

ChemBioChem

Supporting Information

The Total Synthesis of Glycolipids from *Streptococcus pneumoniae* and a Re-evaluation of Their Immunological Activity**

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1. Supplementary Figures

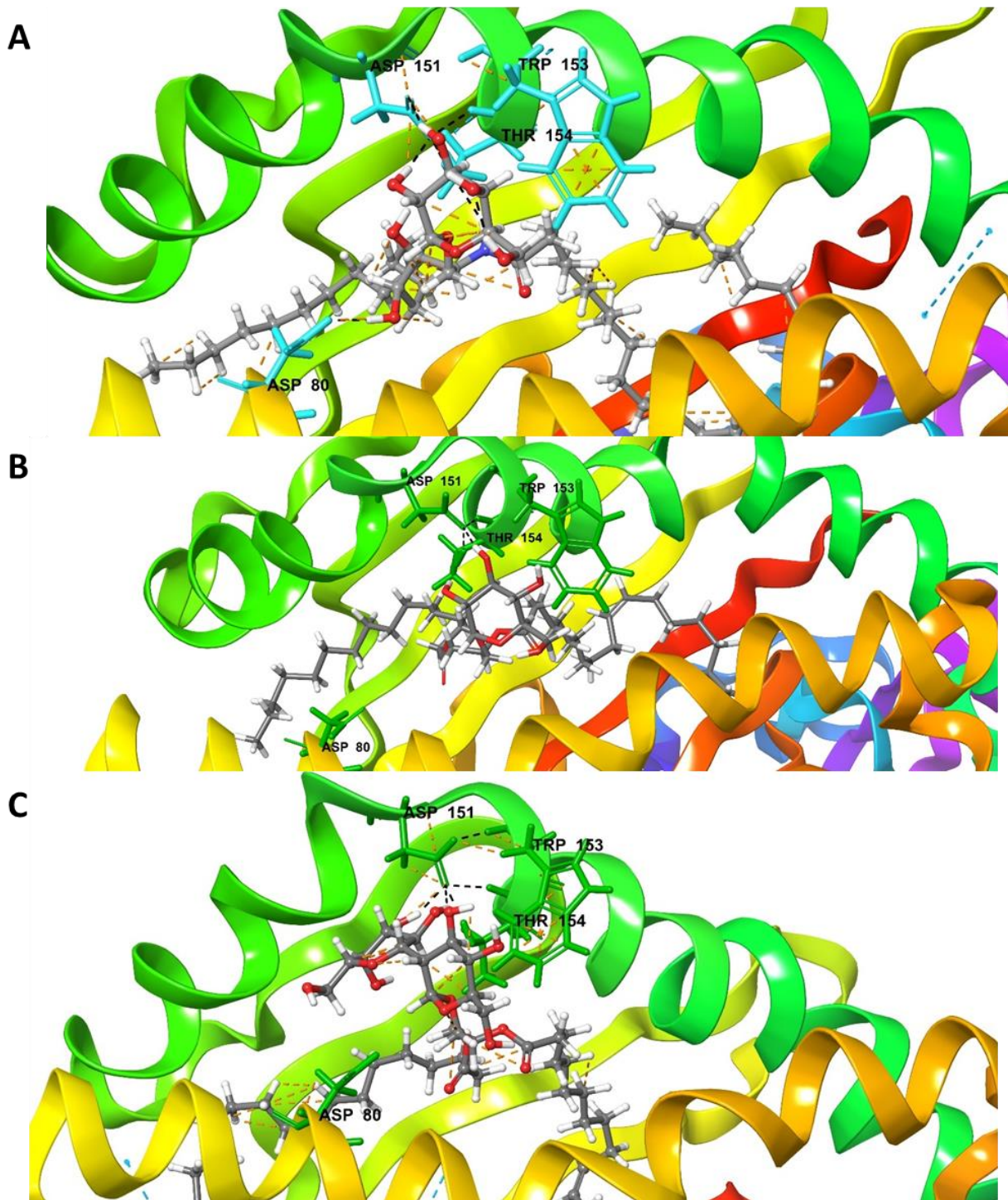


Figure S1. Highlighting key interactions at the mouth of the CD1d binding groove with A) KRN7000, B) Disaccharide **3**, and C) Monosaccharide **2**.

Docking Study:

To evaluate which pose best replicates the important interactions characteristic of the human CD1d with α -Galactosylceramide we reported both the S-score with the lowest value (the first series of docking posed that superimposed together; Figure S3) and the least value of RMSD (RMSD between the docked and the input structure). The lowest energetic values of both the "S score" and the "E_refine" as well as a low RMSD of conformer 1 is selected as the best pose and used for further MD simulation. The RMSD of above 2 Å reflects the significant differences between the different poses. The lowest energy pose is extremely similar to the X-ray crystal structure, although the carbohydrate adopts a slightly different pose when exposed to the water solvent.

	Conformer 1	Conformer 2
S score	-16.0875	-14.6502
E_refine	-55.6458	-45.2061
RMSD	2.0928	3.0557

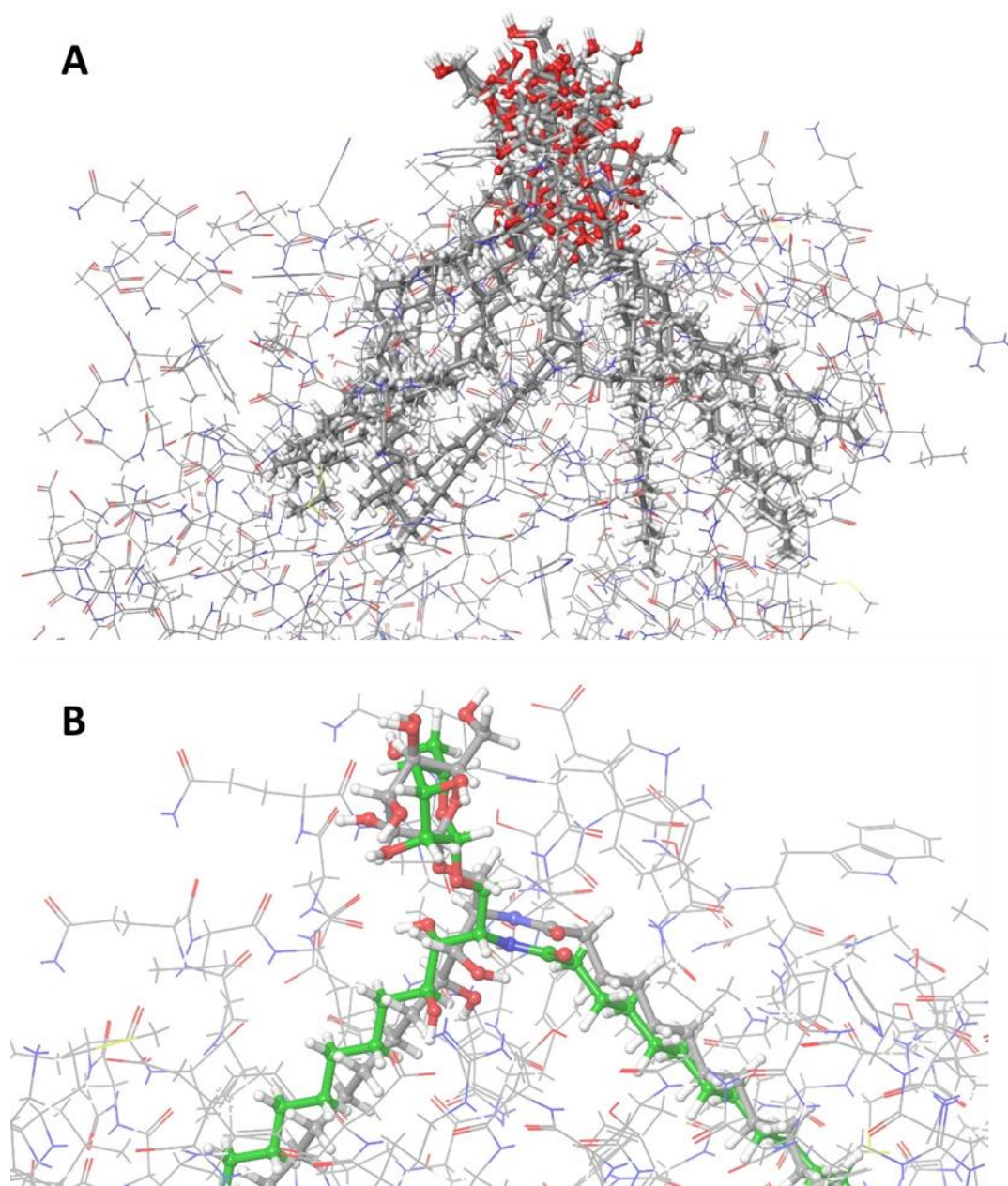


Figure S2. **A)** The superimposed binary structure of diverse docking poses obtained from rigid docking results for KRN7000 (1ZT4; The crystal structure of human CD1d with α -Galactosylceramide). These structures obtained are comparable to those in the crystal structure. The lowest energy docked structure is essentially identical with the crystal structure of the dimeric complex; **B)** The crystal structure of KRN7000 (green) superimposed with the optimal docked structure (grey).

