

Supplementary Materials

Chain-branched Polyhydroxylated Octahydro-1*H*-indoles, as Potential Leads against Lysosomal Storage Diseases

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Figure S1. Single Crystal XRD- for compound **5**,
with thermal ellipsoids drawn at the 50% probability
level and CCDC: **1885010**

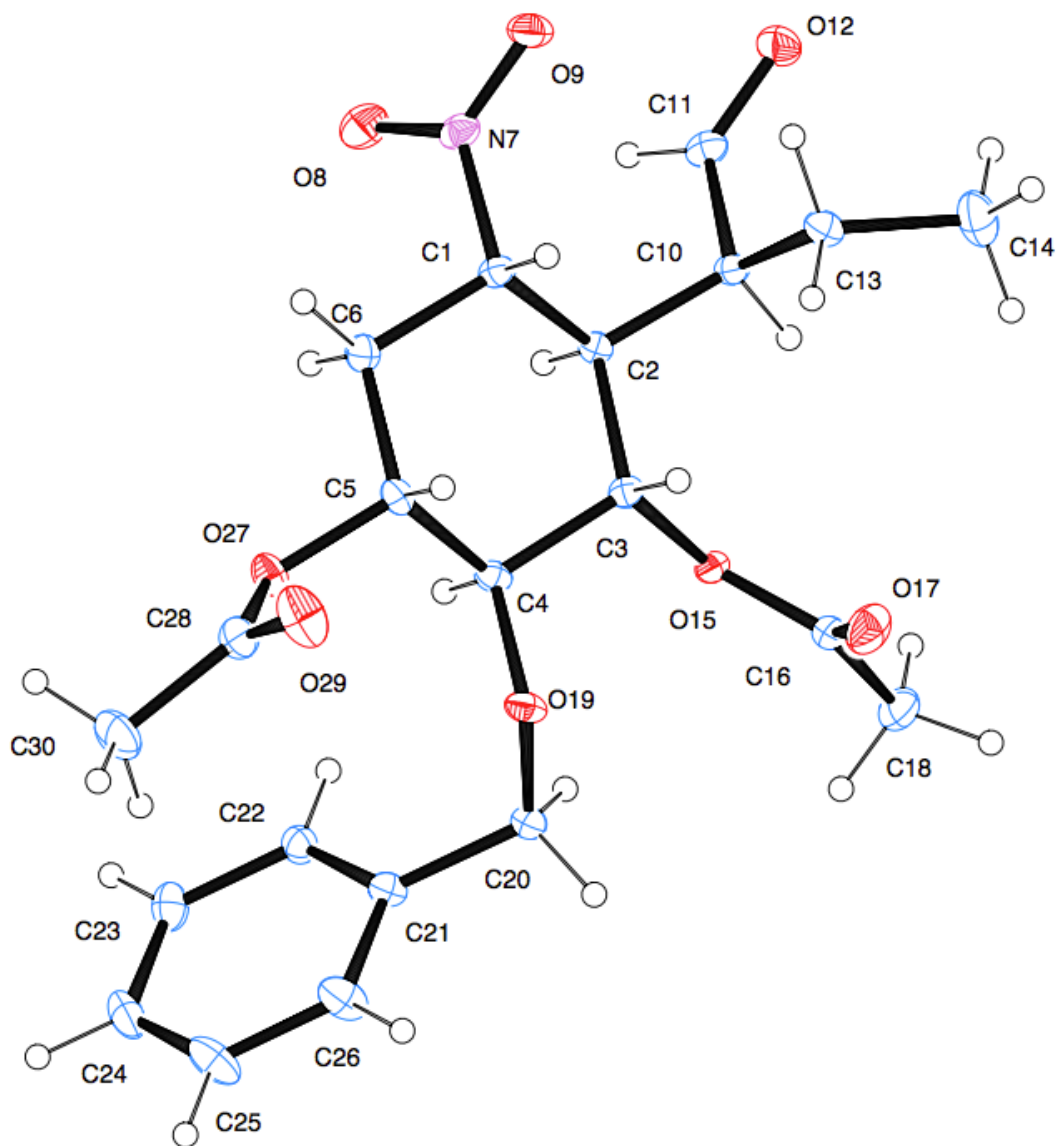


Table S1. Crystal data and structure refinement for compound **5**, and CCDC:
1885010

Experimental data 5 (2011re02mge01)

Crystal data	
Chemical formula	C ₂₁ H ₂₇ NO ₈
Temperature (K)	421.44
Crystal system, space group	Monoclinic <i>P</i> 2 ₁
Temperature (K)	100(2) K
<i>a</i> , <i>b</i> , <i>c</i> (Å)	<i>a</i> = 10.4104(6) Å α = 90° <i>b</i> = 8.8682(5) Å β = 101.541(3)° <i>c</i> = 11.6487(6) Å γ = 90°
<i>V</i> (Å ³)	1053.68(10) Å ³
<i>z</i>	2
Radiation type	<i>MoKα</i>
μ (mm ⁻¹)	0.102 mm ⁻¹
Crystal size (mm)	0.42 x 0.14 x 0.09 mm ³
Data collection	
Diffractometer	BRUKER APPEX-II CCD
Absorption correction	Multi-scan BRUKER SADABS
<i>T</i> _{min} , <i>T</i> _{max}	0.9253-0.9853
No. of measured, independent and observed (<i>I</i> > 2σ(<i>I</i>)) reflections	18089, 2777, 2302
Rint	0.052
(sin(θ)/λ) _{max} (Å ⁻¹)	0.667
Refinement	
<i>R</i> [<i>F</i> ² > 2σ(<i>F</i> ²)], <i>wR</i> [<i>F</i> ²], <i>S</i>	0.0390, 0.0878, 1.038
No. of reflections	2777
No. of parameters	274
H-atom treatment	H atoms treated by constrained refinement
Δ <i>r</i> _{max} , Δ <i>r</i> _{min} (e Å ⁻³)	0.199, -0.193
Absolute structure	Absolute structure cannot be determined reliably.
Absolute structure parameter	N/A

Computer programs: APPEX2 (BRUKER AXS, 2005), *S/R97* (Giacovazzo *et al.*, 1999), *SHELXL97* (Sheldrick, 1997), *ORTEP-3 for Windows* (Farrugia, 1997), *WinGX* publication routines (Farrugia, 1999).

Figure S2. Single Crystal XRD- for compound 7,
with thermal ellipsoids drawn at the 50% probability
level and CCDC: **1885009**

