

Supplementary Information

1. 18S rDNA Sequence Information of the Strain Z-4

The amplification by the primers of NS1 (5'-GTAGTCATATGCTTGTCTC-3') and NS8 (5'-TCCGCAGGTTACCTACGGA-3') obtained 18S rDNA sequence information of Z-4 as follows:

GGTCGCATGTCTAGTATATGCACTTTATACCGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATT
TGATAGTACCTTACTACATGGATACCTGTGGTAATTCTAGAGCTAATACATGCTAAAAACCCCGACTTCGG
AAGGGGTGTATTTATTAGATAAAAAACCAATGCCCTTCGGGGCTCCTTGGTGATTGATAATAACTTAACGA
ATCGCATGGCCTTGCGCCGGCGATGGTTCATTCAAATTTCTGCCCTATCAACTTTTCGATGGTAGGATAGTG
GCCTACCATGGTGGCAACGGGTAACGGGGAATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG
CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATA
AATACTGATACGGGGCTCTTTTGGGTCTCGTAATTGGAATGAGTACAATTTAAATCCCTTAACGAGGAACA
ATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTTGC
AGTTAAAAAGCTCGTAGTTGAACCTTGGGTCTGGCTGGCCGGTCCGCCTCACCGCGAGTACTGGTCCGG
CTGGACCTTTCTTCTGGGGAATCCCATGGCCTTCACTGGCTGTGGGGGGAACCAGGACTTTTACTGTGA
AAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAATACATTAGCATGGAATAATAGAATAGGACGTGCG
GTTCTATTTTGTGTTTCTAGGACCGCCGTAATGATTAATAGGGATAGTCGGGGGCGTCAGTATTCAGCT
GTCAGAGGTGAAATCTTGGATTTGCTGAAGACTAACTACTGCGAAAGCATTGCGCAAGGATGTTTTTCAT
TAATCAGGGAACGAAAGTTAGGGGATCGAACGATCAGATACCGTCGTAGTCTTAACCATAAACTATGCCG
ACTAGGGATCGGGCGGTGTTTCTATGATGACCCGCTCGGCACCTTACGAGAAATCAAAGTTTTTGGGTTC
TGGGGGGAGTATGGTCGCAAGGCTGAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGC
CTGCGGCTTAATTTGACTCAACACGGGGAACTCACCAGGTCCAGACAAAATAAGGATTGACAGATTGA
GAGCTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAA
TTGCGATAACGAACGAGACCTCGGCCCTTAAATAGCCCGGTCCGCATTTGCGGGCCGCTGGCTTCTTAGG
GGGACTATCGGCTCAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGG
CCGCACGCGCGCTACACTGACAGGGTCAGCGAGTACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGT
TAAACCCTGTCTGTGCTGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAGGCACG
AGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG
CTCGGTGAGGCCTTCGGACTGGCTCAGGAGGGTTGGCAACGACCCCCCAGAGCCGGAAAGTTGGTCAA
ACCCGGTCATAGAGAAGAAAGTATT

Figure S1. Comparing the Sequence with Those in NCBI Gene Bank.

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
NW_001884680.1	Aspergillus oryzae RIB40 contig SC206	3051	3051	99%	0.0	99%
NW_001849579.1	Aspergillus oryzae RIB40 contig rDNA_te13	3051	3051	99%	0.0	99%
NT_166520.1	Aspergillus niger CBS 513.88 supercontig An03	3046	1.025e+04	99%	0.0	99%
NC_007197.1	Aspergillus fumigatus Af293 chromosome 4, whole genome shotgun	3046	4439	99%	0.0	99%
NT_165929.1	Aspergillus terreus NIH2624 scaffold_6 genomic scaffold, whole genome	2972	2972	99%	0.0	98%
NW_001510400.1	Aspergillus clavatus NRRL 1 1099423829788 genomic scaffold, whole genome	2918	2918	94%	0.0	99%
NW_002990118.1	Talaromyces stipitatus ATCC 10500 scf_1105507295515, whole genome	2915	2915	99%	0.0	98%
NW_003101676.1	Ajellomyces dermatitidis SLH14081 genomic scaffold supercont1.7	2824	1.493e+04	99%	0.0	97%
NW_003217216.1	Paracoccidioides brasiliensis Pb01 supercont1.72 genomic scaffold	2813	9289	99%	0.0	97%
NW_003217281.1	Paracoccidioides brasiliensis Pb01 supercont1.7 genomic scaffold	2813	8440	99%	0.0	97%

