

Supporting Information

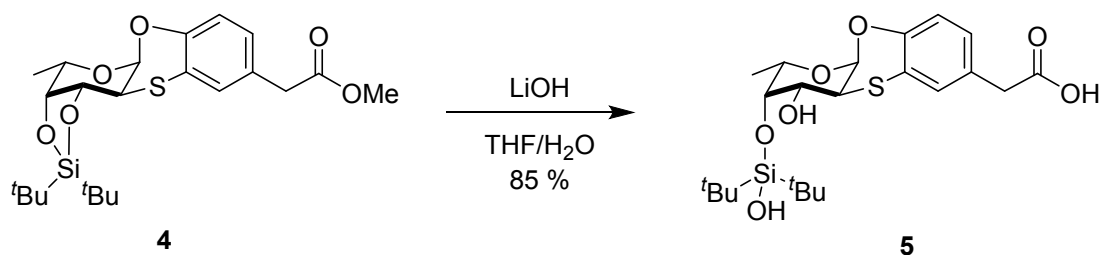
Fucosylated Ubiquitin and Orthogonally Glycosylated Mutant A28C: Conceptually New Ligands for Burkholderia ambifaria Lectin (BamBL)

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Table of content

Synthesis of compound 5	Pag.	S2
Synthesis of compound 6	pag.	S2
Synthesis of compound 3	pag.	S3
Synthesis of compound 9	pag.	S4
Synthesis of compound 10	pag.	S4
Synthesis of compound 11	pag.	S5
Synthesis of compound 7	pag.	S6
Synthesis of compound 14	pag.	S7
Synthesis of compound 13	pag.	S7
Procedure for lysine functionalization	pag.	S8
Expression and purification of Ub	pag.	S9
X-ray crystallography	pag.	S9
Table S1	pag.	S10
Isothermal Titration Calorimetry	pag.	S11
Figure S1	pag.	S12
Figure S2	pag.	S13
Surface Plasmon Resonance	pag.	S14
NMR measurements	pag.	S15
Figures S4-S7	pag.	S16-S18
SEC-MALS-QELS analysis	pag.	S18
Figure S8	pag.	S19
Cell culture	pag.	S19
TNF- α evaluation	pag.	S20
Statistical analysis	pag.	S20
Figure S9	pag.	S21
NMR and ESI-MS spectra	pag.	S22-S45
References	pag.	S46-S47

Synthesis of compound 5:



Aqueous solution of LiOH (1M, 3.9 eq, 10 mL) was added to a solution of **4** (1.26 g, 2.60 mmol) in THF (96 mL) and H₂O (38 mL). The mixture was stirred at room temperature for 2 hours then the solvents were removed *in vacuo* and the crude mixture was purified via flash chromatography on silica gel (DCM/MeOH/formic acid: 90/10/0.1) yielding **5** as a white solid (1.04 g, 85%).

MW: (C₂₂H₃₄O₇SSi) 470.65

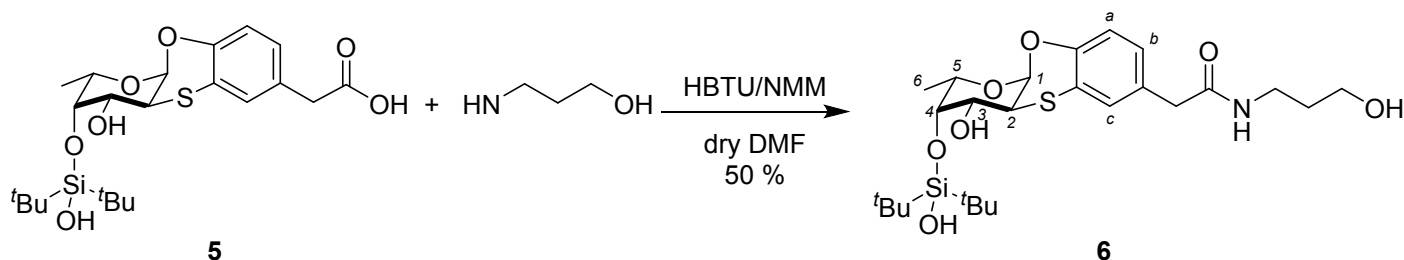
m.p. 73.3-75.7 °C

ESI-MS: *m/z* (%) 493 (100) [M + Na]⁺

[α]_D²² = - 65.10 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, CD₃OD) δ 7.03 (d, *J*_{c-b} = 2.1 Hz, 1H, CH-c), 6.95 (dd, *J*_{b-a} = 8.3 Hz, *J*_{c-b} = 2.1 Hz, 1H, CH-b), 6.78 (d, *J*_{b-a} = 8.3 Hz, 1H, CH-a), 5.62 (d, *J*₁₋₂ = 2.8 Hz, 1H, CH-1), 4.30 (d, *J* = 1.9 Hz, 1H, CH-4), 4.28 (q, *J*_{5-Me} = 6.5 Hz, 1H, CH-5), 3.73 (dd, *J*₂₋₃ = 10.9 Hz, *J* = 2.5 Hz, 1H, CH-3), 3.49-3.46 (m, 3H, CH₂+CH-2), 1.33 (d, *J*_{5-Me} = 6.5 Hz, 3H, CH₃-5), 1.07 (s, 18H, C(CH₃)₃).
¹³C NMR: (125 MHz, CD₃OD) δ 175.56 (CO), 152.44 (C_q-f), 129.90 (C_q-d), 128.72 (CH-c), 128.28 (CH-b), 118.83 (CH-a), 115.81 (C_q-e), 96.95 (CH-1), 76.68 (CH-4), 70.95 (CH-5), 69.26 (CH-3), 41.70 (CH-2), 41.00 (CH₂), 28.54-28.15 (C(CH₃)₃), 22.28-21.65 (C(CH₃)₃), 17.60 (CH₃-5).

Synthesis of compound 6:



HBTU (174 mg, 0.46 mmol) and NMM (46.5 mg, 51 μL, 0.46 mmol) were dissolved in 2.3 mL dry DMF and stirred at room temperature for 20 minutes. This mixture was then added to a solution of **5** (100 mg, 0.23 mmol) in 1.15 mL DMF. The mixture was stirred at room temperature for 20 minutes after which 3-amino-1-propanol (35 mg, 0.46 mmol, 35 μL in 180 μL dry DMF) was

added. After 2 hours, solvents were removed *in vacuo*. The crude mixture was purified via Flash Chromatography (DCM/MeOH: 95/5) to yield 57 mg of the pure product as a white solid (50%)

MW: (C₂₅H₄₁NO₇SSi) 527.75 g/mol

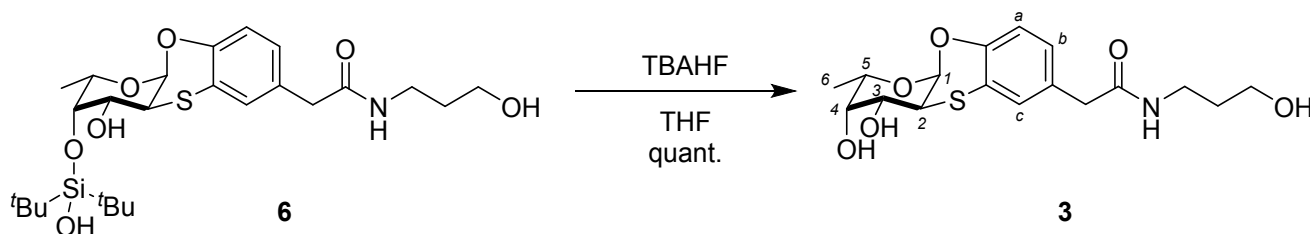
ESI-MS: *m/z* (%) 550.50 (100) [M+Na]⁺

[α]_D²² = - 58 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, CDCl₃) δ 6.99 (d, *J*_{c-b} = 1.91 Hz, 1H, CH-c), 6.87 (dd, *J*_{b-a} = 8.75 Hz, *J*_{c-b} = 1.91 Hz, 1H, CH-b), 6.82 (d, *J*_{b-a} = 8.75 Hz, 1H, CH-a), 6.58 (t, *J* = 5.77 Hz, 1H, NH), 5.68 (d, *J*₁₋₂ = 2.8 Hz, 1H, CH-1), 5.41 (bs, 1H), 5.11 (bs, 1H), 4.27 (m, 1H, CH-5, 1H, CH-4), 3.85 (bs, 1H), 3.72 (d, *J*₂₋₃ = 11.1 Hz, 1H, CH-3), 3.56 (bt, 2H, CH₂), 3.53 (dd, *J*₁₋₂ = 2.76 Hz, *J*₂₋₃ = 11.12 Hz, 1H, C-H₂), 3.39 (s, 2H), 3.28 (m, 2H), 1.62 (bt, 2H), 1.38 (d, *J*₆₋₅ = 6.55 Hz, 3H, C-H₆), 1.07 (s, 18H, C(CH₃)₃).

¹³C NMR: (125 MHz, CDCl₃) δ 172.40, 151.33, 128.36, 128.01, 17.38, 118.35, 114.44, 95.50, 74.50, 69.89, 67.75, 59.92, 42.40, 40.04, 37.13, 31.60, 27.95, 27.67, 21.43, 20.70, 17.17

Synthesis of compound 3:



100 μL of a 2M solution of TBA.HF in THF (0.19 mmol) was added to a solution of **6** (50 mg, 0.095 mmol) in 1 mL THF. The solution was stirred at 40°C overnight, after which another equivalent of TBA.HF was added (50 μL of a 2M solution in THF) and the reaction mixture was stirred at 40°C for another night. The formed precipitate was filtered and further washed with THF to yield the pure product as a white solid (35 mg, quantitative).

MW: (C₁₇H₂₃NO₆S) 369.43

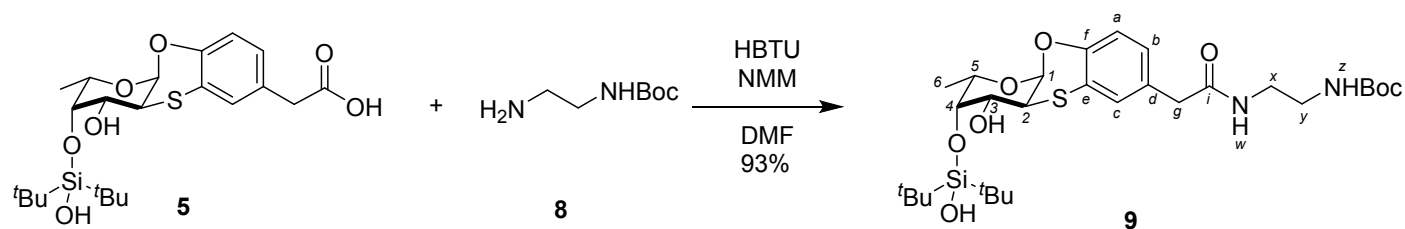
ESI-MS: *m/z* (%) 370.33 (100) [M+H]⁺, 392.33 (50) [M+Na]⁺

[α]_D²² = - 36 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, MeOD) δ 7.05 (d, *J*_{c-b} = 1.84 Hz, 1H, CH-c), 6.97 (dd, *J*_{b-a} = 8.42 Hz, *J*_{c-b} = 1.84 Hz, 1H, CH-b), 6.79 (d, *J*_{b-a} = 8.42 Hz, 1H, CH-a), 5.61 (d, *J*₁₋₂ = 2.82 Hz, 1H, CH-1), 4.25 (q, CH-5, *J*₅₋₆ = 6.53 Hz, 1H), 3.71 (bd, 1H), 3.66 (dd, *J*₃₋₄ = 2.91 Hz, *J*₃₋₂ = 10.82 Hz, 1H, C-H₃), 3.57 (t, *J* = 6.35, 2H, CH₂), 3.44 (dd, *J*₁₋₂ = 2.83 Hz, *J*₂₋₃ = 11.0 Hz, 1H, C-H₂), 3.38 (bs, 2H), 3.27 (t, 6.89, 2H, CH₂), 1.71 (q, 6.52, 2H, CH₂), 1.30 (d, *J*₆₋₅ = 6.54 Hz, 3H, C-H₆)

¹³C NMR: (125 MHz, MeOD) δ 172.77, 151.13, 129.25, 127.11, 126.52, 117.48, 114.74, 95.56, 71.67, 68.67, 67.33, 59.01, 41.51, 39.85, 36.23, 31.72, 15.45

Synthesis of compound 9:



HBTU (302 mg, 0.80 mmol) and NMM (188 mg, 1.86 mmol) were added to a solution of **5** (250 mg, 0.53 mmol), in DMF (10 mL)). After 20 minutes, **8** (127 mg, 0.80 mmol) was added. The mixture was stirred at room temperature for 3 hours after which organic solvents were dried *in vacuo* and the crude mixture was purified via flash chromatography (DCM/EtOAc: 7/3 to EtOAc), yielding 306 mg of pure product as a white solid (93%).

MW: (C₂₉H₄₈N₂O₈SSi) 612.85

m.p.: 105-110 °C

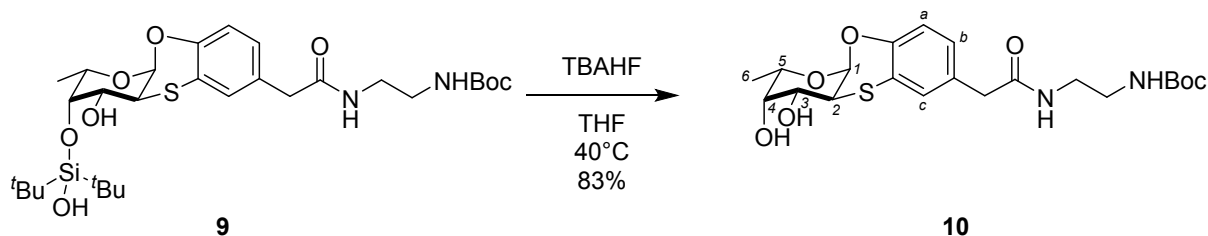
ESI-MS: *m/z* (%) 635 (100) [M + Na]⁺

[α]_D²⁵ = -121.5 (c 0.001 in CH₃OH)

¹H NMR: (400 MHz, CDCl₃) δ 6.97 (d, J_{c-b} =1.9 Hz, 1H, *H*-c), 6.88 (dd, J_{b-a} = 8.4 Hz, J_{c-b} =1.9 Hz, 1H, *H*-b), 6.80 (d, J_{b-a} = 8.4 Hz, 1H, *H*-a), 6.48 (bs, 1H, *NH*-w), 5.68 (d, J_{1-2} = 2.6 Hz, 1H, *CH*-1), 5.07 (bs, 1H, *NH*-z), 4.87 (bs, 1H, *OH* -3), 4.78 (s, 1H, *OH* -Si), 4.31-4.23 (m, 2H, *CH*-4 + *CH*-5), 3.75 (d, J_{2-3} = 11.1 Hz, 1H, *CH*-3), 3.53 (dd, J_{2-3} = 11.1 Hz, J_{1-2} = 2.6 Hz, 1H, *CH*-2), 3.36 (s, 2H, *CH*₂-g), 3.31-3.09 (m, 4H, *CH*₂-x + *CH*₂-y), 1.42 (s, 9H, OC(CH₃)₃), 1.38 (d, J_{5-Me} = 6.5 Hz, 3H, *CH*₃-5), 1.06 (s, 18H, SiC(CH₃)₃).

¹³C NMR: (100 MHz, CDCl₃) δ 171.88 (CO-i), 151.25 (CO + Cq-f), 128.43 (Cq-d), 128.06 (CH-c), 127.49 (CH-b), 118.49 (CH- a), 110.49 (Cq-e), 95.31 (CH-1), 79.93 (C(CH₃)₃), 74.00 (CH-4), 69.86 (CH-5), 67.80 (CH-3), 42.42 (CH₂-g), 40.73 (CH₂-x), 39.96 (CH₂-y), 39.89 (CH-2), 28.37 (OC(CH₃)₃), 27.68 (C(CH₃)₃), 27.9 (C(CH₃)₃), 21.43 (C(CH₃)₃), 20.71 (C(CH₃)₃), 17.20 (CH₃-5).