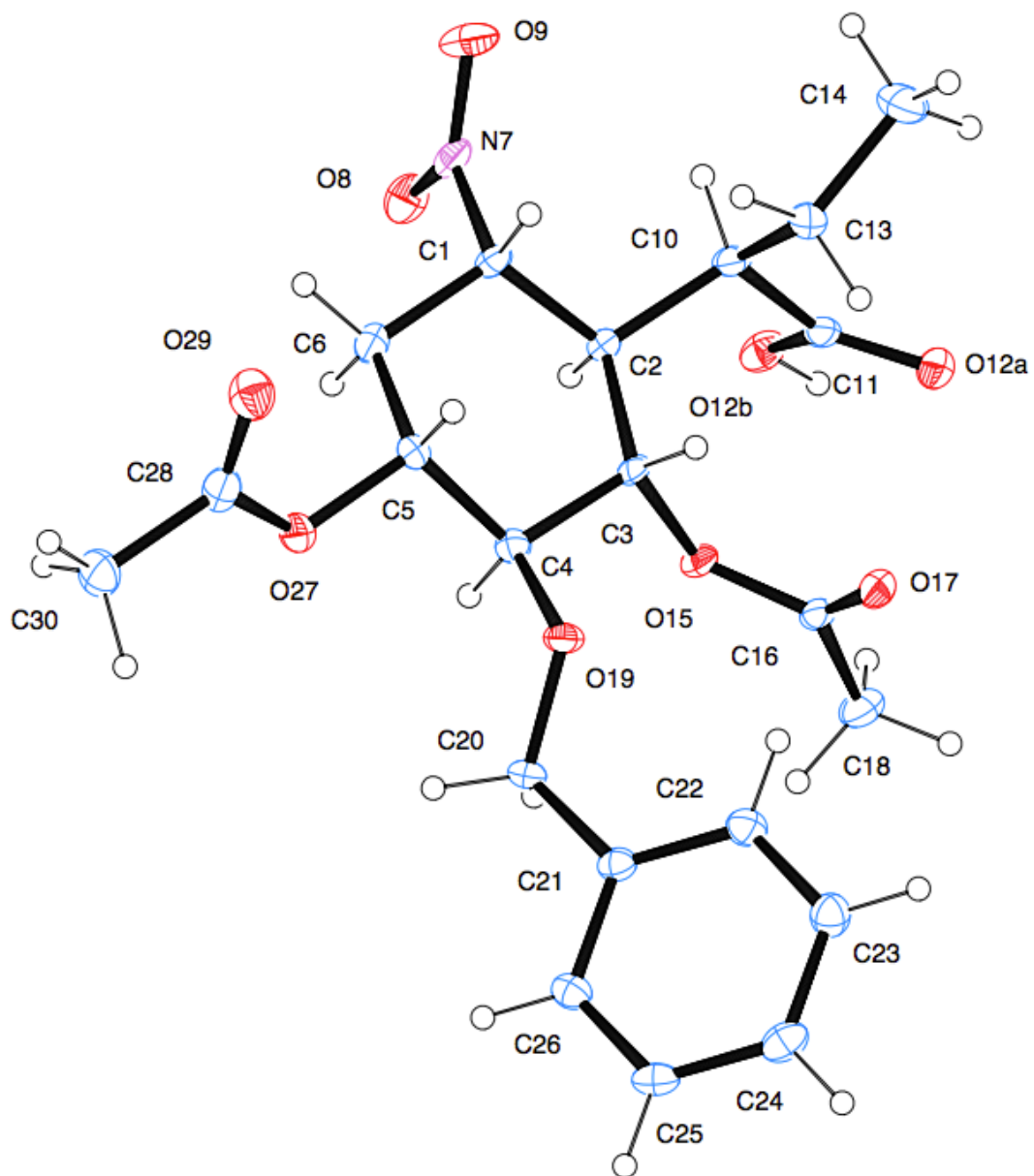


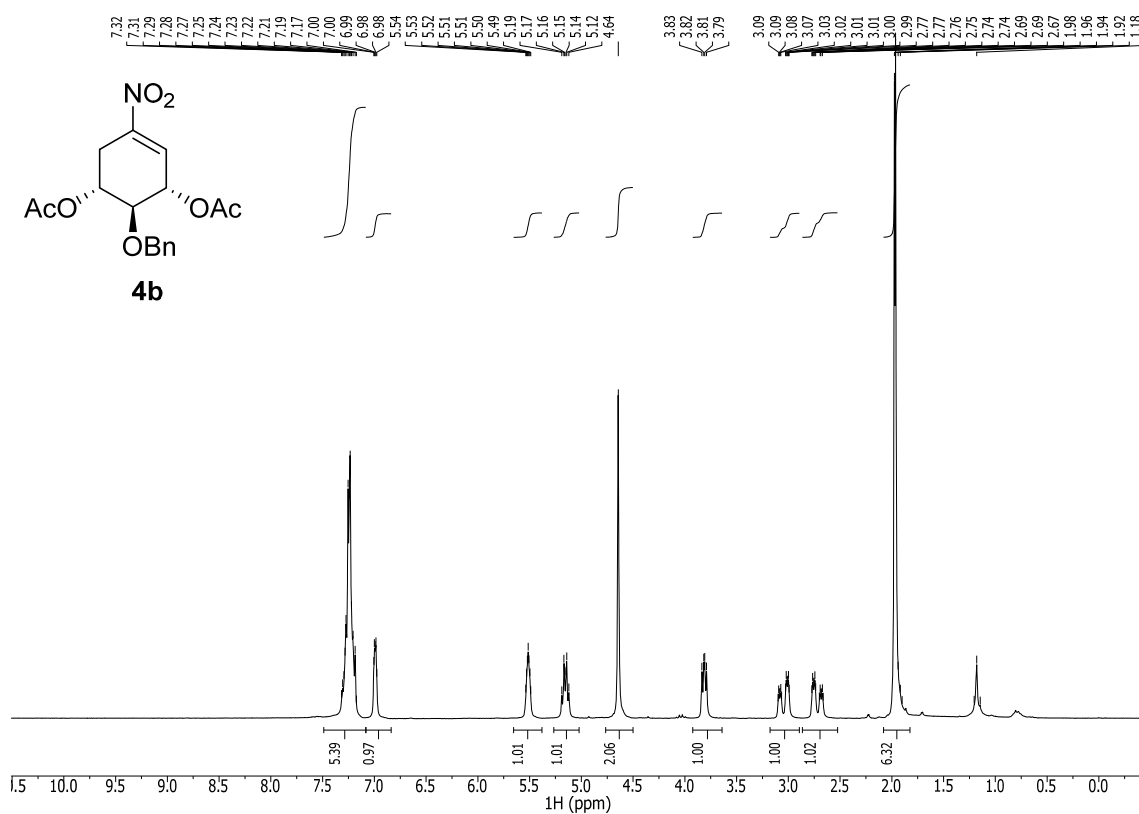
Table S2. Crystal data and structure refinement for compound **7**, and
CCDC: 1885009

Experimental data 7 (2011re03mgc02)

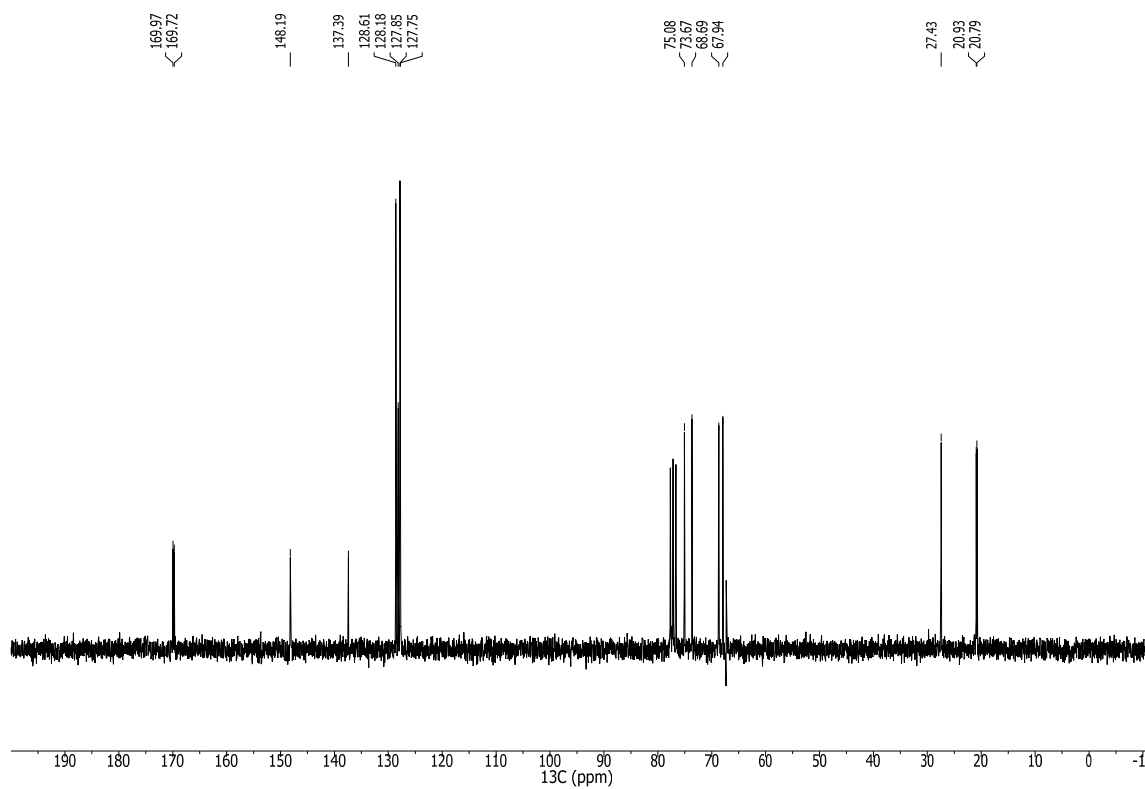
Crystal data	
Chemical formula	C ₂₁ H ₂₇ NO ₉
Temperature (K)	437.44
Crystal system, space group	Monoclinic <i>P</i> 2 ₁
Temperature (K)	100(2) K
<i>a, b, c</i> (Å)	<i>a</i> = 9.7916(13) Å α = 90° <i>b</i> = 9.2932(12) Å β = 99.230(8)° <i>c</i> = 12.3910(17) Å γ = 90°
<i>V</i> (Å ³)	1112.9(3) Å ³
<i>z</i>	2
Radiation type	<i>MoKα</i>
μ (mm ⁻¹)	0.103 mm ⁻¹
Crystal size (mm)	0.35 x 0.12 x 0.04 mm ³
Data collection	
Diffractometer	BRUKER APPEX-II CCD
Absorption correction	Multi-scan BRUKER SADABS
T _{min} , T _{max}	0.8784-0.9866
No. of measured, independent and observed (<i>I</i> > 2 σ (<i>I</i>)) reflections	21663, 2417, 1945
R_{int}	0.0602
(<i>sin</i> (θ)/ λ) _{max} {Å ⁻¹ }	0.625
Refinement	
<i>R</i> [<i>F</i> ² > 2 σ (<i>F</i> ²)] , <i>wR</i> (<i>F</i> ²), <i>S</i>	0.0384, 0.0913, 1.067
No. of reflections	2417
No. of parameters	287
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{\text{max}}$, $\Delta\rho_{\text{min}}$ {e Å ⁻³ }	0.171, -0.205
Absolute structure	Absolute structure cannot be determined reliably.
Absolute structure parameter	N/A

