Electronic Supplementary Material (ESI) for RSC Advances.

Tetrocarcins N and O, glycosidic spirotetronates from a marine-derived *Micromonospora* sp. identified by PCR-based screening

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Supporting Information

Contents

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ChaH1          -MRILITGGAGFIGSHFVRSLLDDRYAGWEGARVTVLDKLTYAGNRASLP--ASHPRLTF 60
ChlC2          -MRYFVTGGAGFIGGHYVRALLAGAYPGTAGCEVTVLDKLTYAAHLDNLP--LDHDRLTF 60
ChmAII         -MRVLVTGAAGFIGSHFVRQLLSGSYPELAGAHVLSLDKLTYAGNTENLAEVAGHPRHTF 60
ChryE          TTHLLVTGGAGFIGSHYVRTLLSPEGP--GDISVTVLDALTYAGNPANLDPVRAHPGFTF 60
LanH           MKKILITGGAGFIGSHYVRTLLNDGYEDWKGAHVTVLDKLTYAGNRDNLP--EAHPRLTF 60
PdmY           -MRILVTGGAGFIGSHYVRSVLAGRYPAVADALVTVVDKLTYAGNTDNLP--IGDPRLTF 60
RhoH           -MNIPVTGAAGFIGSHFVRTLLSGGYPGHEDDRVTVVDKLTYAGTLNNLP--PRHPRLTF 60
StrE           ATRLLVTGGAGFIGSHYVRTLLGPDGP--PDAVVTVLDALSYAGNLANLDPVRDHPPVRF 60
TcaB2          SKRVVVTGGAGFIGSHYVRQLIGGAYPAFADASVVVLDKLTYAGNLDNLAAVSGDERFEL 60
UrdH           -MNILVTGAAGFIGSHFVRSLLADTYSGWEGARVTALDKLTYAGNRNNLP--PSNPRLEF 60
dTGD_5-297a    ---------------------------------VVVLDKLTYAGNLDNLAAVSGDERFEL 60
dTGD_5-297b    -------------------------YVGFEDCHVTVLDKLTYASDRNNLP--AHHPRLTF 60
                                         *  :* *:**.   .*    .    :

ChaH1          VQGDVCDSALLREVLPGHDAVVHFAAESHVDRSITGAAEFFRTNVLGTQALLDAVLATGV 120
ChlC2          VRGDICDAGLLADLLPGHDAVVHFAAESHVDRSLADGTPFVTTNVLGTQILLDACARTGV 120
ChmAII         LHGDICDPPTVAQALRGTDLVVHFAAESHVDRSITDSAAFVTTNVLGTQTLLRSALEAGV 120
ChryE          VRGDICDAPLVRSLARRADQIVHFAAESHVDRSITDPAAFTRTNVMGTQILLDAALRAGT 120
LanH           VQGDICDFELLLELLPGHDAVVHFAAESHVDRSLESAEEFVHTNVTGTQRLLDAVLATRV 120
PdmY           VKGDICDVPLLRELLPGHDAVVHFAAESHVDRSLVSAGEFAVTNVLGTQSLLDCCVLAGI 120
RhoH           VHGDICDTPLLGKVFPGHEAVVHFAAESHVDRSVAGAEAFVRTNVLGTQALLEAALRHGT 120
StrE           VHGDICDADLVRVMAG-QDQVVHLAAESHVDRSLLDAAAFVRTNAGGTQTLLDAALRHGV 120
TcaB2          VVGDICDAQLLAGLLPGADVVVHFAAESHVDRSIVGAADFMHTNVQGTYTVLQACLDAGV 120
UrdH           VRGDVCDRALLRELLPGHHAVVHFAAESHVDRSLEGAGEFFRTNVLGTQTLLDAVLDSGV 120
dTGD_5-297a    VVGDICDAQLLAGLLPGADVVVHFAAESHVDRSIVGAADFMHTNVQGTYTVLQACLDAGV 120
dTGD_5-297b    VRGDICDRPLLADLVPGHDALVHFAAESHVDRSIDDPAPFFETNVMGSHHLLAACARAAV 120
               : **:**   :       . :**:*********: .   *  **. *:  :* .

ChaH1          ERVVHVSTDEVYGSIEEGAWTEEWPLLPNTPYAASKAGSDLVARSYWRTHGVDVSVTRCS 180
ChlC2          PRFVHVSTDEVYGSLRHGSWTEDTLLEPNSPYAASKAASDLMARAYWRTSDVAVSITRCS 180
ChmAII         SRFVHVSTDEVYGSIPEGSSTEADPLDPNSPYAASKASSDLLALAFHRTHGLDVRVTRCS 180
ChryE          RTFVHISTDEVYGSIDEGSWPEDHPLRPSSPYAASKASSDLLALSHHHTHGLDVRVTRCS 180
LanH           KRVVHVSTDEVYGSIDEGSWTEEWPLAPNSPYSASKAASDLLARSYWRTHGLDLSITRCS 180
PdmY           GRVVHVSTDEVHGSIDTGSWDEAAPVDPRSPYAASKAASDHFALAYHHTHRLPVMITRCS 180
RhoH           GVFVQVSTDETYGSIAEGSWTEDEPLLPNSPYAASKASADLIARSYWRTHGLDVRVTRCA 180
StrE           APFVQVSTDEVYGSLETGSWTEDEAVRPNSPYAASKASGDLLALAMHVSHGLDVRITRCS 180
TcaB2          GRVVQVSTDEVYGSIATGSWPESDPLEPNSPYSASKACGDLIARSYFRTYGLPVCLTRCS 180
UrdH           ERVVHVSTDEVYGSIEQGSWTEDWPLQPNSPYAASKACSDLVARAYCAPTEVDLSITRCS 180
dTGD_5-297a    GRVVQVSTDEVYGSIATGSWPESDPLEPNSPYSASKACGDLIARSYFRTYGLPVCLTRCS 180
dTGD_5-297b    GRVVHVSTDEVYGSITDGSWTERCVLEPNSPYAASKAASDCVVRSYWRTYDVDVSITRCA 180
                 .*::****.:**:  *:  *   : * :**:**** .* .. :   .  : : :***:

ChaH1          NNYGPYQHPEKLIPLFITNLLEGRPVPLYGDGRNVREWMHVDDHCRALHLVLNNGRAGEV 240
ChlC2          NNYGTHQFIEKVVPLFVTNLLDGLDVPLYGDGHHVREWLHVEDHCRALHLVLTEGRAGEI 240
ChmAII         NNYGPHQHPEKVVPLFVTHLLEGLRLPLYGDGLHRRDWLHVDDHCRGIAMVAARGRAGEV 240
ChryE          NNYGHHHFPEKAIPLFVTRLLDGRKVPLYGDGRNVRDWLHIDDHVRAVELVRTSGRPGEV 240
LanH           NNYGPYQHPEKLIPLFVTNLLEGEQVPLYGDGGNIREWLHVDDHCRAIDLVLNKGRAGEI 240
PdmY           NNYGPYQFPEKVIPLFVTNLLAGRPVPLFGDGLHRRQWLHVSDHCDAVQRVLEDGAPGEV 240
RhoH           NNYGPGQHPEKLVPLFVTRLLDGQPVPLYGDGSNLREWLHVDDHCRAVRLVLDEGRPGEI 240
StrE           NNYGPYQFPEKLVPRFVTLLLEGRKVPLYGDGLHVRDWLHVDDHVRGIEAVRARGRAGRV 240
TcaB2          NNYGPHQYPEKIIPLFITNLLDGRPVPLYGDGHNVRDWLHVDDHCRAIQLVVEGGRPGEV 240
UrdH           NNYGPHQHPEKVIPRFVTNLLEGRQVPLYGDGRNVREWLHVEDHCRGIHLVLNKGQAGEI 240
dTGD_5-297a    NNY------------------------------------------------------------ 240
dTGD_5-297b    NNY------------------------------------------------------------ 240
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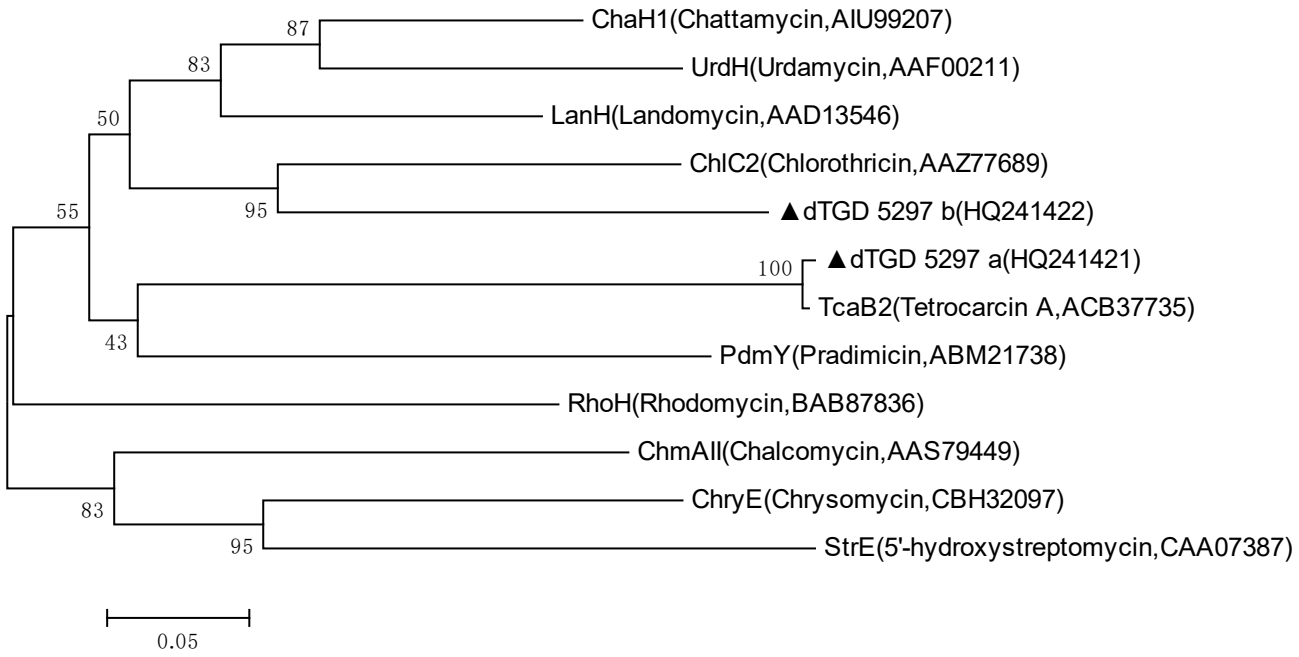
(a)



(**b**)