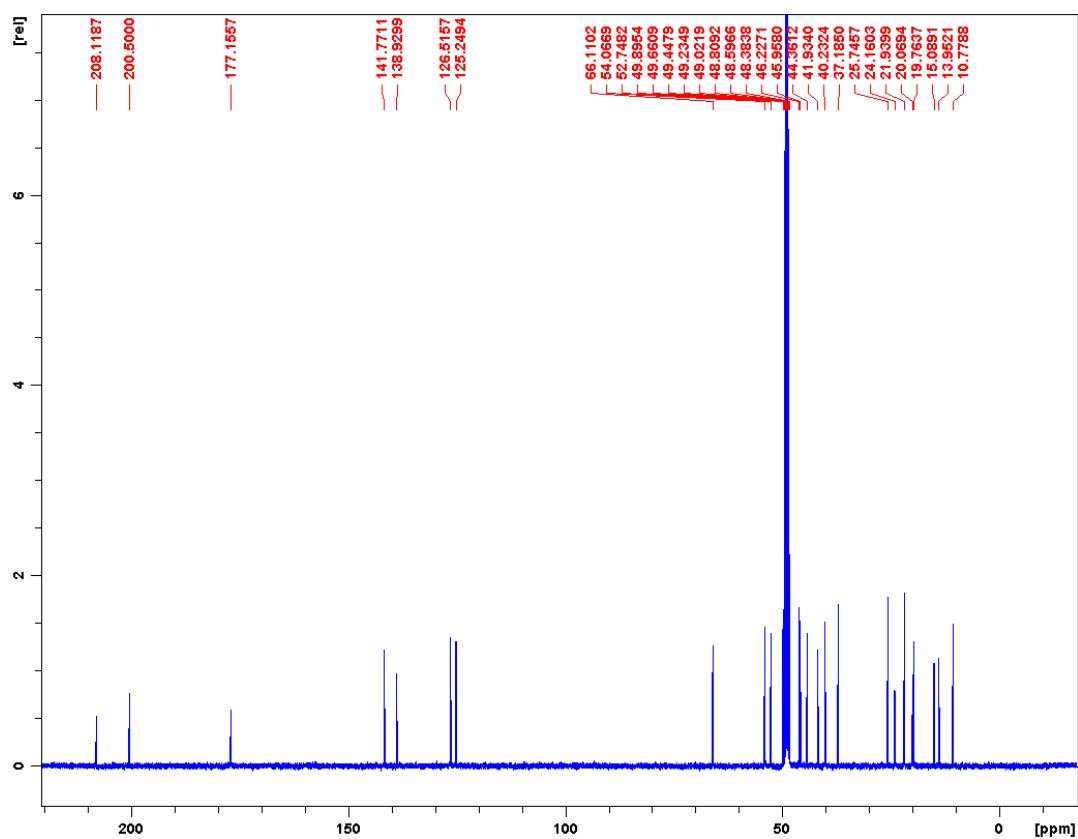


Figure S4. DEPT135 Spectrum for Compound 1.