Computer programs: APPEX2 (BRUKER AXS, 2005), *S/R97* (Giacovazzo *et al.*, 1999), *SHELXL97* (Sheldrick, 1997), *ORTEP-3 for Windows* (Farrugia, 1997), *WinGX* publication routines (Farrugia, 1999).

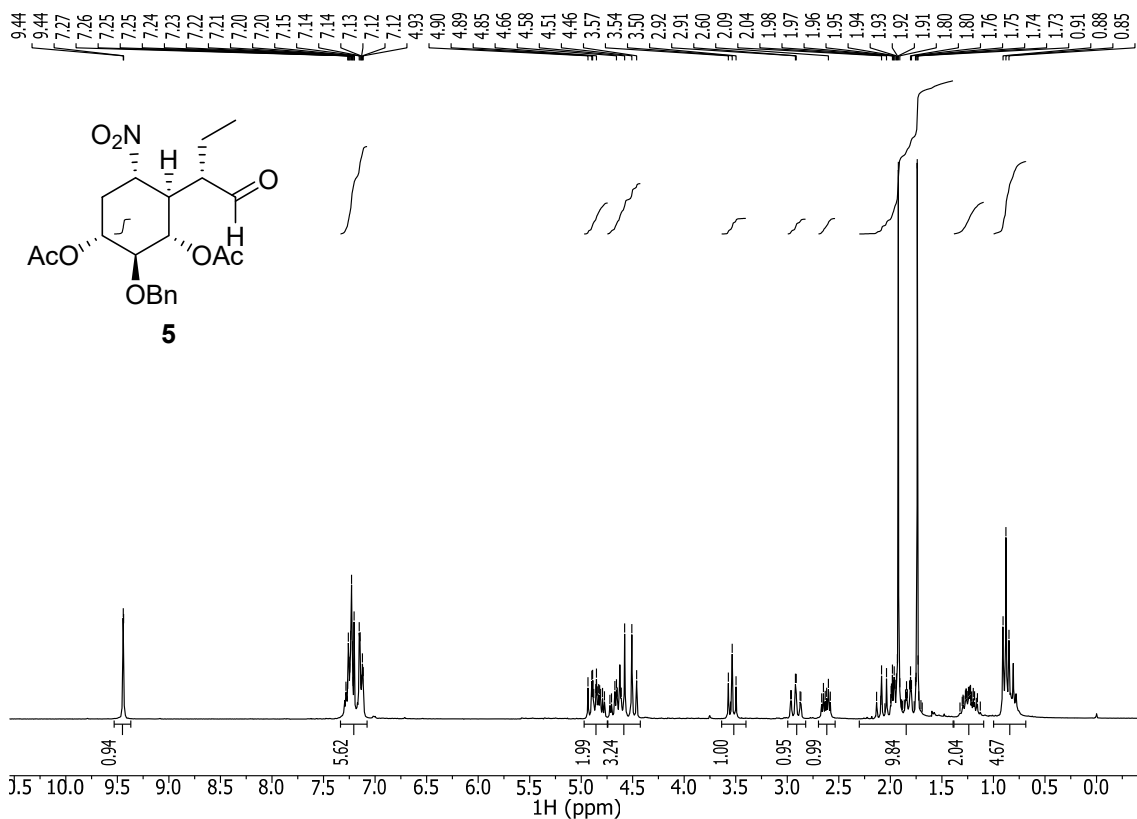
SI6. ^1H NMR (250 MHz, Cl_3CD , **4b**)



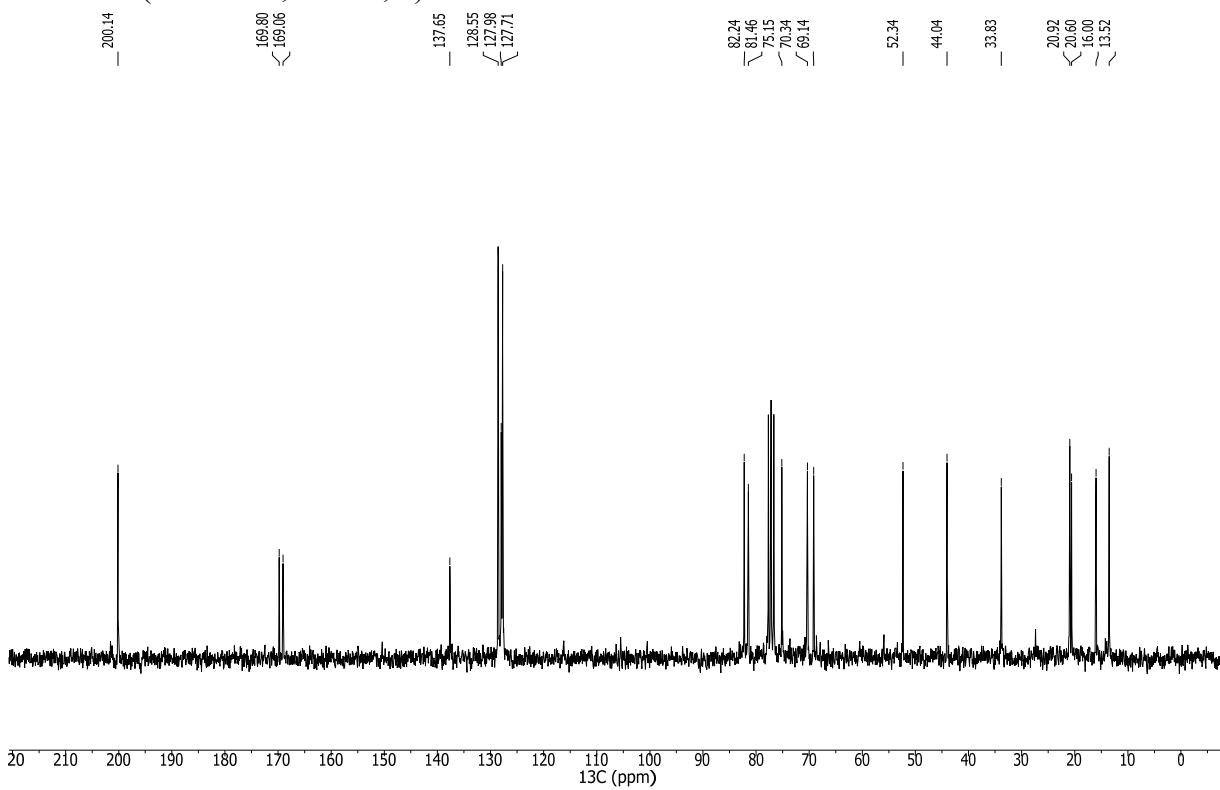
^{13}C NMR (62.5 MHz, Cl_3CD , **4b**)