Figure S1. The amino acid sequence alignment (**a**) and the phylogenetic tree (**b**) of cloned dTDP-Glucose-4,6-dehydratase fragments with their known analogues. dTGD 5-297a (NCBI accession no. HQ241421) and dTGD 5-297b (accession no. HQ241422) are the cloned dTDP-glucose-4,6-dehydratase gene fragments identified from *Micromonospora* sp. 5-297; ChaH1 (accession no. AIU99207) for chattamycin biosynthesis from *Streptomyces chattanoogensis*; UrdH (accession no. AAF00211) for urdamycin A biosynthesis *S. fradiae*; LanH (accession no. AAD13546) for landomycin biosynthesis from *S. cyanogenus*; ChlC2 (accession no. AAZ77689) for chlorothricin biosynthesis from *S. antibioticus*; PdmY (accession no. ABM21738) for pradimicin biosynthesis from *Actinomadura hibisca*; TcaB2 (accession no. ACB37735) for tetrocarcin A biosynthesis from *Micromonospora chalcea*; RhoH (accession no. BAB87836) for rhodomycin biosynthesis from *S. violaceus*; ChmAII (accession no. AAS79449) for chalcomycin biosynthesis from *S. bikiniensis*; ChryE (accession no. CBH32097) for chrysomycin biosynthesis from *S. albaduncus*; StrE (accession no. CAA07387) for 5'-hydroxystreptomycin biosynthesis from *S. glaucescens*.

m/z	Theo. Mass	Delta (mmu)	RDB equiv.	Composition
1339.6581	1339.6558	2.26	18.5	$C_{67}H_{100}O_{24}N_2Na$