Synthesis of compound 10:



A 2M solution (1.42 mL) of TBAHF was added to a solution of **9** (582 mg, 0.95 mmol) in THF (6.5 mL) and the mixture is stirred at 40°C for 48 hours. The white suspension was filtered on #3 frit and the solid was washed with THF to yield 291 mg of pure product. The filtrate was evaporated and resuspended in THF, filtered, then the precipitate was washed with THF yielding another 66 mg of pure product as a white solid (total yield 83%).

MW: (C₂₁H₃₀N₂O₇S) 454.54 g/mol

m.p.: 217-219 °C

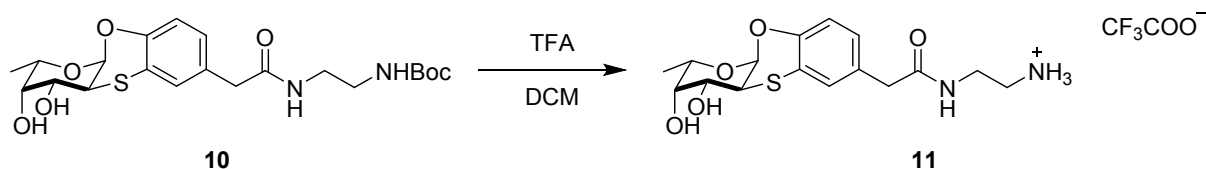
ESI-MS *m/z* (%) 477 (100) [M + Na]⁺

[α]_D²² = -58.1 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, DMSO-d₆) δ 7.99 (bs, 1H, NH-x), 6.98 (d, *J*_{b-c} = 2.0 Hz, 1H, CH-c), 6.89 (dd, *J*_{a-b} = 8.4 Hz, *J*_{b-c} = 2.0 Hz, 1H, CH-b), 6.80 (bs, 1H, NH-y), 6.77 (d, *J*_{a-b} = 8.4 Hz, 1H, CH-a), 5.56 (d, *J*₁₋₂ = 2.7 Hz, 1H, CH-1), 5.24 (d, *J*_{OH-3} = 6.9 Hz, 1H, OH-3), 4.87 (d, *J*_{OH-4} = 4.9 Hz, 1H, OH-4), 4.11 (q, *J*_{5-Me} = 6.6 Hz, 1H, CH-5), 3.58-3.53 (m, 1H, CH-4), 3.52-3.47 (m, 1H, CH-3), 3.39 (dd, *J*₂₋₃ = 11.0 Hz, *J*₁₋₂ = 2.7 Hz, 1H, CH-2), 3.27 (s, 2H, CH₂-g), 3.09-3.02 (m, 2H, CH₂-x), 3.00-2.93 (m, 2H, CH₂-y), 1.38 (s, 9H, OC(CH₃)₃), 1.17 (d, *J*_{5-Me} = 6.6 Hz, 3H, CH₃-5).

¹³C NMR: (125 MHz, DMSO-d₆) δ 170.73 (CO-i), 156.08 (CO-l), 150.82 (C_q-e), 130.30 (C_q-f), 127.41 (CH-c), 127.01 (CH-b), 117.92 (CH-a), 115.12 (C_q-d), 95.59 (CH-1), 78.14 (C(CH₃)₃), 71.57 (CH-4), 69.16 (CH-5), 67.33 (CH-3), 41.80 (CH₂-g), 40.58 (CH₂-g), 39.30 (CH₂ x+y), 28.70 (C(CH₃)₃), 17.02 (CH₃-5).

Synthesis of compound 11:



TFA (0.9 mL, 15 eq) was added dropwise to a suspension of **10** (134 mg, 0.30 mmol) in DCM (3 mL) at 0°C. The solution was stirred at room temperature for 2 hours after which TFA and DCM were removed *in vacuo*. The crude mixture was used without further purification.

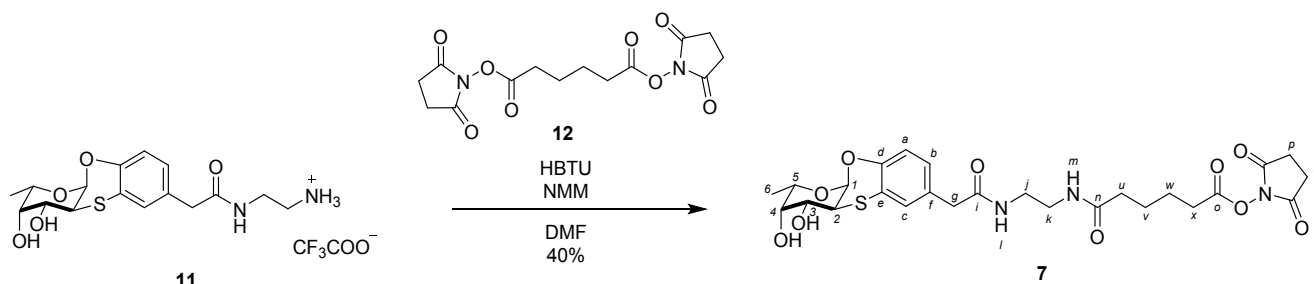
M.W.: (C₁₈H₂₃F₃N₂O₇S) 468.44 g/mol

ESI-MS *m/z* (%) 355.5 (100) [M]⁺

¹H NMR: (400 MHz, D₂O) δ 7.13 (d, *J* = 1.9 Hz, 1H), 7.05 (dd, *J* = 8.5 Hz, *J* = 1.9 Hz, 1H), 6.91 (d, *J* = 8.5 Hz, 1H), 5.79 (d, *J* = 3.0 Hz, 1H), 4.34 (q, *J* = 6.5 Hz, 1H), 3.85 (d, *J* = 3.0 Hz, 1H),

3.76 (dd, $J = 11.1$ Hz, $J = 2.9$ Hz, 1H), 3.55 (s, 2H), 3.53-3.43 (m, 3H), 3.17-3.10 (m, 2H), 1.29 (d, $J = 6.5$ Hz, 3H).

Synthesis of compound 7:



NMM (0.20 mL, 1.84 mmol) was added to a solution of **11** (239 mg, 0.51 mmol) in dry DMF (5 mL). After 20 mins, **12** (695 mg, 2 mmol) was added. The mixture was stirred at room temperature for 18 hours after which the suspension was filtered on #3 frit and washed with DMF. The filtrate was evaporated to dryness and purified via Flash Chromatography (DCM/Acetone: 65/35 to Acetone) to yield 110 mg of the pure product as a white solid (40% yield over two steps)

M.W.: (C₂₆H₃₃N₃O₁₀S) 579.62 g/mol

m.p.: 156-159 °C

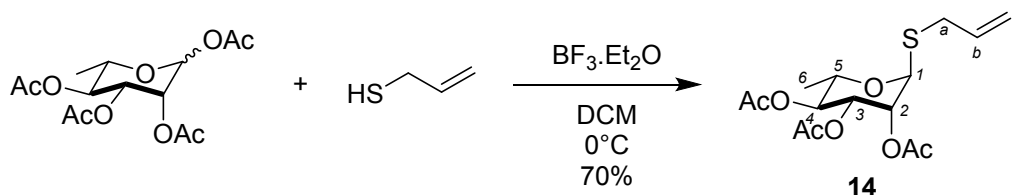
ESI-MS m/z (%) 602 (100) [M + Na]⁺, 637 (55) [M + K]⁺

[α]_D²⁵ = -55.7 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, DMSO -d₆) δ 8.01 (bs, 1H, NH-l), 7.85 (bs, 1H, NH-m), 6.98 (d, $J_{c-b} = 2.0$ Hz, 1H, CH-c), 6.89 (dd, $J_{a-b} = 8.4$ Hz, $J_{b-c} = 2.0$ Hz, 1H, CH-b), 6.78 (d, $J_{a-b} = 8.4$ Hz, 1H, CH-a), 5.56 (d, $J_{1-2} = 2.7$ Hz, 1H, CH-1), 5.25 (bs, 1H, OH-3), 4.88 (bs, 1H, OH-4), 4.10 (q, $J_{5-Me} = 6.4$ Hz, 1H, CH-5), 3.55 (bs, 1H, CH-4), 3.49 (d, $J_{2-3} = 10.7$ Hz, 1H, CH-3), 3.39 (dd, $J_{2-3} = 10.7$ Hz, $J_{1-2} = 2.7$ Hz, 1H, CH-2), 3.27 (s, 2H, CH₂-g), 3.08 (bs, 4H, CH₂-j + CH₂-k), 2.81 (s, 4H, CH₂-p + CH₂-q), 2.70-2.65 (m, 2H, CH₂-x), 2.12-2.07 (m, 2H, CH₂-u), 1.59 (bs, 4H, CH₂-w + CH₂-v), 1.17 (d, $J_{5-Me} = 6.4$ Hz, 3H, CH₃-5).

¹³C NMR: (125 MHz, DMSO -d₆) δ 172.37 (CO-n), 170.77 (CO-o), 170.73 (CO-i), 169.37 (CO NHS), 150.84 (C_q-e), 130.27 (C_q-f), 127.41 (C_q-c), 127.03 (C_q-b), 117.92 (CH-a), 115.11 (C_q-d), 95.59 (CH-1), 71.56 (CH-4), 69.16 (CH-5), 67.33 (CH-3), 41.81 (CH₂-g), 40.40 (CH-2), 38.98 + 38.71 (CH₂-j + CH₂-k), 35.22 (CH₂-u), 30.40 (CH₂-x), 25.90 (CH₂-p + CH₂-q), 24.72 (CH₂-v), 24.31 (CH₂-w), 17.02 (CH₃-5).

Synthesis of compound 14:



Allyl mercaptan (1.01 mL, 1.25 mmol) and $\text{BF}_3 \cdot \text{Et}_2\text{O}$ (1.65 mL, 13.37 mmol) were added to a solution of peracetylated rhamnose (3.7 g, 11.14 mmol) in DCM (110 mL) at 0°C . Reaction mixture was stirred at room temperature for 4 hours, after which it was diluted with DCM and washed with sat. NaHCO_3 (4 times) and brine (1 time). The organic layer was dried over NaSO_4 and solvents were removed *in vacuo*. The crude mixture was purified via Flash Chromatography (DCM/MeOH: 85/15) yielding 2.7 g of pure **14** as a colorless oil (70%).

M.W.: ($\text{C}_{15}\text{H}_{22}\text{O}_7\text{S}$) 346.39 g/mol

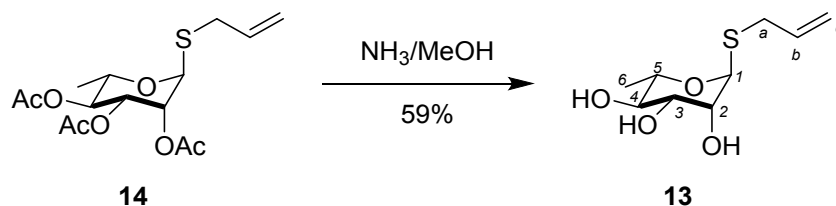
ESI-MS: m/z (%) 369 (100) $[\text{M} + \text{Na}]^+$

$[\alpha]_{\text{D}}^{22} = -152$ ($c = 0.001$ in CH_3OH)

^1H NMR: (500 MHz, CDCl_3) δ 5.85-5.75 (m, 1H, CH-a), 5.35 (dd, $J = 1.5$ Hz, $J_{1-2} = 3.4$ Hz, 1H, CH-1), 5.24 (dd, $J_{2-3} = 10.1$ Hz, $J_{1-2} = 3.4$ Hz, 1H, CH-2), 5.21-5.08 (m, 4H, CH-3, CH-4, CH-b, CH-c), 4.26-4.19 (dq, $J_{\text{Me-5}} = 6.2$ Hz, $J = 9.7$ Hz, 1H, CH-5), 3.27-3.12 (m, 2H, CH_2), 2.16 (s, 3H, CH_3 Ac), 2.07 (s, 3H, CH_3 Ac), 2.00 (s, 3H, CH_3 Ac), 1.25 (d, $J_{\text{Me-5}} = 6.2$ Hz, 3H, CH_3 -5).

^{13}C NMR: (125 MHz, CDCl_3) δ 169.98 (C_q Ac), 169.958 (C_q Ac), 169.84 (C_q Ac), 132.82 (CH-a), 118.35 (CH_2 -b+c), 80.67 (CH-3), 71.35 (CH-1), 71.28 (CH-4), 69.69 (CH-2), 67.13 (CH-5), 33.31 (CH_2), 20.94 (CH_3 Ac), 20.80 (CH_3 Ac), 20.66 (CH_3 Ac), 17.40 (CH_3 -5).

Synthesis of compound 13:



Compound **14** (2 g, 5.77 mol) was dissolved in 5 mL of a 4M solution of NH_3 in MeOH. The mixture was stirred at room temperature for 24 hours after which the reaction mixture was

evaporated to dryness and purified via flash chromatography (DCM/MeOH: 9/1) to yield 750 mg of product as a colourless oil (59%).

M.W.: (C₉H₁₆O₄S) 220.28 g/mol

ESI-MS: *m/z* (%) 243 (100) [M + Na]⁺ 463 (80) [2M + Na]⁺

[α]_D²² = -182 (c = 0.001 in CH₃OH)

¹H NMR: (500 MHz, CD₃OD) δ 5.89-5.79 (m, 1H, CH-a), 5.17 (dd, *J*_{trans} = 17.0 Hz, *J*_{gem} = 1.0 Hz, 1H, CH-c), 5.12 (d, *J*_{cis} = 7.7 Hz, 1H, CH-b), 5.11 (bs, 1H, CH-1), 3.97-3.91 (m, 1H, CH-5), 3.90 (dd, *J*₂₋₃ = 3.2 Hz, *J*₁₋₂ = 1.3 Hz, 1H, CH-2), 3.61 (dd, *J*₃₋₄ = 9.5 Hz, *J*₂₋₃ = 3.2 Hz, 1H, CH-3), 3.43 (t, *J*₃₋₄ = 9.5 Hz, 1H, CH-4), 3.25 (dd, *J*_{gem} = 13.8 Hz, *J*_{CH2-a} = 8.4 Hz, 1H, CH₂), 3.17 (dd, *J*_{gem} = 13.8 Hz, *J*_{CH2-a} = 5.7 Hz, 1H, CH₂), 1.29 (d, *J*_{Me-5} = 6.2 Hz, 3H, CH₃-5).

¹³C NMR: (125 MHz, CD₃OD) δ 133.78 (CH-a), 116.34 (CH₂-b+c), 83.46 (CH-1), 72.84 (CH-4), 72.41 (CH-2), 71.80 (CH-3), 68.91 (CH-5), 32.54 (CH₂), 16.54 (CH₃-5).

Procedure for lysine functionalization:

Compound **7** was dissolved in a minimal amount of 150 mM sodium phosphate (NaPi) pH 7.5 buffer and the solution (70 equivalents, 10 equivalents per lysine) was added to a solution of ubiquitin (450 μM in sodium phosphate 150 mM, pH 7.5). The mixture was stirred overnight at 4 °C and then washed with 20 mM sodium phosphate, 1 mM TCEP, pH 7.5 buffer by cyclical dilution/concentration steps using 3 kDa MWCO Amicon Ultra Centrifugal Filters. The occurrence of the reaction was controlled by SDS-PAGE, 1D ¹H and 2D ¹H-¹⁵N-HSQC NMR experiments. The number of functionalized lysine was confirmed with MALDI/TOF-TOF analysis.

