

Supporting Information

A 'catch-and-release' receptor for the cholera toxin

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Characterisation of polymer **P1**

The molecular weight and monomer composition of **P1** was determined by end-group analysis, comparing the integration of the terminal CH_3 protons with the $CH(CH_3)_2$ protons of NIPAm and the $CHCH_2$ and $CHCH_2$ protons of NIPAm and **M1**. The monomer composition of **P1** was determined to be 4:1 NIPAm:**M1**, in contrast to the feed ratio of 8:1 NIPAm:**M1**, most likely as a consequence of a difference in reactivity of the two monomers.

polymer	chain transfer agent	monomers	initiator	solvent	time / h	temp / °C	M_n^a / g mol ⁻¹	M_n^b / g mol ⁻¹	M_w^b / g mol ⁻¹	PDI ^b (M_w/M_n)
P1	DDMAT (1 eq)	NIPAm (160 eq) M1 (20 eq)	AIBN (0.2 eq)	DMSO	18	70	13,400	20,300	22,700	1.12

Table 1 Characterisation of copolymer **P1**. ^a As determined by ¹H NMR spectroscopy. ^b As determined by gel permeation chromatography in DMF (0.6 mL/min) calibrated against near monodisperse methyl methacrylate standards. AIBN: azobis(isobutyronitrile), DMSO: dimethylsulfoxide, DMA: *N,N*-dimethylacrylamide, DDMAT: *S*-1-dodecyl-*S'*-(α,α -dimethyl- α' -acetic acid)trithiocarbonate.

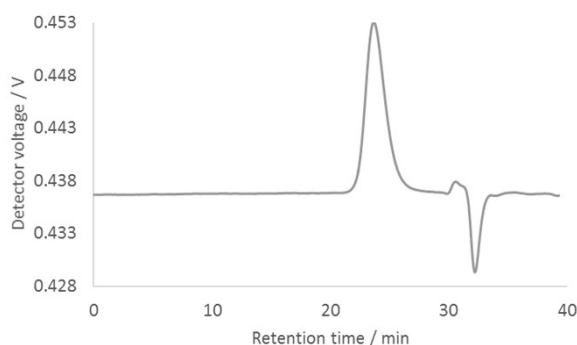


Fig. S1 Differential refractive index gel permeation chromatography (GPC) trace of **P1** in DMF (0.6 mL/min, containing 1.0 g/L LiBr).

Characterisation of GM1os functionalised polymer P2-GM1os

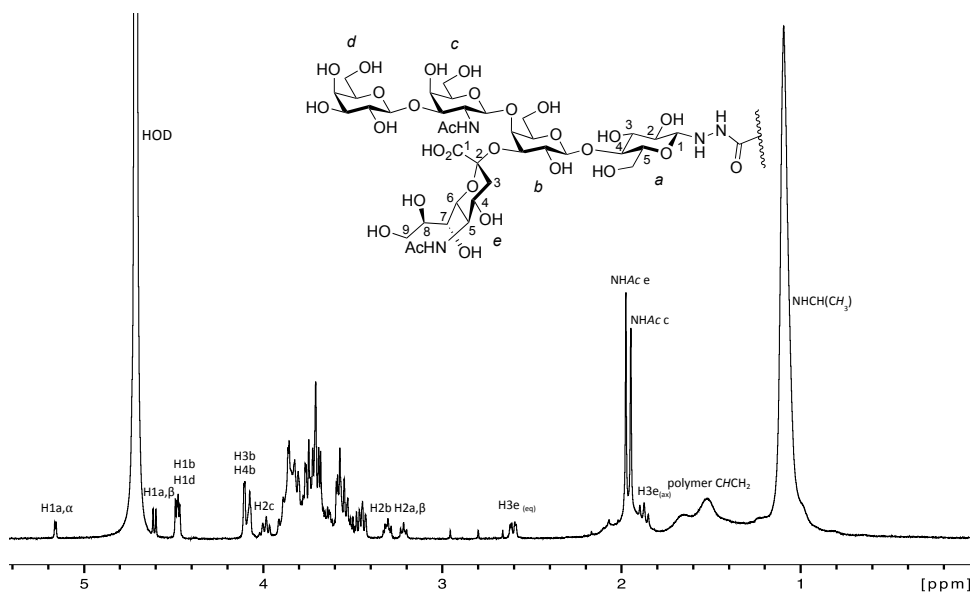


Fig S2 ¹H NMR spectrum of **P2-GM1os** (500 MHz, D₂O)