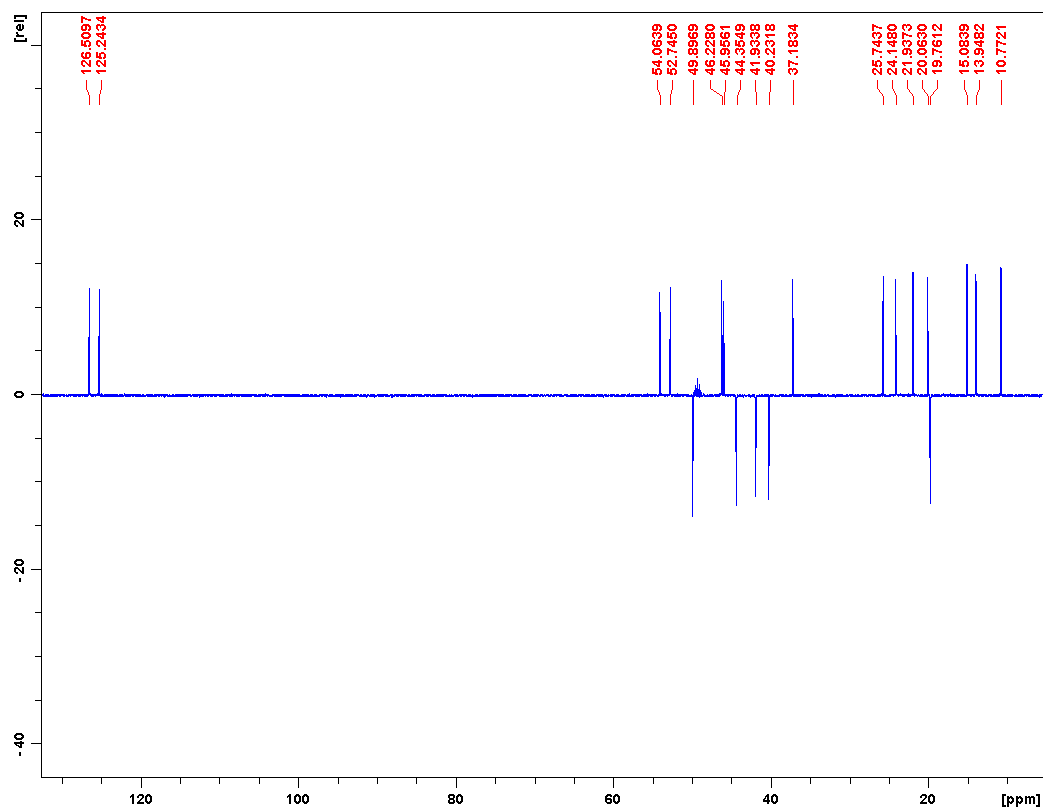


Figure S5. DEPT90 Spectrum for Compound 1.