Procedure for cysteine functionalization of Ubi-A28C with **13:**

Five equivalents of **13** (in solution, 1 mg/10 μL in water) and 5 equivalents of DPAP (in solution, 1 mg/10 μL in DMSO) were added to a solution of ubiquitin mutant A28C (450 μM in 150 mM NaPi, pH 7.5). Argon was gently bubbled in the solution for 5 minutes and the reaction mixture was irradiated by UV light at 365 nm (UVGL-55 Mineralight 26W). Cysteine-functionalization was complete after 20 minutes, as revealed by NMR experiments (1D ¹H and 2D ¹H-¹⁵N-HSQC). The obtained glycoconjugates were washed from the excess of **13** by cyclical

dilution/concentration steps using 3 kDa MWCO Amicon Ultra Centrifugal Filters with 20 mM NaPi, 1 mM TCEP, pH 7.5 buffer, and NMR experiments were recorded again.

Expression and Purification of Ubiquitin WT and A28C:

E. coli BL21(DE3) Gold cells were transformed with pET-21a(+) plasmid encoding for ubiquitin (WT or A28C). The cells were cultured in a minimal medium (M9) supplied with 1.2 g/L of ¹⁵N-labelled ammonium sulfate, 3 g/L of glucose, 0.2 mM CaCl₂, 2.0 mM MgSO₄ and 0.1 mg/mL of ampicillin at 37 °C until OD₆₀₀ reached the value 0.6, then induced with 1 mM IPTG for 16 hours at 37 °C. Cells were harvested by centrifugation and resuspended in a 20 mM Tris-HCl pH 7.2 buffer (20 mL per liter of culture) supplied with 12.5 µg/mL DNase and 20 mM MgSO₄. The disruption of the cells was performed by sonication. After centrifugation, the lysate was treated with a concentrated HClO₄ solution until reaching pH 4.5. The precipitate formed during acidic treatment was removed via centrifugation and the protein contained in the solution was purified by cationic exchange chromatography (5 mL HiTrap SP FF column). Fractions of purified protein were identified by SDS-PAGE. A second purification step was performed by gel filtration chromatography (HiPrep Superdex 75 PG E26/60 Column). The protein was finally eluted in 50 mM NaPi, pH 7.5 buffer (supplied with 1 mM TCEP in the case of A28C mutant)

X-ray crystallography

Molecular cloning, expression and purification of BamBL were performed as previously described.^{1,2} The protein was lyophilized and stored at -20 °C prior to crystallization experiment. The lyophilized protein was dissolved in a buffer pH 7.5 containing 20 mM Tris-HCl, 100 mM NaCl, and 100 µM CaCl₂. 1 µL of **3** (100 mM in 100% DMSO) was aliquot onto a siliconized glass circle cover slides (22 mm, Hampton research) and left to complete dryness at room temperature. 2 µL of the protein solution was mixed with 2 µL of a reservoir solution (200 mM trisodium citrate, 100 mM sodium acetate pH 5.0 and 24% PEG 8000, 1% DMSO) and the mixture was deposited on the dried compound **3**. Crystallization was performed by the hanging drop vapor diffusion method on a 24-well plate with sealant (Hampton Research) at 19 °C, and the protein crystals were observed after 2-3 days. The protein crystals were cryo-protected in 30% PEG8000, 1% DMSO, 100 mM sodium acetate pH 5, 200 mM trisodium citrate and flashed cooled in liquid nitrogen. X-ray diffraction data were collected at SOLEIL-PROXIMA1 (Saint Aubin, France) using a Pilatus

6M hybrid photon counting detector (Dectris). The recorded data were indexed, integrated and scaled using XDS³ and merged using AIMLESS.⁴ The structures were solved by molecular replacement using 3ZW0 as a searching template in PHASER,⁵ followed by further iterations of manual rebuilding in COOT⁶ and restrained refinement in REFMAC5.⁷ **3** model was manually built in ACEDRG in CCP4i2 suite.⁸ The final models were validated with MOLPROBITY,⁹ PDB-redo (<https://pdb-redo.eu/>) and wwPDB validation service (<http://validate.rcsb-1.wwpdb.org/>). All structural figures were prepared using CCP4MG.¹⁰

Table S1. X-ray data collection and processing of BambL structure in complex with compound **3**

Data set	BambL-3 (PDB code:6ZFC)
<u>Data Collection</u>	
Beamline	PROXIMA1 (SOLEIL)
Wavelength (Å)	0.9786
Detector	Pilatus 6M
Resolution (Å) ^a	45.21-1.65 (1.68-1.65)
Space Group	I 1 2 1
a, b, c (Å)	109.09, 49.16, 115.10
α, β, γ (°)	90.0, 91.4, 90.0
Total observations	502,219
Unique reflections	72,307
Multiplicity ^a	6.9 (7.1)
Mean $I/\sigma(I)$ ^a	11.8 (1.5)
Completeness (%) ^a	98.1 (96.5)
R_{merge} ^{a,b}	0.088 (1.260)
$CC_{1/2}$ ^{a,c}	1.0 (0.6)
<u>Refinement</u>	
Reflections: working/free ^d	72,306/3,534
$R_{\text{work}}/R_{\text{free}}$ ^e	0.177/0.209
Ramachandran plot: allowed/favoured/outliers (%) ^f	3/97/0
R.m.s. bond deviations (Å)	0.0115
R.m.s. angle deviations (°)	1.687
Mean <i>B</i> -factors: protein/ligand ^f / /water (Å ²)	25/26/31

^a Values for the outer resolution shell are given in parentheses.

^b $R_{\text{merge}} = \sum_{\text{hkl}} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle| / \sum_{\text{hkl}} \sum_i I_i(\text{hkl})$.

^c $CC_{1/2}$ is the correlation coefficient between symmetry-related intensities taken from random halves of the dataset.

^d The data set was split into "working" and "free" sets consisting of 95 and 5% of the data, respectively. The free set was not used for refinement.

^e The R-factors R_{work} and R_{free} are calculated as follows: $R = \sum(|F_{\text{obs}} - F_{\text{calc}}|) / \sum |F_{\text{obs}}|$, where F_{obs} and F_{calc} are the observed and calculated structure factor amplitudes, respectively

^f refers to ligands bound in the active site and potential surface binding sites

Isothermal Titration Calorimetry:

Purified and lyophilized BambL and AFL were dissolved in buffer (20 mM Tris-HCl, 150 mM NaCl, 100 μ M CaCl_2 buffer containing 2.5% DMSO) and degassed. Compound **3** and α MeFuc were dissolved directly into the same buffer degassed, and placed in the injection syringe (concentration from 2 to 6 mM). Isothermal titration calorimetry was performed with an ITC-200 (MicroCal Inc - Malvern). BambL and AFL were placed in the 200 μ M sample cell, at 25 $^{\circ}\text{C}$, at concentrations of 50 to 150 μ M. Glyco-compounds were injected by 10 μ L steps every 300 s. Data were fitted with MicroCal Origin 7 software, according to standard procedures. Fitted data yielded the stoichiometry (n), the association constant (K_a) and the enthalpy of binding (ΔH). Other thermodynamic parameters (i.e. changes in free energy, ΔG , and entropy, ΔS) were calculated from the equation $\Delta G = \Delta H - T\Delta S = -RT \ln K_a$ where T is temperature and $R = 8.314 \text{ J mol}^{-1} \text{ K}^{-1}$. Two or three independent titrations were performed for each ligand tested.

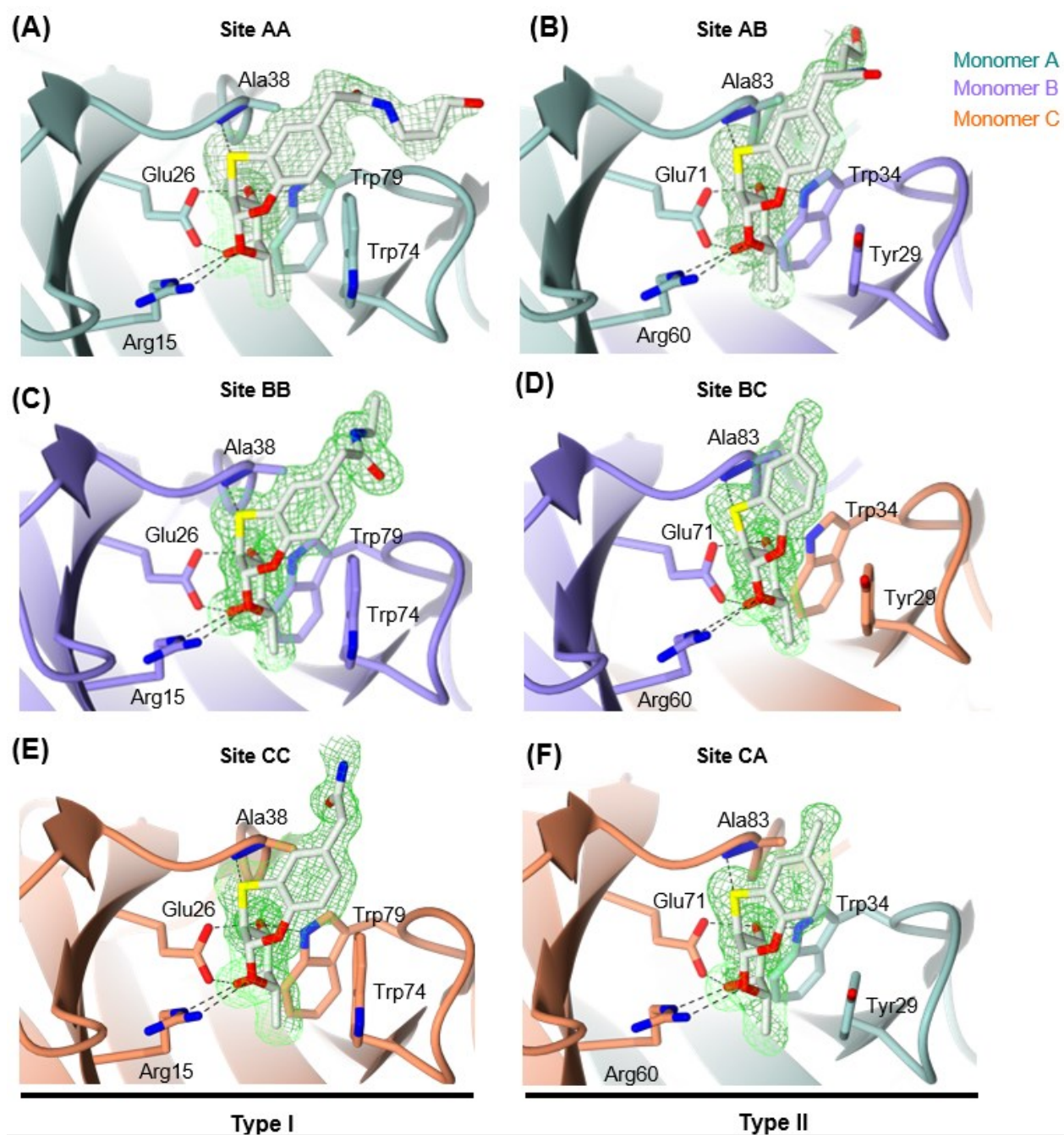


Figure S1. The binding sites of compound **3** in BamBL. The names of the binding sites are indicated in the figure. Green mesh represents the $2mF_o - DF_c$ electron density maps for the ligand contoured at 1σ .

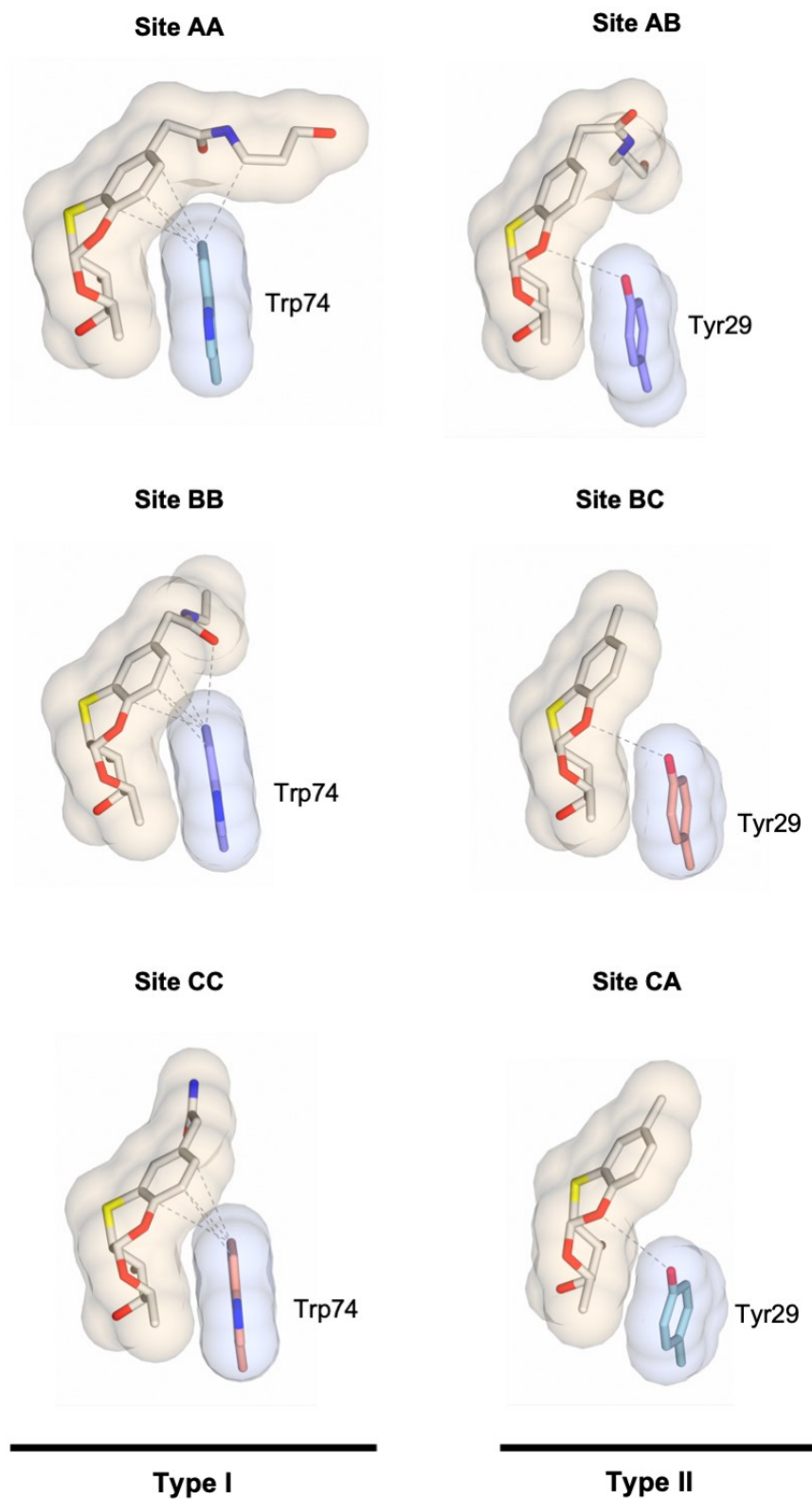


Figure S2. Surface and contact analysis of compound **3** with intra and inter binding sites. The surfaces are shown in blobs and contacts within 4 Å are shown as grey dashes.

MALDI-TOF of Fuc-Ub:

MALDI-TOF measurement were acquired on Bruker Daltonics Ultraflex III TOF/TOF.