The concentration of **P2-GM1os** solutions used for ITC and ELLA experiments was determined by quantification of the trithiocarbonate end groups. Solutions of known concentration of **P2** between 104 μM and 3.26 μM were prepared in triplicate and their absorbance at 309 nm was determined (Fig. S2) allowing the molar extinction coefficient ϵ_{309} to be determined to be 9920 M⁻¹ cm⁻¹.

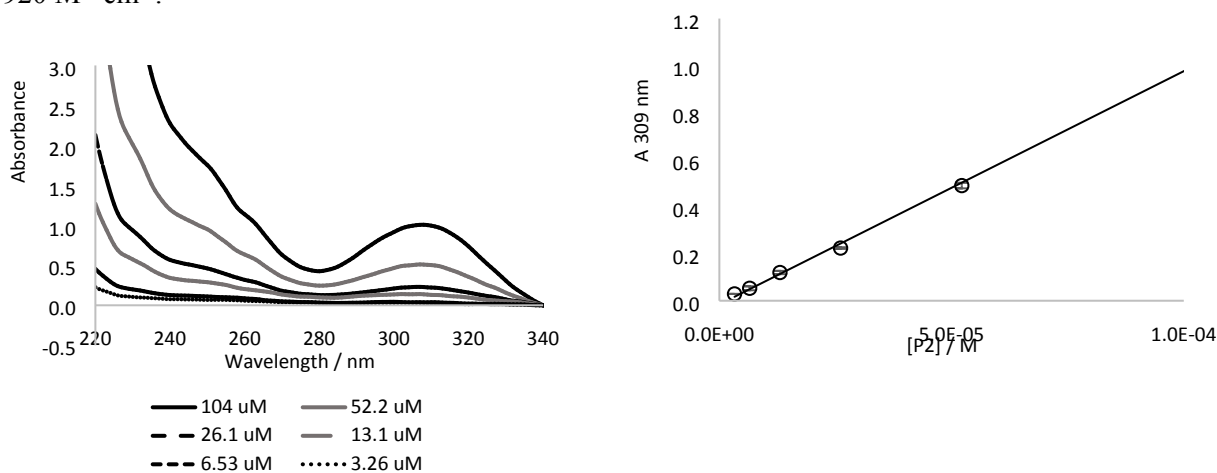


Fig. S3 (a) UV-Vis absorbance spectra for solutions of **P2**. (b) Beer-Lambert plot for **P2**.

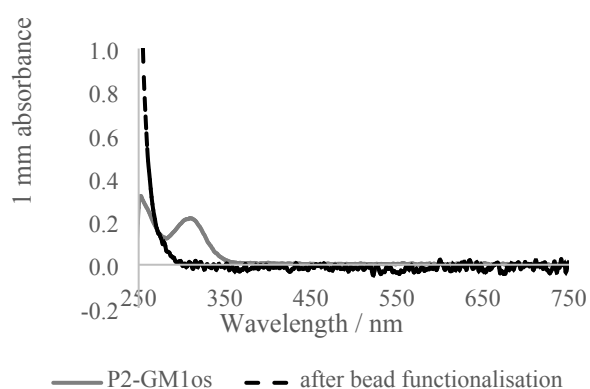


Fig. S4 UV-Vis absorbance spectra for a solution of **P2-GM1os**, and the same solution after aminolysis and exposure to maleimide-functionalise agarose beads.