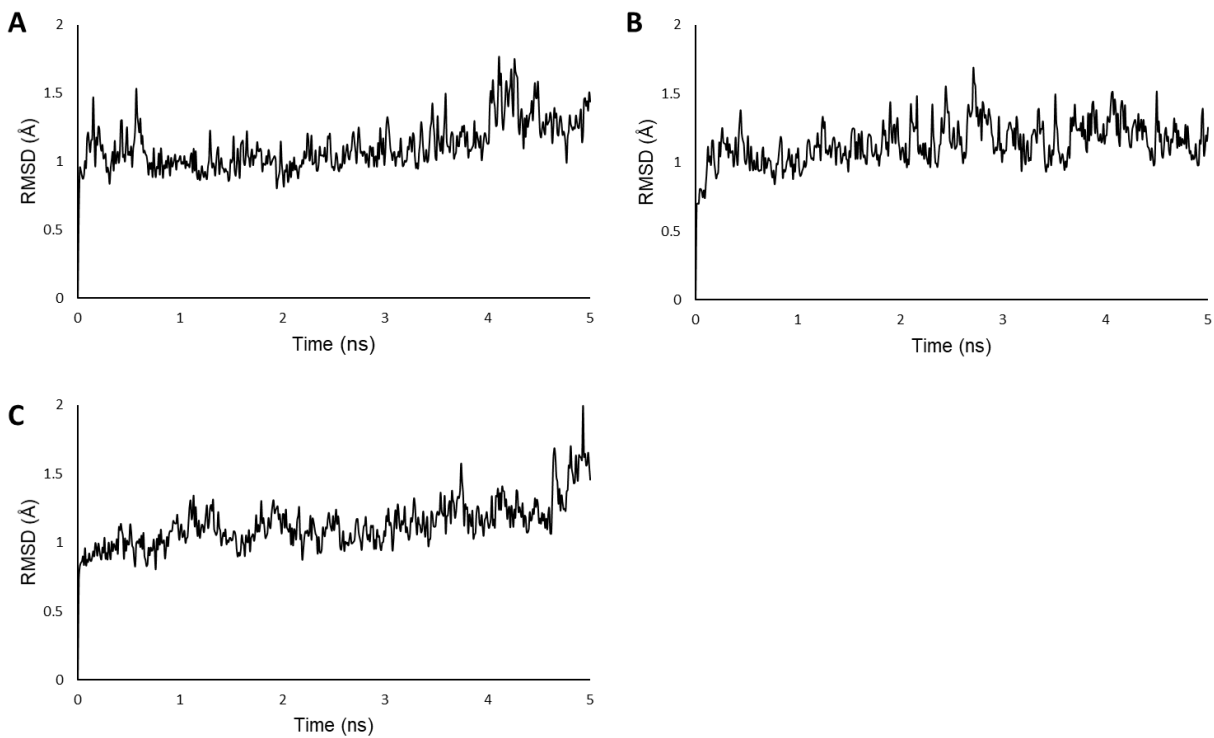


Figure S3. RMSD plot representing the complex of human CD1d bound to A) **KRN7000**; B) monosaccharide **2**; and C) disaccharide **3**.