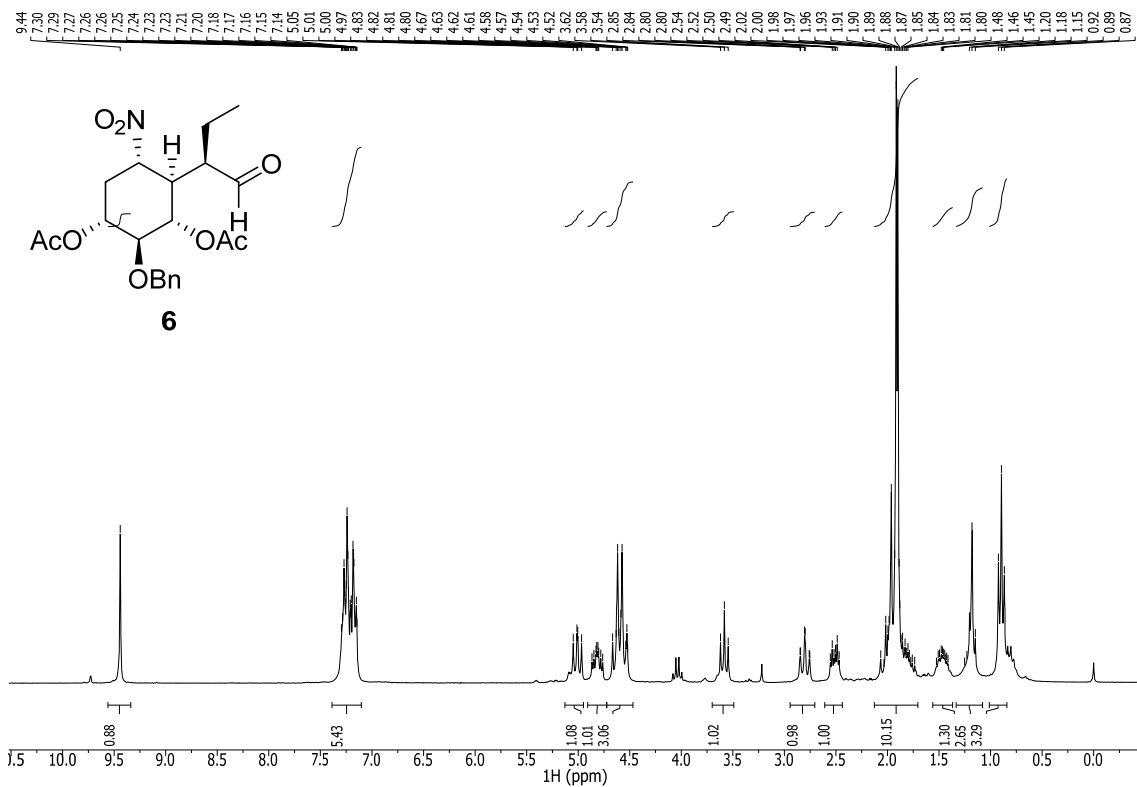
SI6. ^1H NMR (250 MHz, Cl_3CD , **5**)



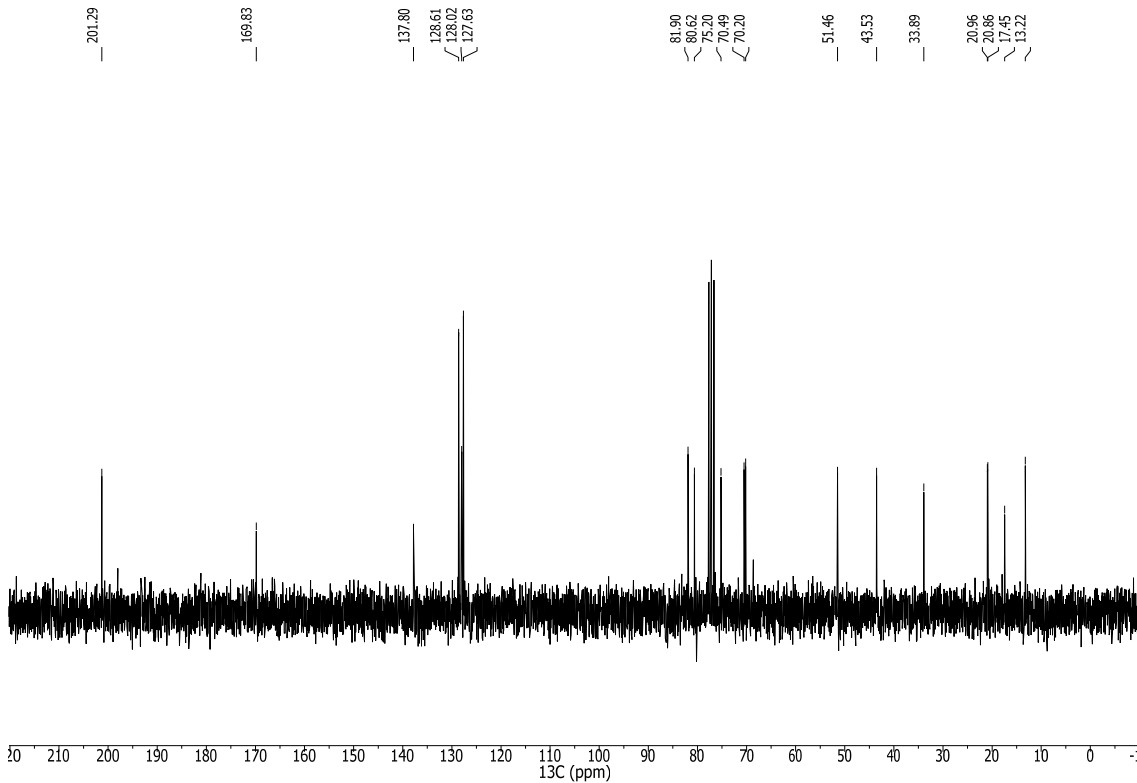
^{13}C NMR (62.5 MHz, Cl_3CD , **5**)



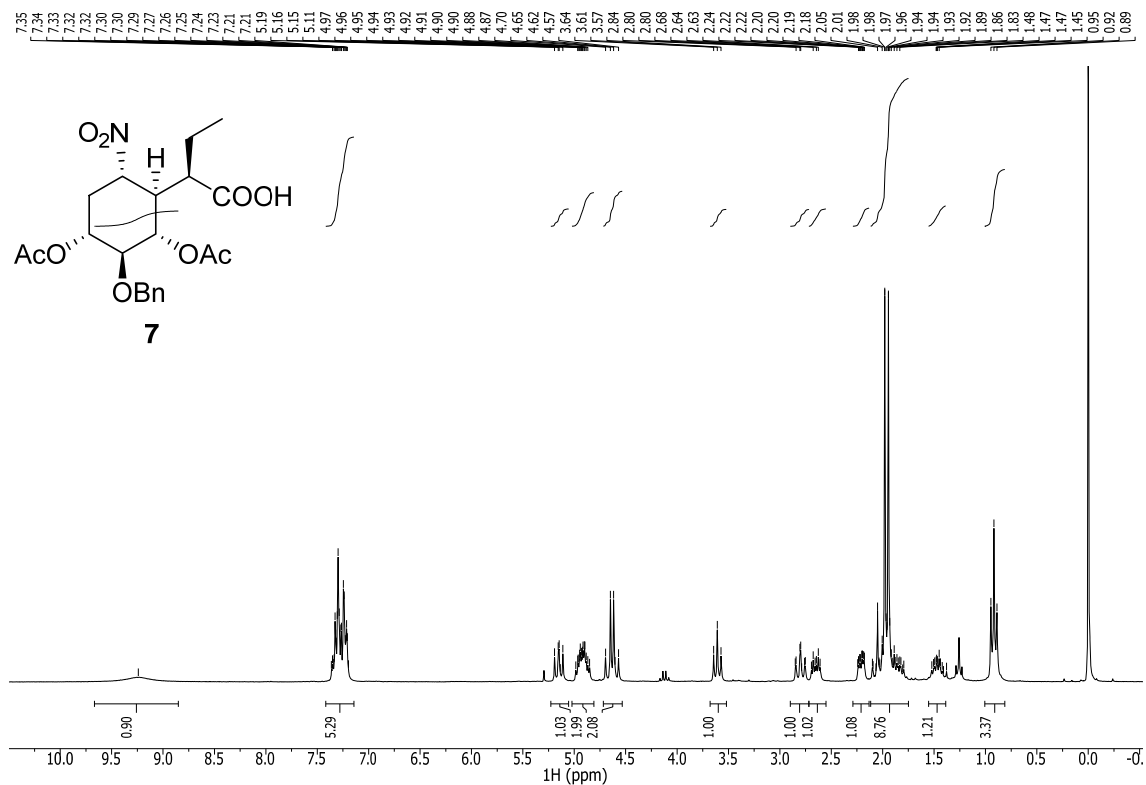
SI6. ¹H NMR (250 MHz, Cl₃CD, **6**)