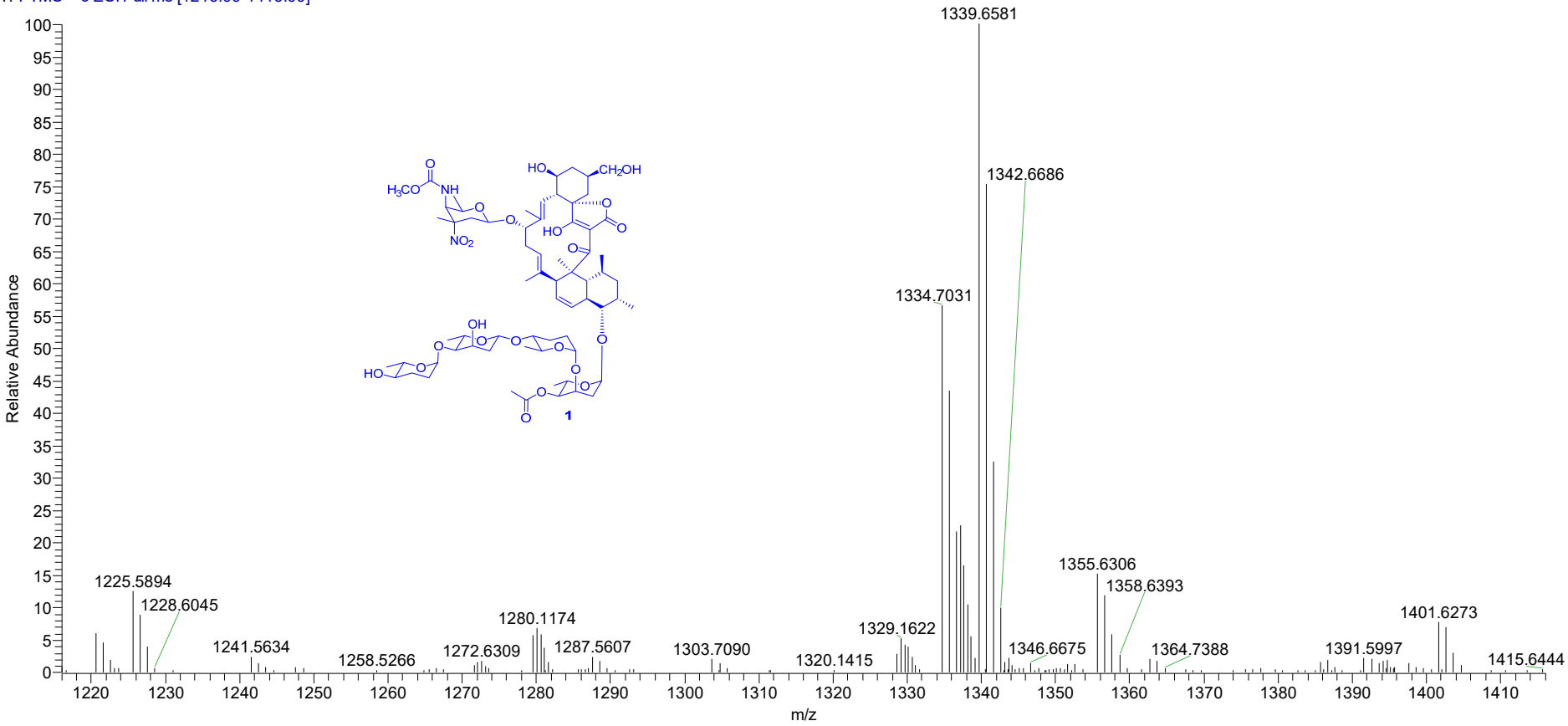


Figure S2. The (+)-HRESIMS spectrum of compound **1**

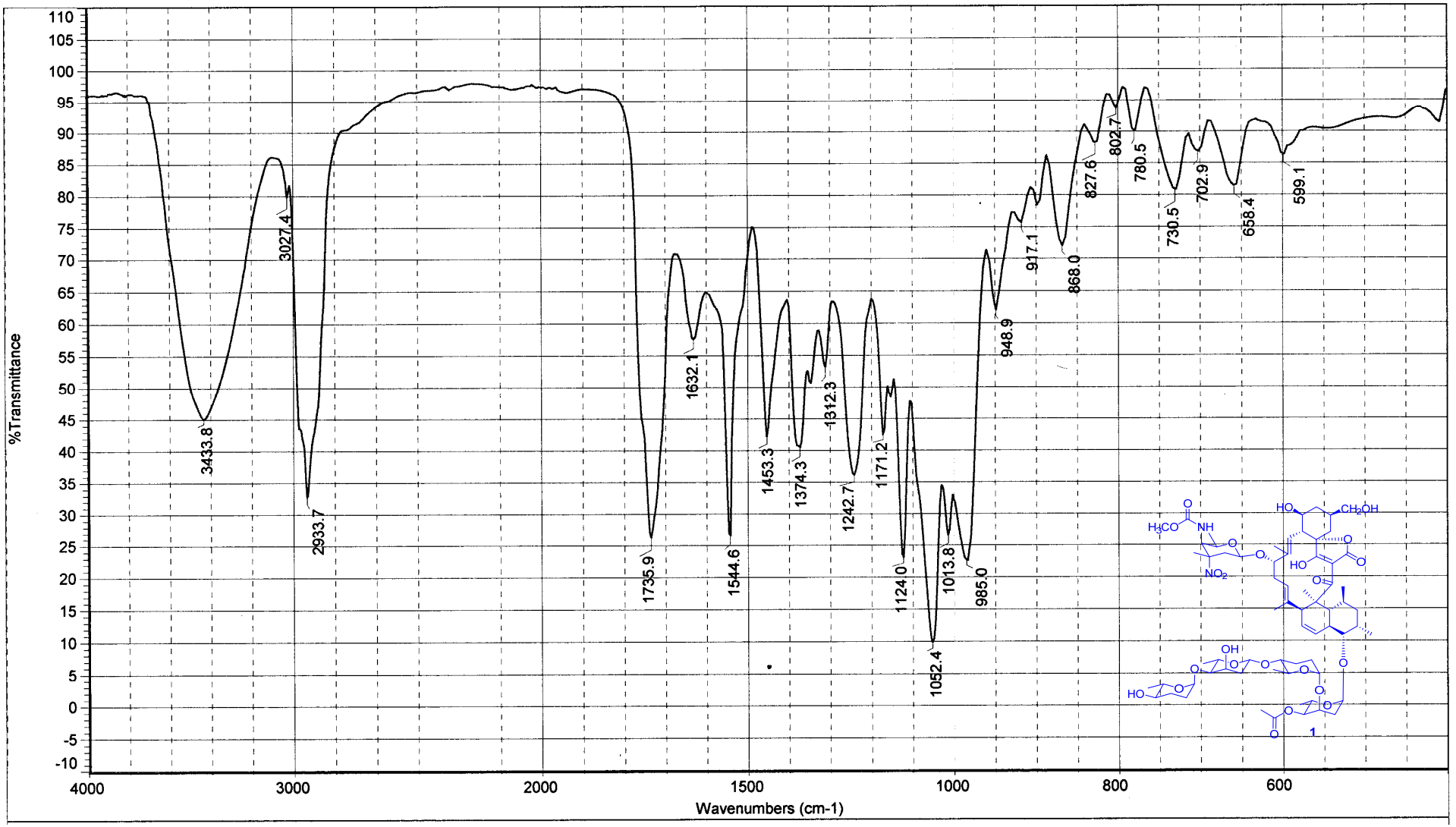


Figure S3. The IR spectrum of compound **1**

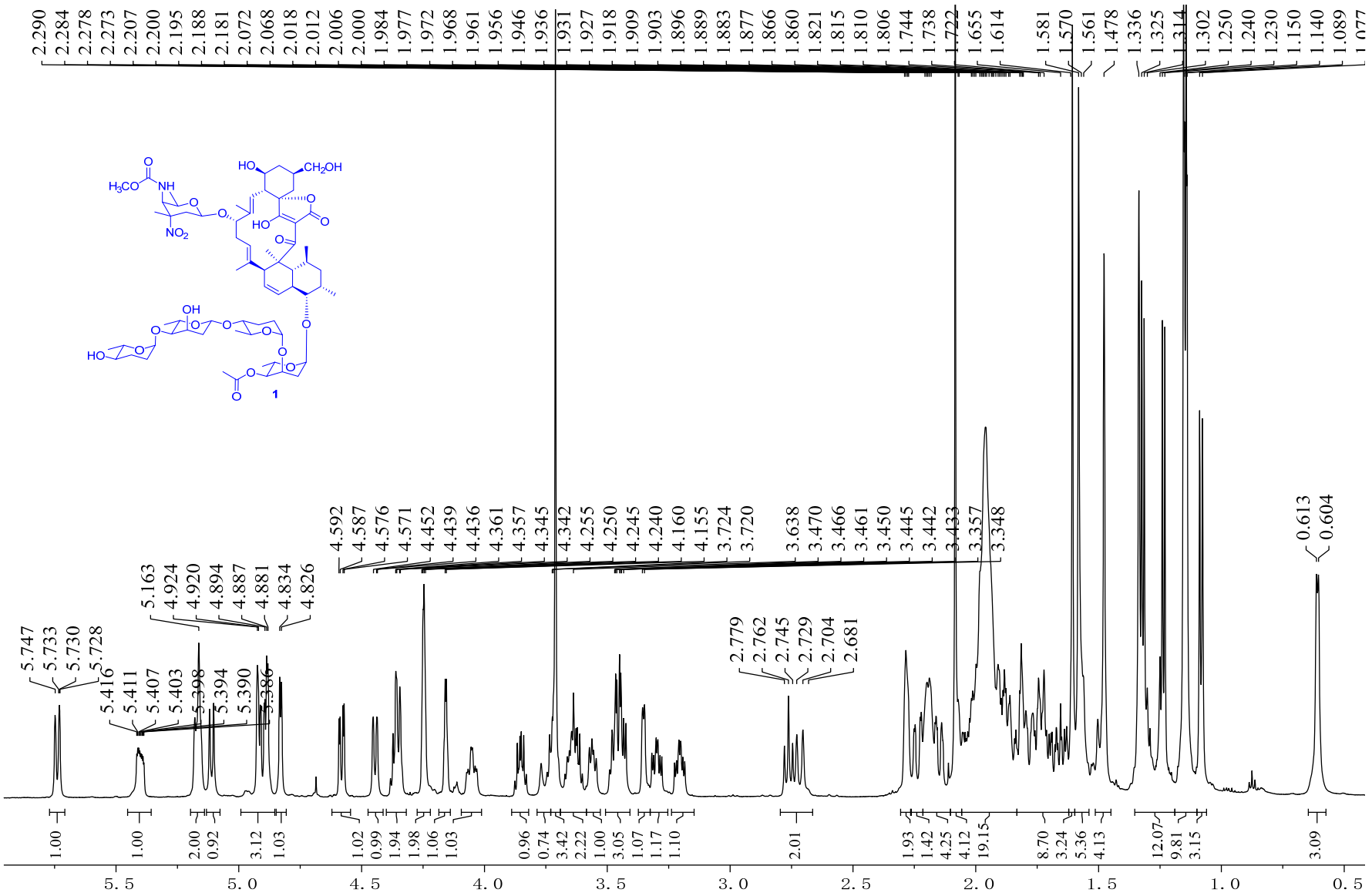


Figure S4. The ^{1}H NMR spectrum of compound **1**

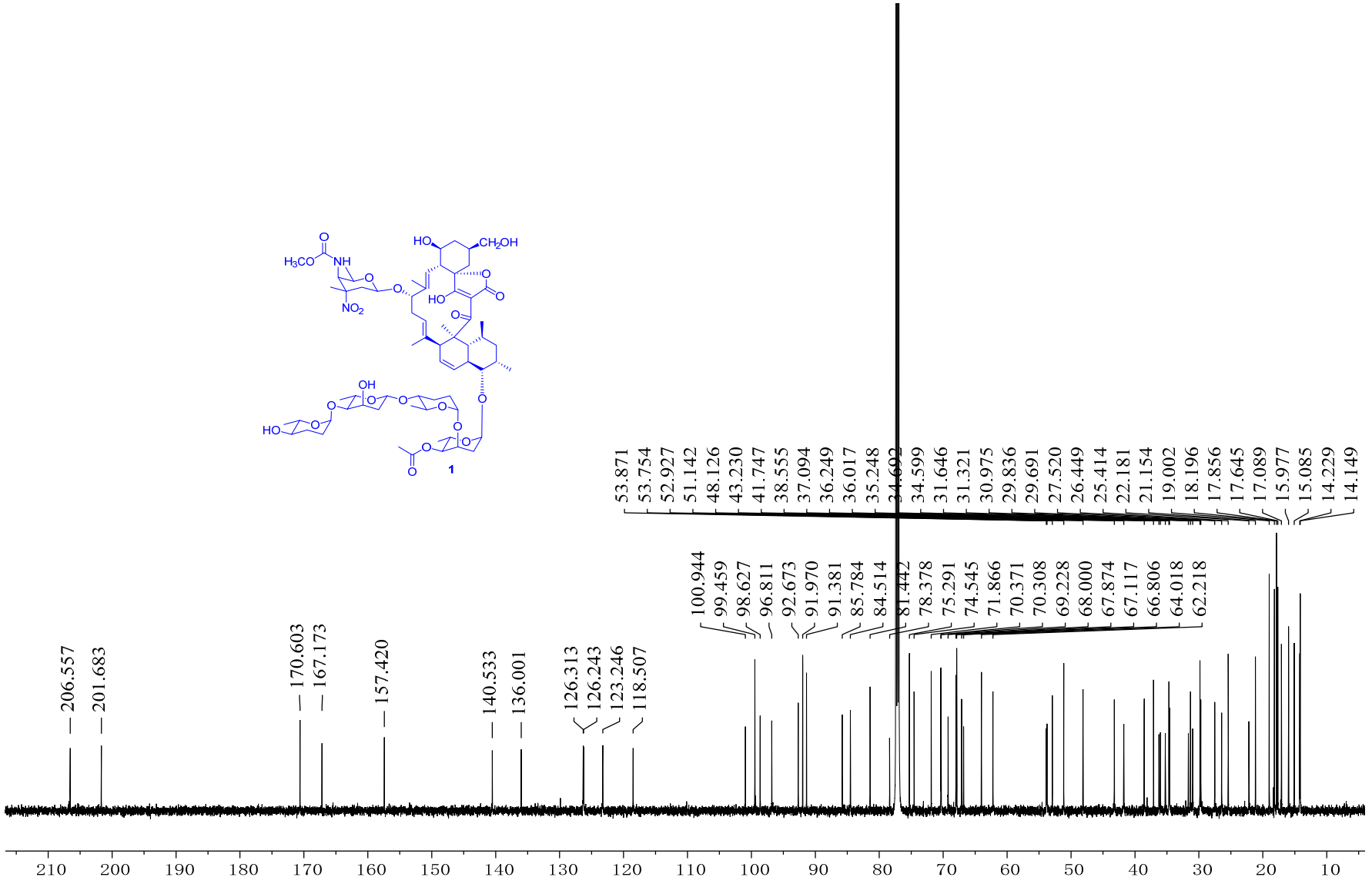