Development of organoid swelling assay

To develop the organoid assay, intestinal organoids were stimulated dose dependently with cholera toxin to select a nonsaturating concentration for inhibitor testing while retaining maximal assay sensitivity (Fig. S5). 3 $\mu\text{g}/\text{mL}$ of cholera toxin was required to induce sufficient swelling of organoids which is 30 times higher than used in the earlier experiments.¹ We next assessed dose-dependent inhibition of cholera toxin-mediated swelling of **P2-GM1os** for binding cholera toxin B subunit. GM1os and free galactose was measured as a reference inhibitors. Organoids were stimulated with cholera toxin, with or without inhibitors.

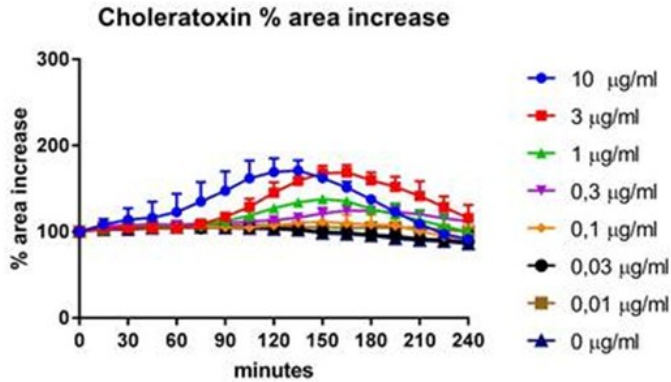
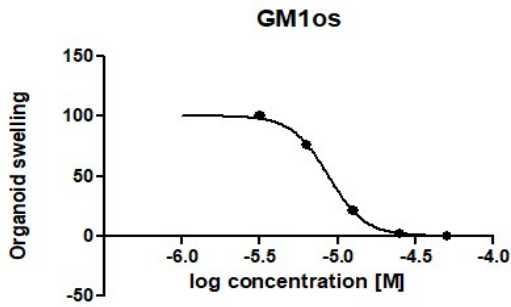
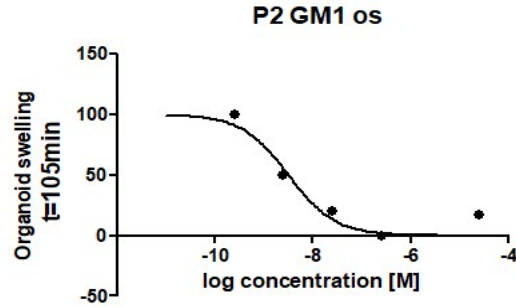


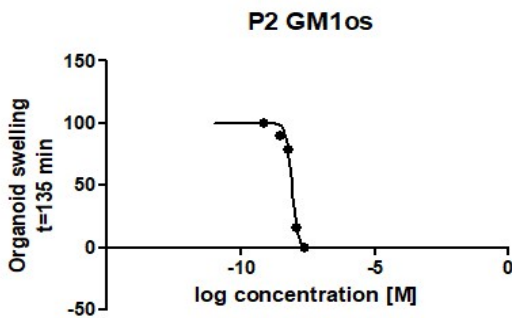
Fig. S5 Organoids were stimulated with cholera toxin as indicated ($\mu\text{g}/\text{mL}$), and organoid swelling was measured by relative area increase in time (t = 0 min: 100%), n = 1 triplicate \pm SD.