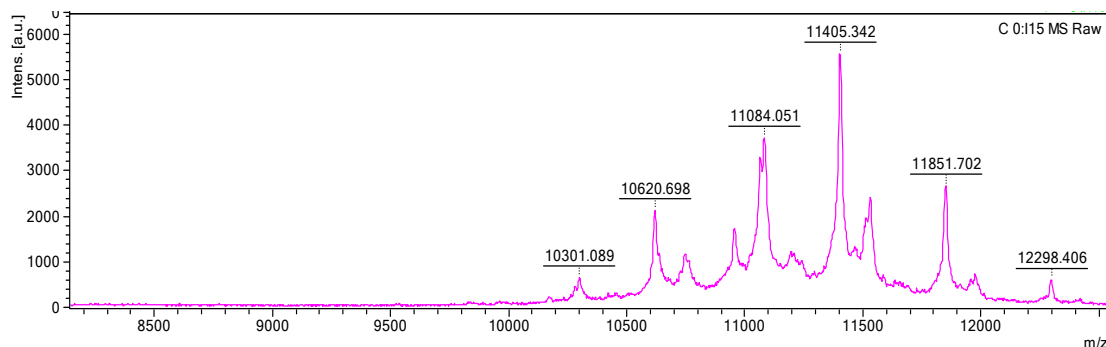


Figure S3: MALDI-TOF analysis of Fuc-Ub conjugates reveals a distribution of 3 to 8 fucose residues conjugated to the protein.

Surface Plasmon Resonance (SPR):

SPR experiments were performed using a Biacore X100 biosensor instrument (GE Healthcare) at 25°C. BambL was immobilized by amine coupling on CM5 chips (GE Healthcare) that were coated previously with streptavidin on flow cell 1 using standard manufacturer's procedures. BambL was diluted to $2 \mu\text{g}\cdot\text{ml}^{-1}$ in HBS-T (HEPES-buffered saline, pH 7.4, with 0.05% Tween 20) before being injected into flow cell 2 of the chip until high immobilization levels of 3385 RU is attained. A reference surface was always present in flow cell 1, thus allowing for the subtraction of bulk effects and non-specific interactions with streptavidin. The running buffer consisted of the same HBS-T. **Fuc-Ub** was injected over the flow cell surface at $30 \mu\text{l}\cdot\text{min}^{-1}$ in a series of 2-fold dilutions. The dissociation of this analyte was achieved by passing running buffer for 4–6 min. Surfaces were regenerated with four consecutive 80 s injections of 1M fucose, also at $30 \mu\text{l}\cdot\text{min}^{-1}$. The information on the affinity was determined by steady state analyses, using the BIACORE evaluation software.

NMR measurements

The NMR spectra for the analysis of Ub conjugates and NMR titration with BambL were acquired on a Bruker AVANCE NEO NMR spectrometer operating at 700 MHz, ^1H Larmor frequency, and equipped with a cryogenically cooled probe. All the spectra were acquired at 298 K. The assignment of the spectra of free Ub was based on the data reported in the Biological Magnetic Resonance Data Bank under the accession code 6457.¹¹ The assignment of the spectra of the functionalized Ub-A28C was helped by the analysis of 3D ^1H - ^{15}N NOESY-HSQC acquired on a Bruker AVANCE MHD NMR spectrometer operating at 950 MHz, ^1H Larmor frequency, and equipped with a cryogenically cooled probe. The titration with BambL was performed using ^{15}N -isotopically enriched **Fuc-Ub** or **Fuc-Rha-A28C** or **Rha-A28C** at the concentration of 100 μM in 20 mM Tris buffer at pH 7.5 and 100 mM NaCl. Two different aliquots of BambL solution (0.6 mM of monomer in 20 mM Tris buffer at pH 7.5, 100 mM NaCl), to reach the final concentrations in solution of 50 and 100 μM , were added to **Fuc-Ub** or **Fuc-Rha-A28C** or **Rha-A28C** and 2D ^1H - ^{15}N HSQC acquired at 700 MHz after each addition. In the titrations involving **Fuc-Ub** or **Fuc-Rha-A28C**, the signal intensity was decreased by more than 50% after the first addition, and the signals completely disappeared after the second.

The spectra were processed with the program Topspin 4.0 and analyzed with CARRA.¹²

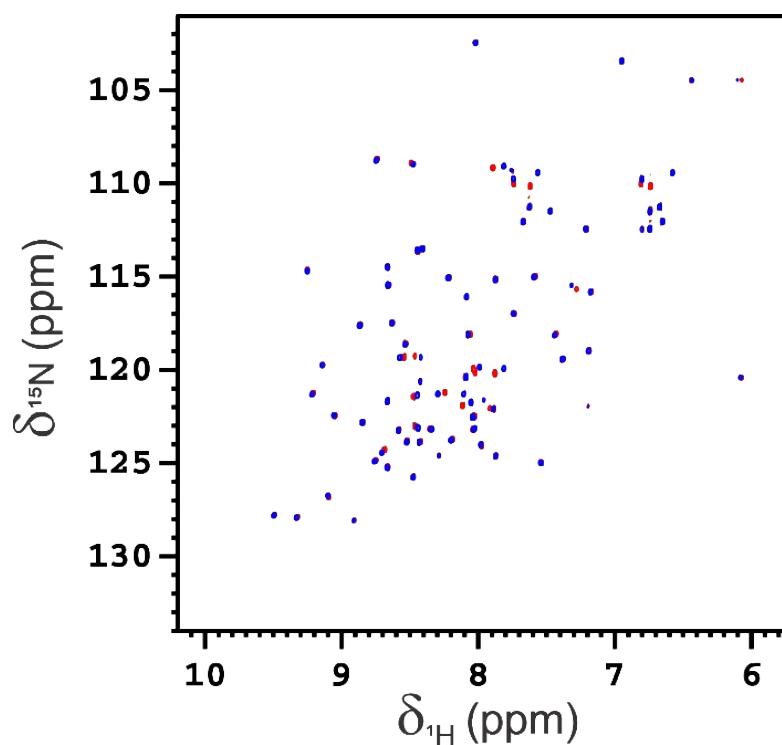


Figure S4. 2D ^1H - ^{15}N HSQC spectra of Ub-A28C (red) and Ub-A28C functionalized with the rhamnose derivative on the cysteine residue (**Rha-A28C**, blue). The protein was 350 μM in 20 mM NaPi buffered solution at pH 7.5.

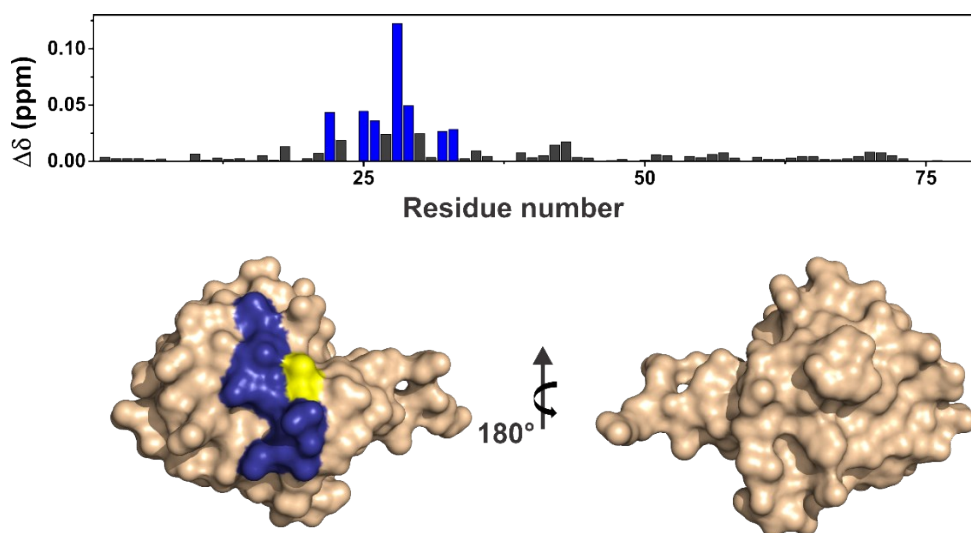


Figure S5. Graphical representation of the per residue chemical shift perturbation (CSP) of Ub-A28C functionalized on the cysteine side chain with rhamnose derivative with respect to the free protein. The CSP has been evaluated according to the formula $\Delta\delta = \frac{1}{2} \sqrt{(\Delta\delta_H)^2 + \left(\frac{\Delta\delta_N}{5}\right)^2}$. The residue exhibiting the

highest CSP have been highlighted in blue in the plot (A) and on the surface representation of the protein (PDB: 1UBQ); the cysteine residue is in yellow.

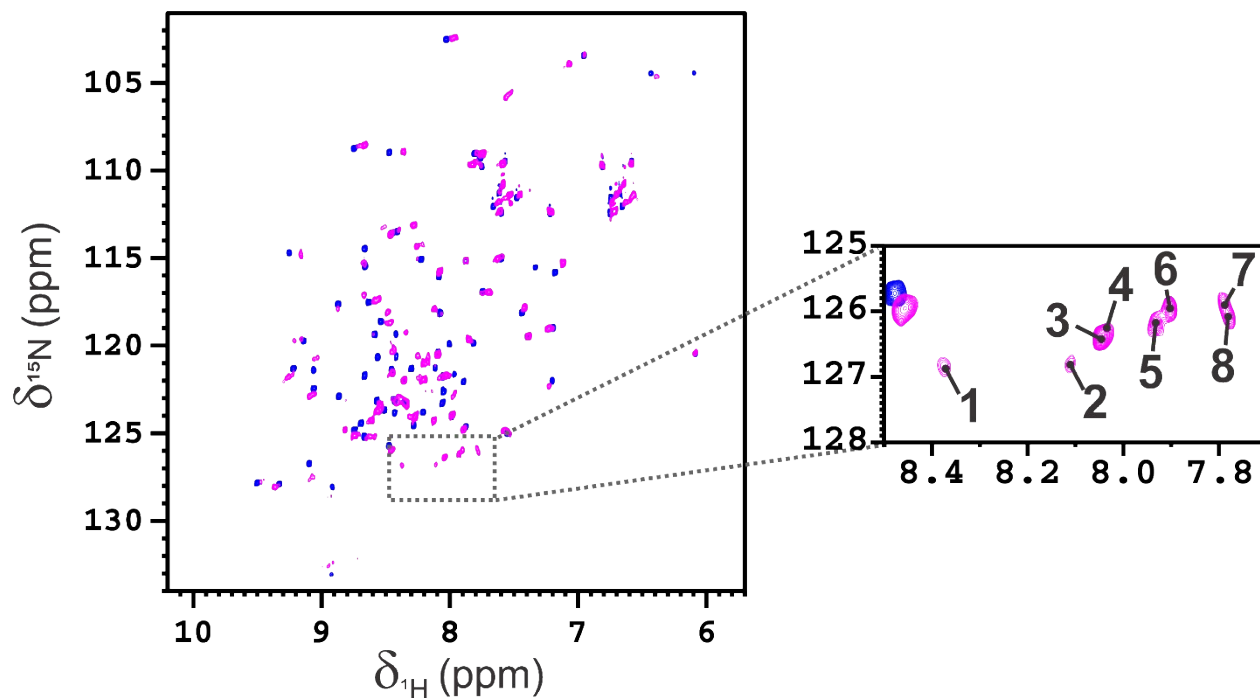


Figure S6. 2D ^1H - ^{15}N HSQC spectra of **Rha-A28C** (blue) and **Fuc-Rha-A28C** (magenta) acquired at 298 K and 700 MHz. The signals in the area, selected by the dashed lines (enlarged on the right), correspond to the new amide groups obtained by the conjugation of the ϵ - NH_2 group of lysine sidechains and the N-terminus with fucoside 7.

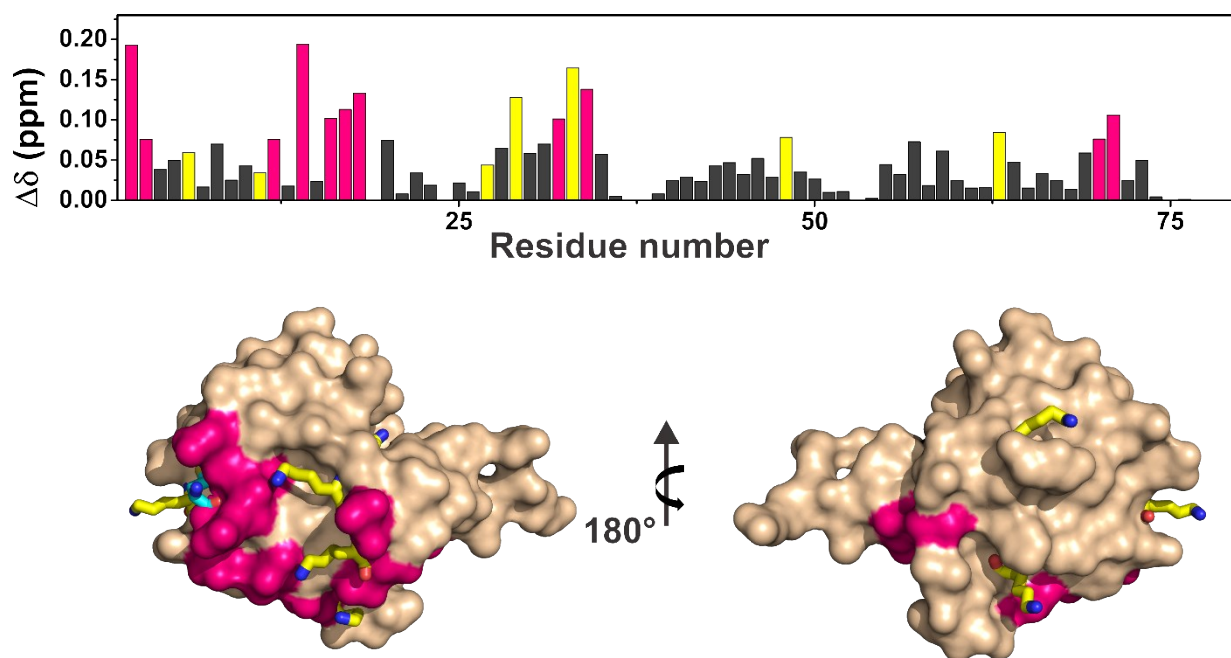


Figure S7. (A) Graphical representation of the per residue chemical shift perturbation (CSP) of **Rha-A28C** with respect to **Fuc-Rha-A28C**. The CSP has been evaluated according to the formula $\Delta\delta = \frac{1}{2} \sqrt{(\Delta\delta_H)^2 + \left(\frac{\Delta\delta_N}{5}\right)^2}$. The residues exhibiting the highest CSPs have been highlighted in pink, while the lysine residues are in yellow. (B) Surface representation of Ub (PDB: 1UBQ) with highlighted in pink the residues exhibiting the highest CSP; the lysine residues are represented as yellow sticks, and the N-terminus as cyan sticks.

SEC-MALS-QELS analysis

SEC-MALS-QELS analysis was performed using a coupled method consisting of a size-exclusion chromatography (SEC) and multiangle light scattering and quasi-elastic light scattering detectors (MALS-QELS). The system was composed of several modules:

- an HPLC system (Knauer) equipped with a Superdex 200 HR 10/30 column (GE Healthcare) and an Optilab rEX interferometric refractometer detector (Wyatt Technology Corporation) for monitoring dRI elution profiles,
- a quasi-elastic light scattering (QELS) module for measuring RH values,
- a DAWN EOS MALS module set at 690 nm for scattering evaluation.

150 μL of the NMR sample of the complex formed using a 1:1 ratio of monomeric BambL:Fuc-Ub were injected onto the column, previously equilibrated with 20 mM Tris-HCl, pH 7.5, 100 mM NaCl buffer. The sample was eluted at 0.6 mL min^{-1} . Data were acquired and processed using the ASTRA 5.4.3 software (Wyatt Technology Corporation) which recorded dRI and scattering profiles and estimated molar mass values. Two main dRI peaks were revealed. The first one (13.5-14.5 mL) corresponded to an average molar mass of 153900 g mol^{-1} , whereas the second one (around 17.5 mL) to a molar mass range of 47570-71460 g mol^{-1} . Since the molar mass of BambL is 28143 g mol^{-1} and average molar mass of Fuc-Ub is 11169 g mol^{-1} , the latter range is compatible with 2 to 4 Fuc-Ub units bound to each trimeric BambL. The presence in solution of a complex where a Fuc-Ub unit bridges two trimeric BambL could be also possible.