Figure S5. The ^{13}C NMR spectrum of compound **1**

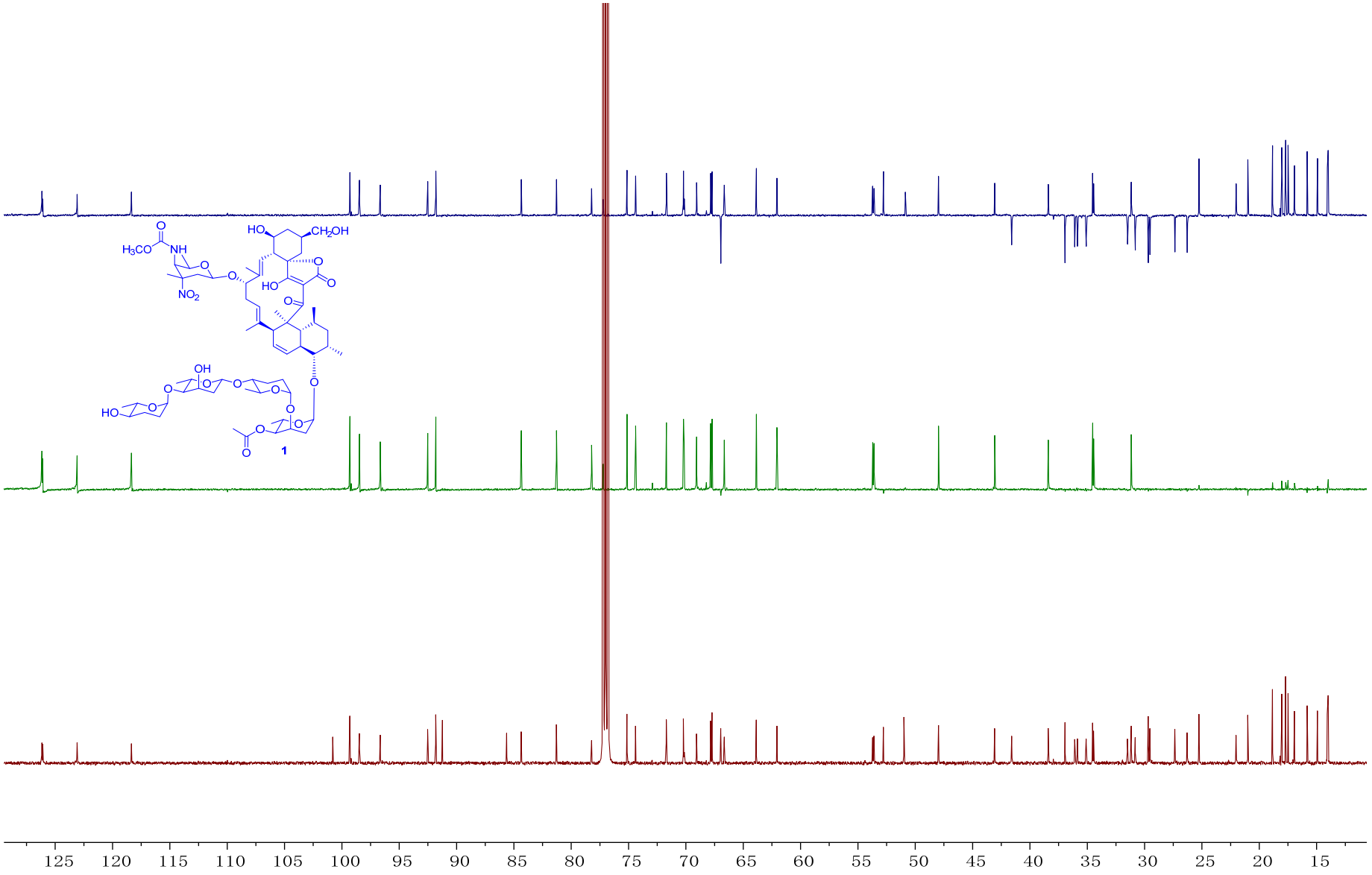


Figure S6. The DEPT spectrum of compound **1**

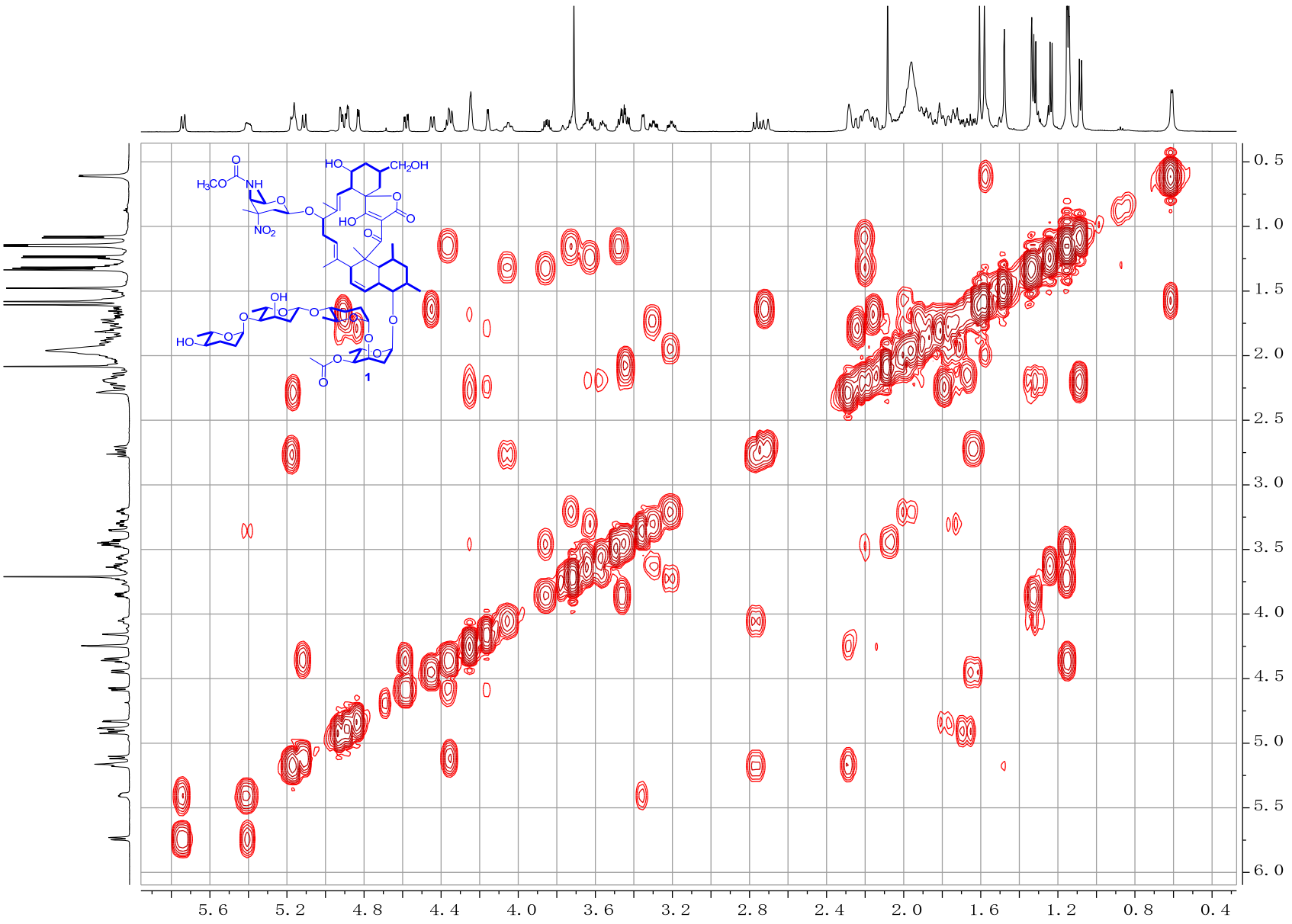


Figure S7. The ^{1}H-^{1}H COSY spectrum of compound **1**

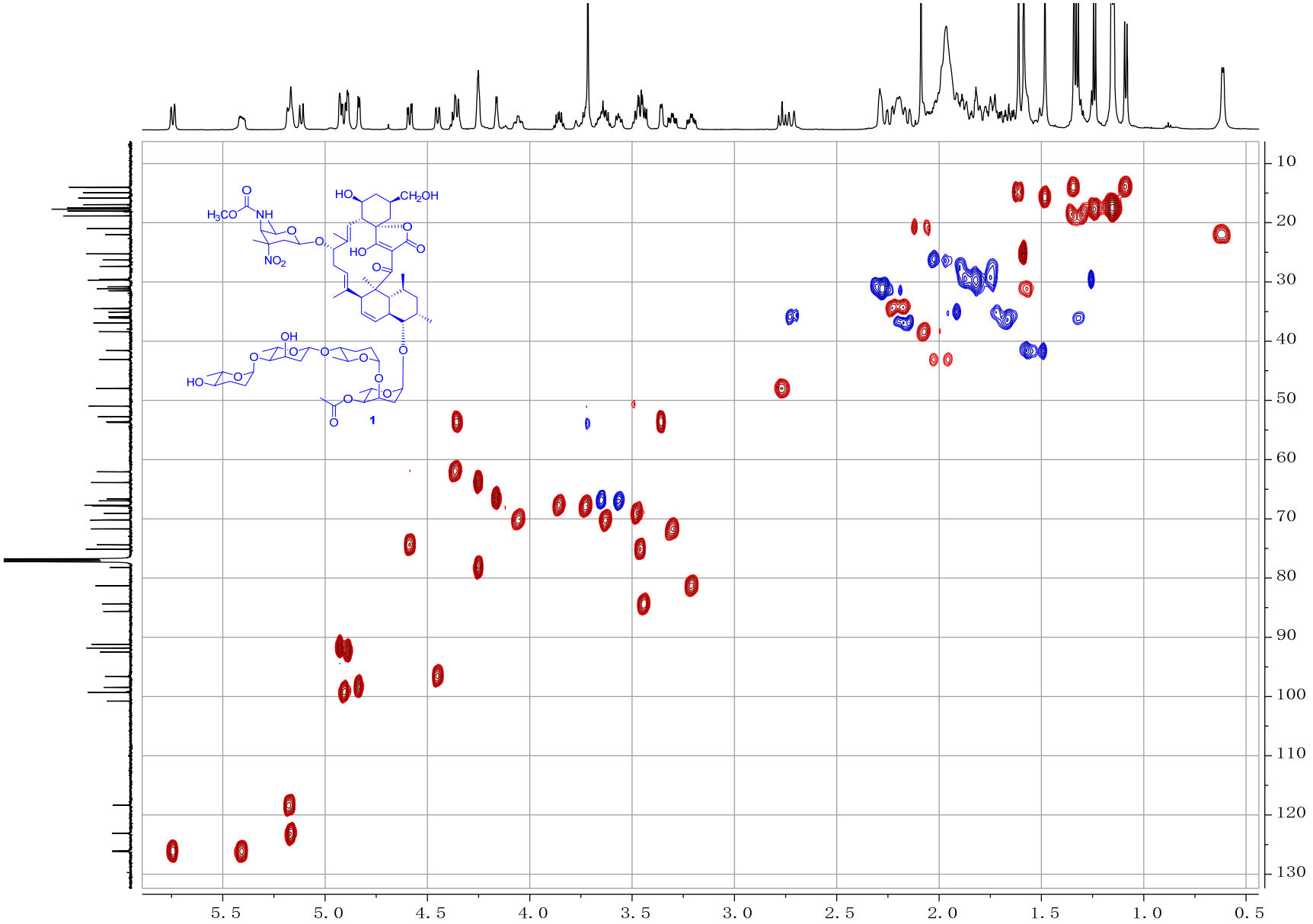