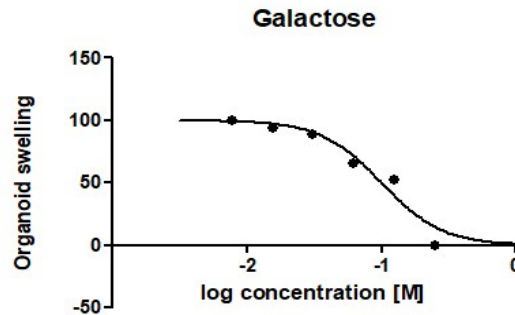
log(inhibitor) vs. response -- Variable slope (met IC50 errors)	
Best-fit values	
BOTTOM	= 0.0
TOP	= 100.0
LOGIC50	-5.059
HILLSLOPE	-3.856
IC50	8.739e-006
Span	= 100.0
Std. Error	
LOGIC50	0.1066
HILLSLOPE	2.453
IC50	2.144e-006
95% Confidence Intervals	
LOGIC50	-5.274 to -4.843
HILLSLOPE	-8.606 to 1.295
IC50	4.412e-006 to 1.307e-005
Goodness of Fit	
Degrees of Freedom	43
R ²	0.2850
Absolute Sum of Squares	187088
Sy.x	65.96
Constraints	
BOTTOM	BOTTOM = 0.0
TOP	TOP = 100.0
Number of points	
Analyzed	45



log(inhibitor) vs. response -- Variable slope (met IC50 errors)	
Best-fit values	
BOTTOM	= 0.0
TOP	= 100.0
LOGIC50	-8.492
HILLSLOPE	-0.9095
IC50	3.222e-009
Span	= 100.0
Std. Error	
LOGIC50	0.1970
HILLSLOPE	0.3547
IC50	1.462e-009
95% Confidence Intervals	
LOGIC50	-8.917 to -8.066
HILLSLOPE	-1.676 to -0.1433
IC50	6.507e-011 to 6.380e-008
Goodness of Fit	
Degrees of Freedom	13
R ²	0.7613
Absolute Sum of Squares	5391
Sy.x	20.36
Constraints	
BOTTOM	BOTTOM = 0.0
TOP	TOP = 100.0
Number of points	
Analyzed	15



log(inhibitor) vs. response -- Variable slope (met IC50 errors)		P2 GM1 os
Best-fit values		
BOTTOM	= 0.0	
TOP	= 100.0	
LOGIC50	-8.089	
HILLSLOPE	-4.098	
IC50	8.149e-009	
Span	= 100.0	
Std. Error		
LOGIC50	0.1267	
HILLSLOPE	3.409	
IC50	2.378e-009	
95% Confidence Intervals		
LOGIC50	-8.363 to -7.815	
HILLSLOPE	-11.46 to 3.267	
IC50	3.013e-009 to 1.328e-008	
Goodness of Fit		
Degrees of Freedom	13	
R ²	0.4725	
Absolute Sum of Squares	27695	
Sy.x	46.16	
Constraints		
BOTTOM	BOTTOM = 0.0	
TOP	TOP = 100.0	
Number of points		
Analyzed	15	



log(inhibitor) vs. response -- Variable slope (met IC50 errors)	
Best-fit values	
BOTTOM	= 0.0
TOP	= 100.0
LOGIC50	-0.9968
HILLSLOPE	-1.920
IC50	0.1007
Span	= 100.0
Std. Error	
LOGIC50	0.07190
HILLSLOPE	0.5772
IC50	0.01668
95% Confidence Intervals	
LOGIC50	-1.141 to -0.8523
HILLSLOPE	-3.080 to -0.7592
IC50	0.06720 to 0.1343
Goodness of Fit	
Degrees of Freedom	50
R ²	0.4959
Absolute Sum of Squares	54894
Sy.x	33.13
Constraints	
BOTTOM	BOTTOM = 0.0
TOP	TOP = 100.0
Number of points	
Analyzed	52

Organoid swelling assays

Fig. S6 Organoid swelling assays indicate the inhibitory potency of **P2-GM1os** compared to GM1os and galactose.