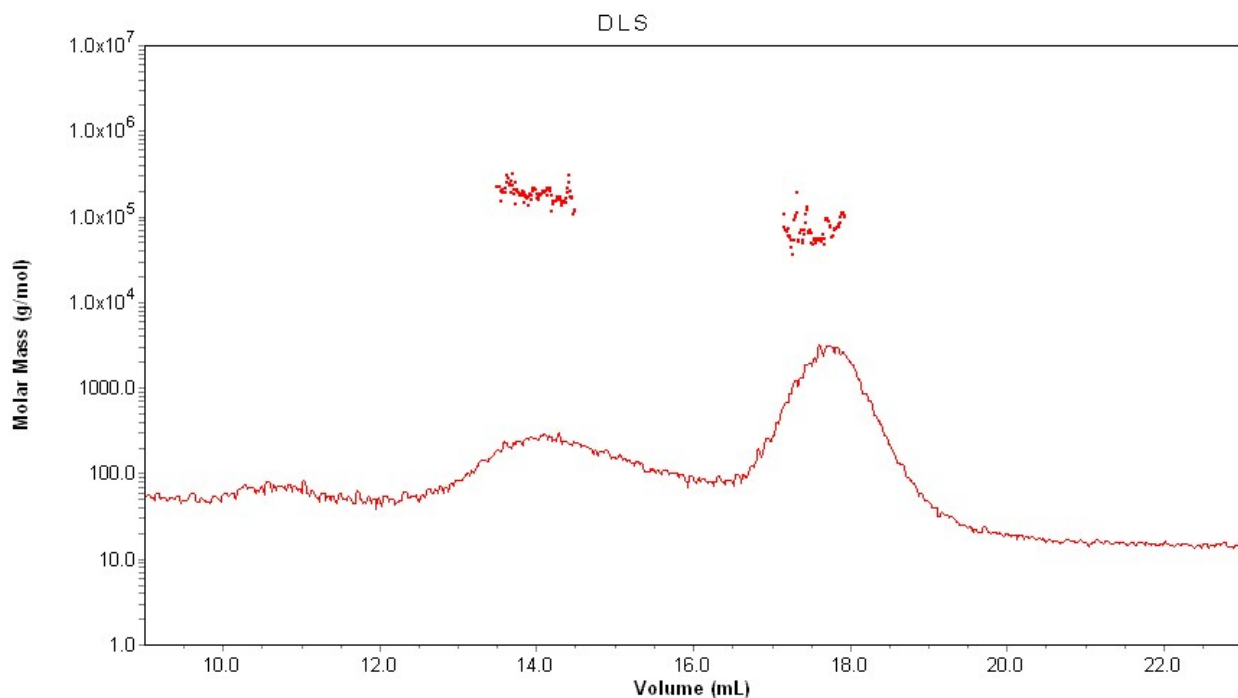


Figure S8. dRI profile (curve) and molar mass values (dots) of the NMR sample of the complex formed using a 1:1 ratio of monomeric BambL:Fuc-Ub.

Cell culture

The mouse monocyte/macrophage cell line RAW 264.7 was cultured in high glucose Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10% heat-inactivated FBS, 2 mM L-glutamine, 100 U/mL penicillin and 100 $\mu\text{g/mL}$ streptomycin in a 37 $^{\circ}\text{C}$ incubator with 5% CO_2 . Cells were grown in 75 cm^2 flasks and sub-cultured by scraping when they reached 90% confluence with a 1:5 or 1:10 ratio in fresh medium. Before each experiment, viable cells were assessed by

trypan blue staining, then, cells were seeded in a complete fresh medium 24 h prior to compound treatments.

Cell viability assay

Cell viability was measured by the 3-(4,5-dimethylthiazol-2-yl)-2,5- diphenyl-tetrazolium bromide (MTT) assay, as previously described. RAW 264.7 cells were seeded (0.5×10^5 cells/ well) in 24-well plates and treated with increasing concentrations (0.01-1 μ M) of test compounds for 24 h at 37 °C in a 5% CO₂ humidified incubator. The percentage of cell viability was calculated as $[100(x-y)/(z-y)]$, where x, y, and z were the absorbance read in compound-treated, resting, and compound-untreated cells, respectively.

TNF- α evaluation

Compounds were tested for their effects on the production of pro-inflammatory mediators, such as tumor necrosis factor (TNF)- α , as previously described. RAW 264.7 cells were seeded at a density of 0.6×10^5 cells/well in 24-well plates. The day of experiment, cells were pre-treated with increasing concentrations (0.01-1 μ M) of each test compound for 1 h and then unstimulated/stimulated with LPS (0.1 μ g/ml) for 24 h. At the end of each experiment, supernatants were collected and stored at -20 °C until assays. The amounts of TNF- α in cell culture medium were assayed using enzyme-linked immunosorbent assay (ELISA) kits (Biolegend), according to the manufacturer's instructions. The concentrations of TNF- α in the samples were determined by extrapolation from specific reference standard curves.

Statistical analysis

Results are expressed as means \pm SEM of at least four different experiments run in triplicate. Statistical significance was evaluated by Student's t-test for unpaired varieties. Differences were considered statistically significant when $p < 0.05$.

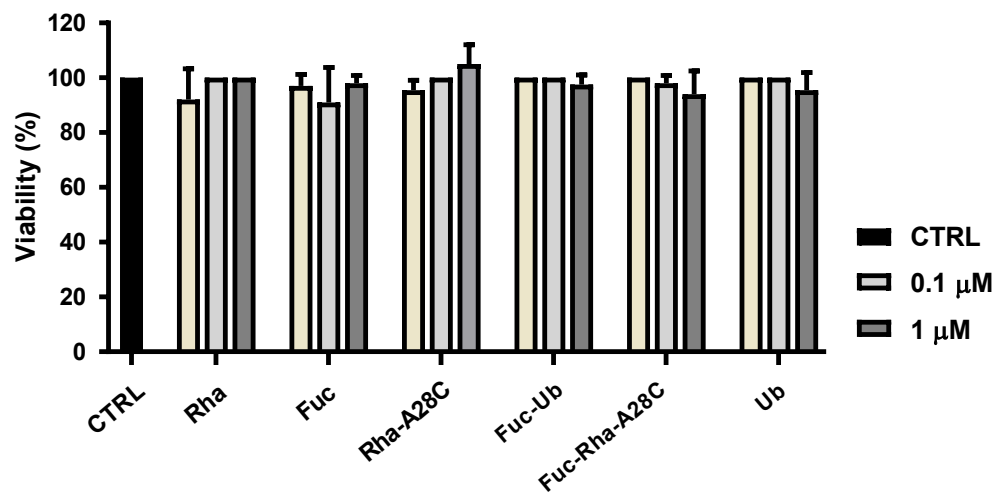
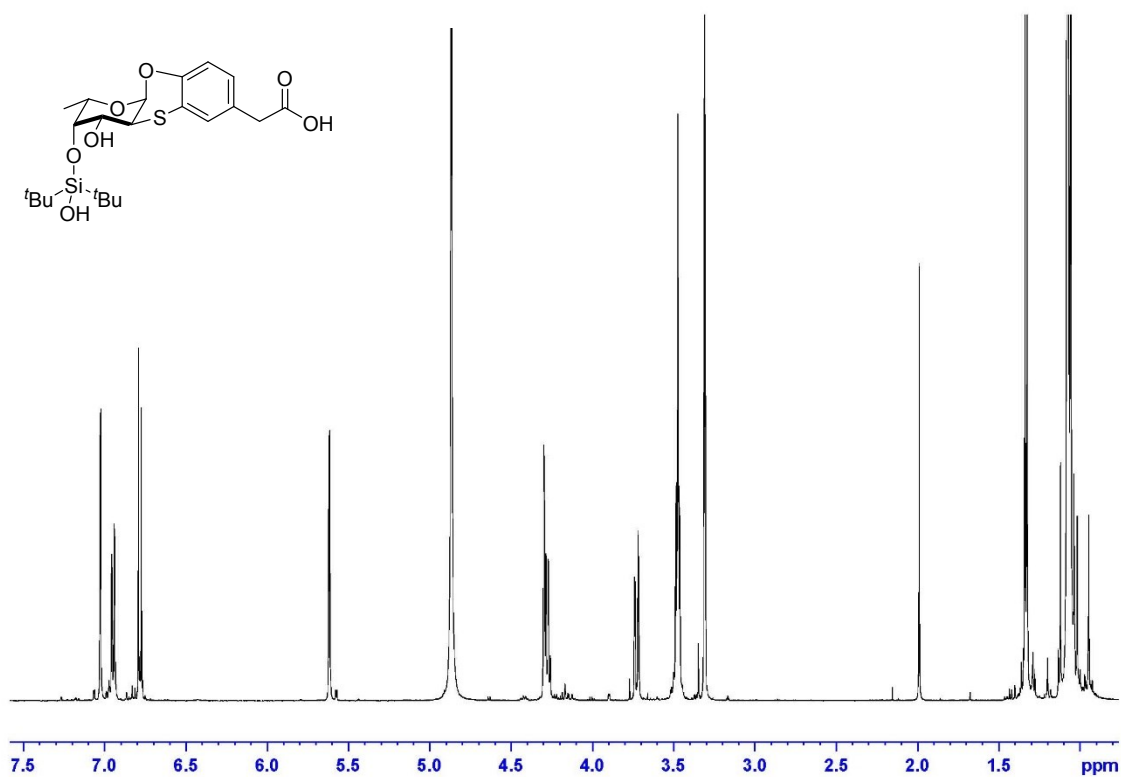


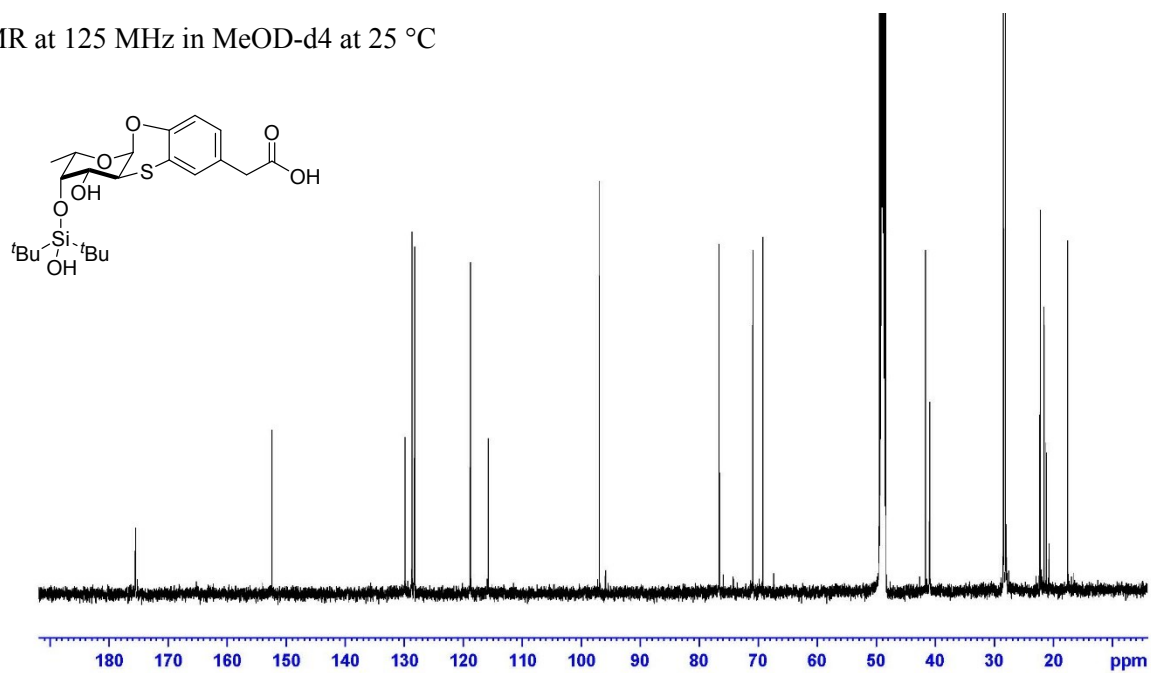
Figure S9. Effects of compounds on cell viability. RAW 264.7 cells were treated with increasing concentrations (0.01-1 μ M) of each compound for 24 h and cell viability was assessed by MTT. The data represent mean \pm SEM of at least three independent experiments run in triplicate.

NMR and ESI-MS Spectra

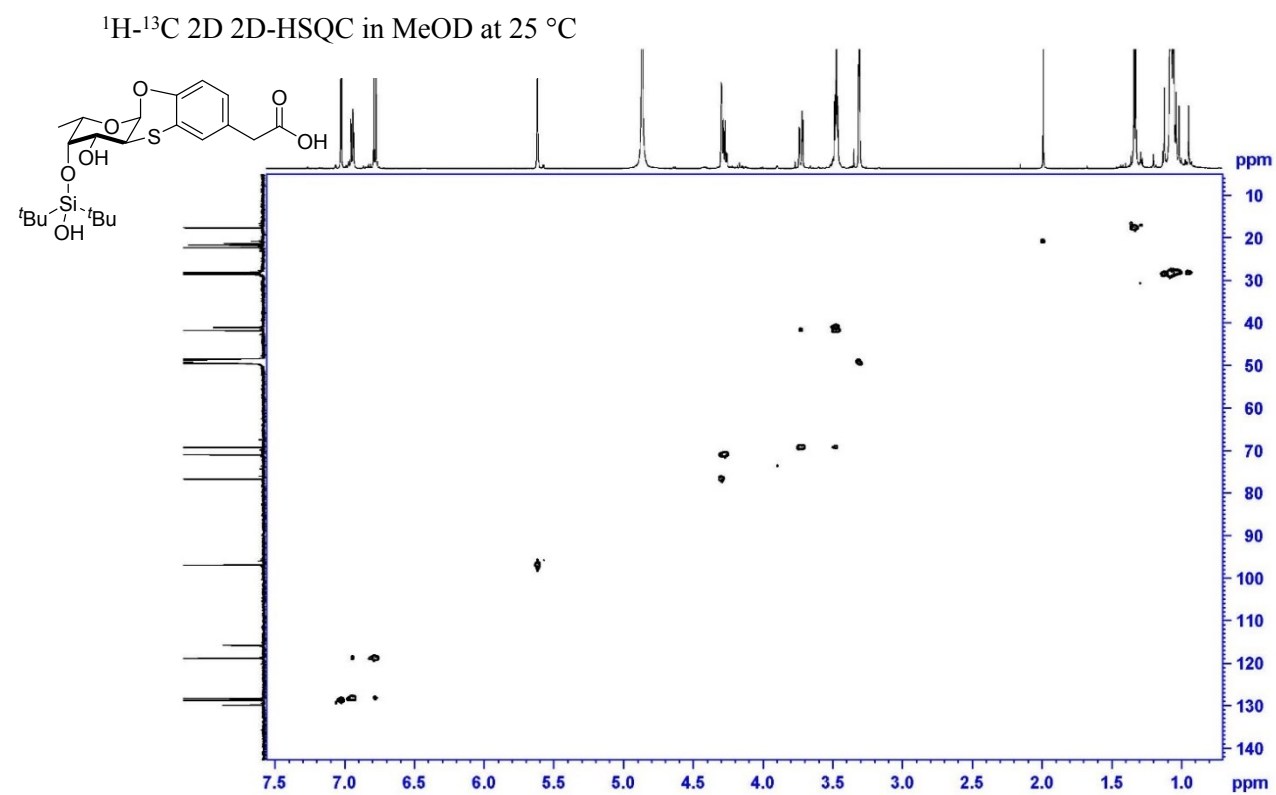
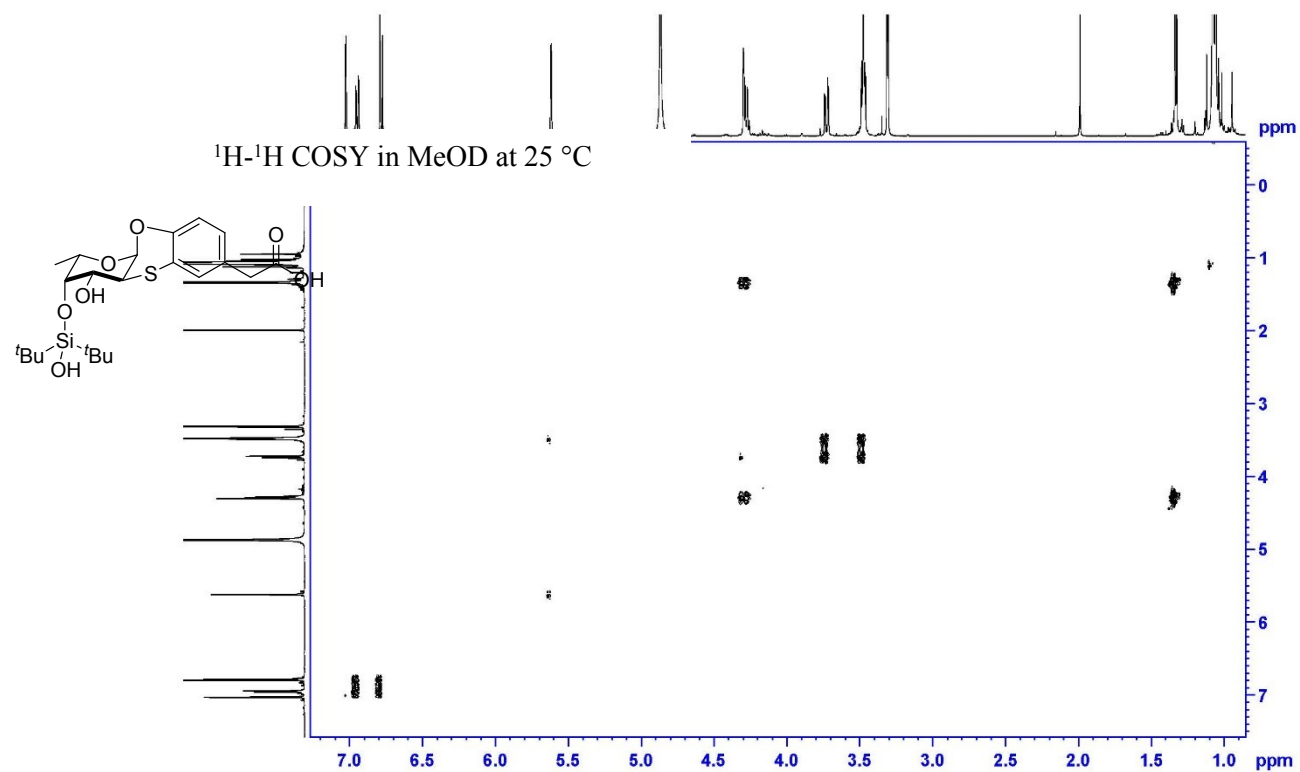
^1H NMR at 500 MHz in MeOD- d_4 at 25 °C