Figure S8. The HSQC spectrum of compound **1**

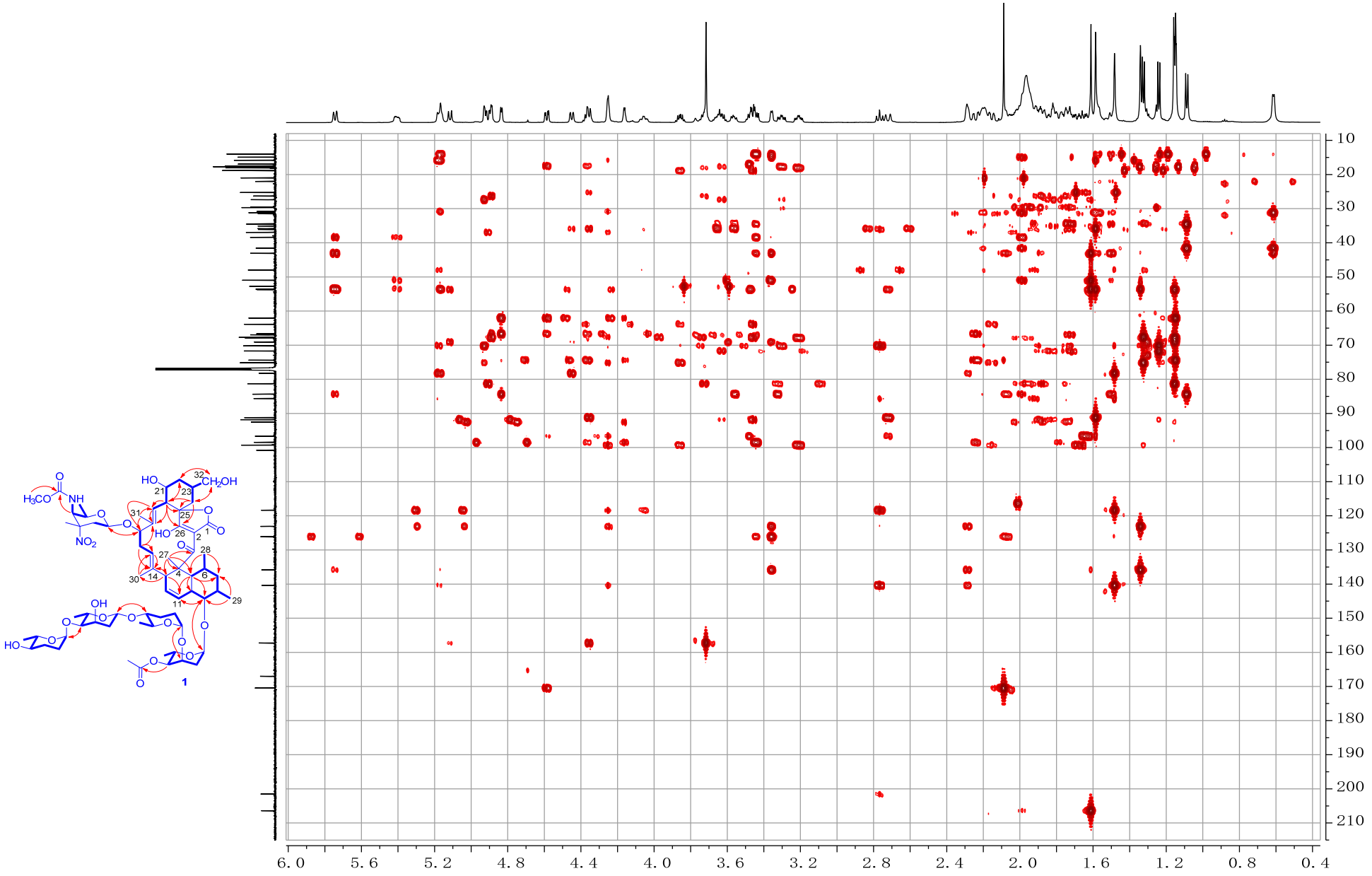


Figure S9. The HMBC spectrum of compound **1**

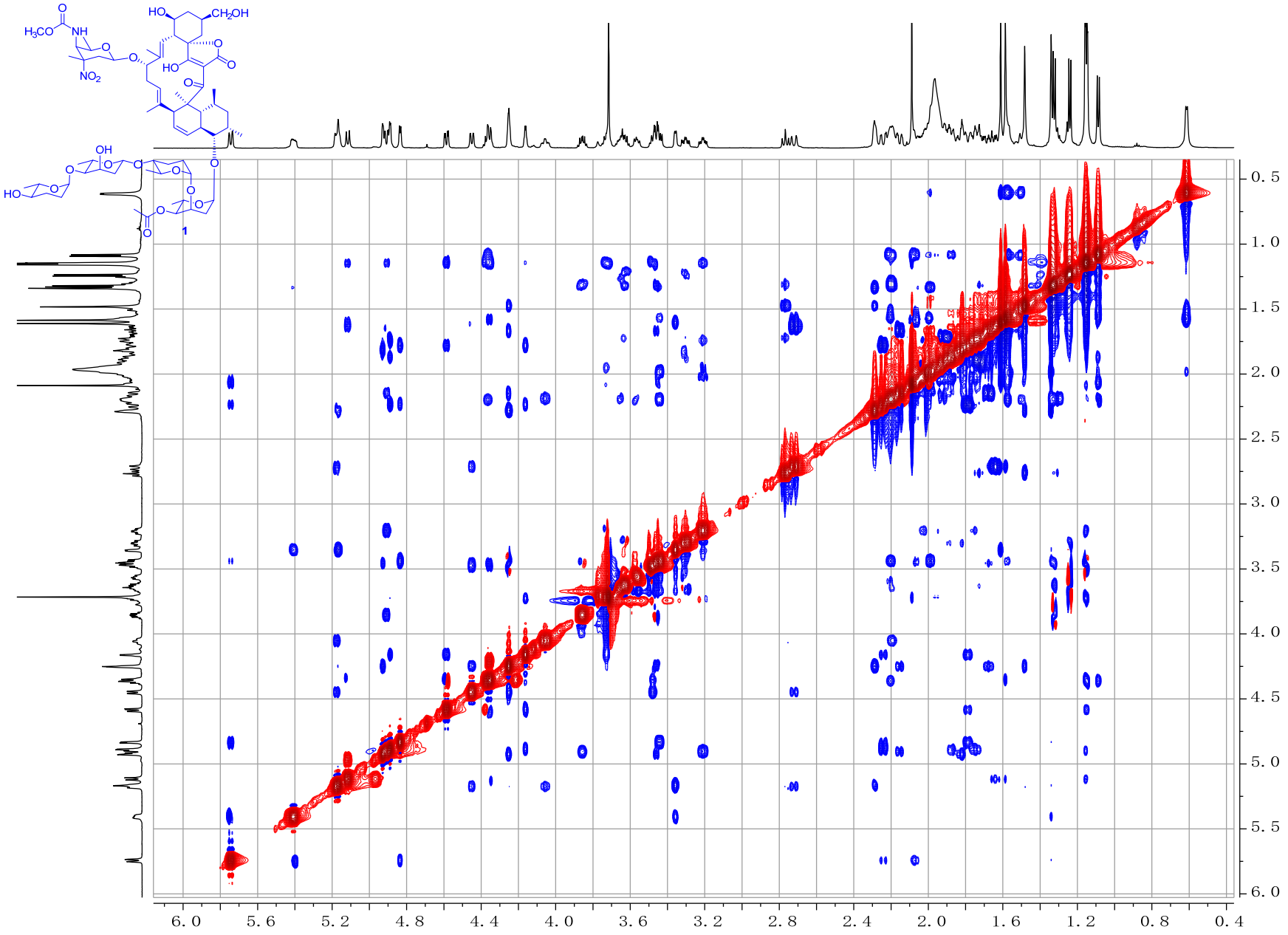


Figure S10. The ROESY spectrum of compound **1**

m/z	Theo. Mass	Delta (mmu)	RDB equiv.	Composition
1225.5894	1225.5877	1.62	17.5	$C_{61}H_{90}O_{22}N_2Na$

