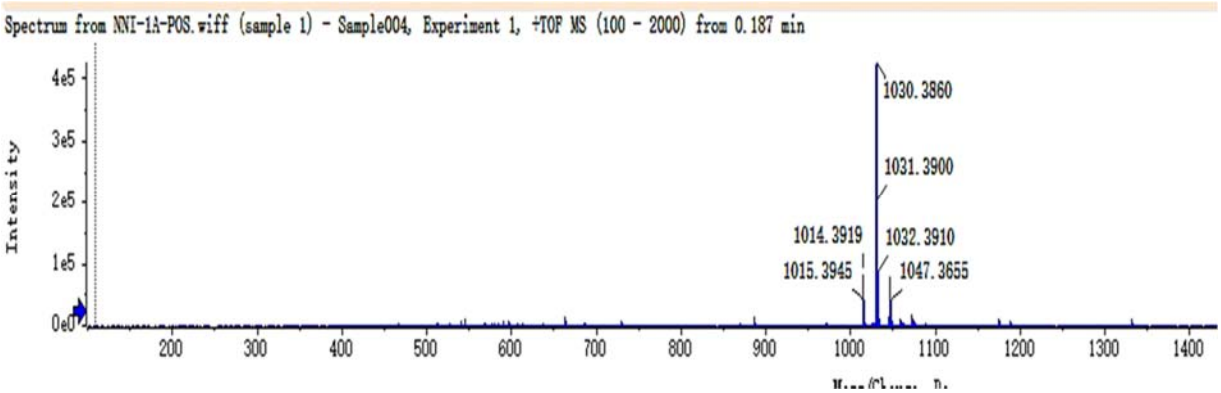

Figure S 30. HR-TOF-MS spectrum in negative mode for compound **2.**

Table S 1. Biological activities of compounds (**1**-**5**) (MIC values are given in μg/mL)

Compounds	MRSA	*Pseudomonas aeruginosa*	*Klebsiella pneumoniae*	*Escherichia coli*	*Bacillus subtilis*
	MIC	MIC	MIC	MIC	MIC
1	16	16	16	16	8-16
2	16	16	16	16	8-16
3	16-32	16-32	16-32	-	-
4	32	16	16	16	16
5	32	16	16	16	16
Tetracycline	16	32	32	16	8

Strain	16S rDNA gene sequence
Streptomyces pratensis NA-ZhouS1	AGGGCGGGCGTGCTTACCATGCAGTCGAACGATGAAGCCTTTCGG GGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCC CTTCACTCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATA ACACTCTGTCCCGCATGGGACGGGGTTAAAAGCTCCGGCGGTGAA GGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGTAATGGCCTAC CAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACA CTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGG GGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGT GAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAG AAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTAC GTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTGTCCGGA ATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGATGT GAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGATACGGGCTAG CTAGAGTGTGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAA ATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCT GGGCCATTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACA GGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTGGGAACTAG GTGTTGGCGACATTCCACGTCGTCGGTGCCGCAGCTAACGCATTAA GTTCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGA ATTGACGGGGGCCCGCACAAGCAGCGGAGCATGTGGCTTAATTCG ACGCAACGCGAAGAACCTTACCAAGGCTTGACATATACCGGAAAG CATCAGAGATGGTGCCCCCCTTGTGGTCGGTATACAGGTGGTGCAT GGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAA CGAGCGCAACCCTTGTTCTGTGTTGCCAGCATGCCCTTCGGGGTGA TGGGGACTCACAGGAGACTGCCGGGGTCAACTCGGAGGAAGGTGG GGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACG TGCTACAATGGCCGGTACAATGAGCTGCGATGCCGCGAGGCGGAG CGAATCTCAAAAAGCCGGTCTCAGTTCGGATTGGGGTCTGCAACTC GACCCCATGAAGTCGGAGTTGCTAGTAATCGCAGATCAGCATTGCT GCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCA CGAAAGTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGG AGGAGCTTCGAAGGTGTACGGCAAGTTTCCCTT