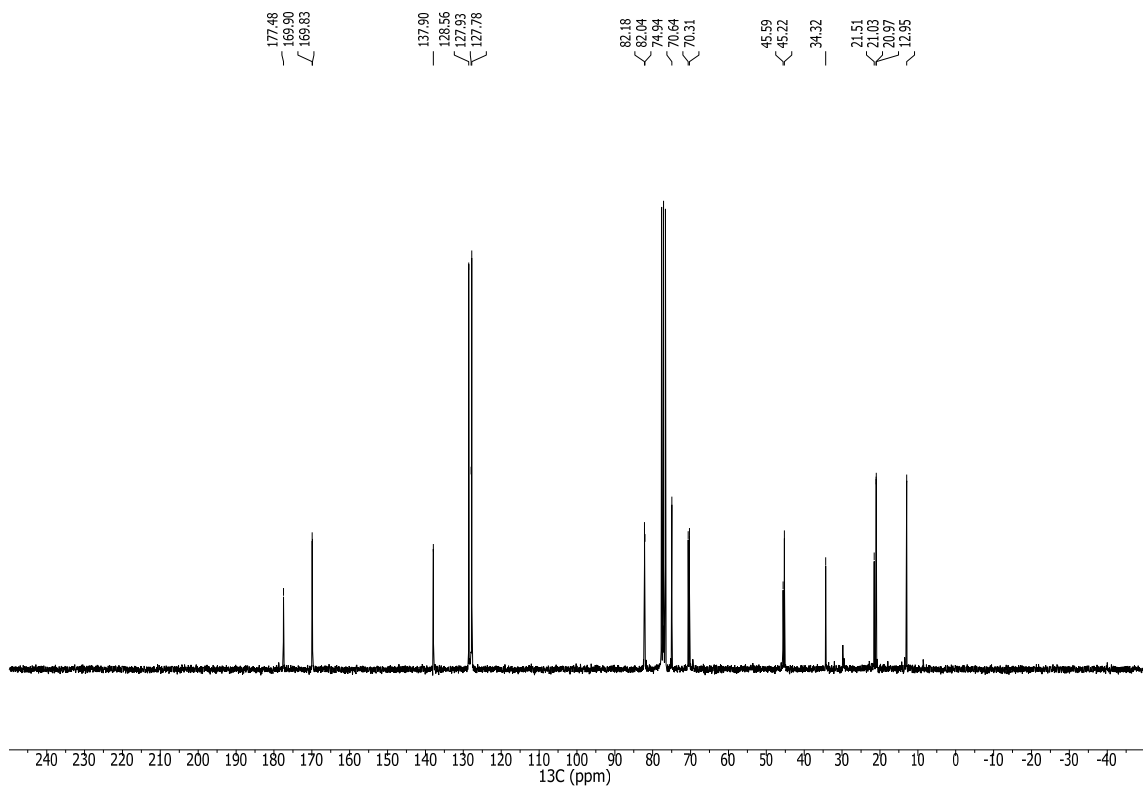
¹³C NMR (62.5 MHz, Cl₃CD, **6**)



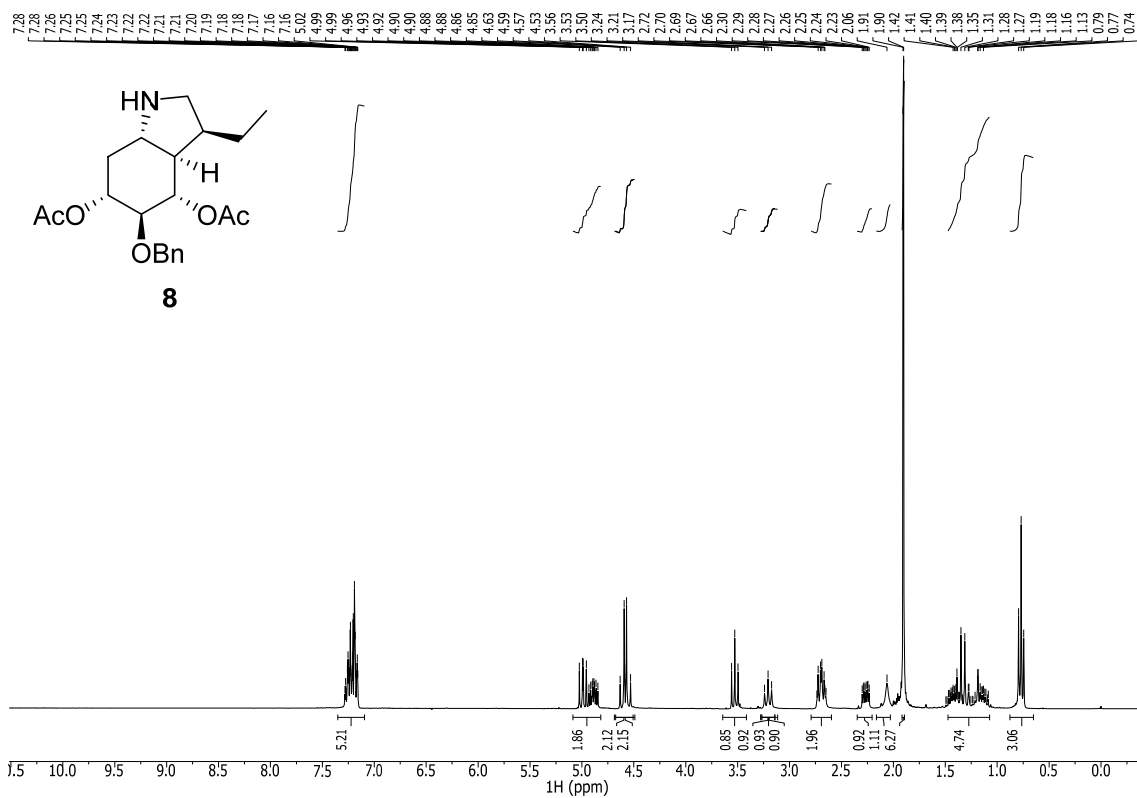
SI6. ¹H NMR (250 MHz, Cl₃CD, 7)