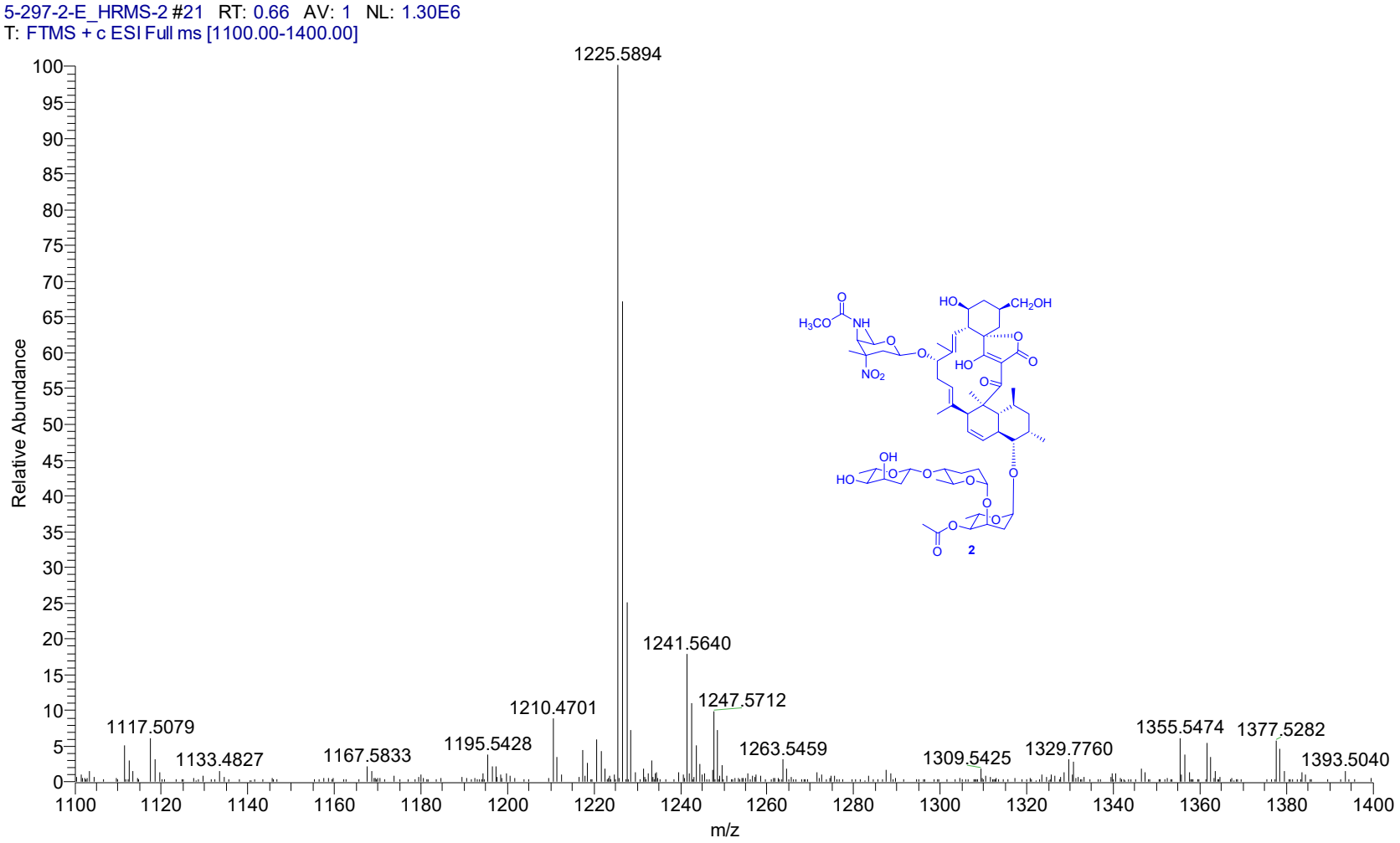


Figure S11. The (+)-HRESIMS spectrum of compound **2**

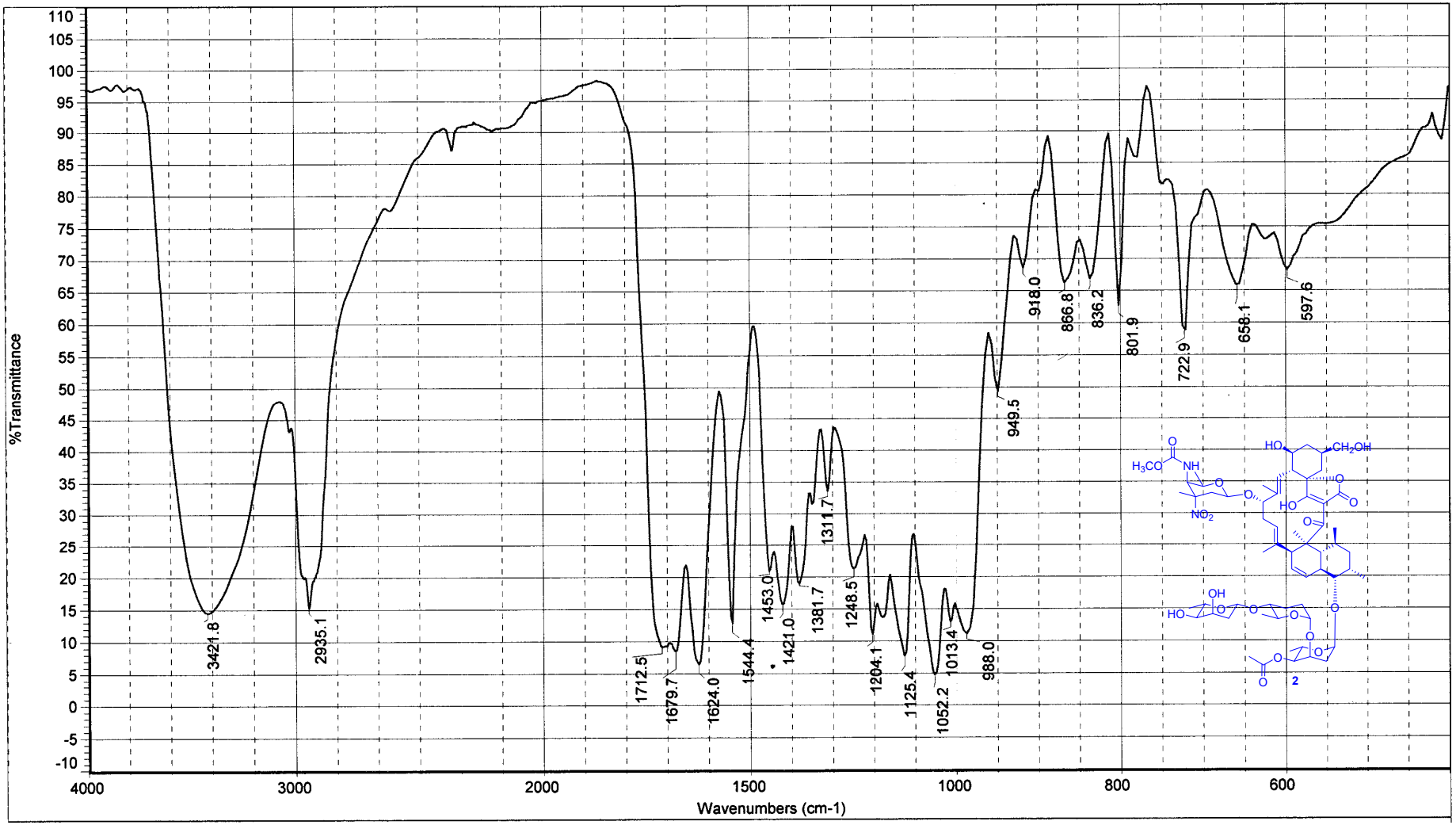


Figure S12. The IR spectrum of compound **2**

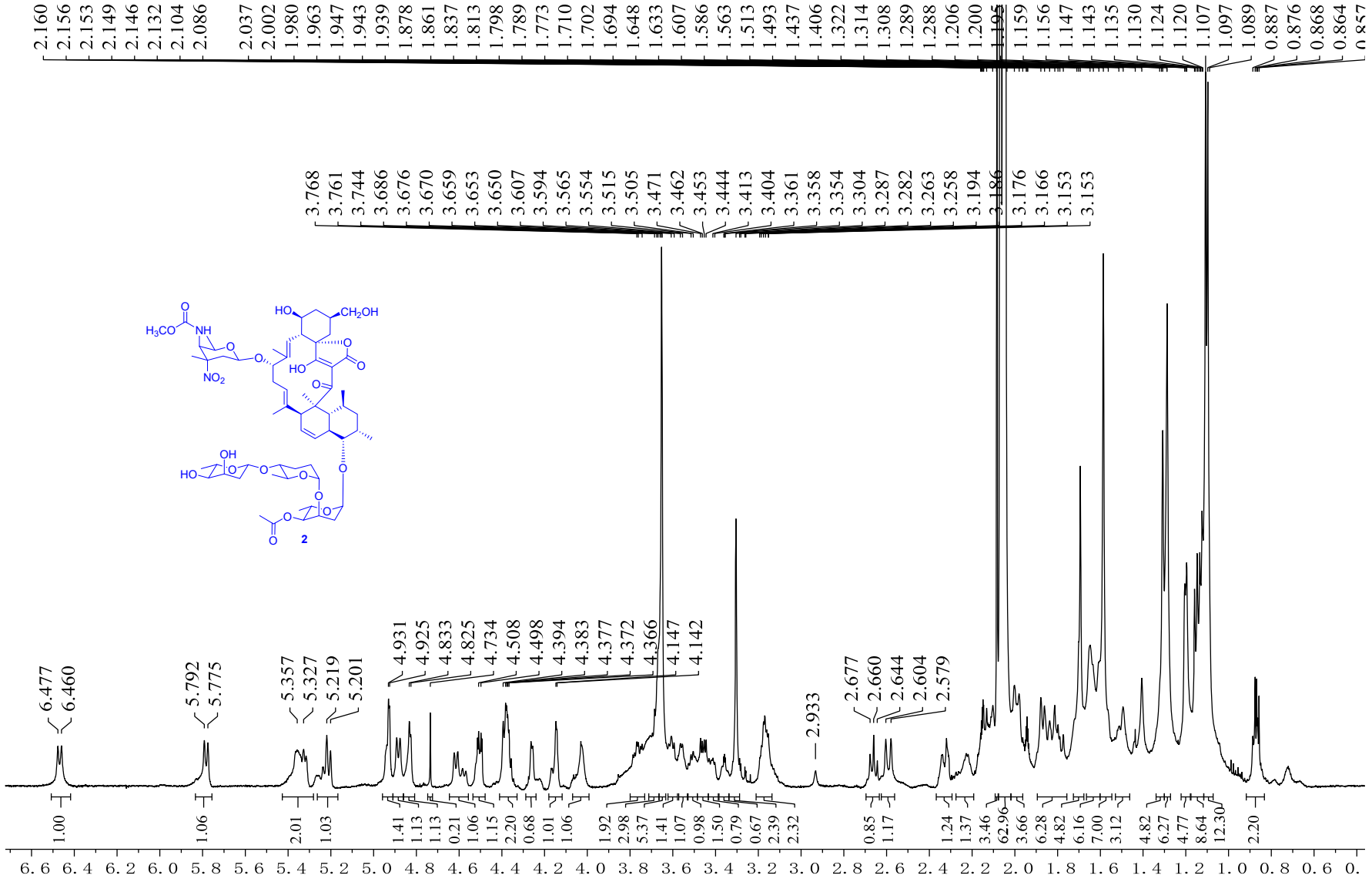


Figure S13. The ^{1}H NMR spectrum of compound **2**

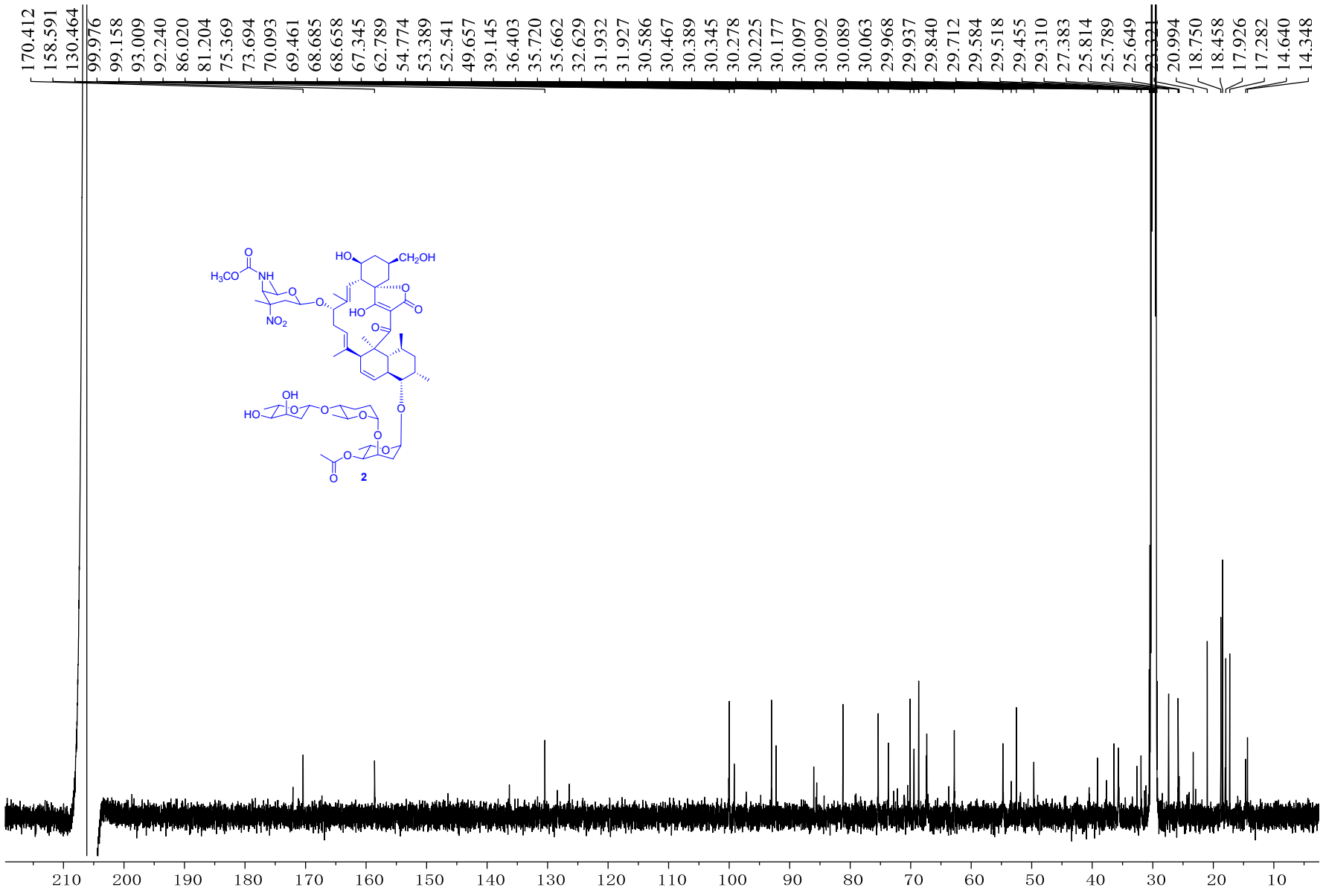