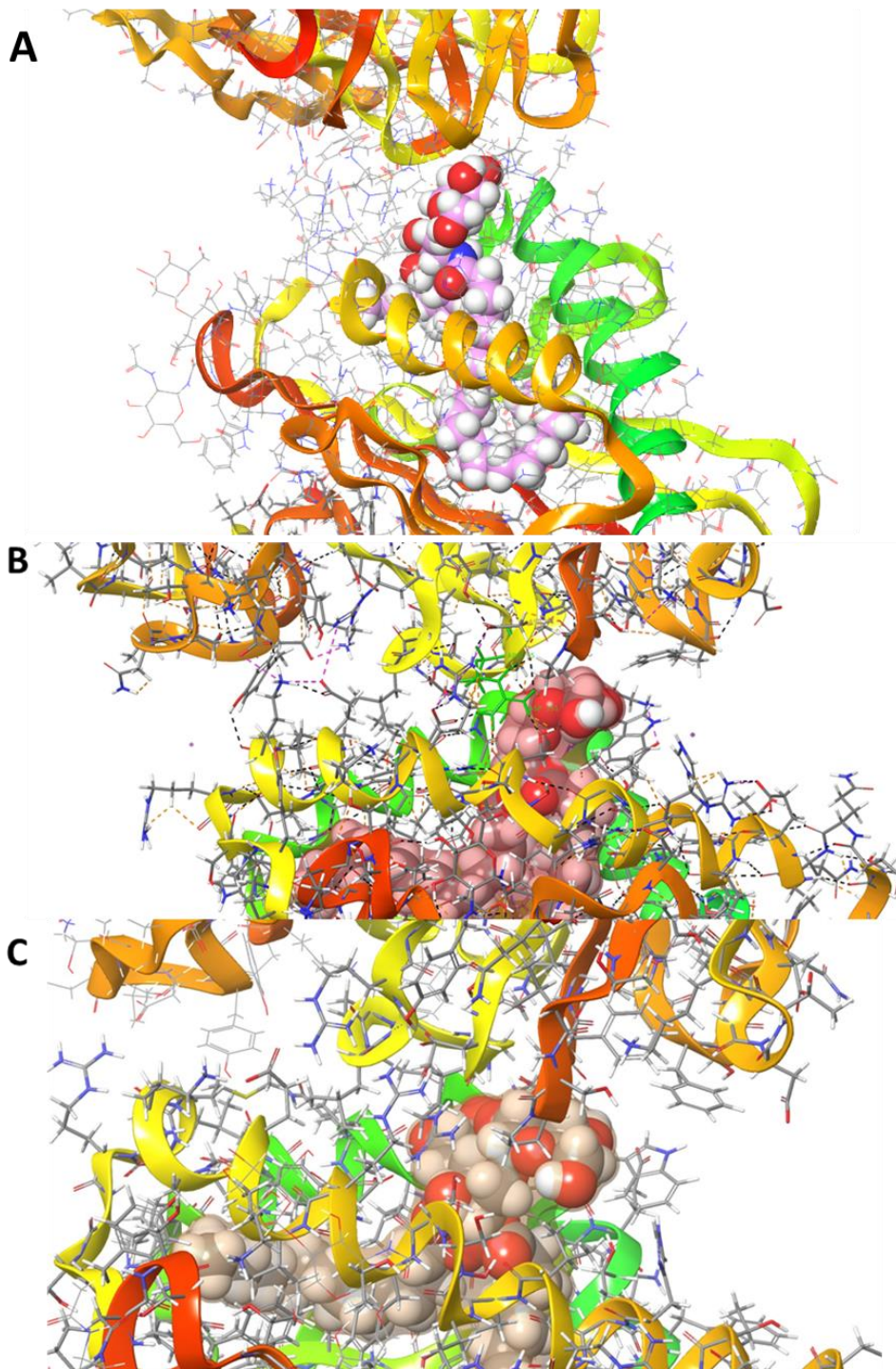
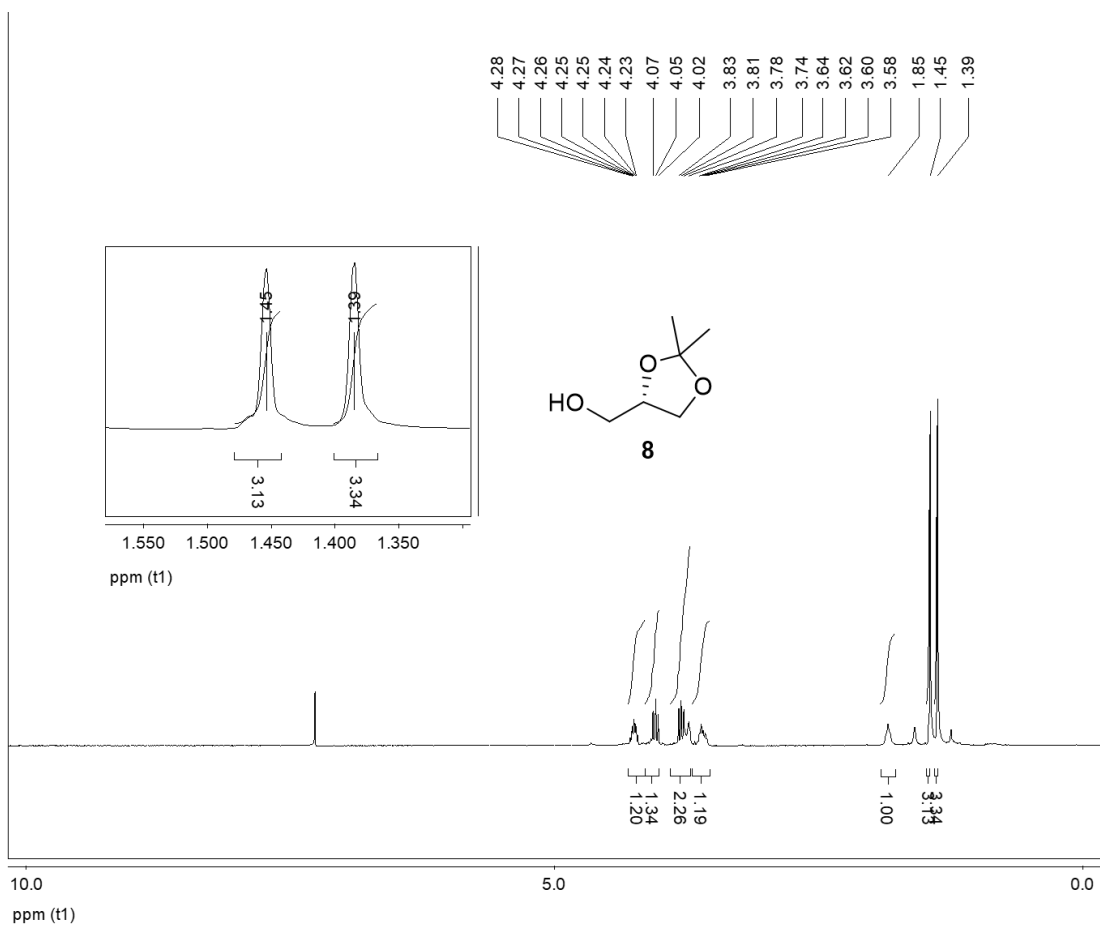
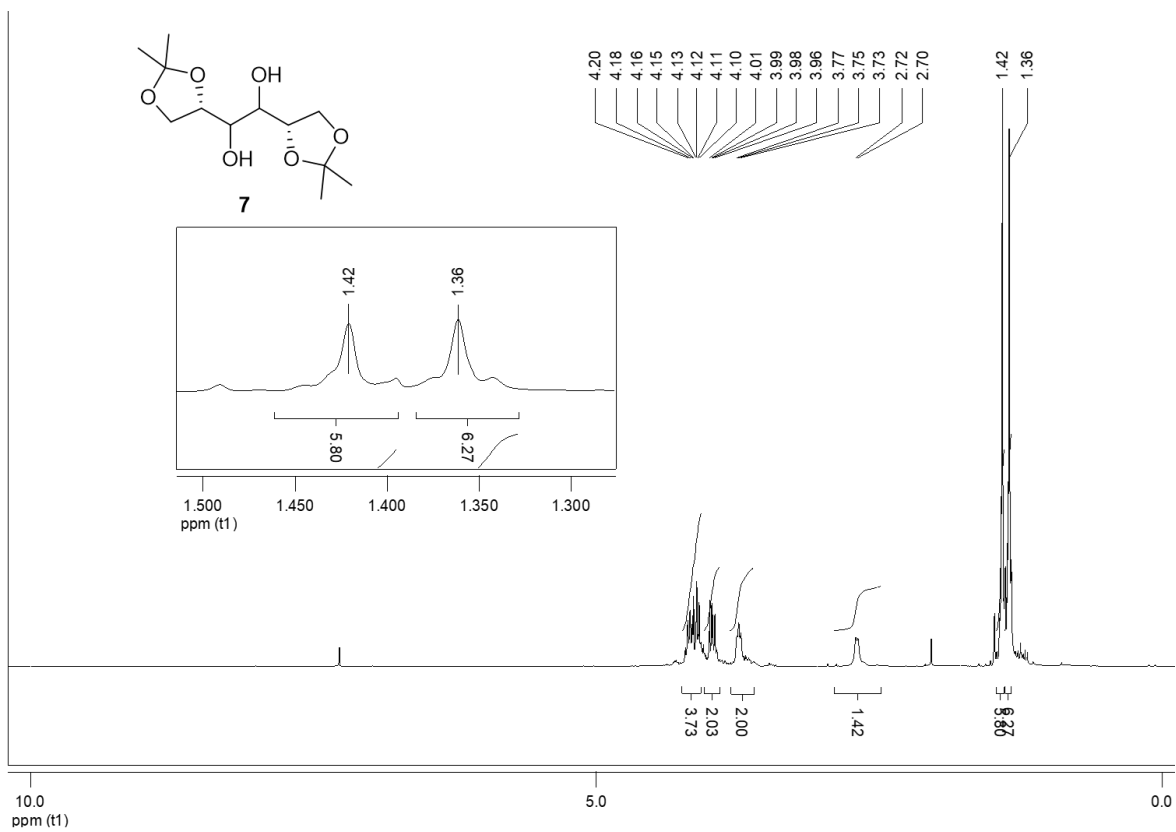
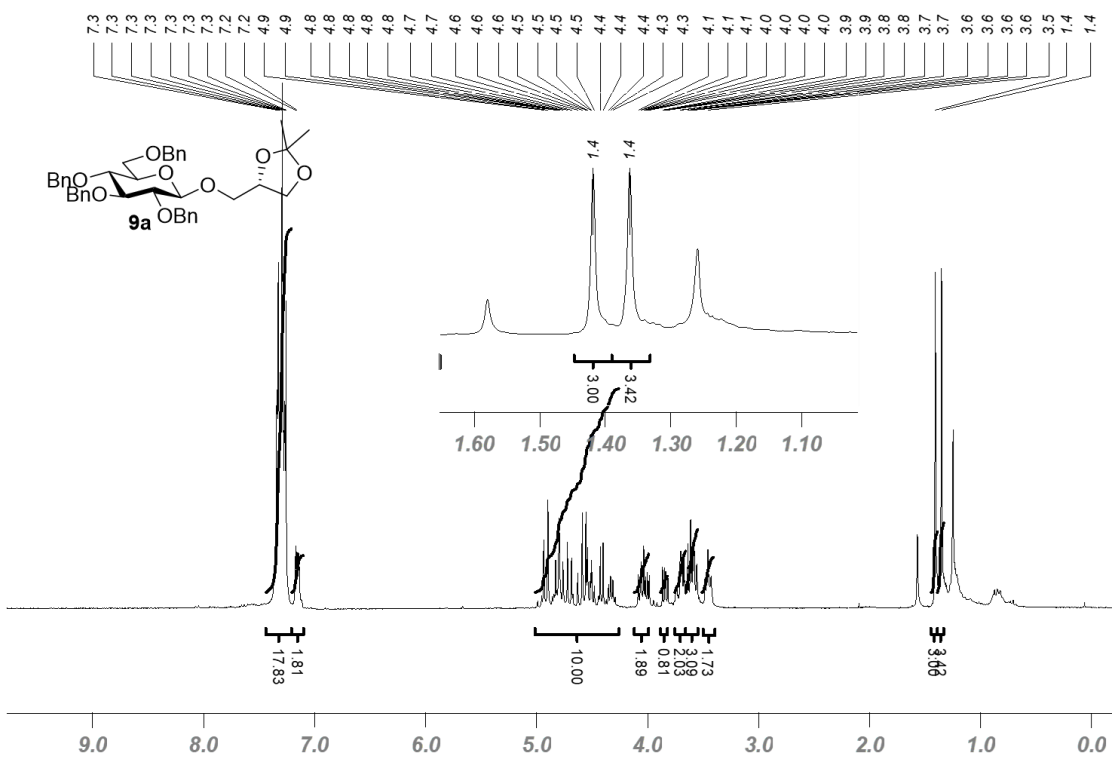
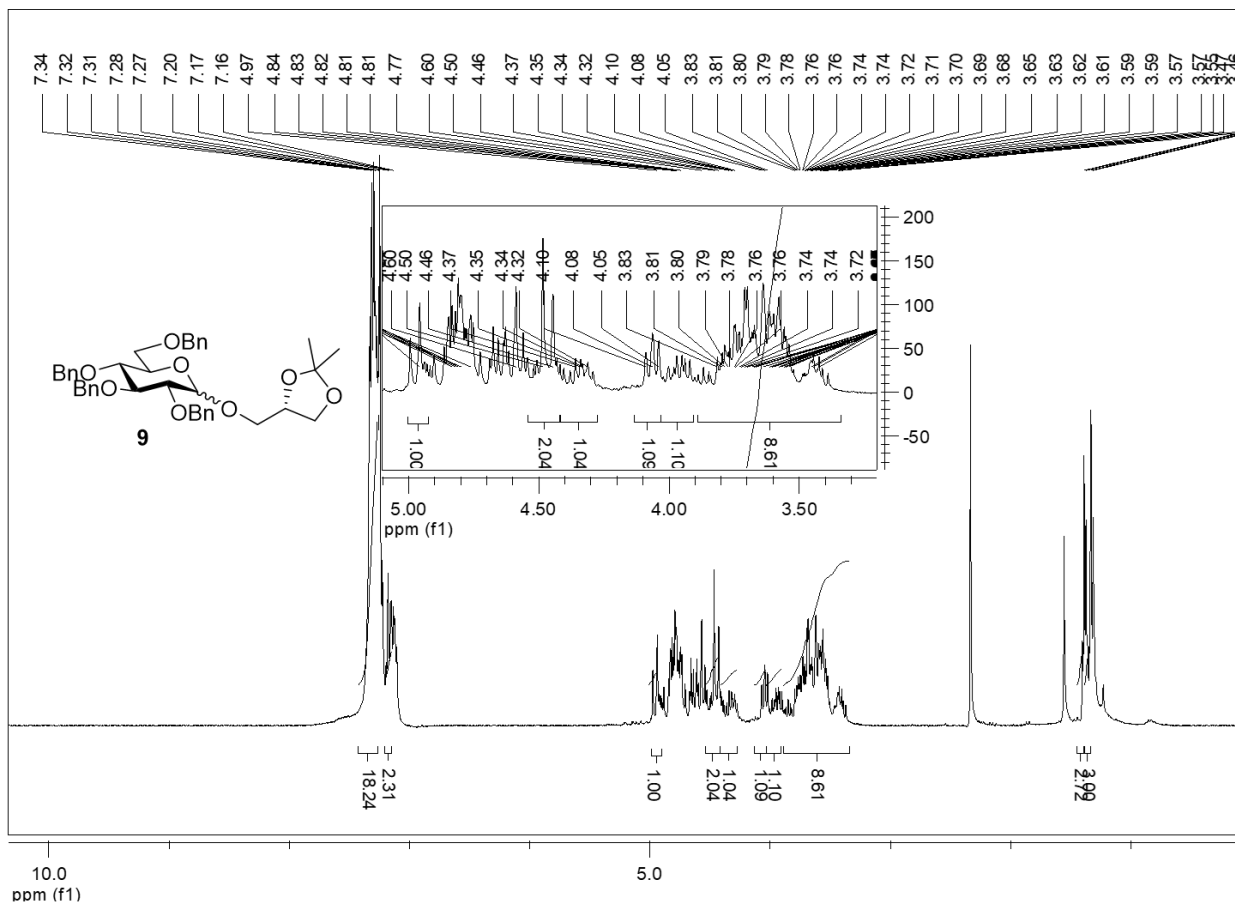