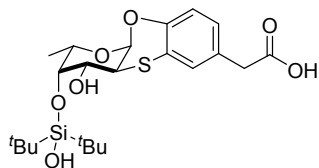
^{13}C NMR at 125 MHz in MeOD- d_4 at 25 °C



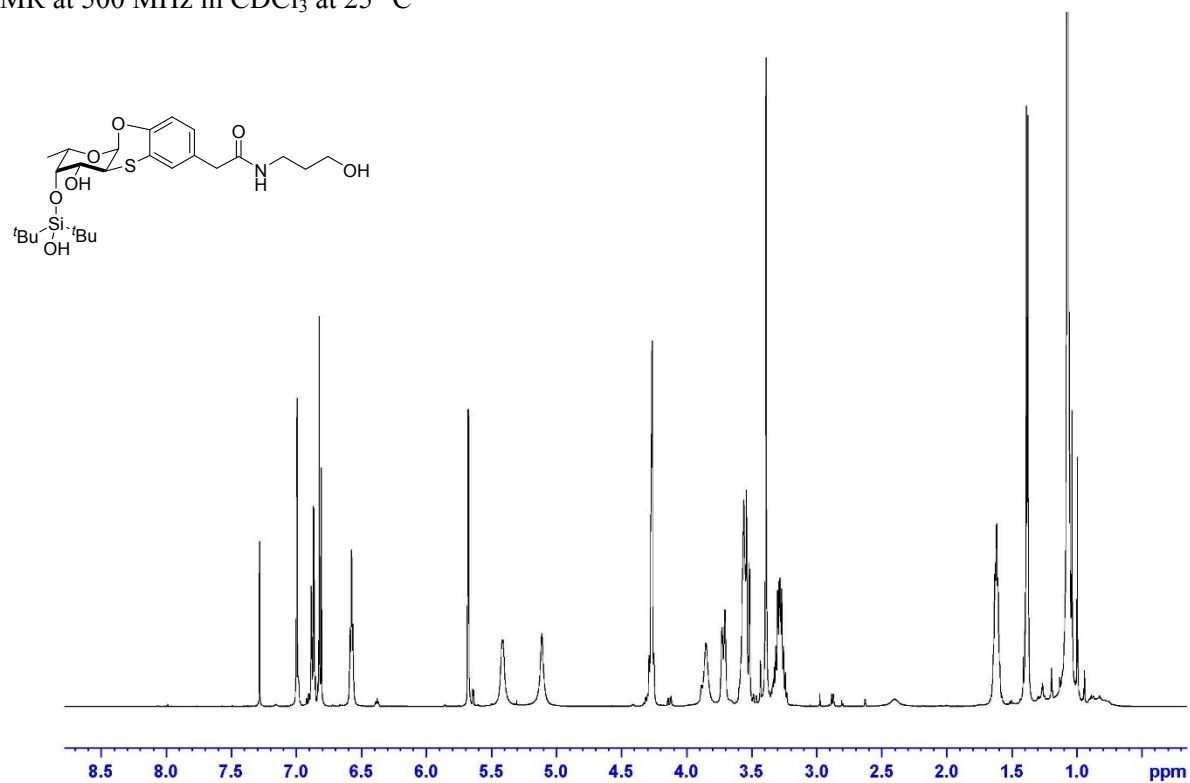
NMR Spectra of compound 5:



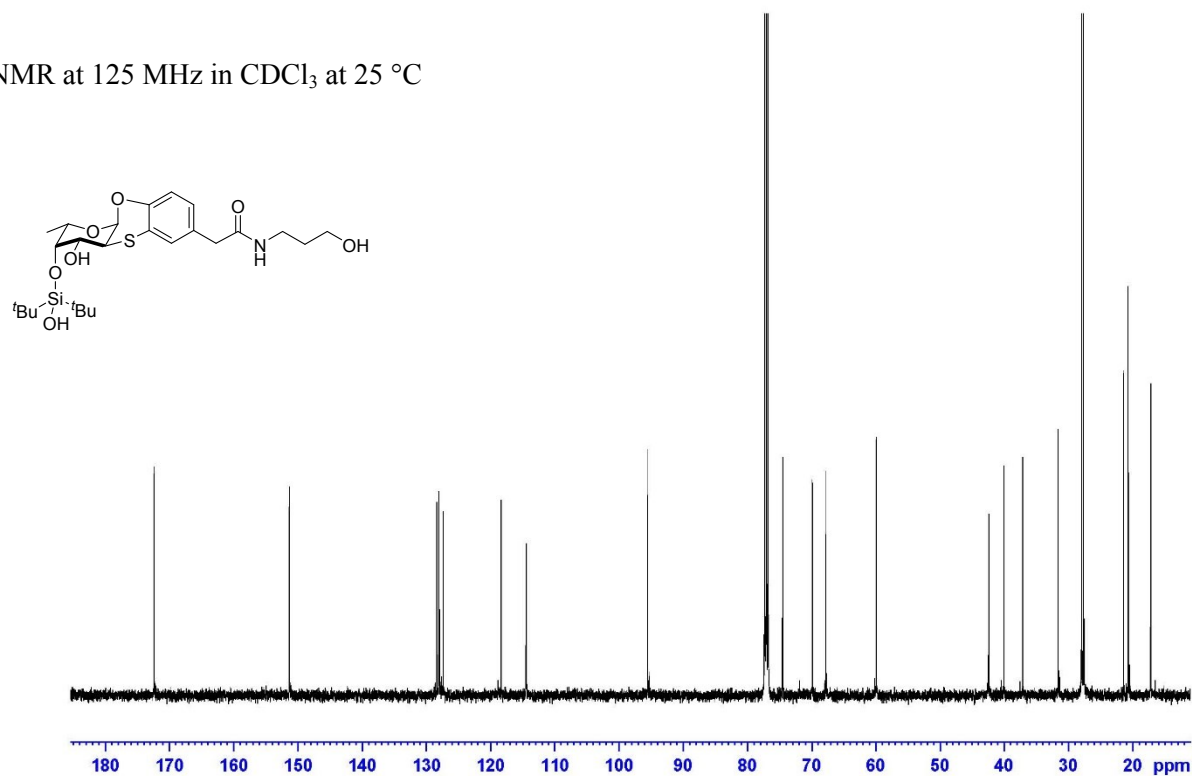
ESI-MS of compound 5:



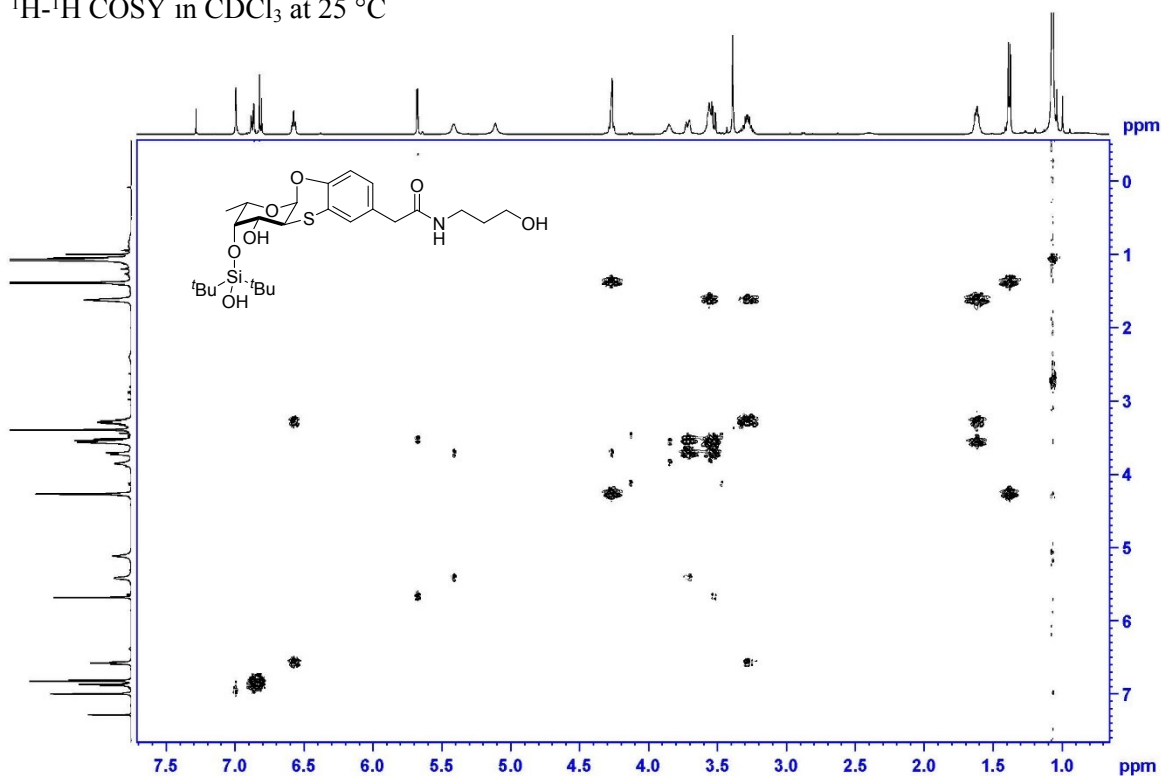
^1H NMR at 500 MHz in CDCl_3 at 25 °C



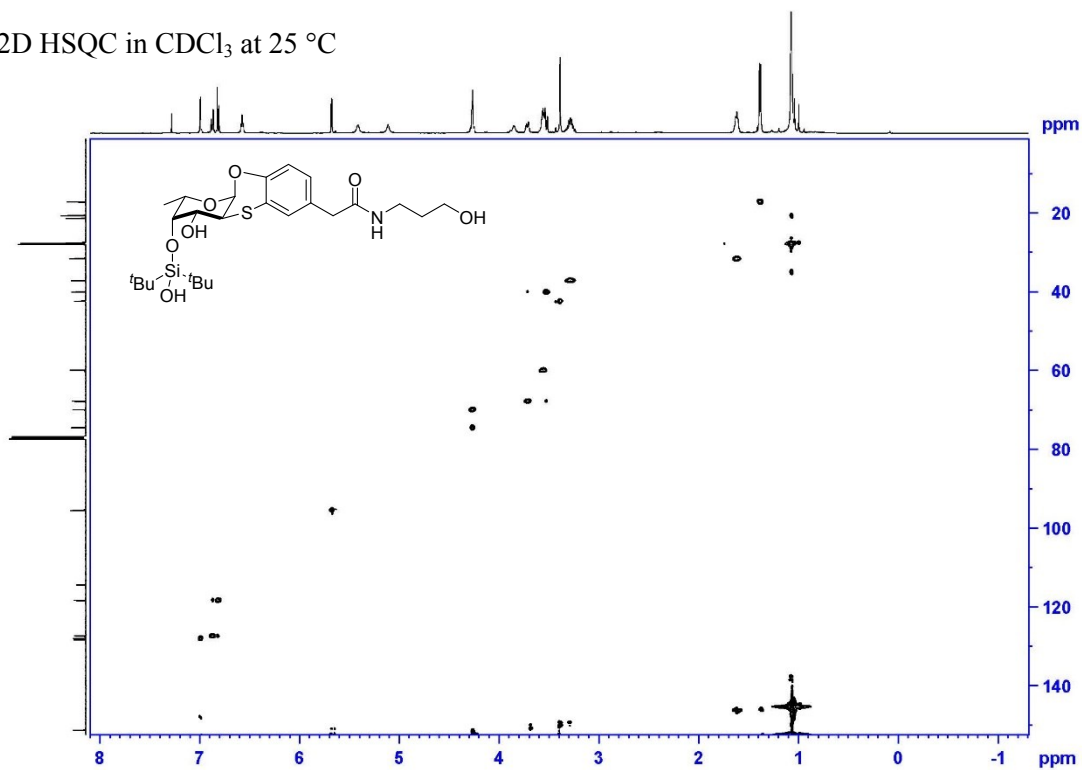
^{13}C NMR at 125 MHz in CDCl_3 at 25 °C