Figure S14. The ^{13}C NMR spectrum of compound **2**

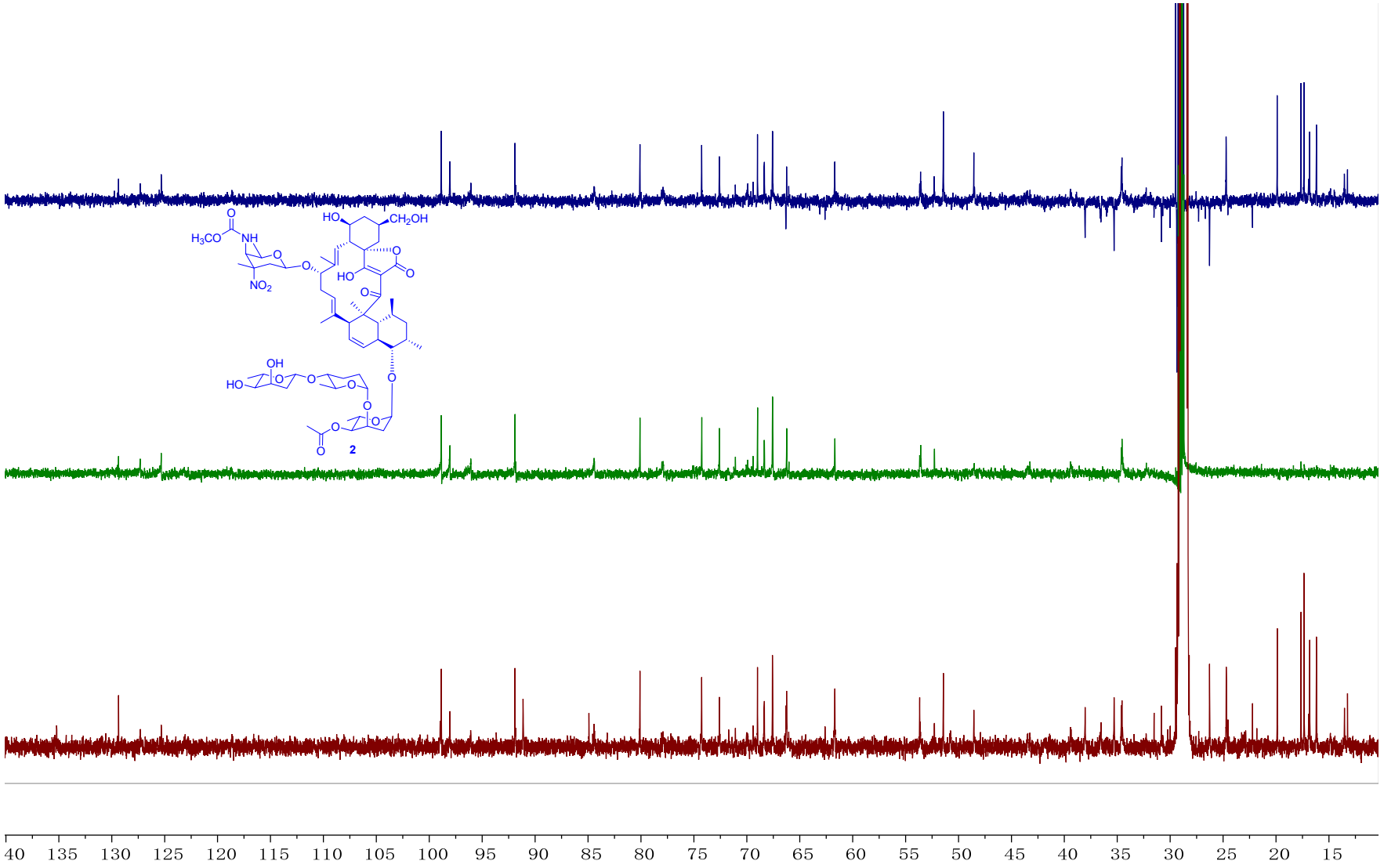


Figure S15. The DEPT spectrum of compound **2**

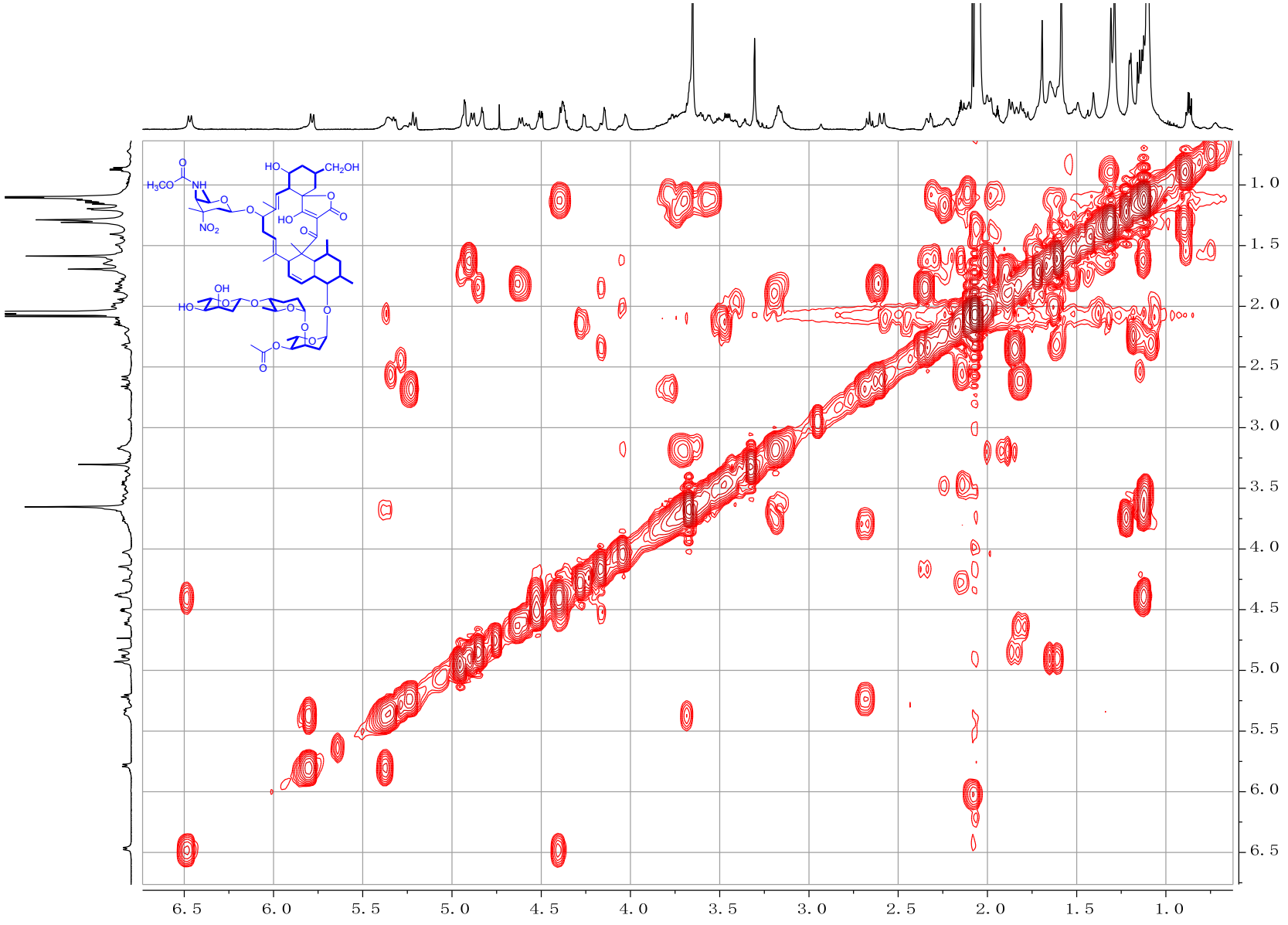


Figure S16. The ^{1}H-^{1}H COSY spectrum of compound **2**

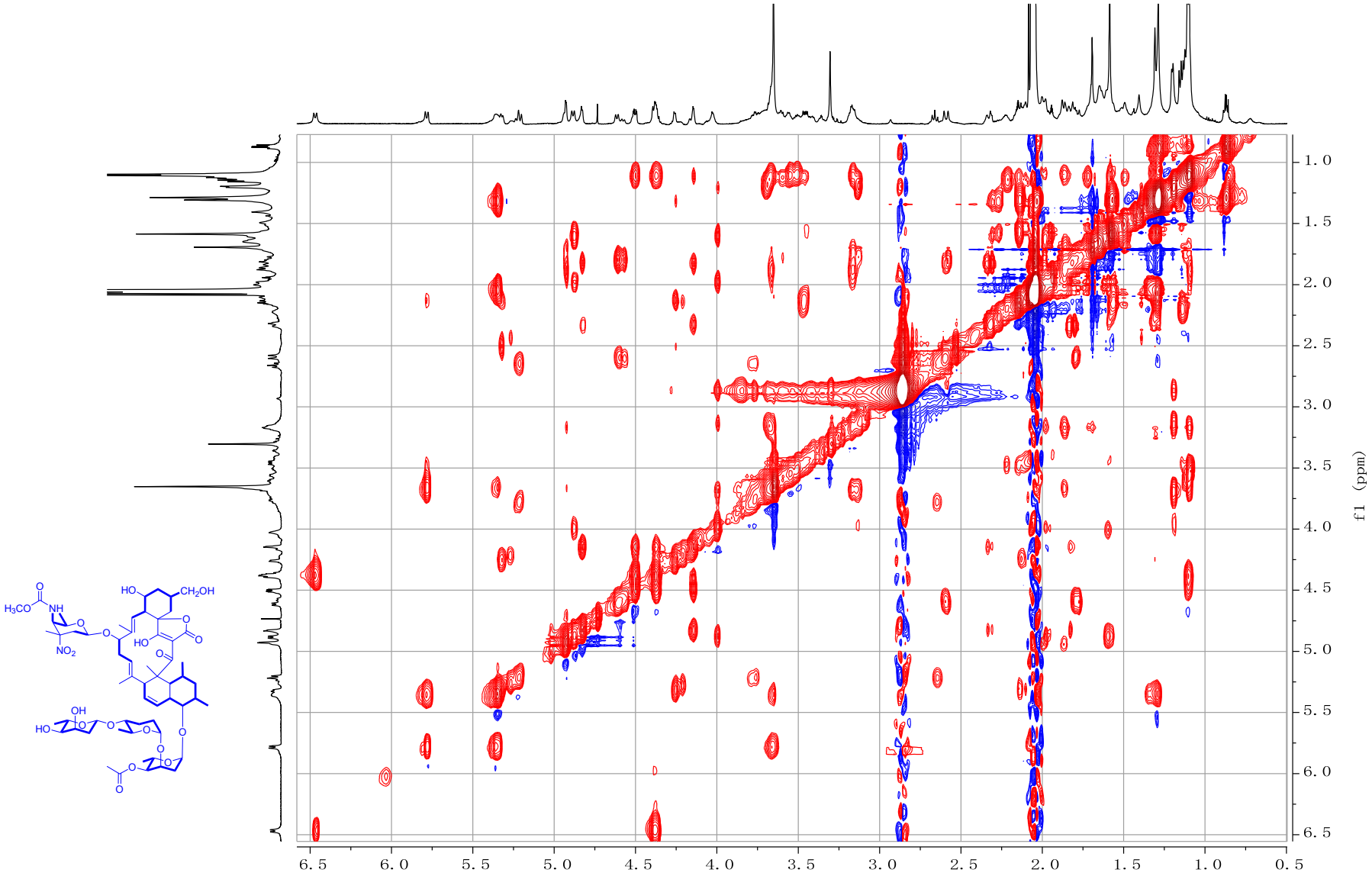


Figure S17. The TOCSY spectrum of compound **2**