Figure S4. Visualization of the modelled ternary complex highlighting differences in key interactions. Structure is obtained from the energy minimum conformation from the MD simulation (extracted from the 5 ns NPT). A) TCR∩KRN7000@CD1d; B) TCR∩2@CD1d ;C) TCR∩3@CD1d





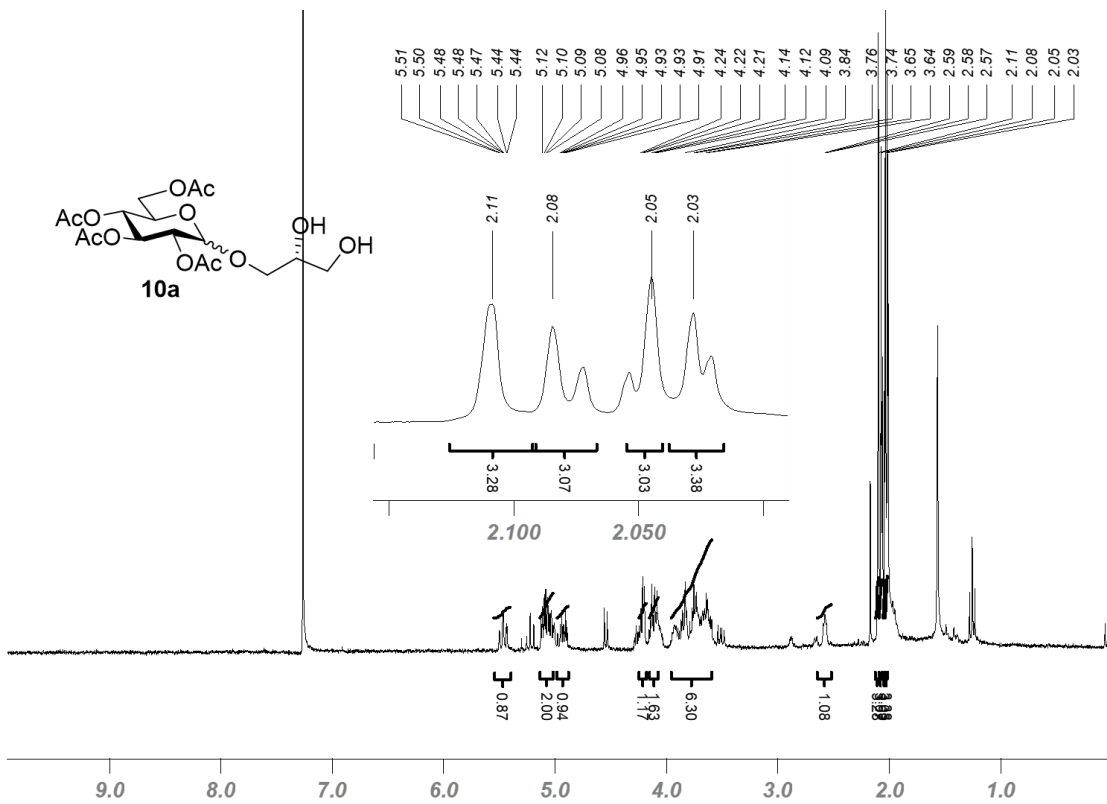


Figure S15. ¹H NMR (300MHz, CDCl₃) of compound **10a**

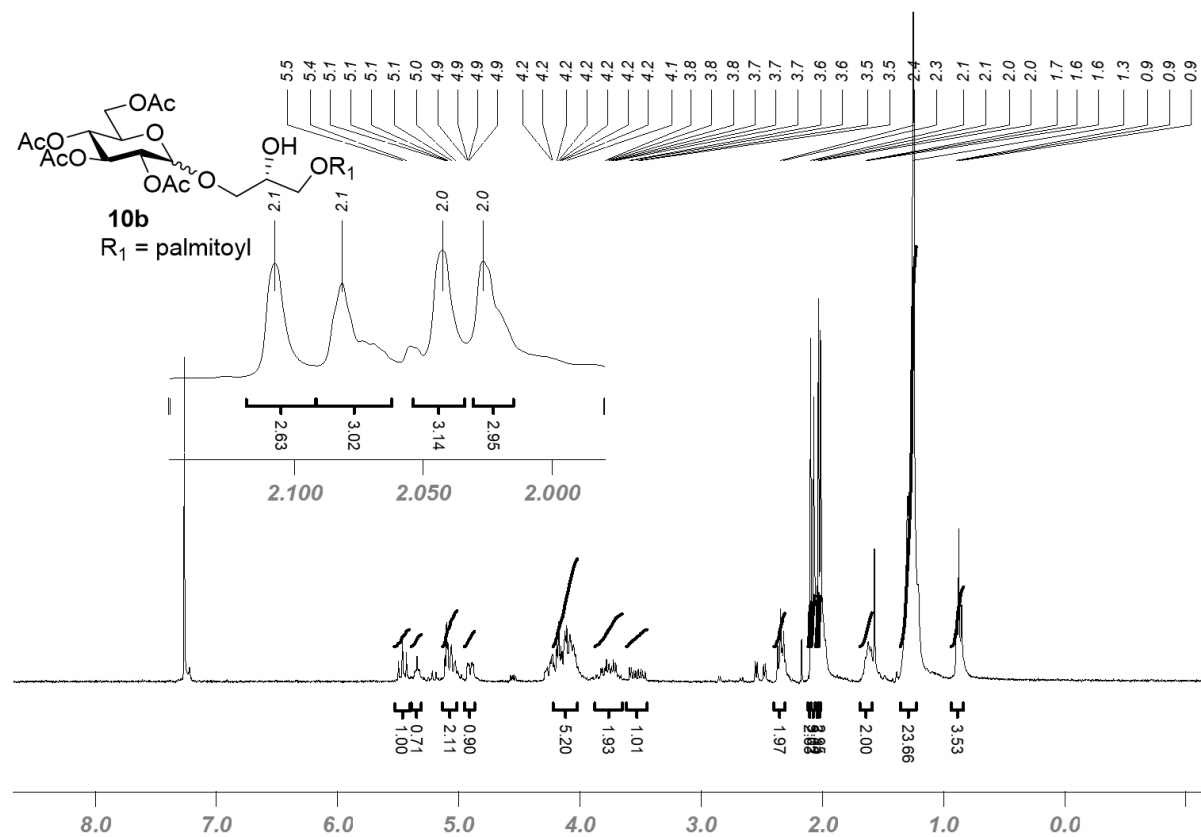