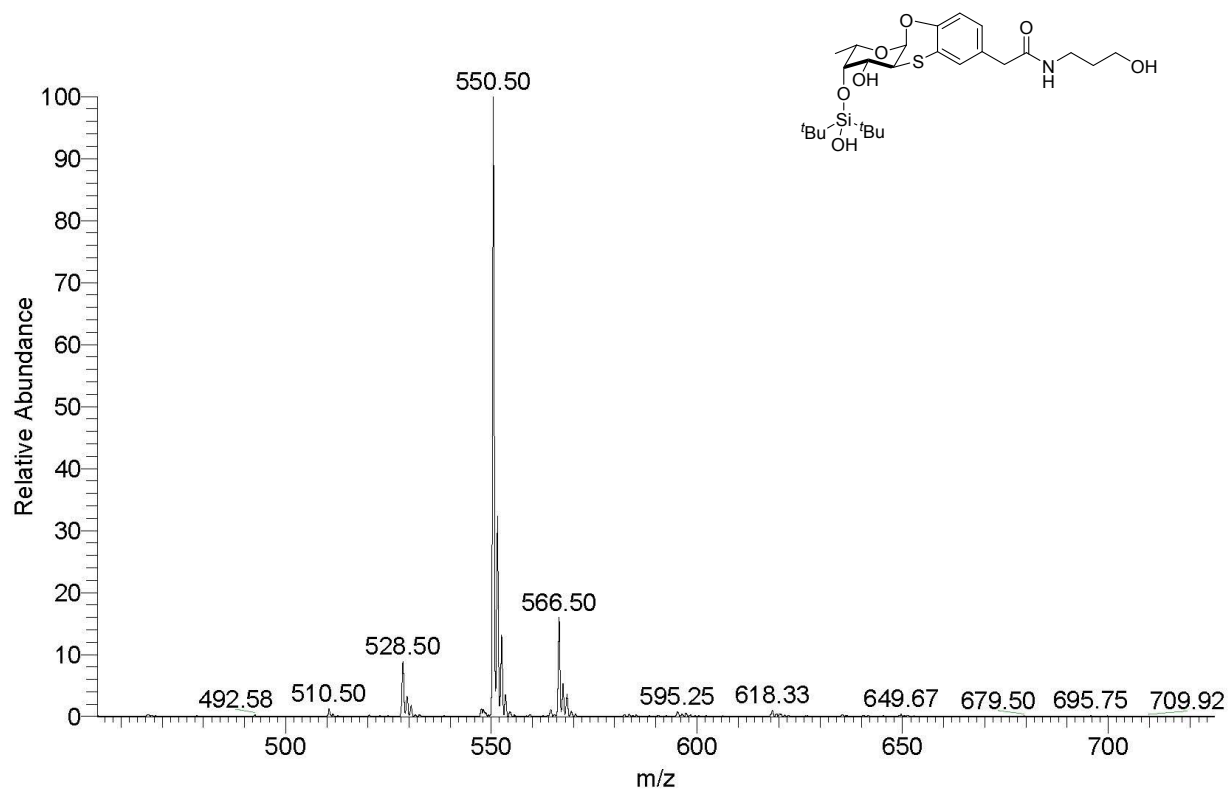
^1H - ^1H COSY in CDCl_3 at 25 °C



^1H - ^{13}C 2D HSQC in CDCl_3 at 25 °C

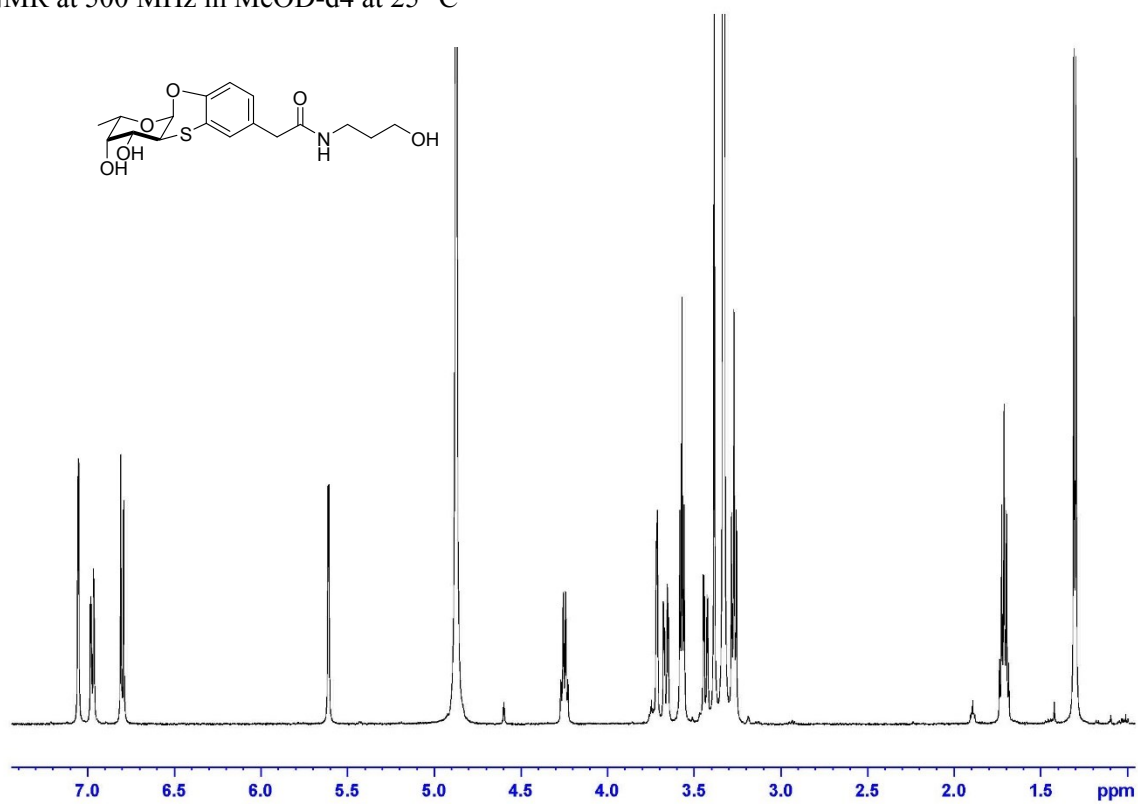


ESI-MS of compound 6:

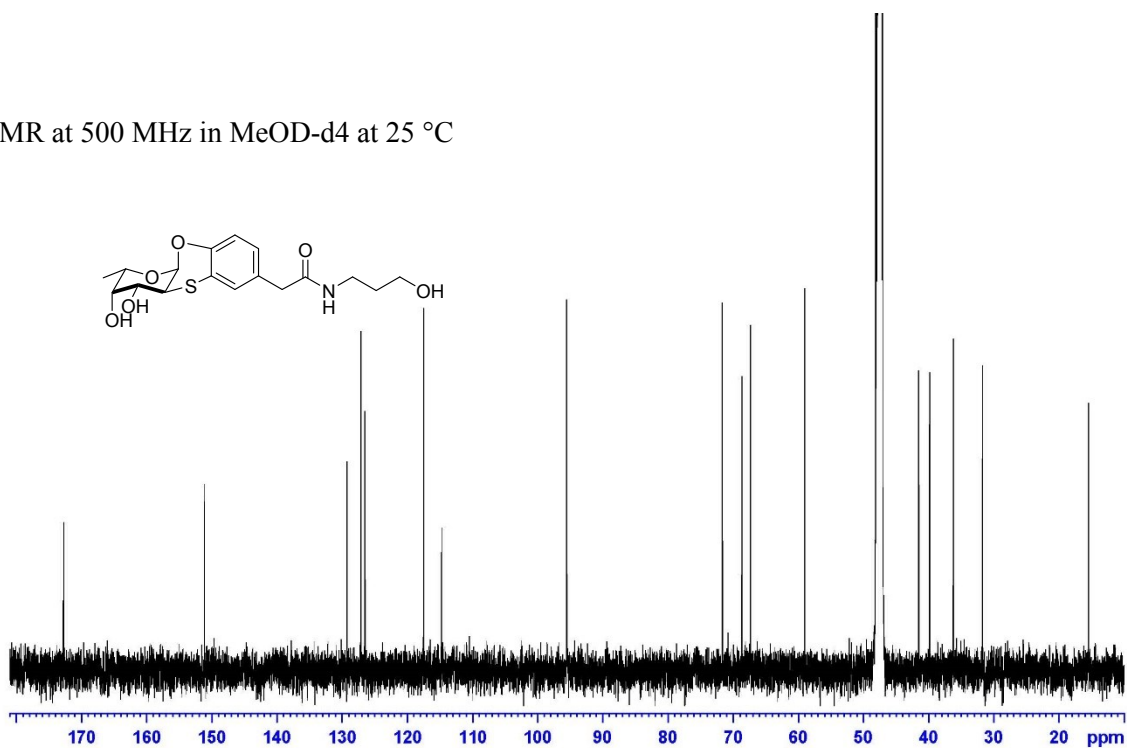


NMR Spectra of compound 3:

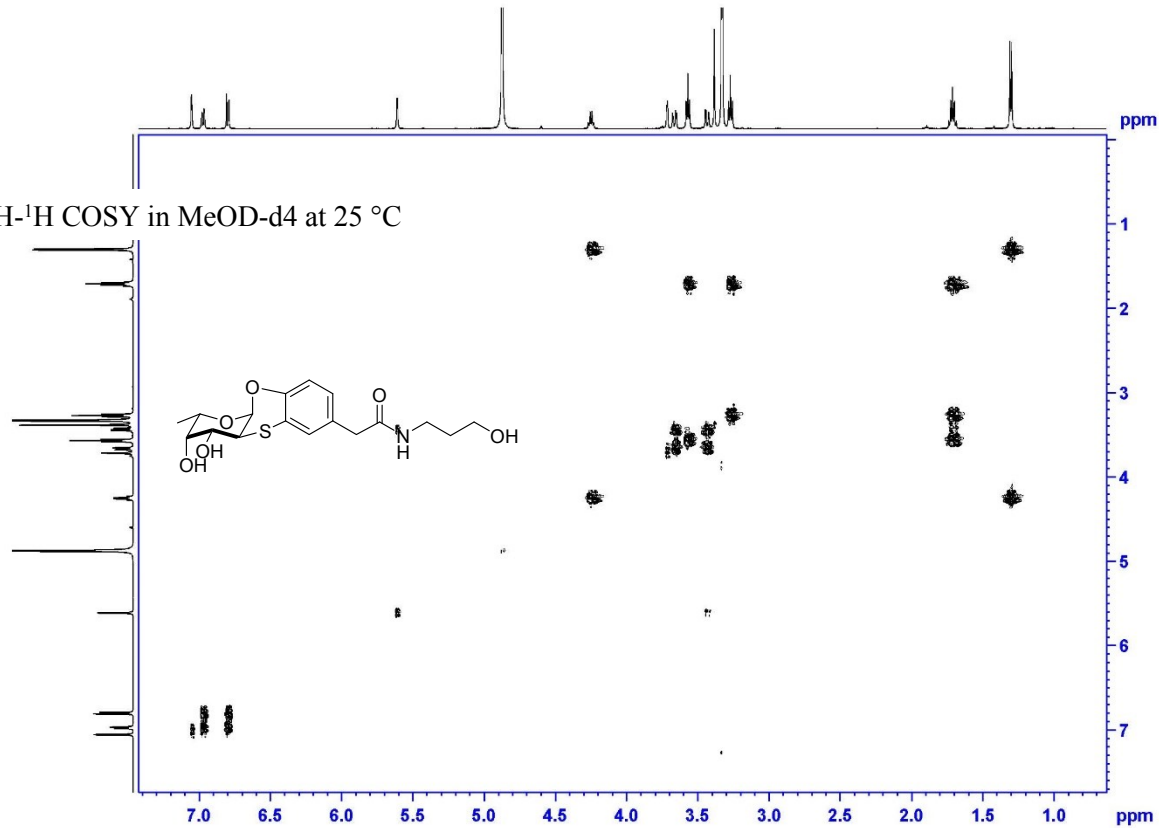
^1H NMR at 500 MHz in MeOD- d_4 at 25 °C



^{13}C NMR at 500 MHz in MeOD- d_4 at 25 °C

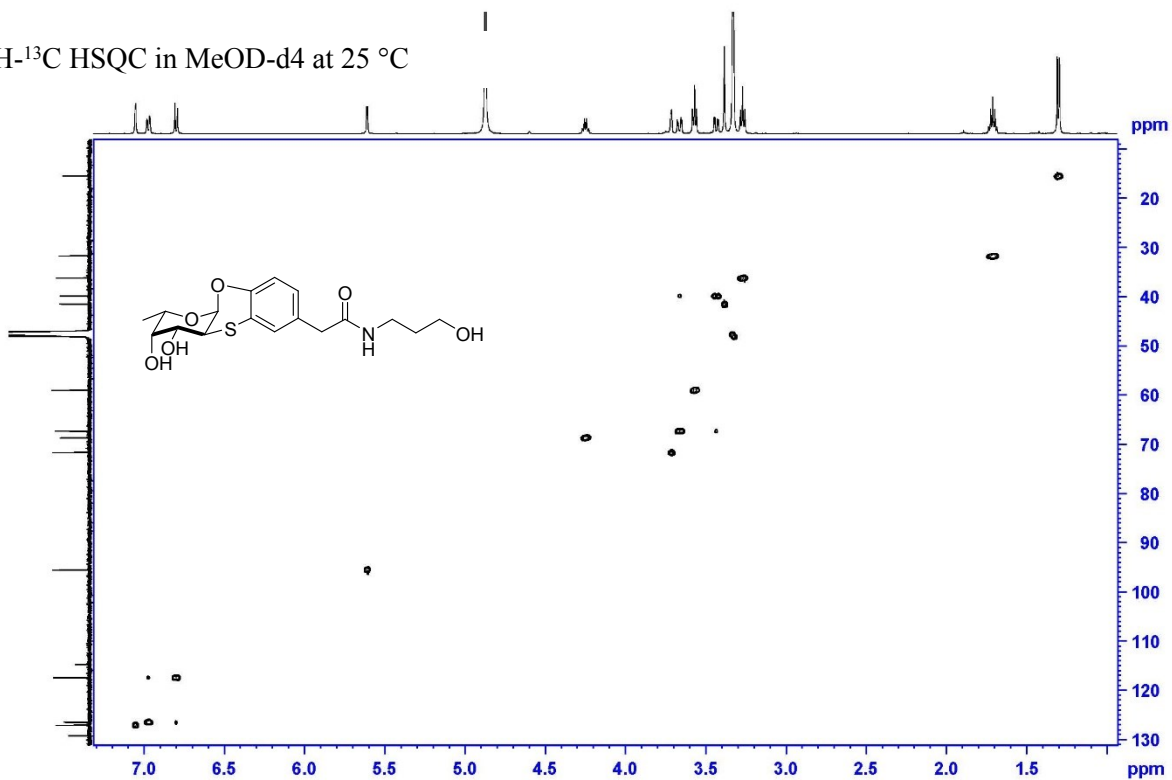


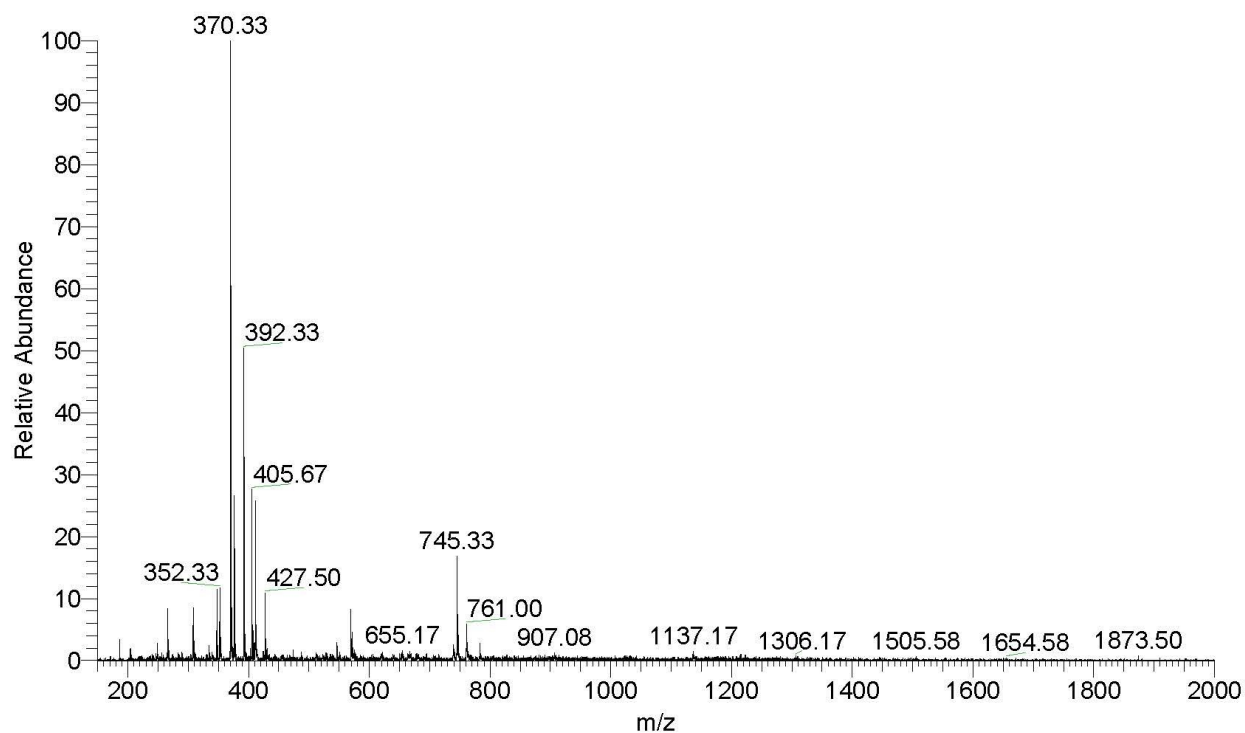
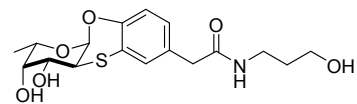
^1H - ^1H COSY in MeOD-d₄ at 25 °C