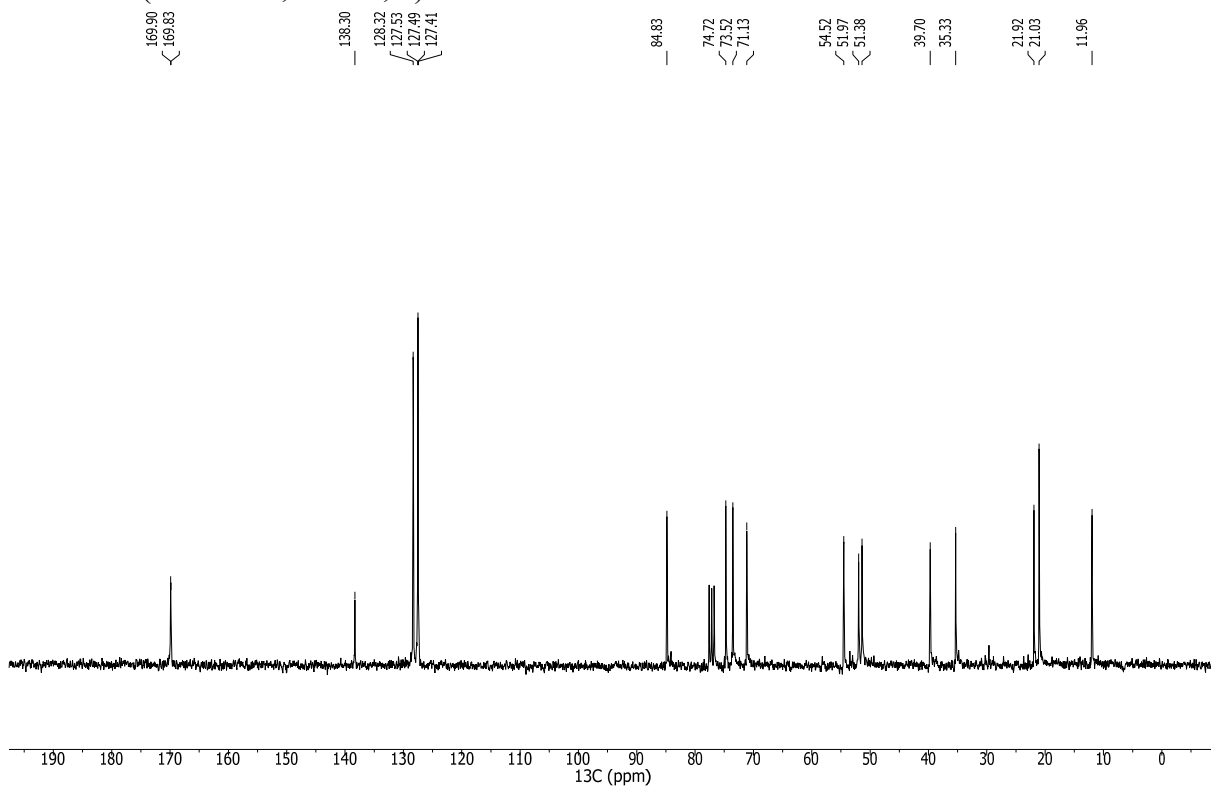
¹³C NMR (62.5 MHz, Cl₃CD, 7)



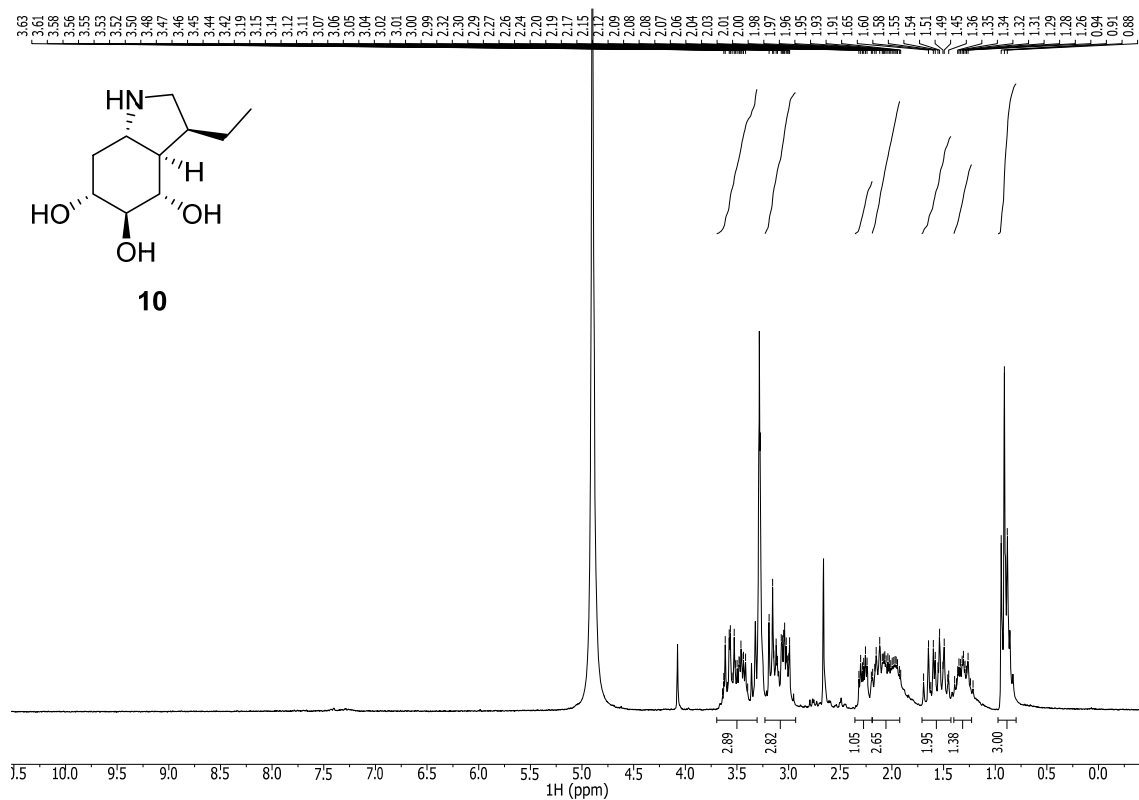
SI6. ^1H NMR (250 MHz, Cl_3CD , **8**)



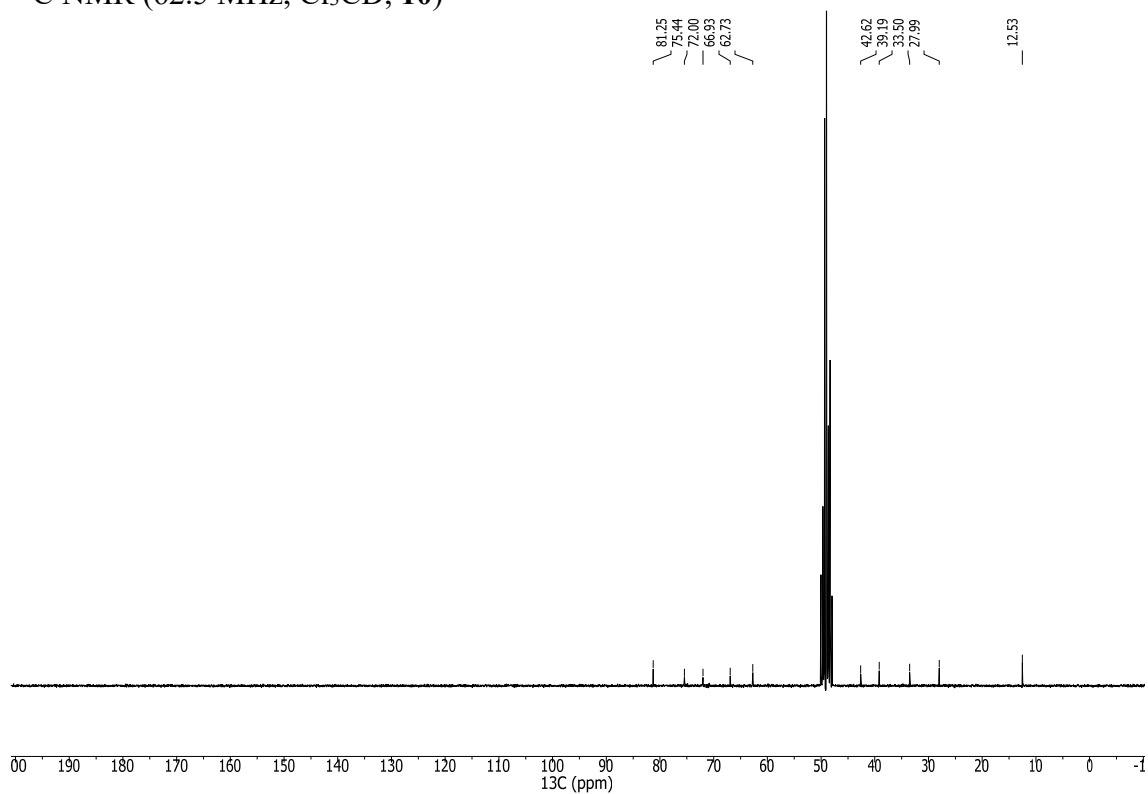
^{13}C NMR (62.5 MHz, Cl_3CD , **8**)