Figure S16. ¹H NMR (300MHz, CDCl₃) of compound **10b**

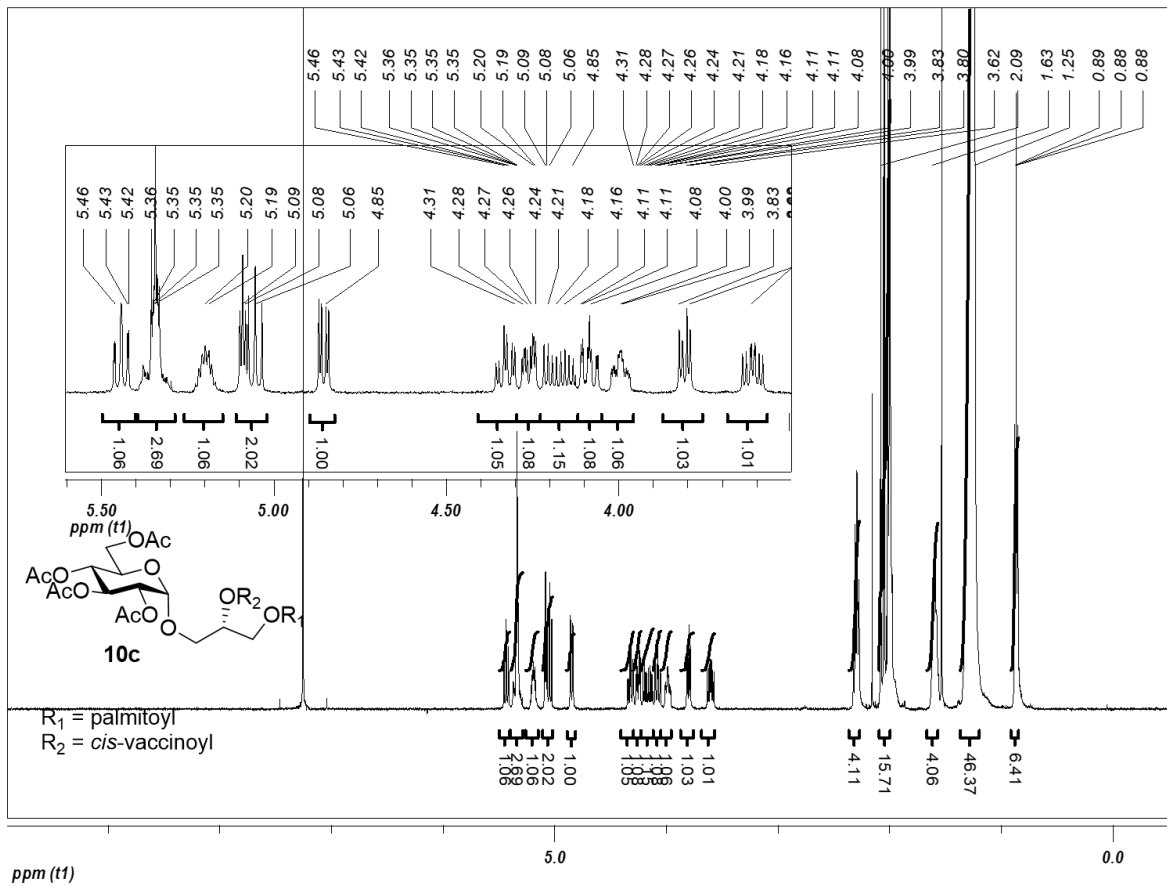


Figure S17. ^1H NMR (300MHz, CDCl_3) of compound **10c**

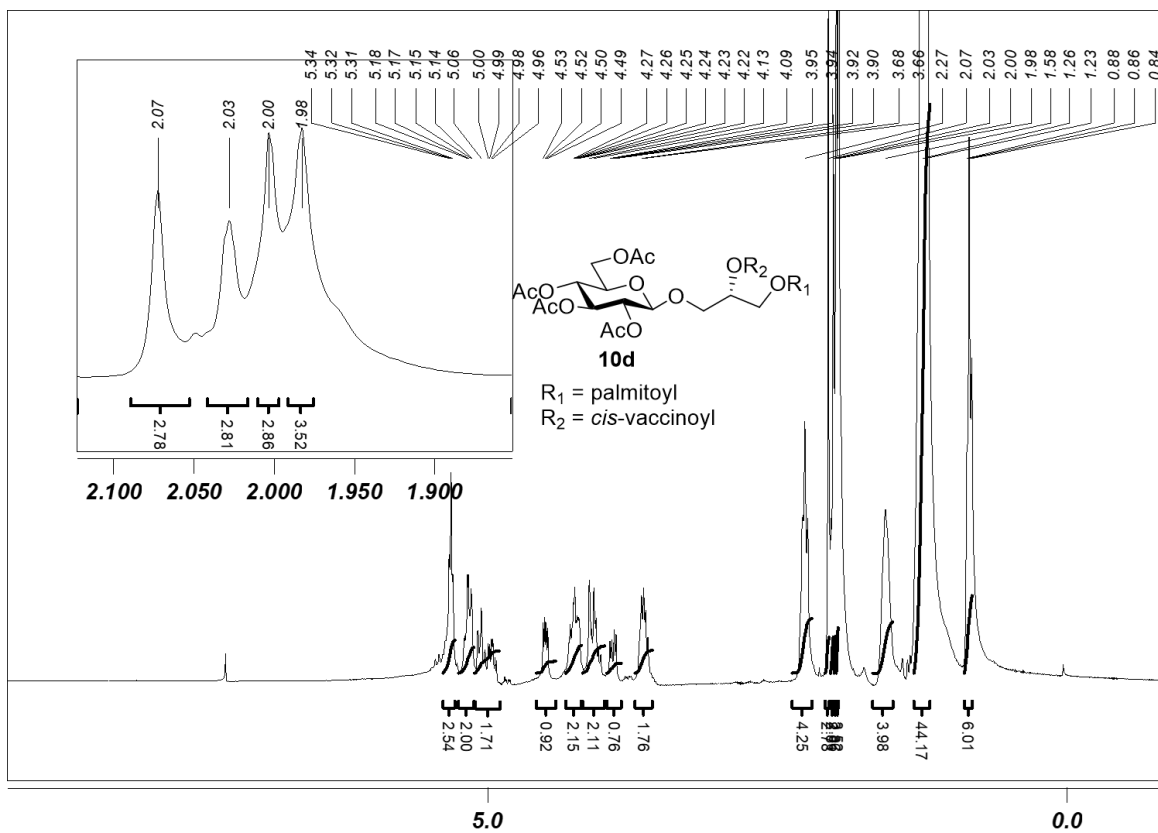


Figure S18. ^1H NMR (300MHz, CDCl_3) of compound **10d**

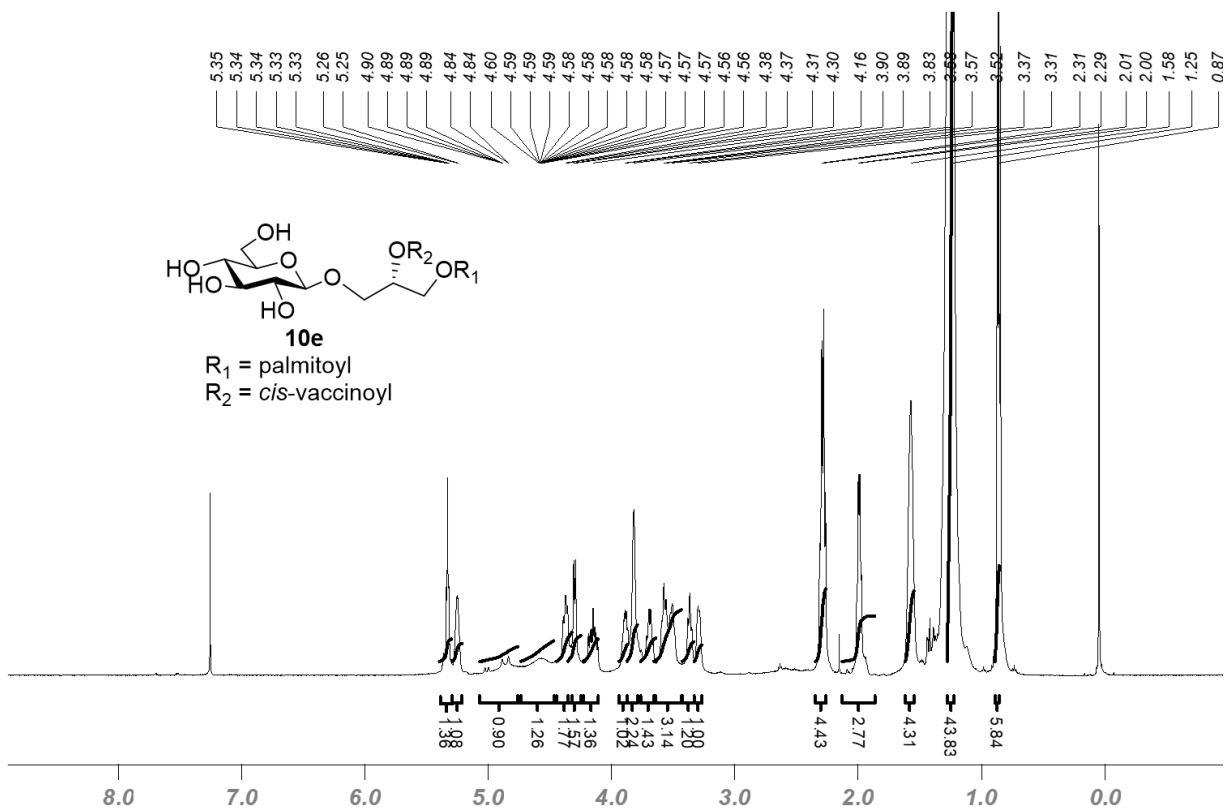


Figure S19. ¹H NMR (300MHz, CDCl₃) of compound 10e

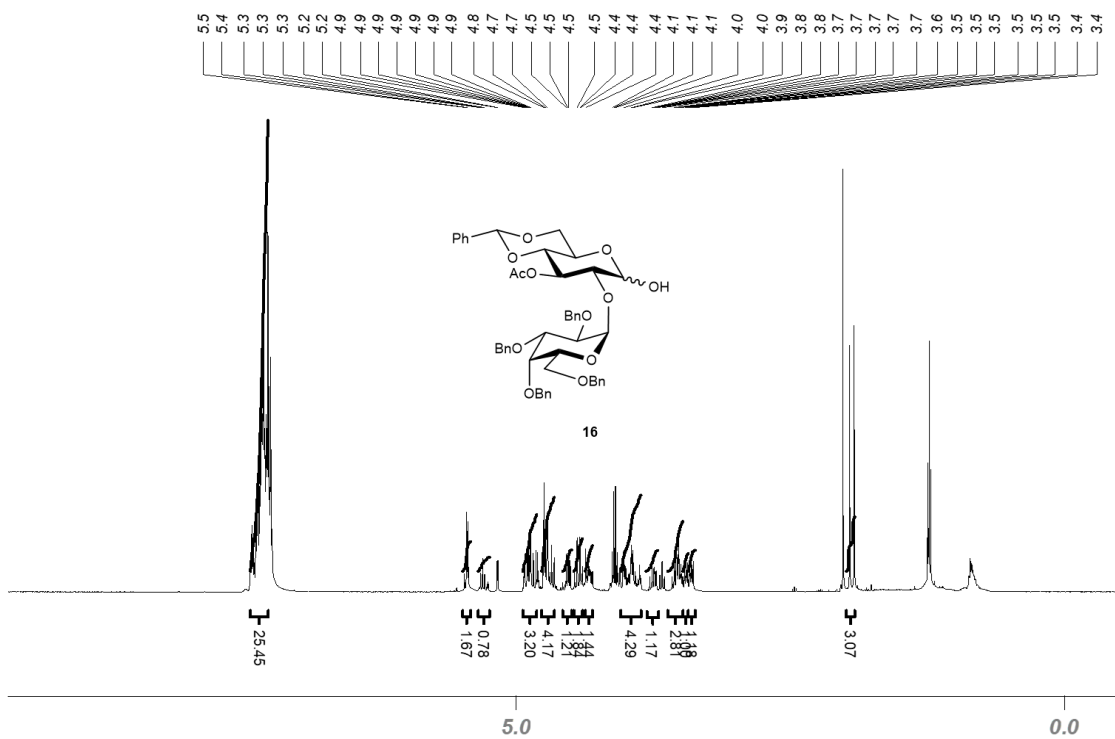


Figure S22. ^1H NMR (500MHz, CDCl_3) of compound 16.