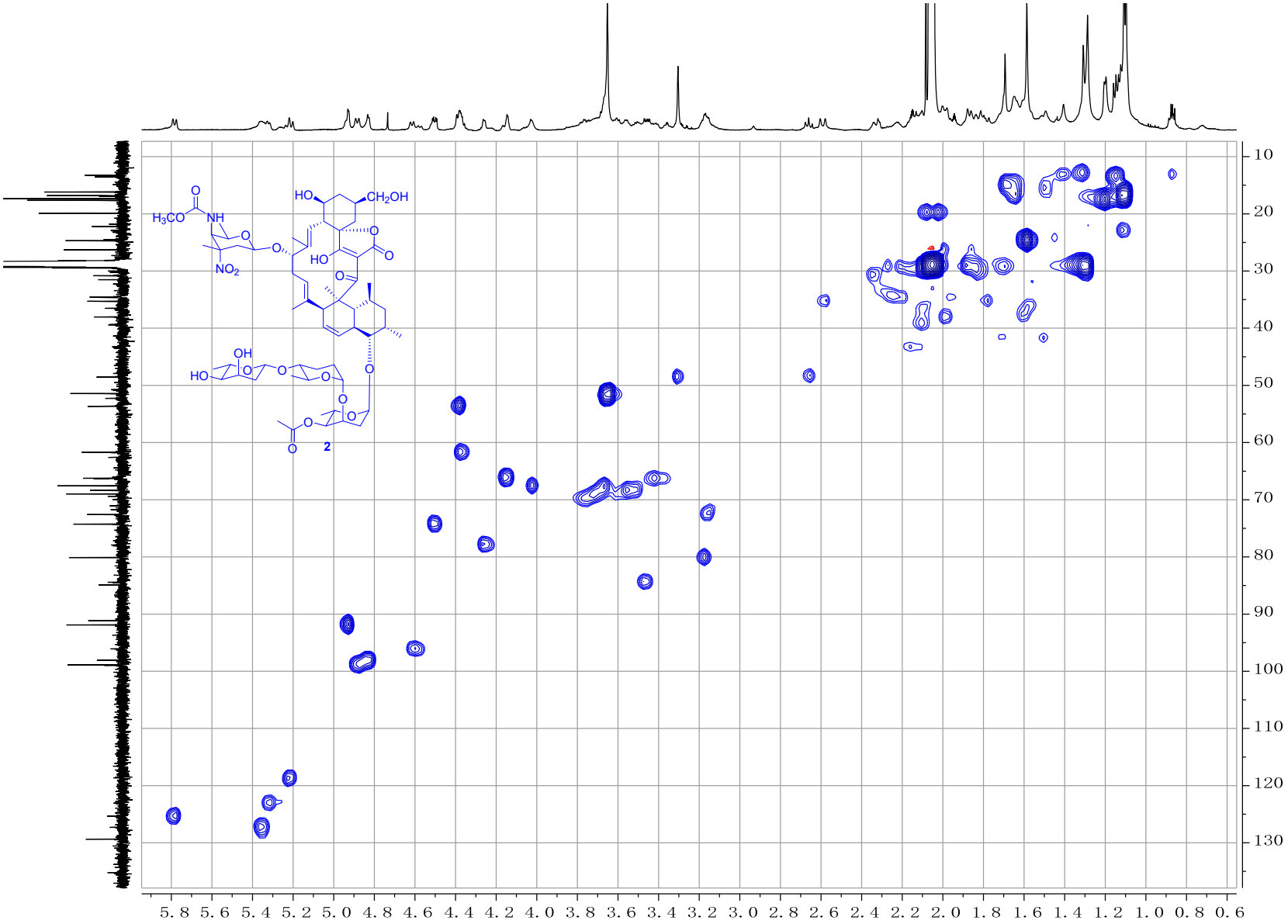


Figure S18. The HSQC spectrum of compound **2**

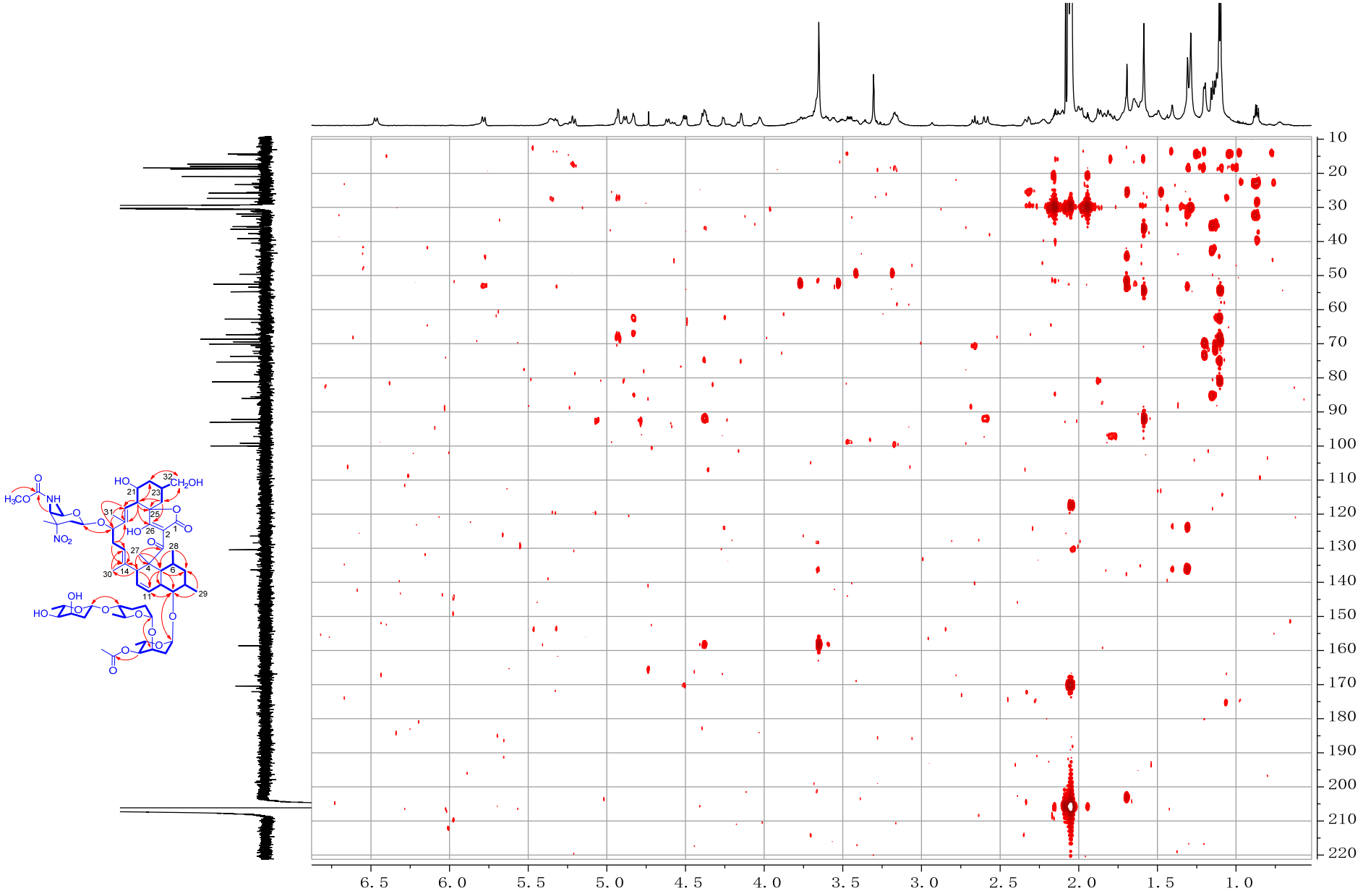


Figure S19. The HMBC spectrum of compound **2**

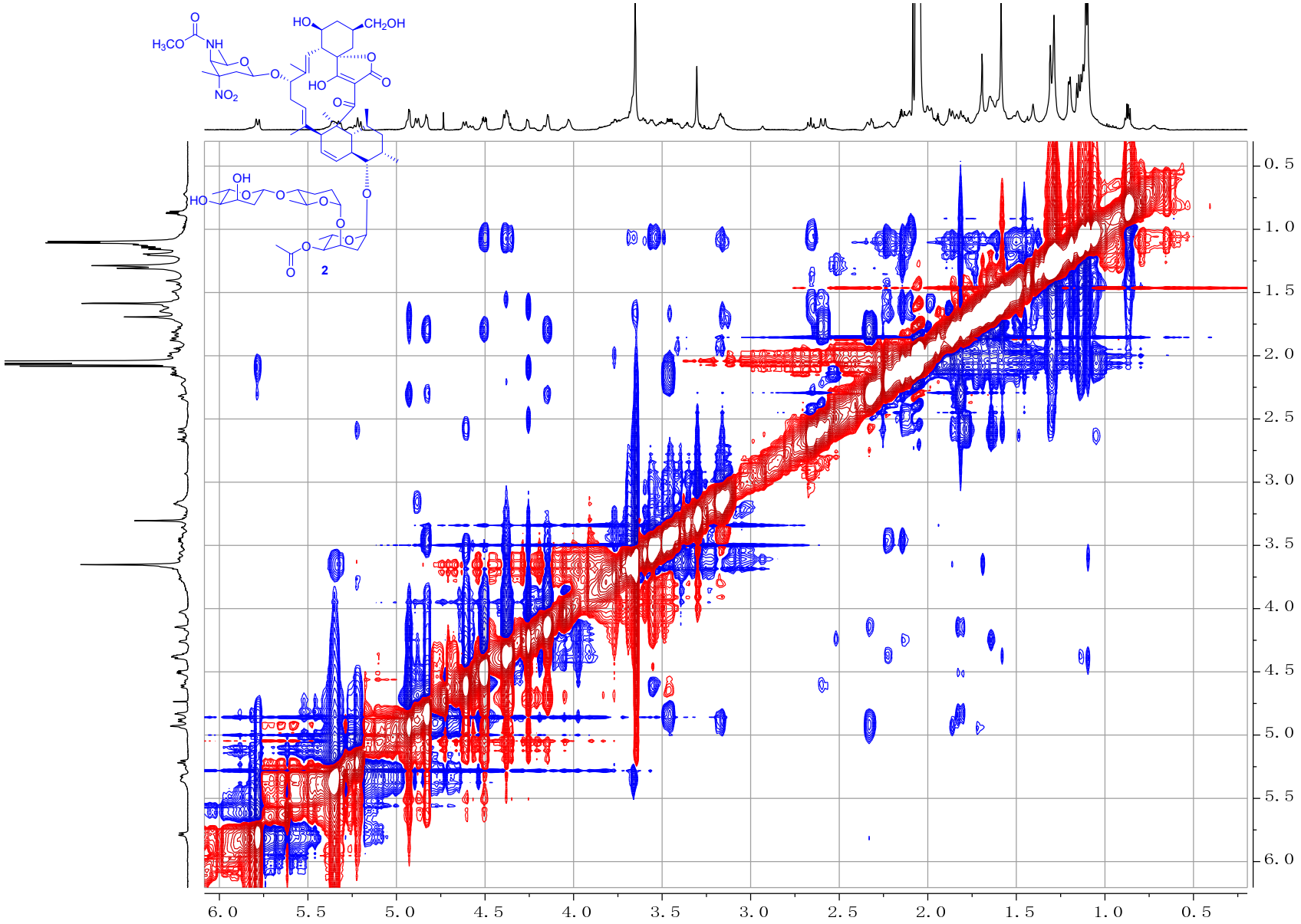


Figure S20. The ROESY spectrum of compound **2**

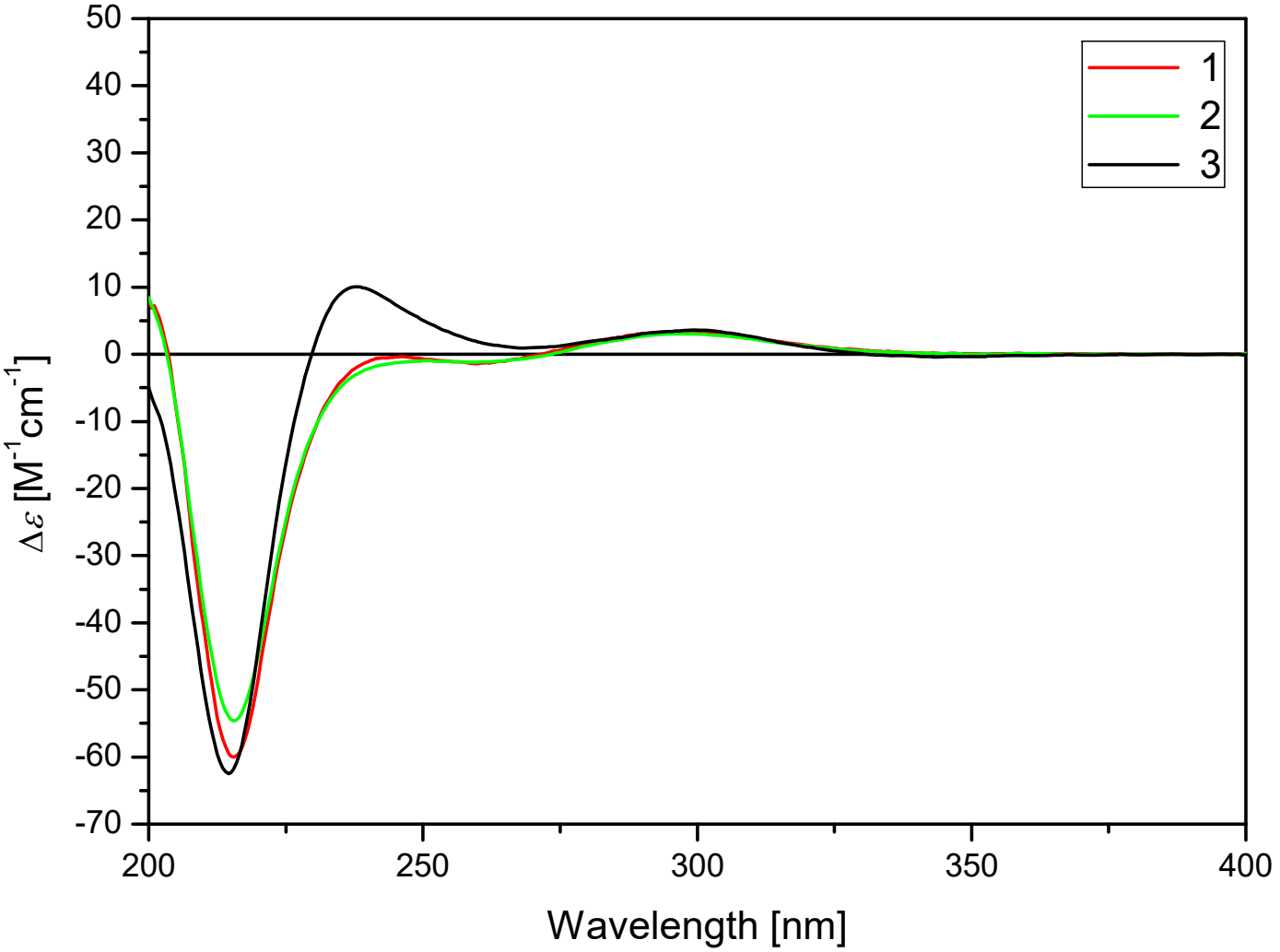


Figure S21. The CD spectra of compounds **1–3**