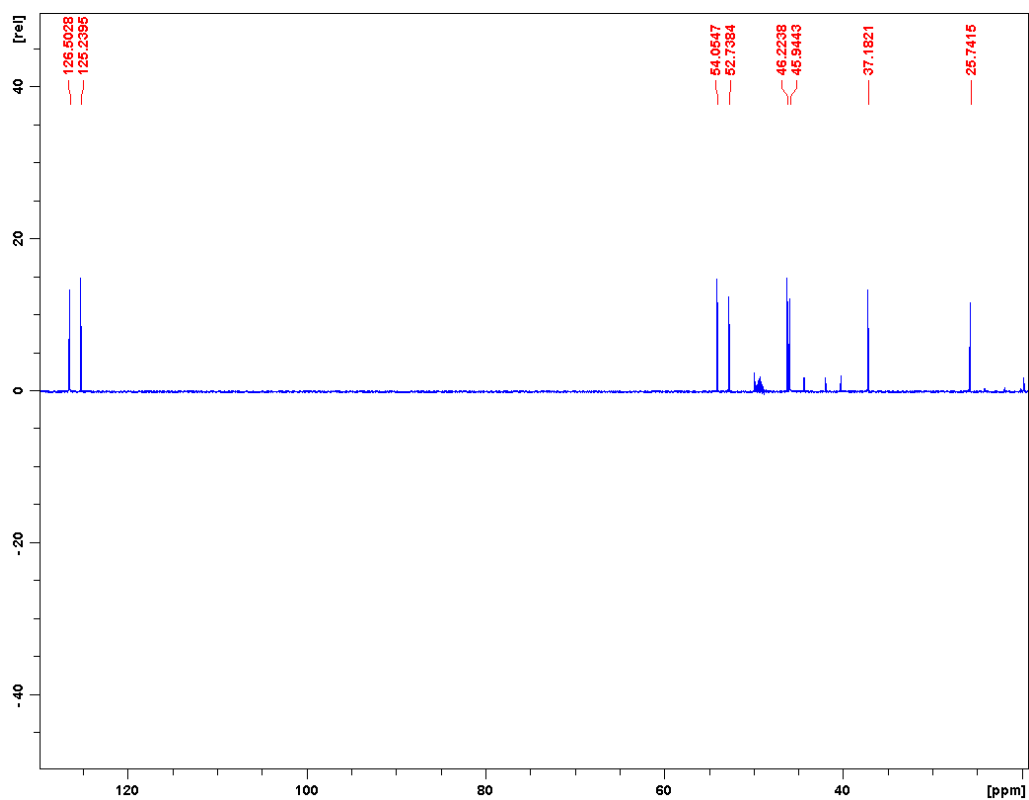


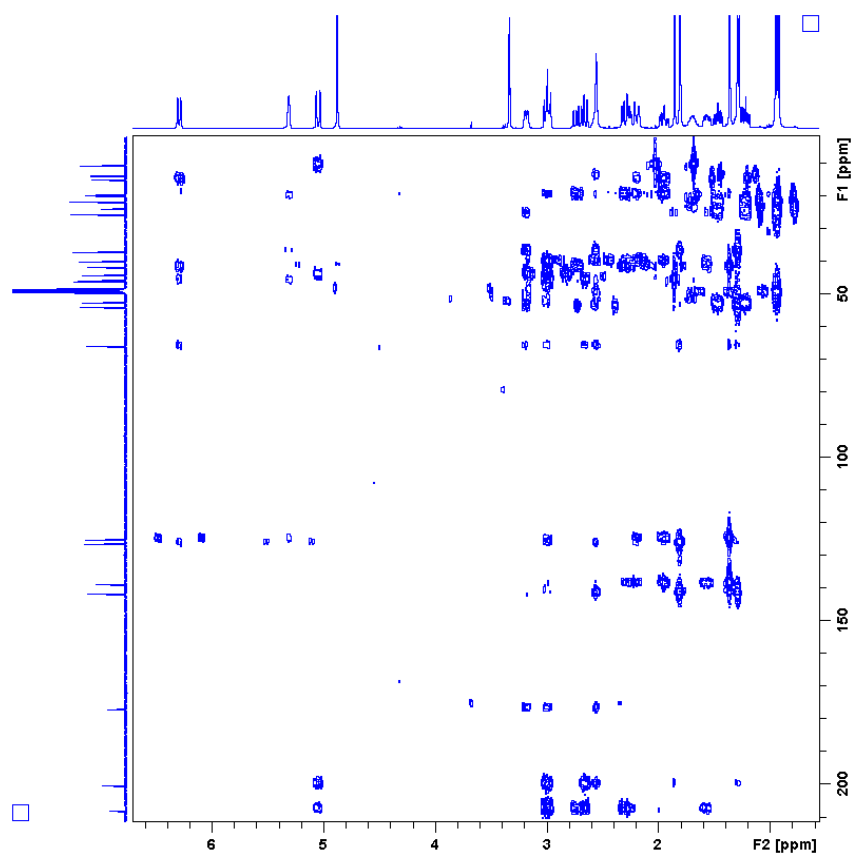
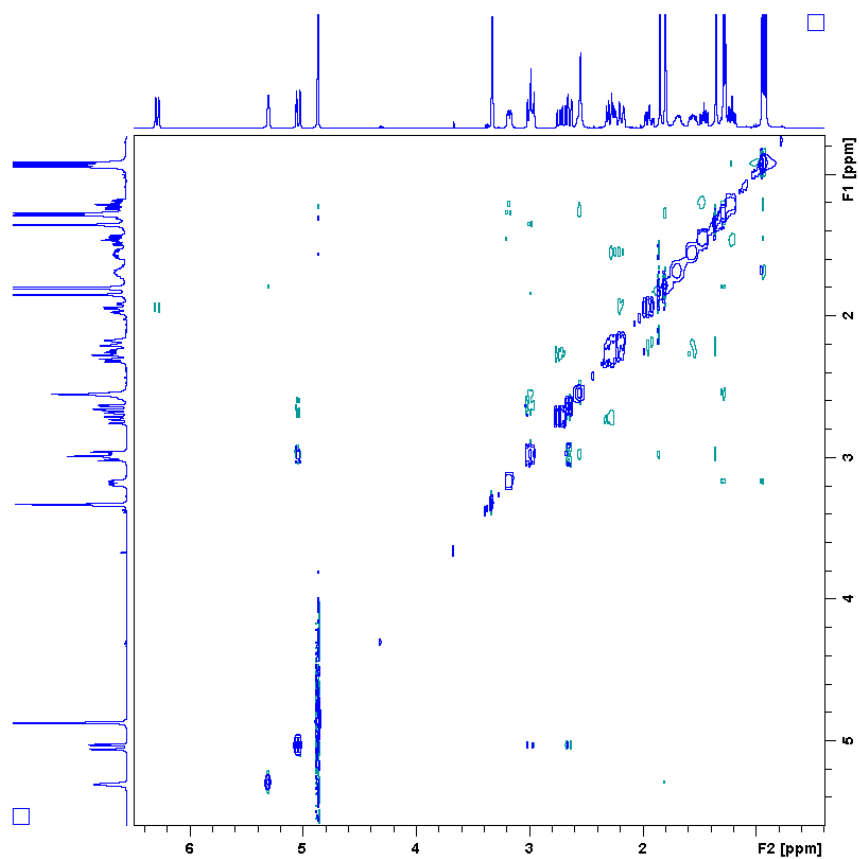
Figure S8. HMBC for Compound 1.**Figure S9.** NOESY for Compound 1.

Figure S10. Proton NMR for Compound 2.