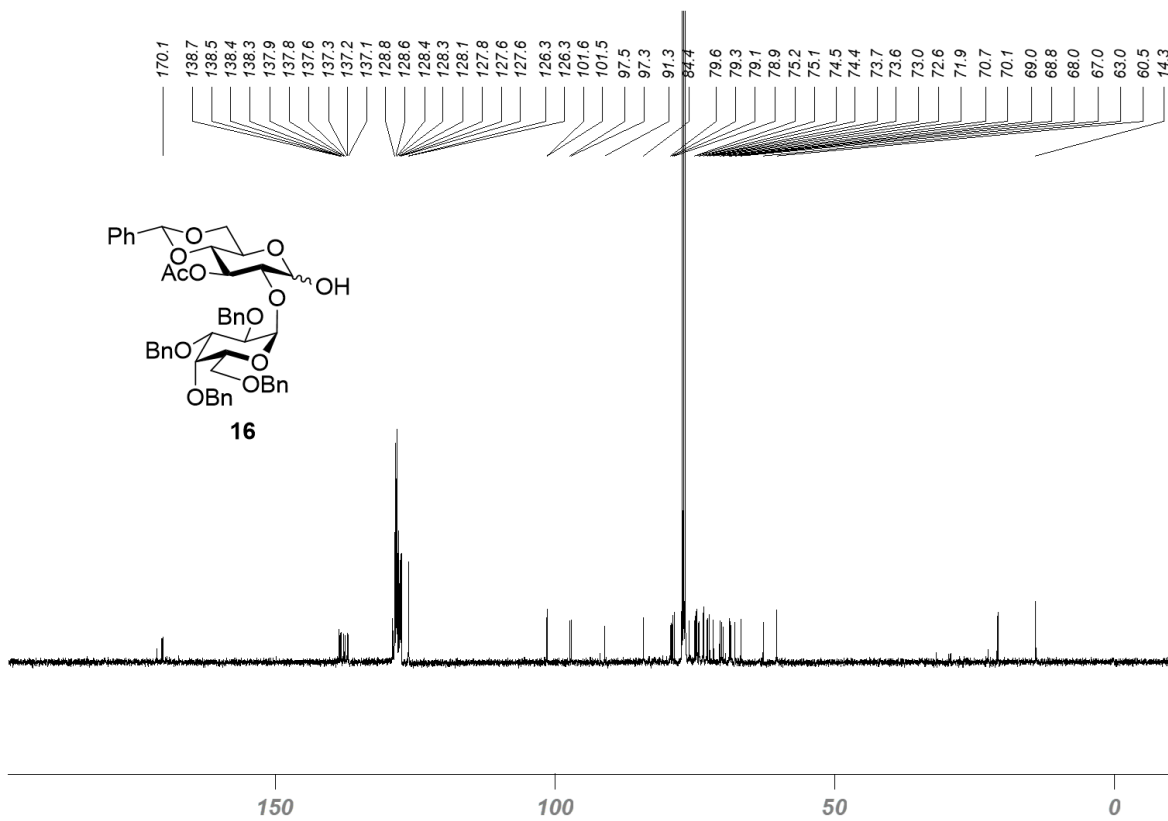
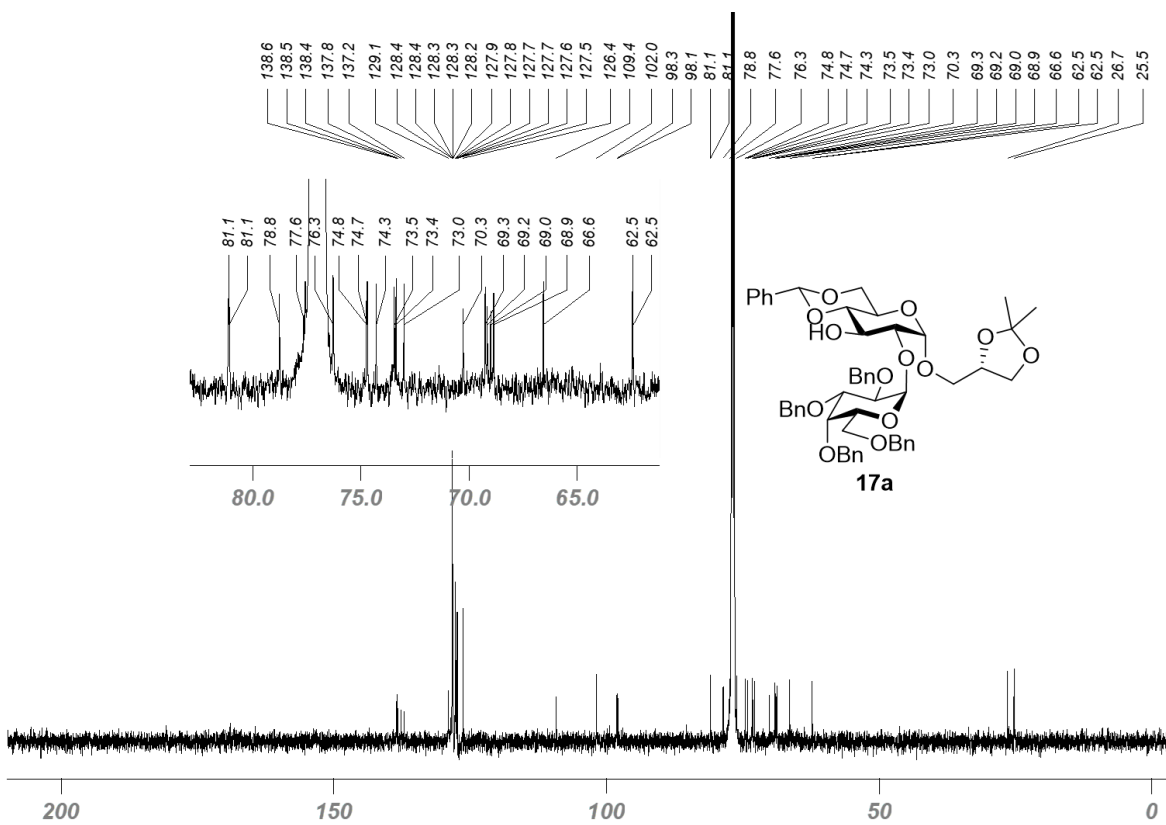
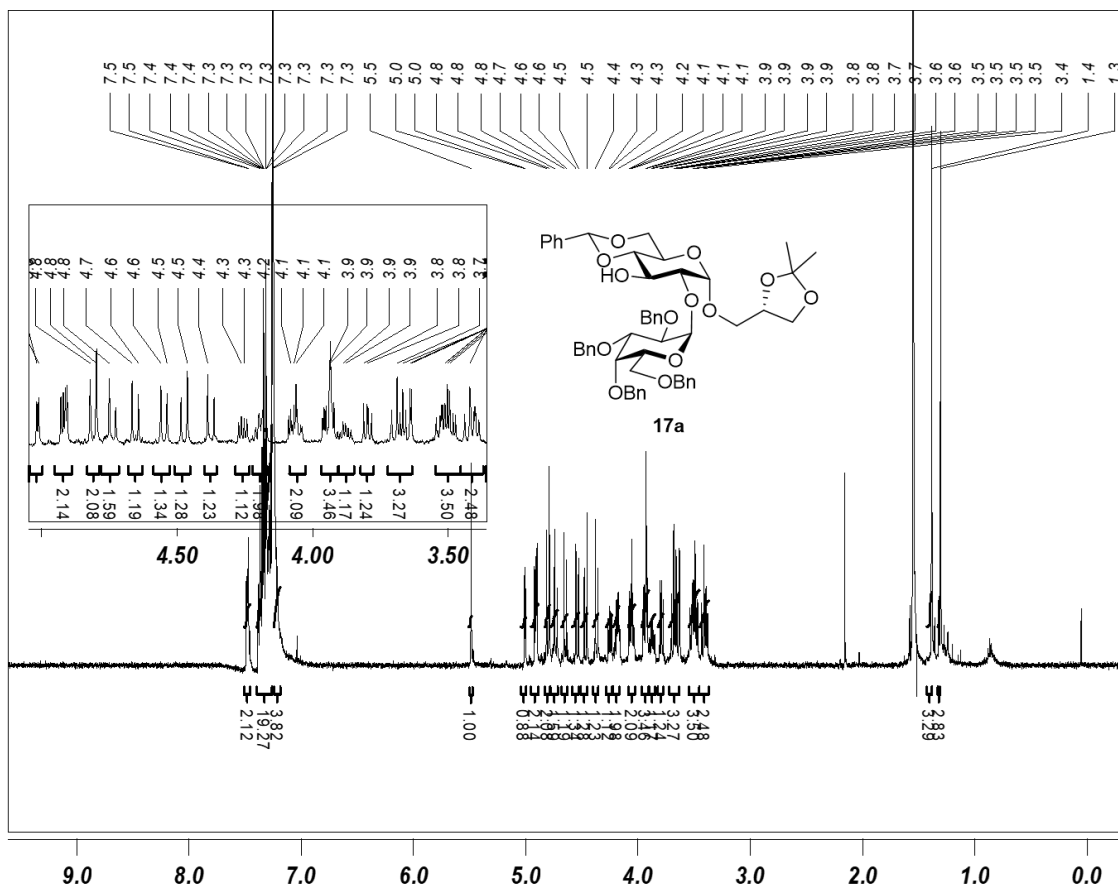


Figure S23. ^{13}C NMR (125MHz, CDCl_3) of compound 16.