NMR spectra

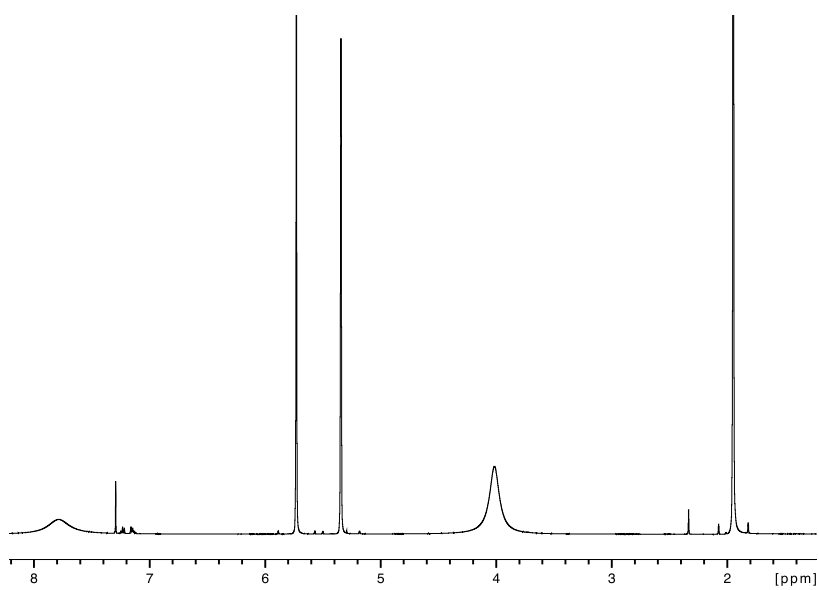


Fig S7 ¹H NMR spectrum of **1** (500 MHz, CDCl₃)

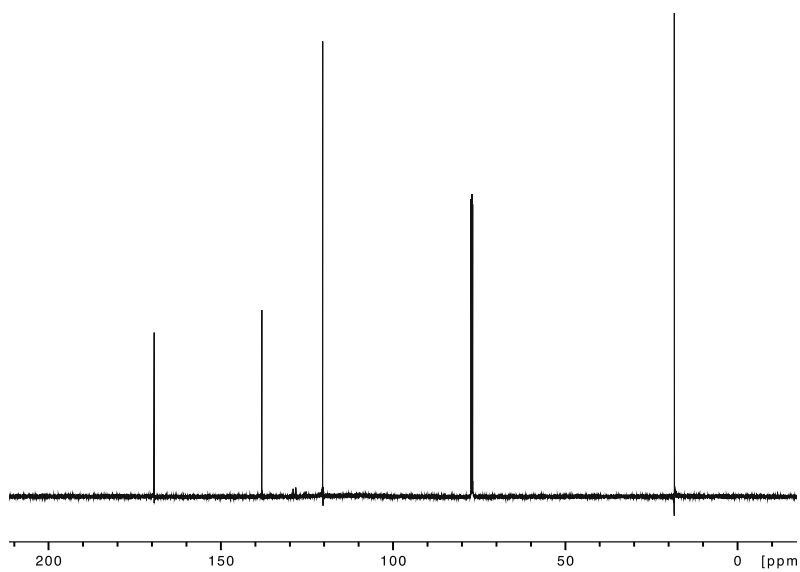


Fig S8 ¹³C NMR spectrum of **1** (125 MHz, CDCl₃)