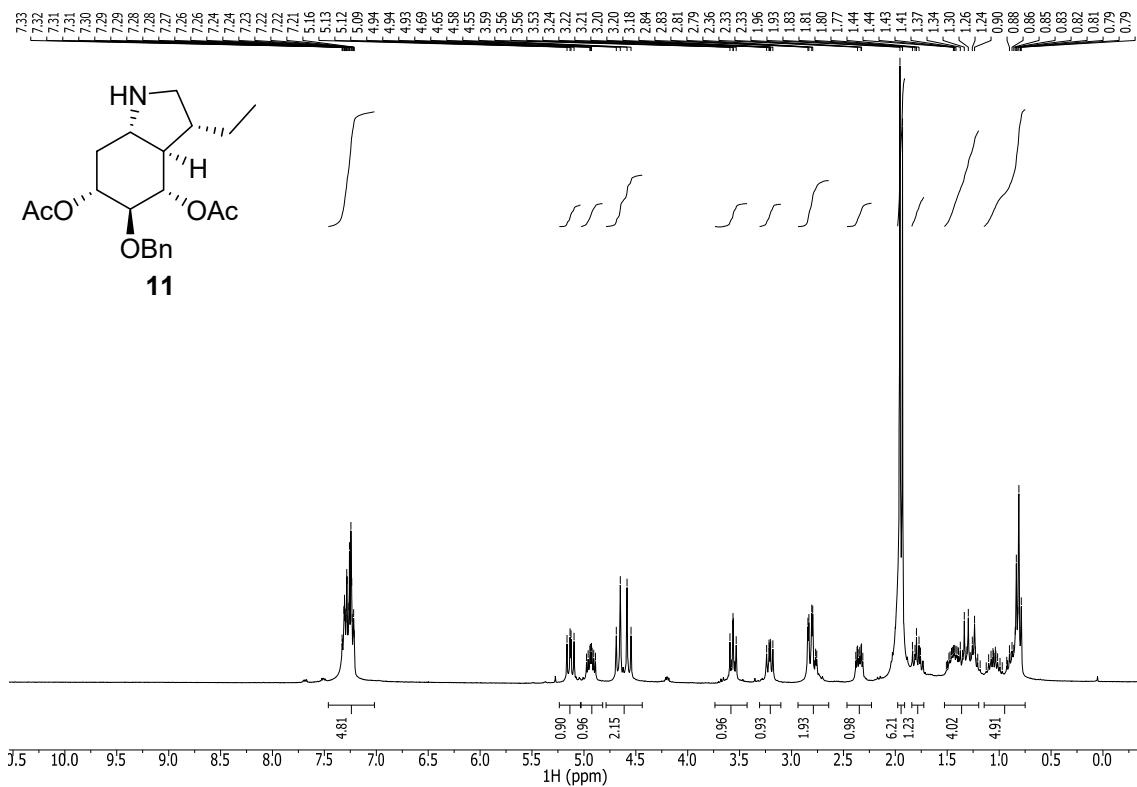
SI6. ^1H NMR (250 MHz, CD_3OD , **10**)



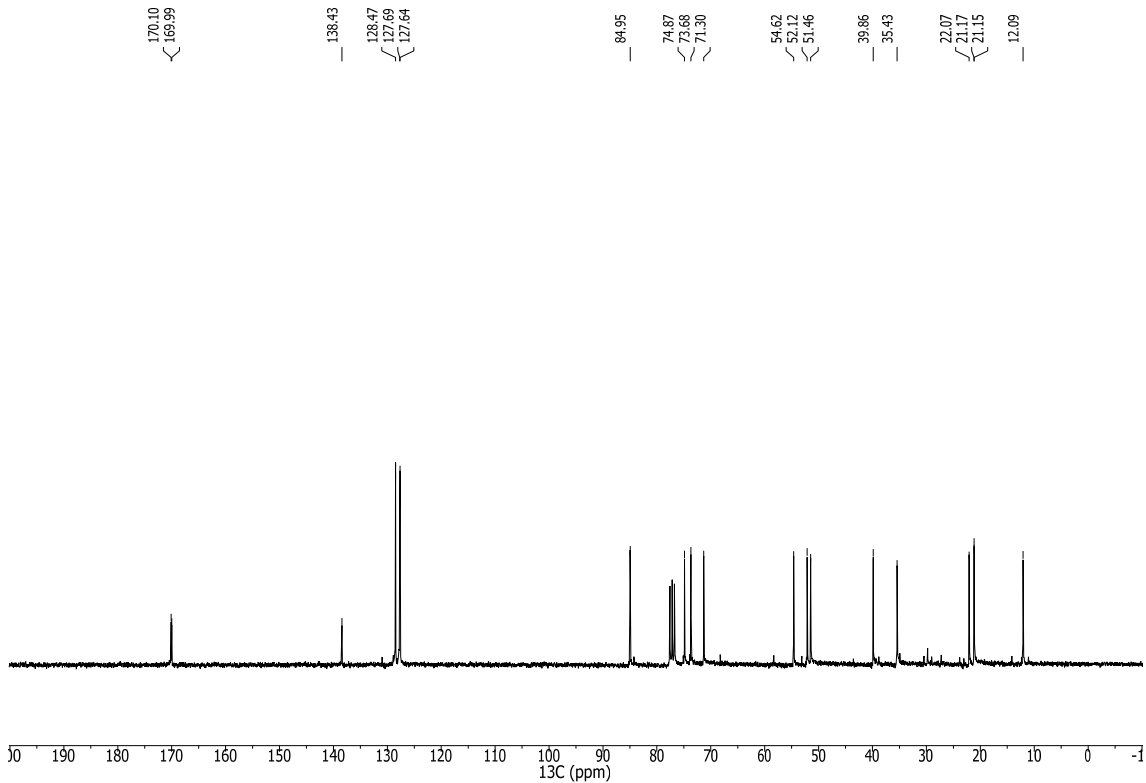
^{13}C NMR (62.5 MHz, Cl_3CD , **10**)