Figure S 31. 16S ribosomal DNA gene, full sequence of Streptomyces sp. NA-ZhouS1

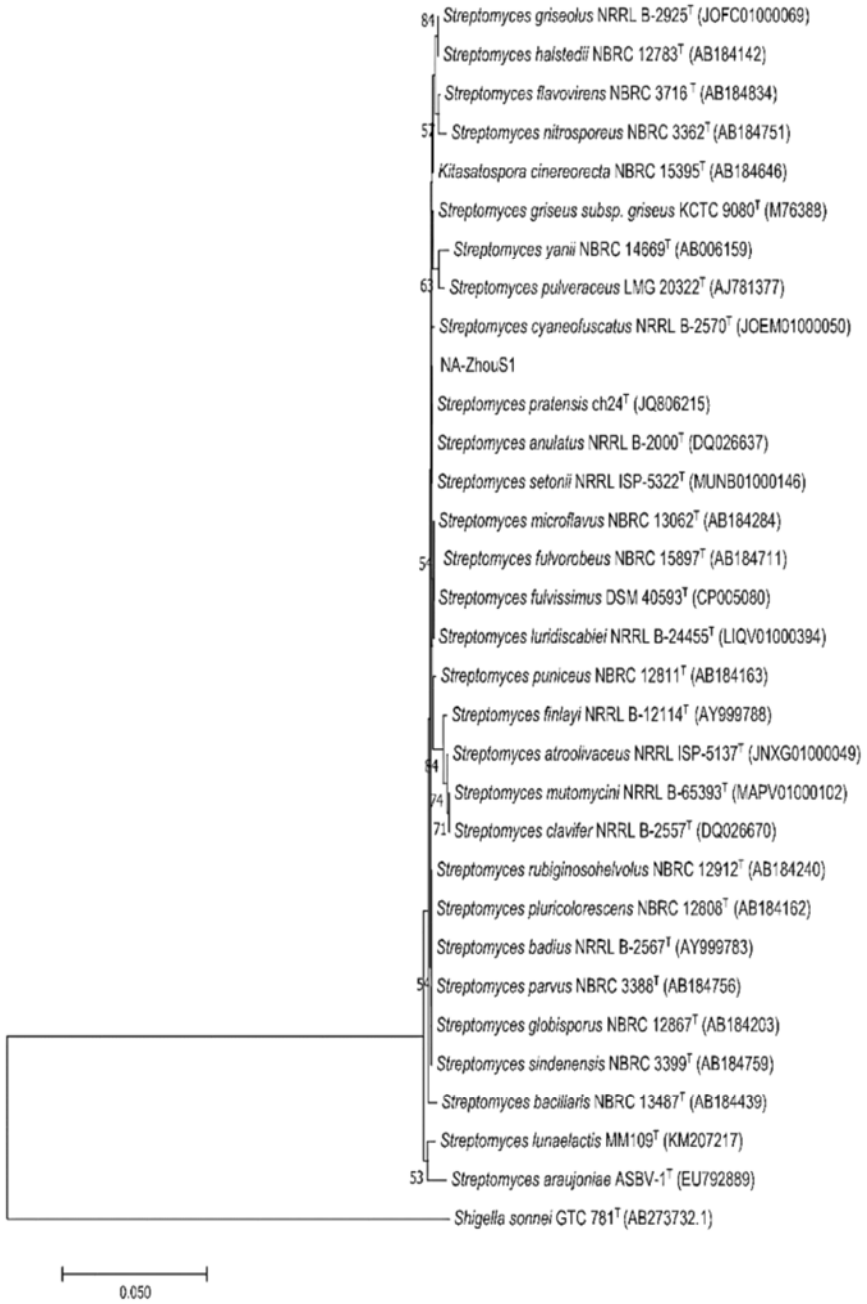

Figure S 32. Neighbor-joining phylogenetic tree of strain NA-ZhouS1 based on 16S rDNA sequences generated by Mega version 7. Numbers at branch points indicate levels of bootstrap (expressed as percentages of 1000 replicates), only values exceeding 50% are given. *Shigella sonnei* GTC 781^T (AB273732.1) was used as an outgroup. Bar, 0.050 substitutions per nucleotide position.