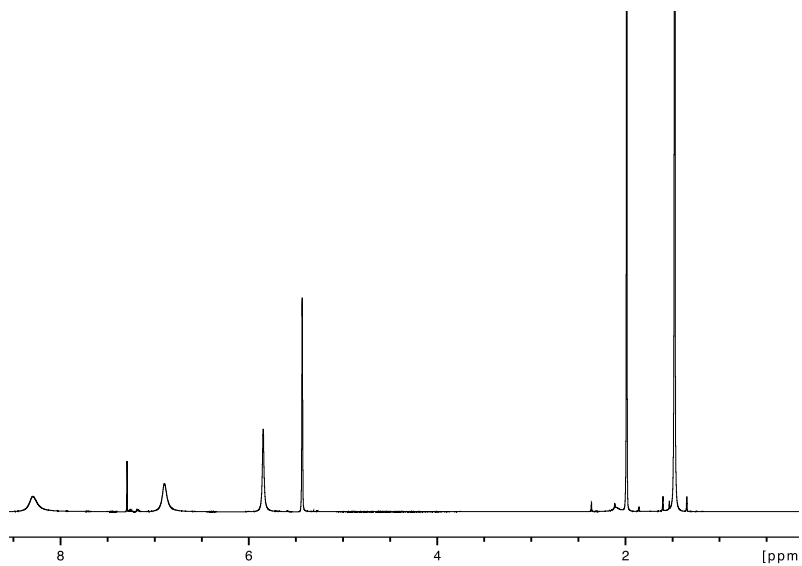


Fig S9 ^1H NMR spectrum of **M1** (500 MHz, CDCl_3)

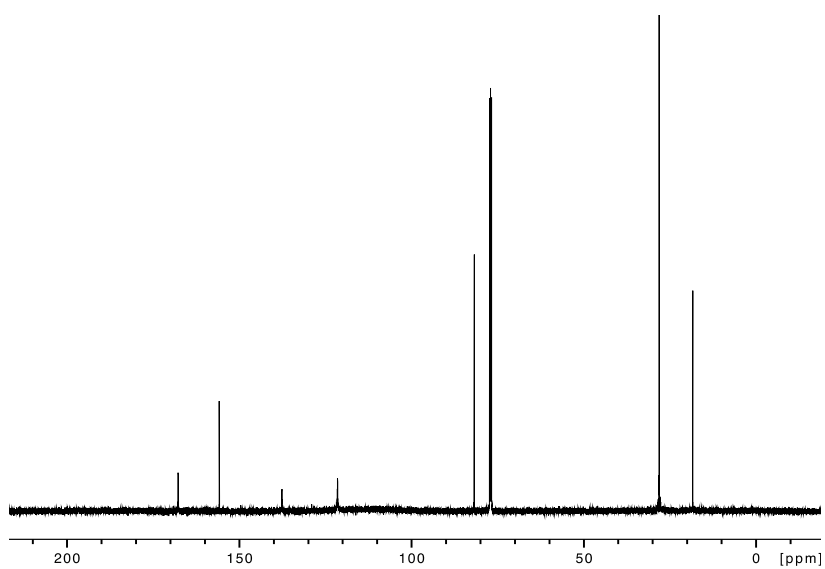


Fig S10 ^{13}C NMR spectrum of **M1** (125 MHz, CDCl_3)

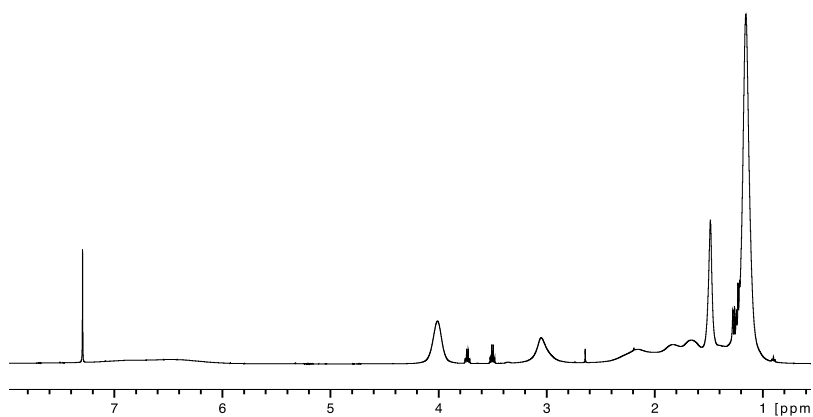


Fig S11 ¹H NMR spectrum of **P1** (500 MHz, CDCl₃)