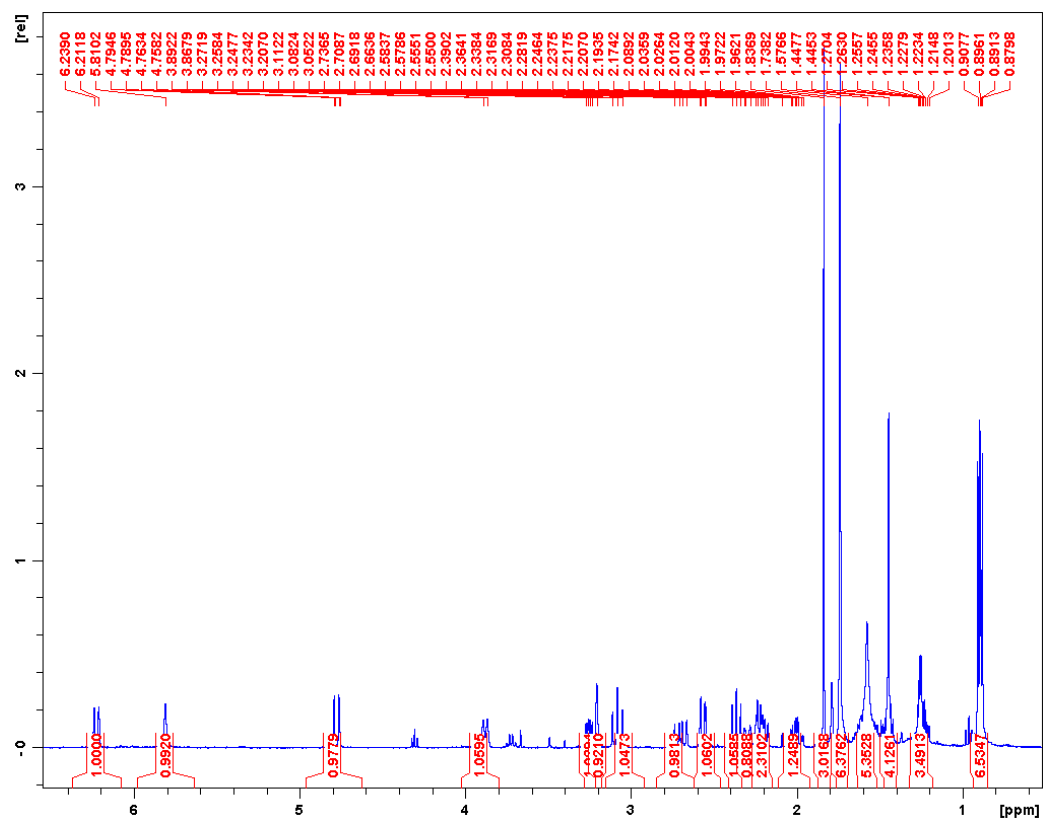


Figure S11. Carbon NMR for Compound 2.