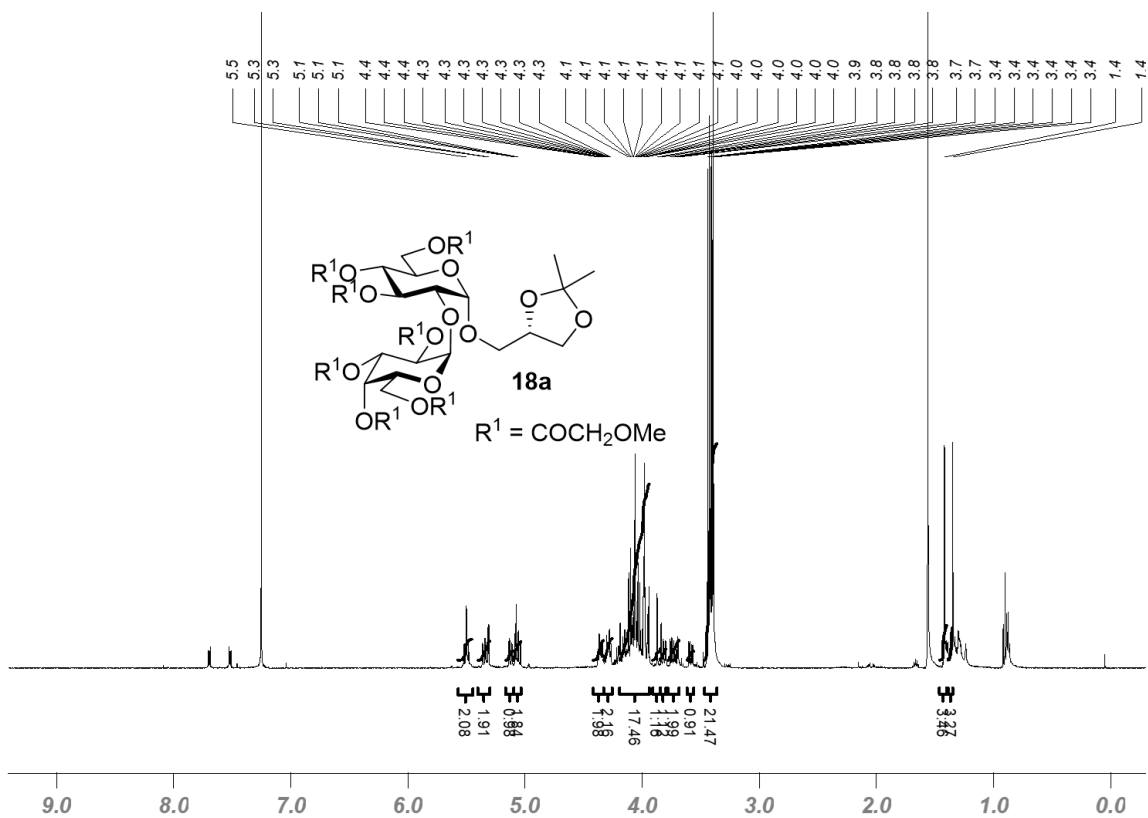


Figure S30. ¹H NMR (500MHz, MeOD) of compound **18a**.

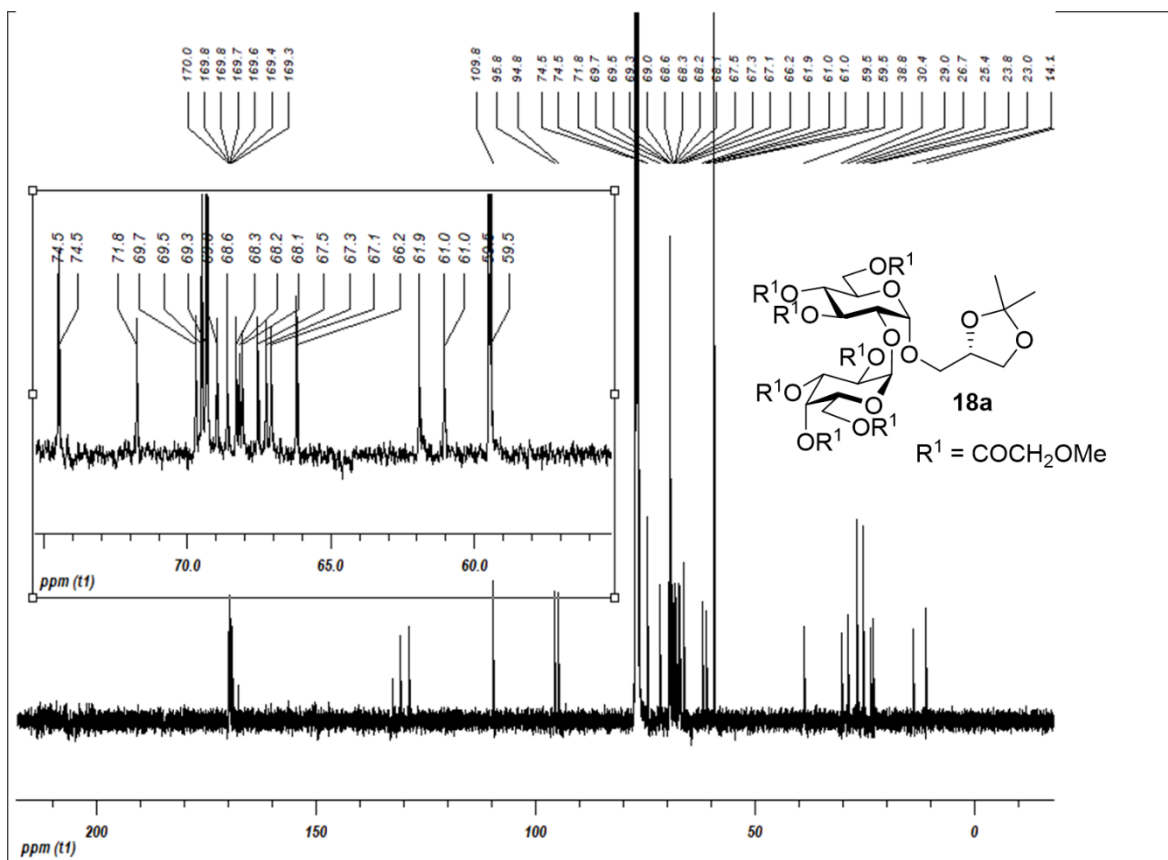
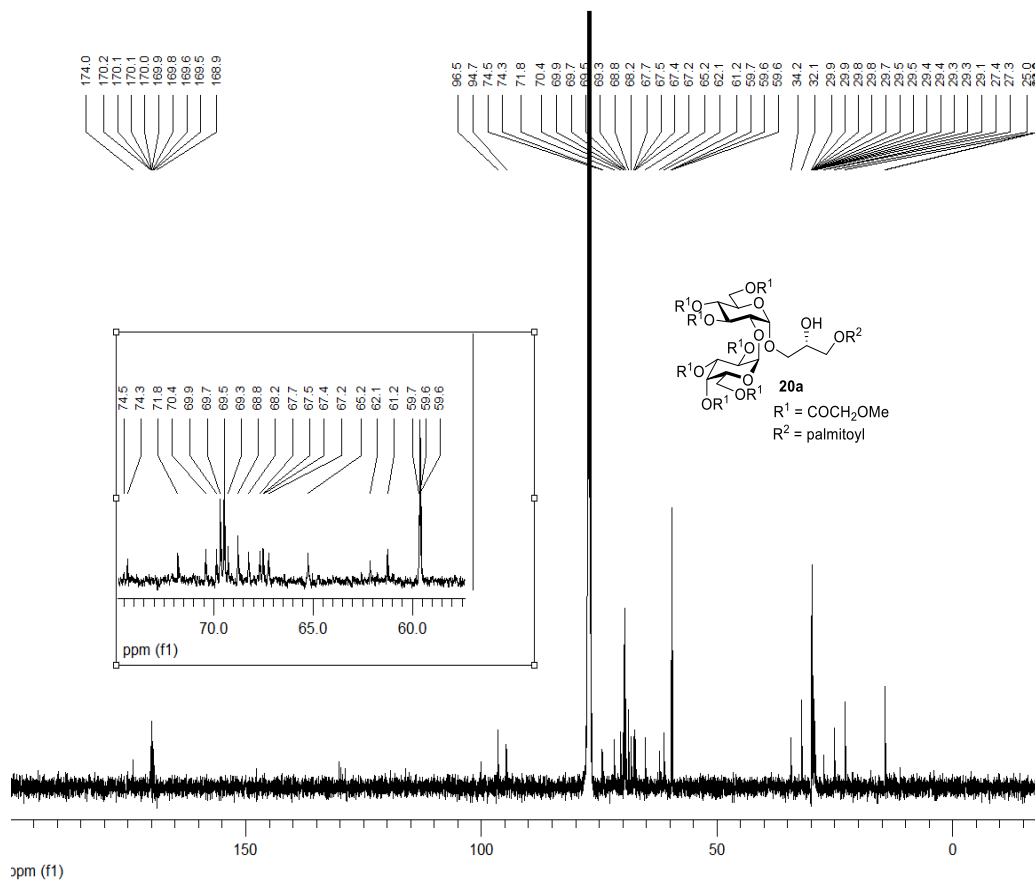
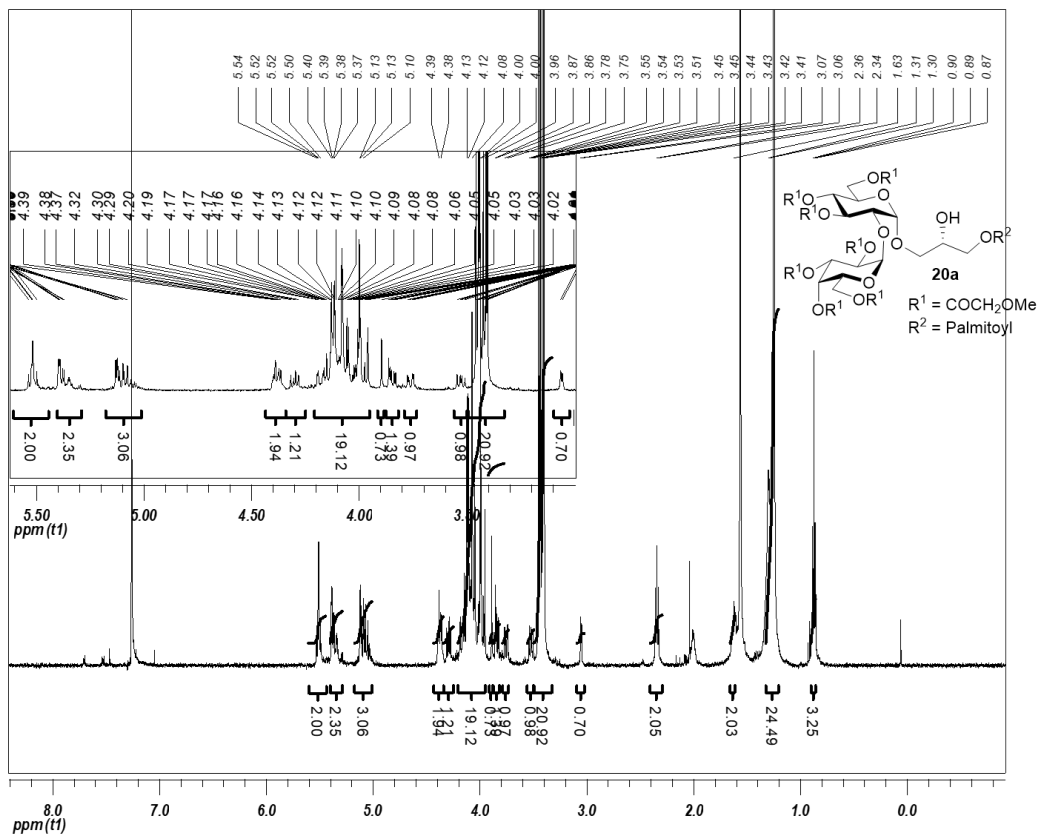