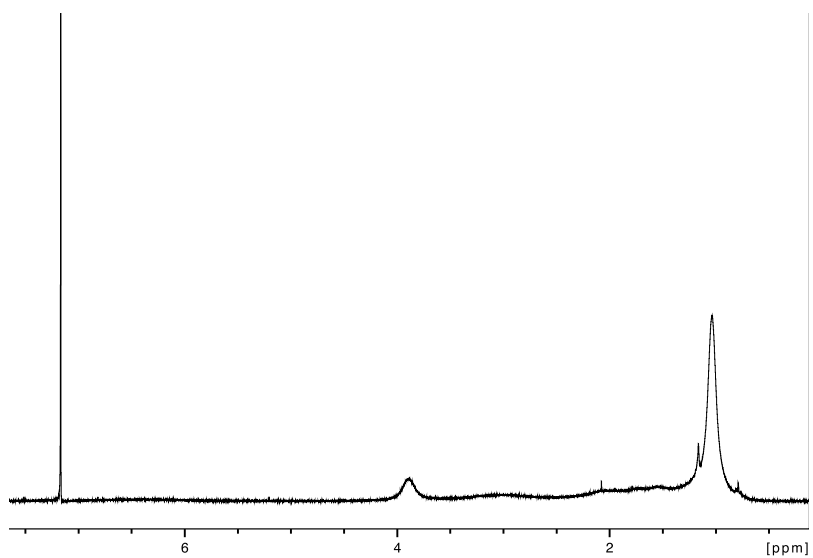


Fig S12 ¹H NMR spectrum of **P2** (500 MHz, CDCl₃)

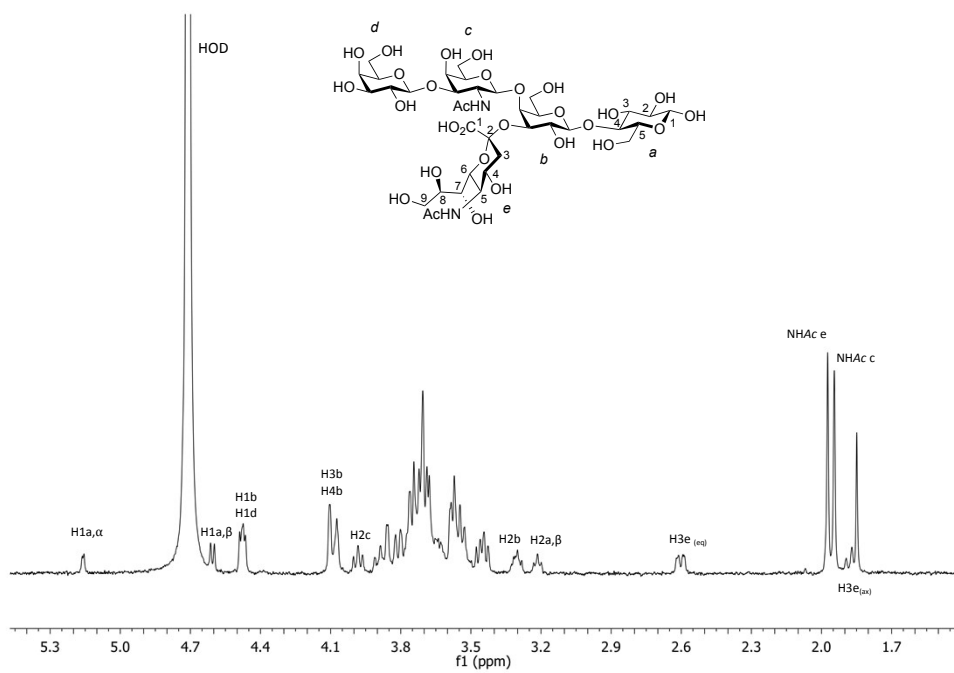


Fig S13 ¹H NMR spectrum of GM1os (500 MHz, D₂O)

References

1. D. D. Zomer-van Ommen, A. V. Pukin, O. Fu, L. H. C. Quarles van Ufford, H. M. Janssens, J. M. Beekman and R. J. Pieters, *J. Med. Chem.*, 2016, **59**, 6968-6972.