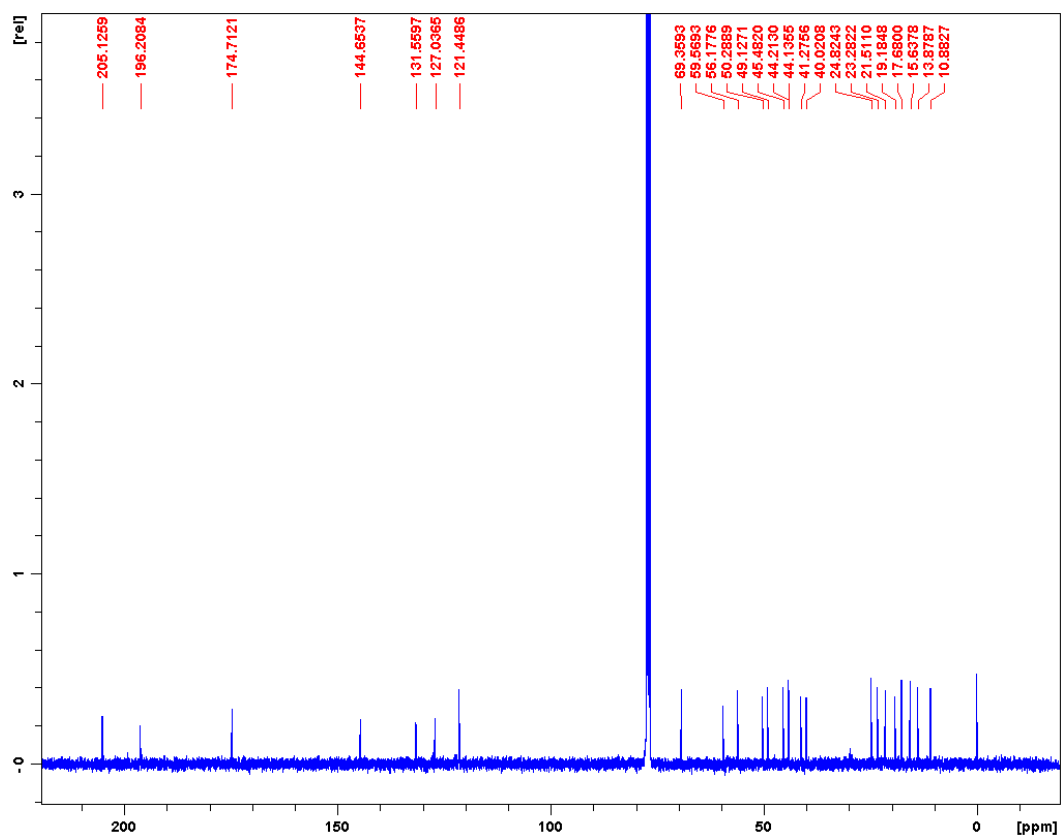


Figure S12. DEPT135 Spectrum for Compound 2.

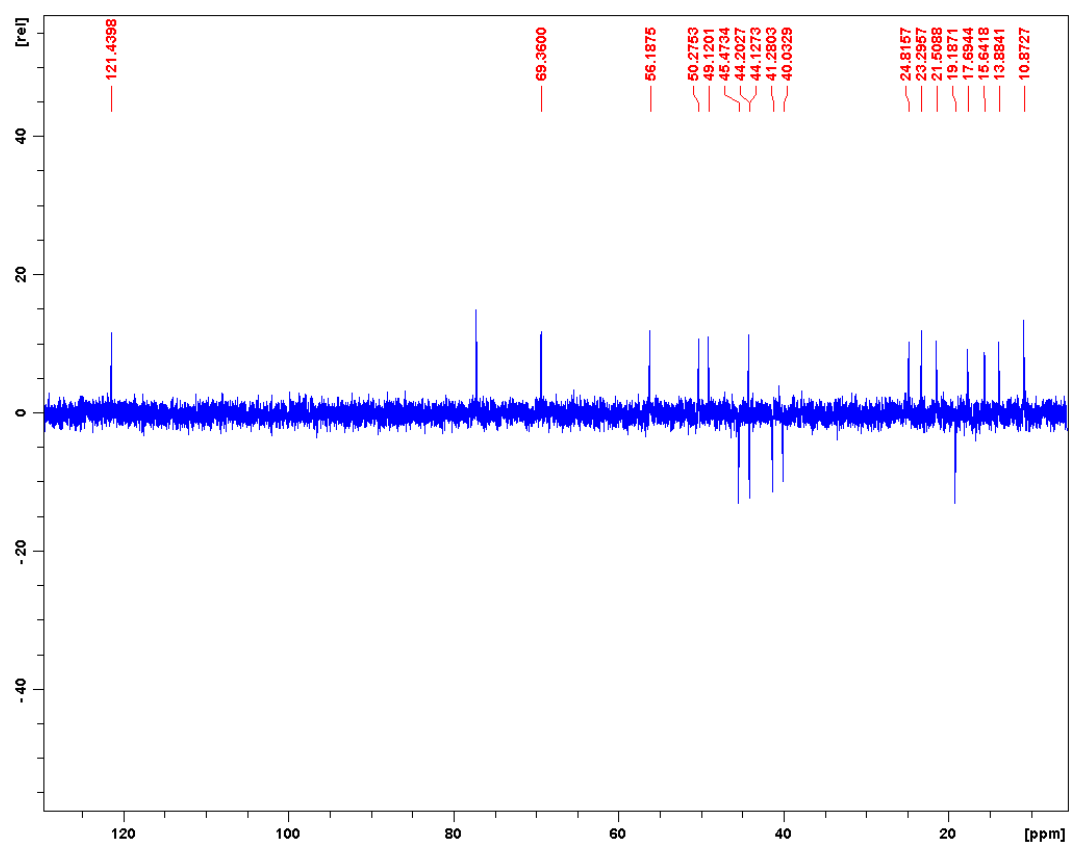


Figure S13. DEPT90 Spectrum for Compound 2.