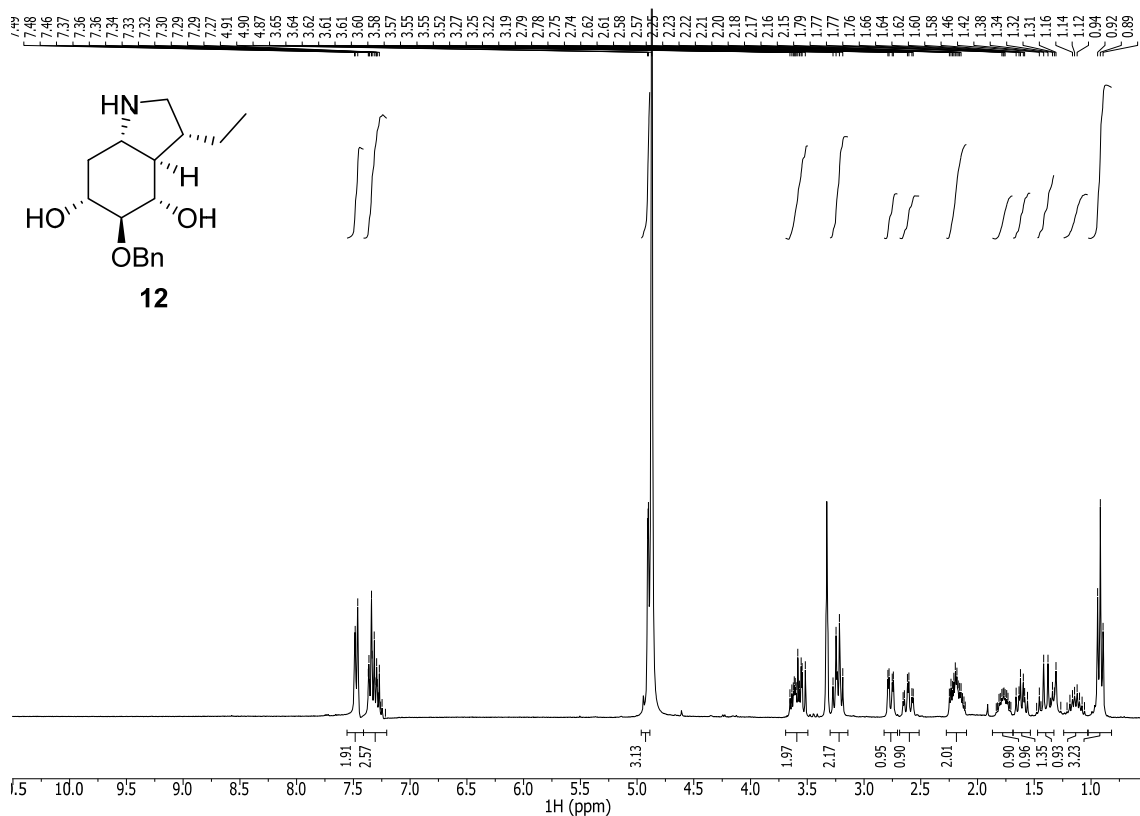
SI6. ^1H NMR (250 MHz, Cl_3CD , **11**)



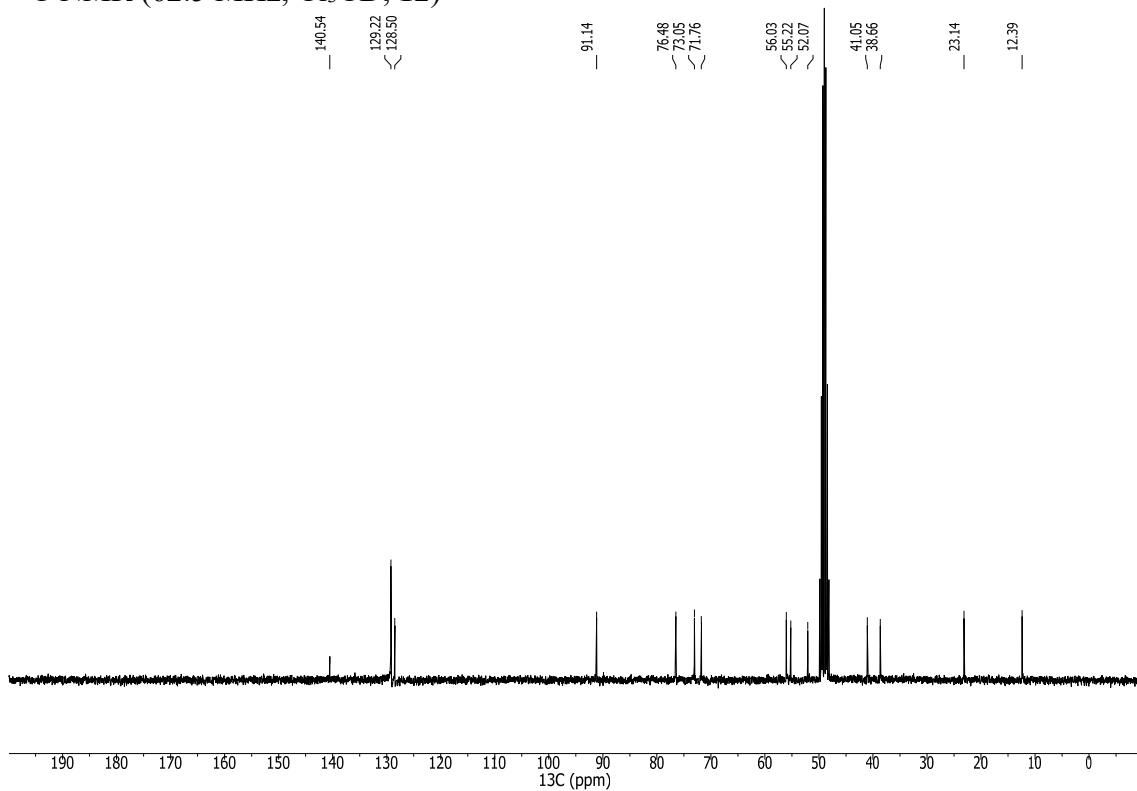
^{13}C NMR (62.5 MHz, Cl_3CD , **11**)



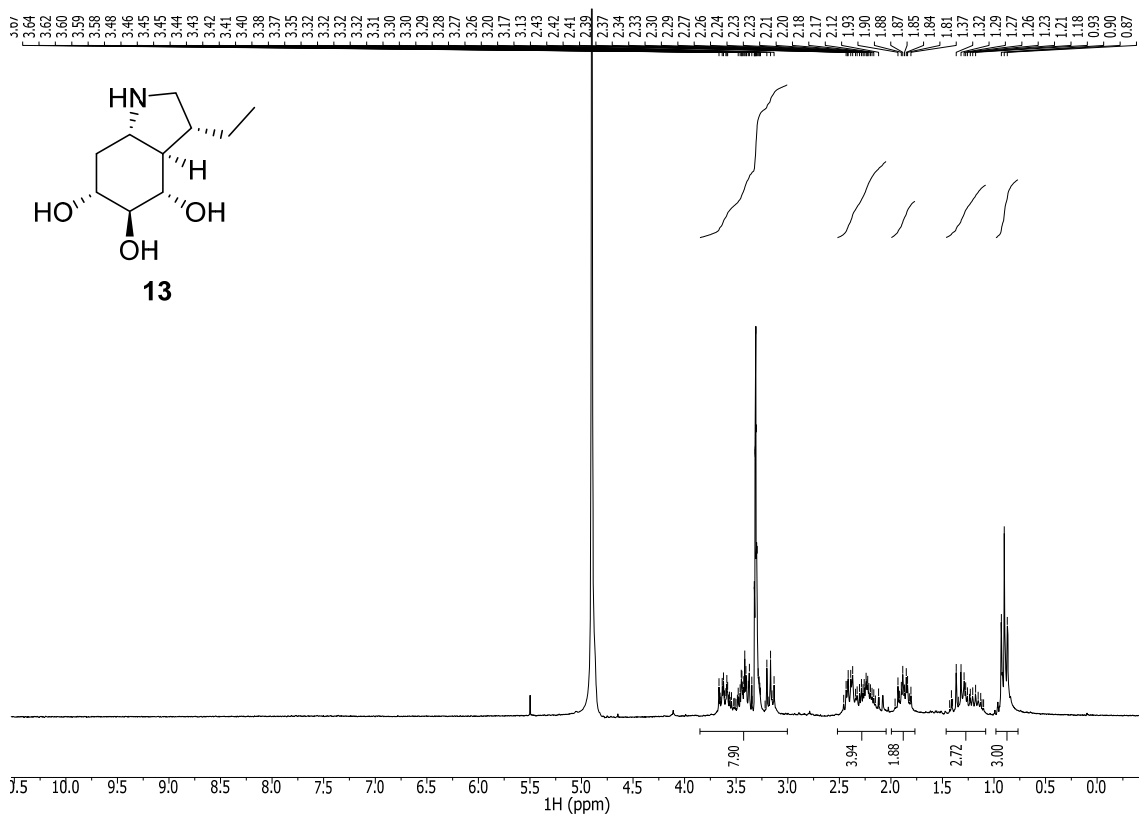
SI6. ¹H NMR (250 MHz, CD₃OD, **12**)



¹³C NMR (62.5 MHz, Cl₃CD, **12**)



SI6. ^1H NMR (250 MHz, CD_3OD , **13**)



^{13}C NMR (62.5 MHz, Cl_3CD , **13**)