Figure S31. ¹³C NMR (125MHz, MeOD) of compound **18a**.



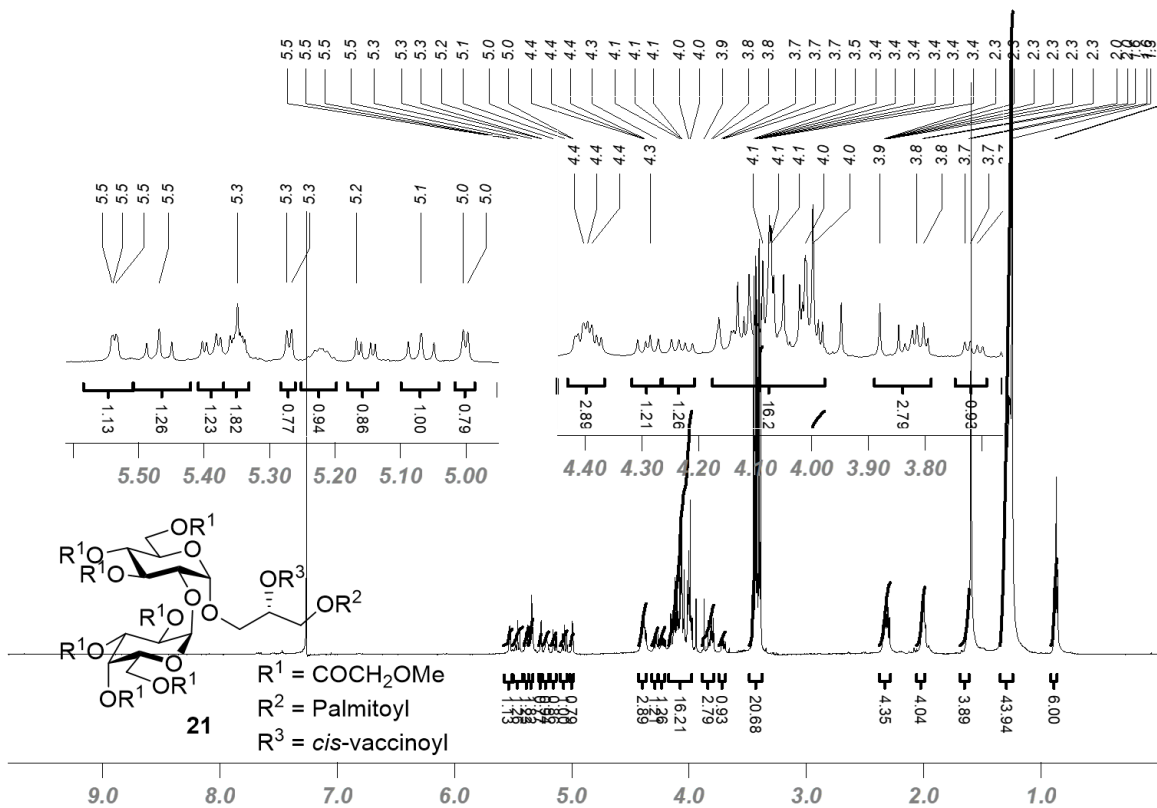
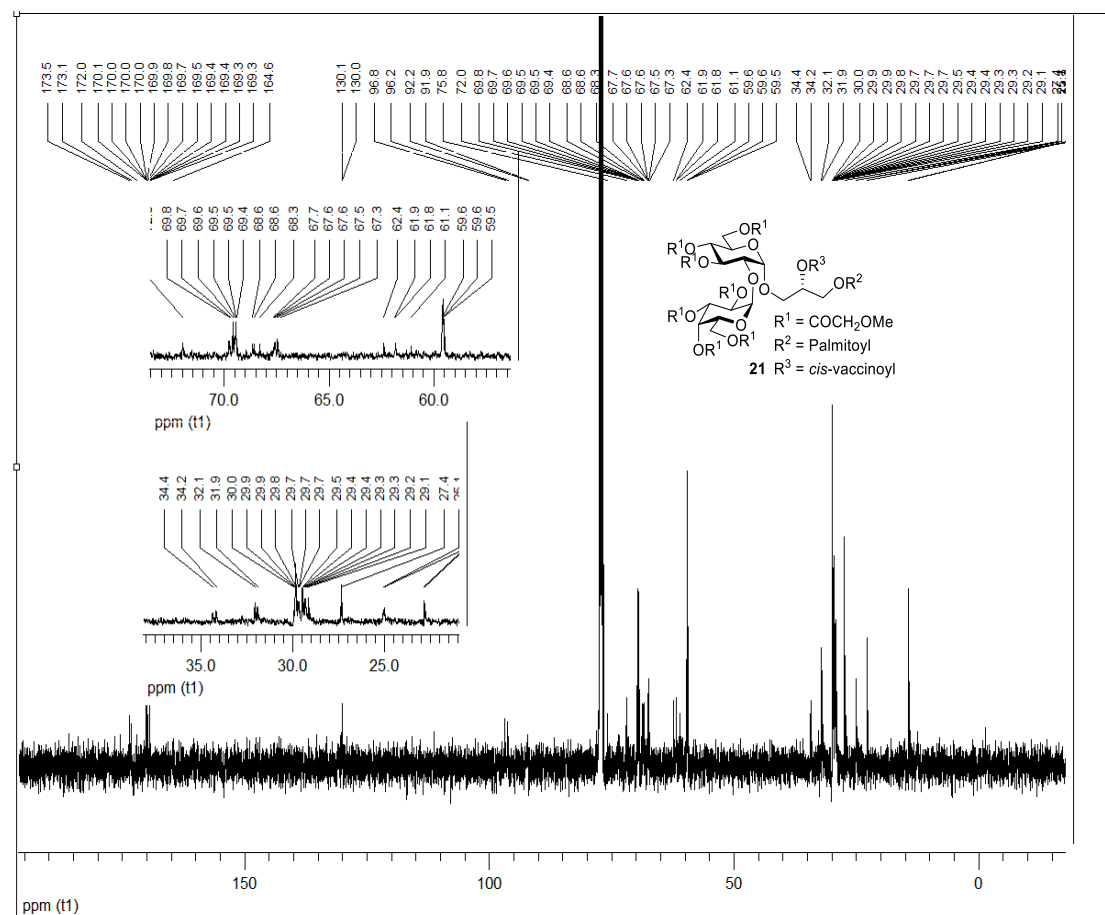


Figure S36. ¹H NMR (500MHz, CDCl₃) of compound 21.



Reference

[1] Y. Kinjo, P. Illarionov, J. L. Vela, B. Pei, E. Girardi, X. Li, Y. Li, M. Imamura, Y. Kaneko, A. Okawara, Y. Miyazaki, A. Gomez-Velasco, P. Rogers, S. Dahesh, S. Uchiyama, A. Khurana, K. Kawahara, H. Yesilkaya, P. W. Andrew, C.-H. Wong, K. Kawakami, V. Nizet, G. S. Besra, M. Tsuji, D. M. Zajonc and M. Kronenberg, *Nat. Immunol.* **2011**, *12*, 966-974.