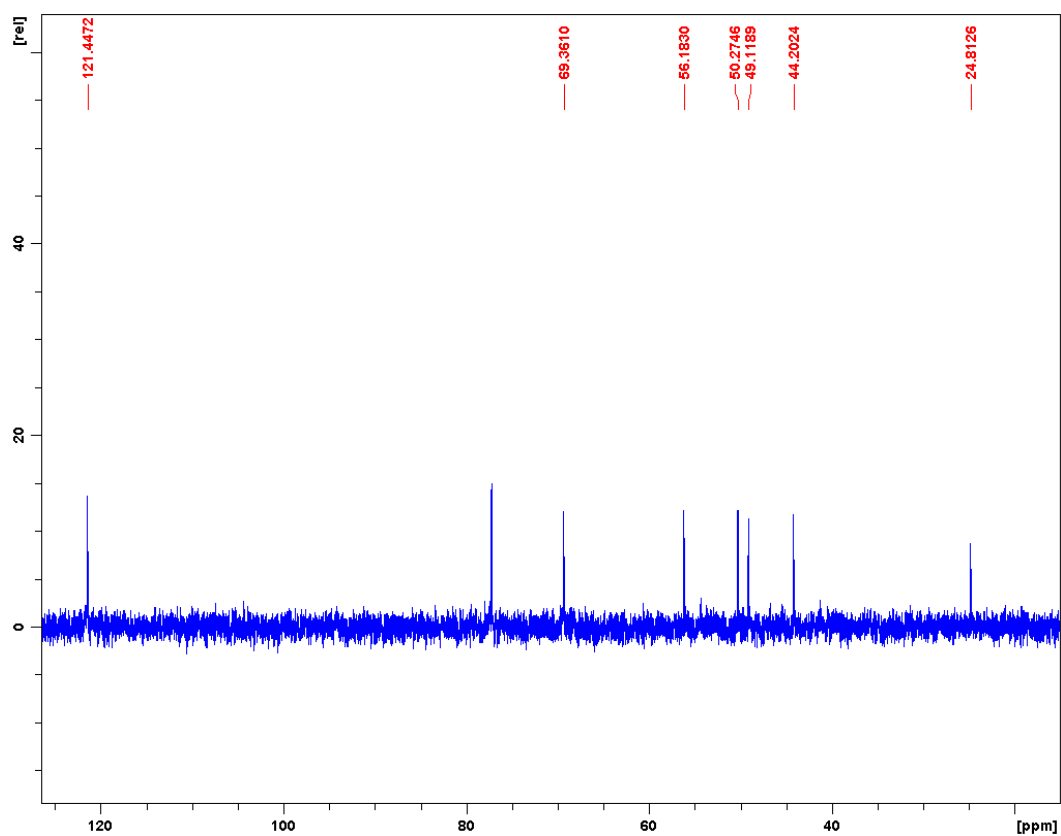


Figure S14. HMQC for Compound 2.

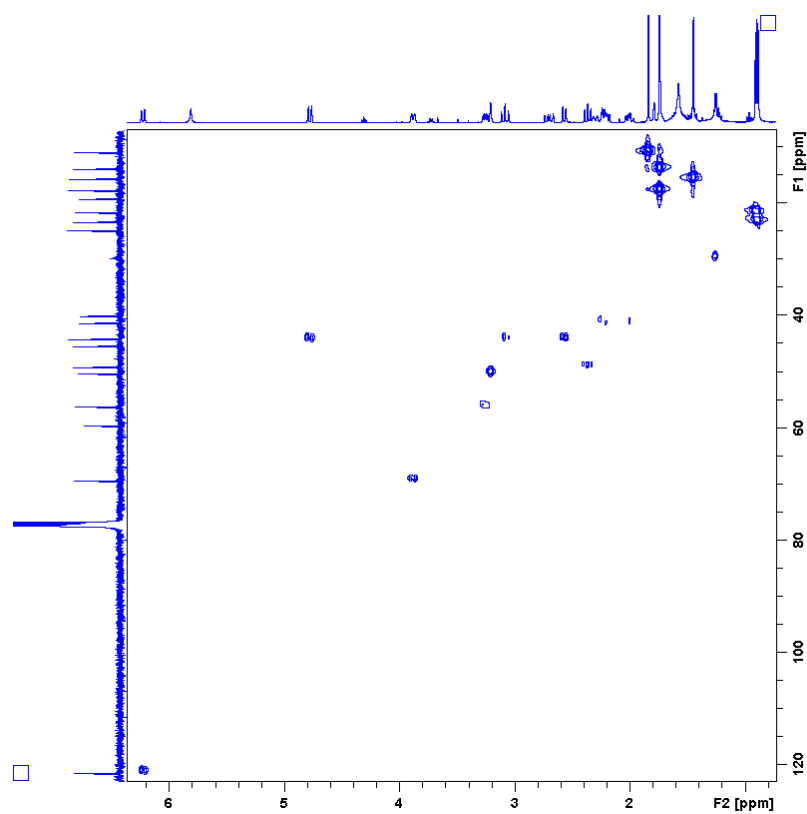


Figure S15. HMBC for Compound 2.

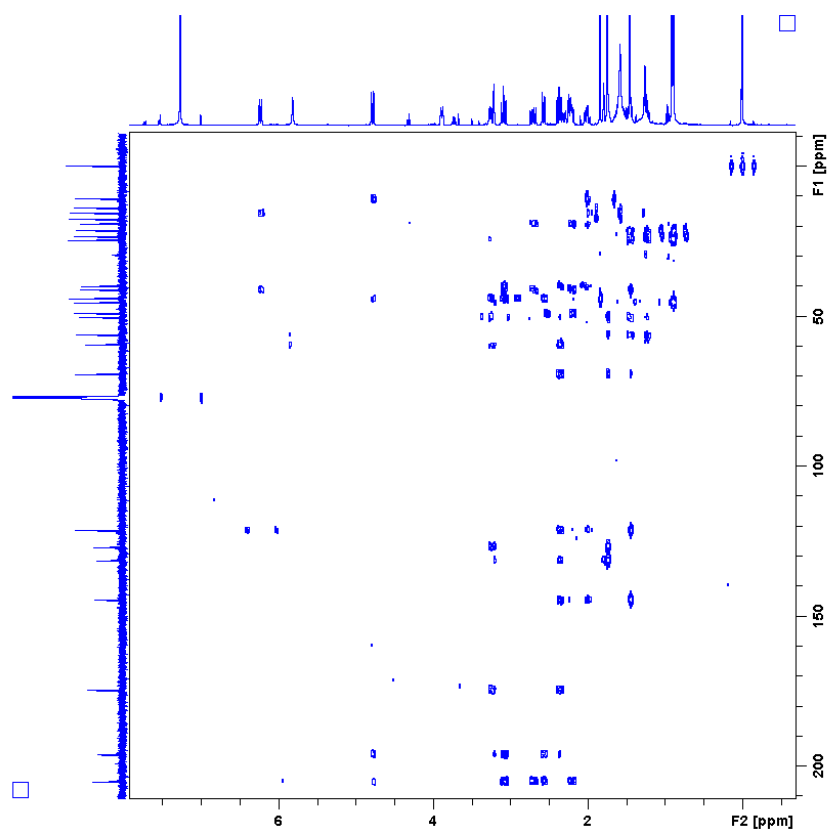
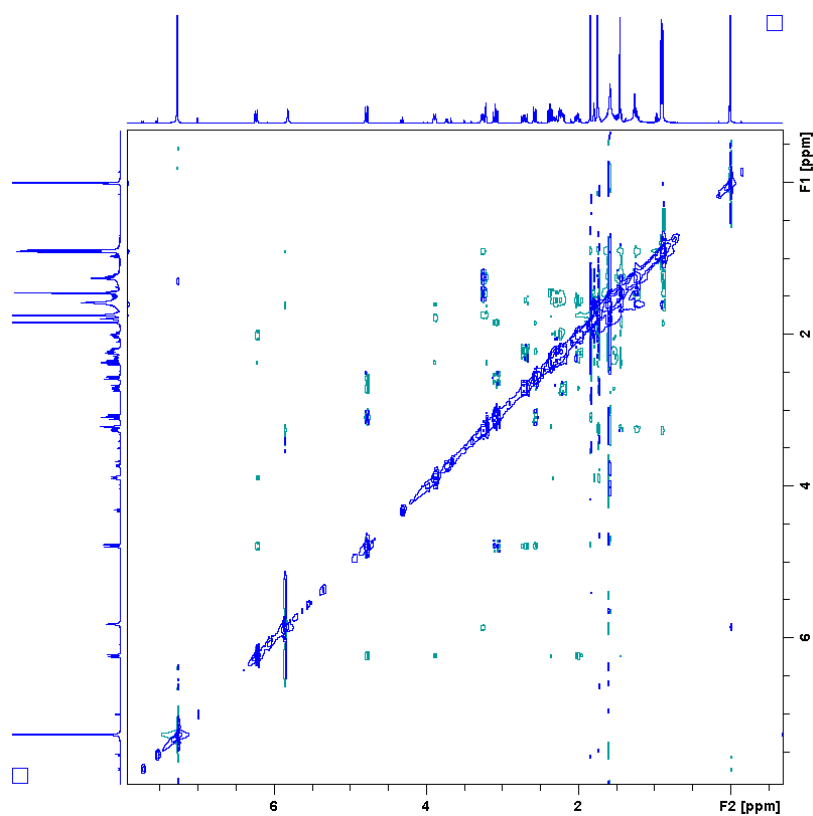


Figure S16. NOESY for Compound 2.

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