ESI-MS of compound 3:

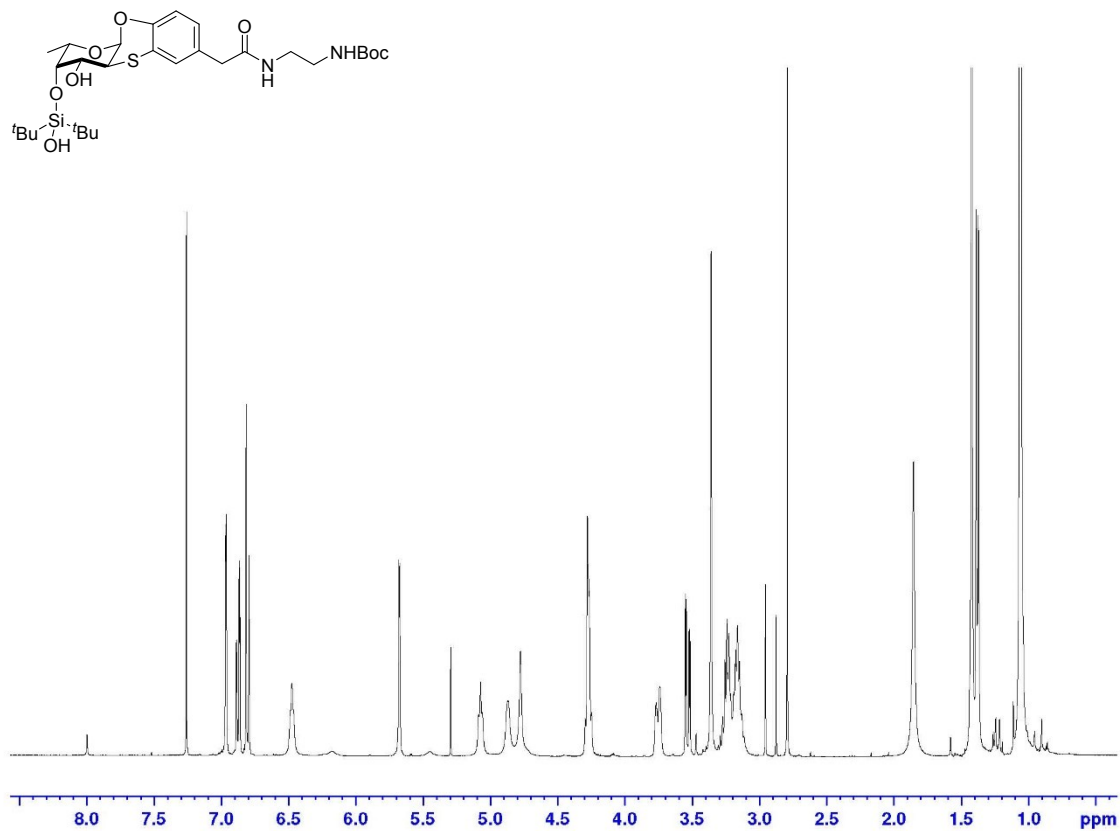
^1H - ^{13}C HSQC in MeOD-d₄ at 25 °C



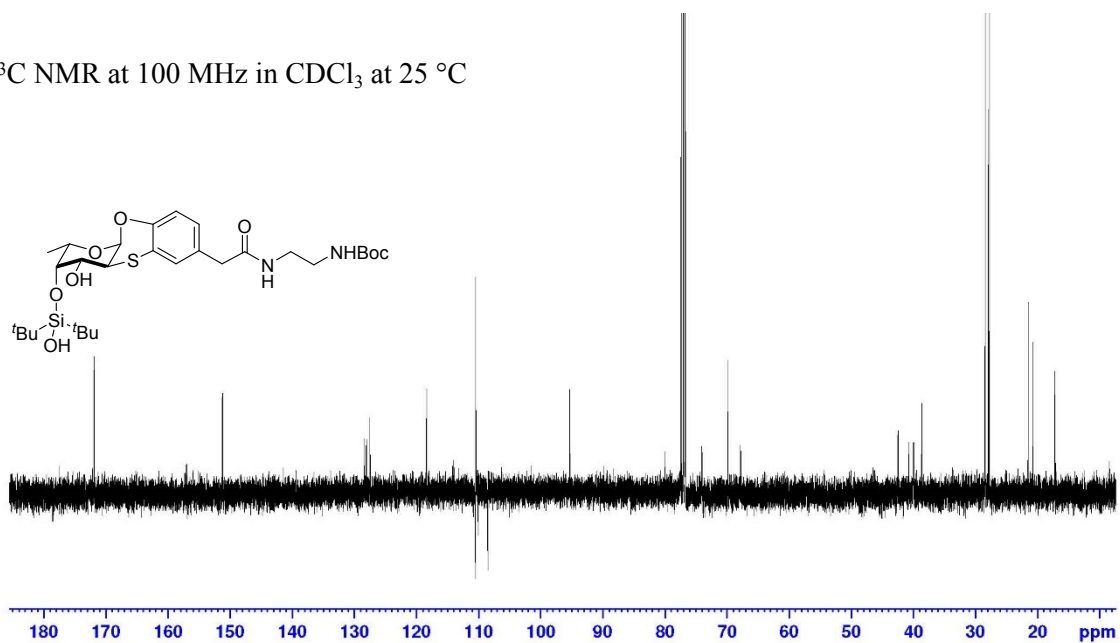


NMR of compound 9:

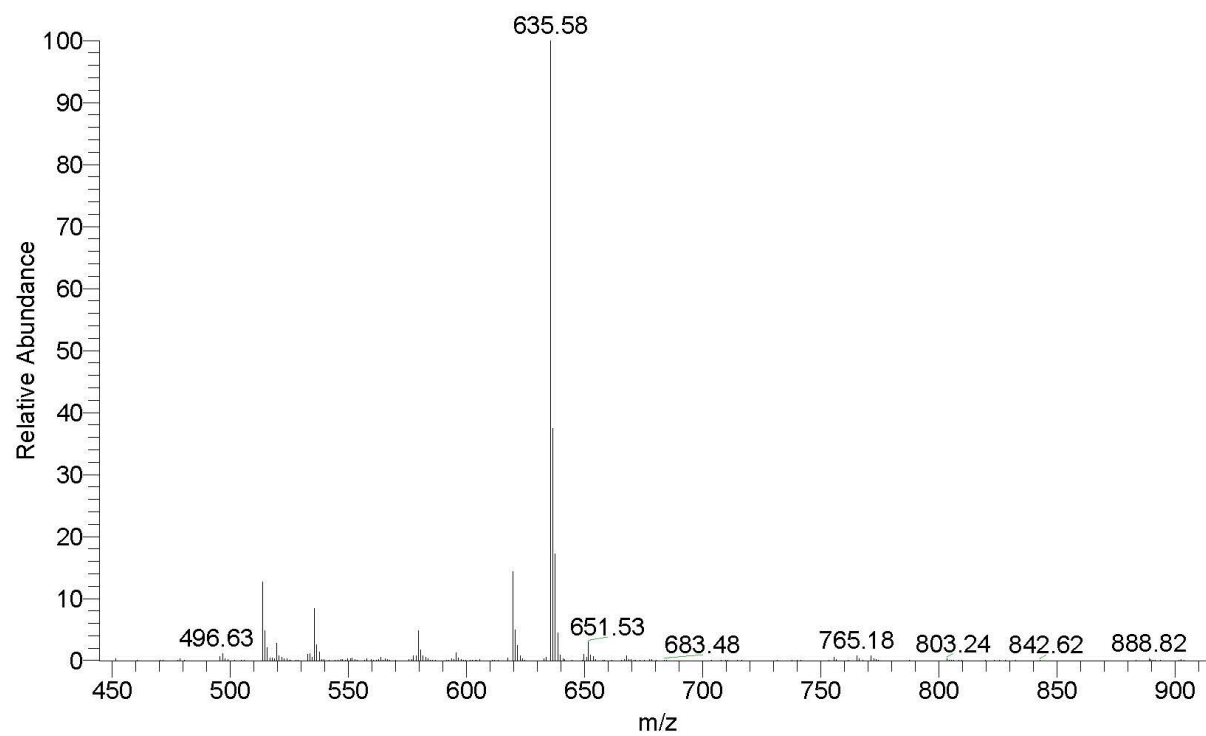
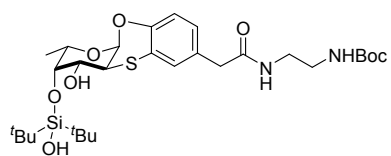
^1H NMR at 400 MHz in CDCl_3 at 25 °C



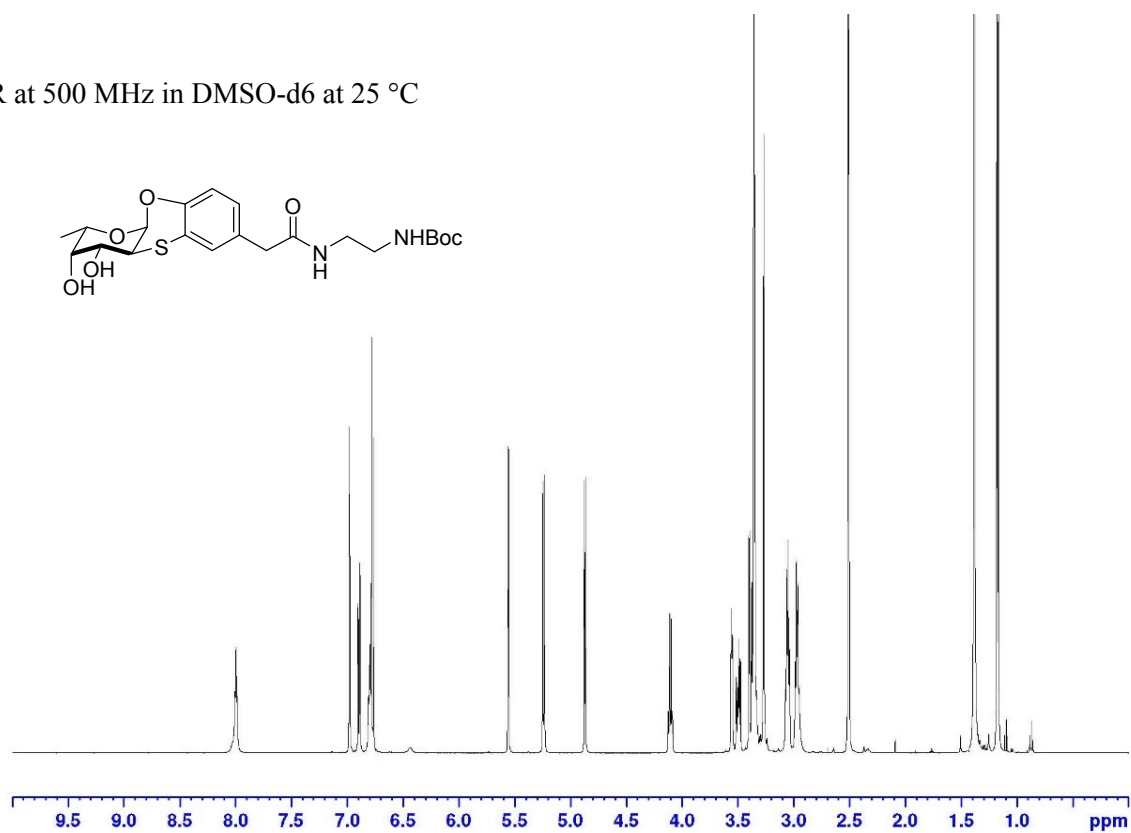
^{13}C NMR at 100 MHz in CDCl_3 at 25 °C



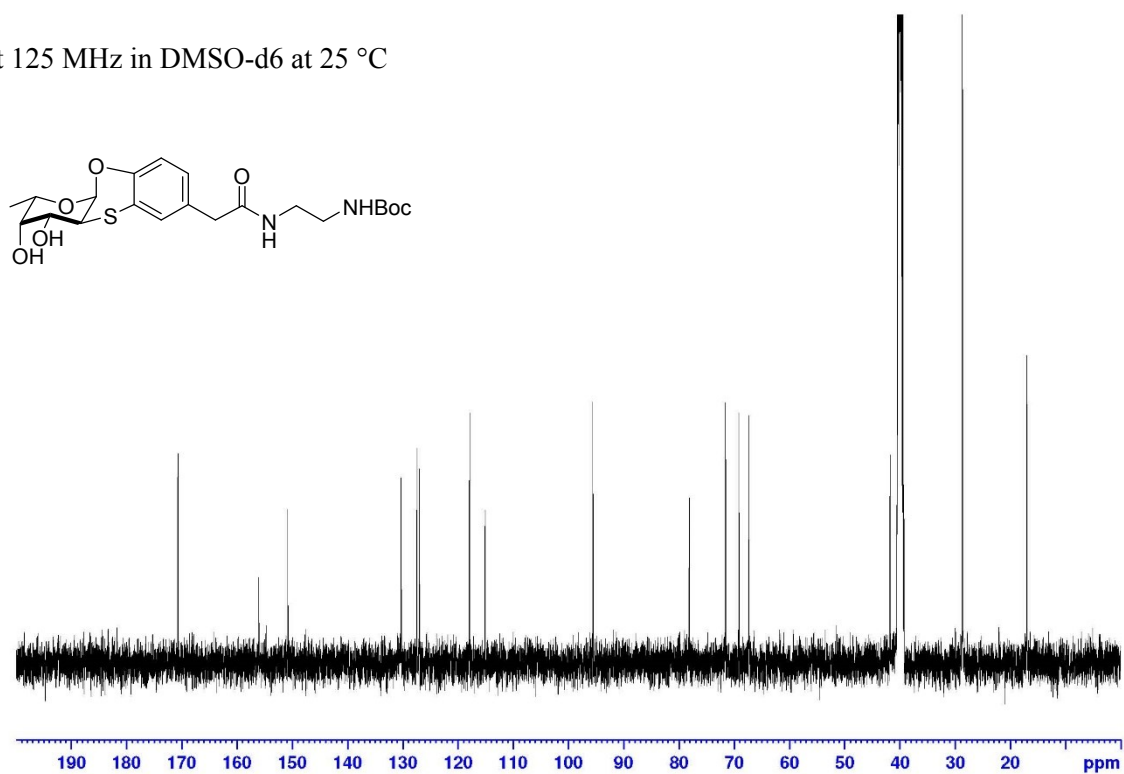
ESI-MS of compound 9:



^1H NMR at 500 MHz in DMSO- d_6 at 25 $^\circ\text{C}$

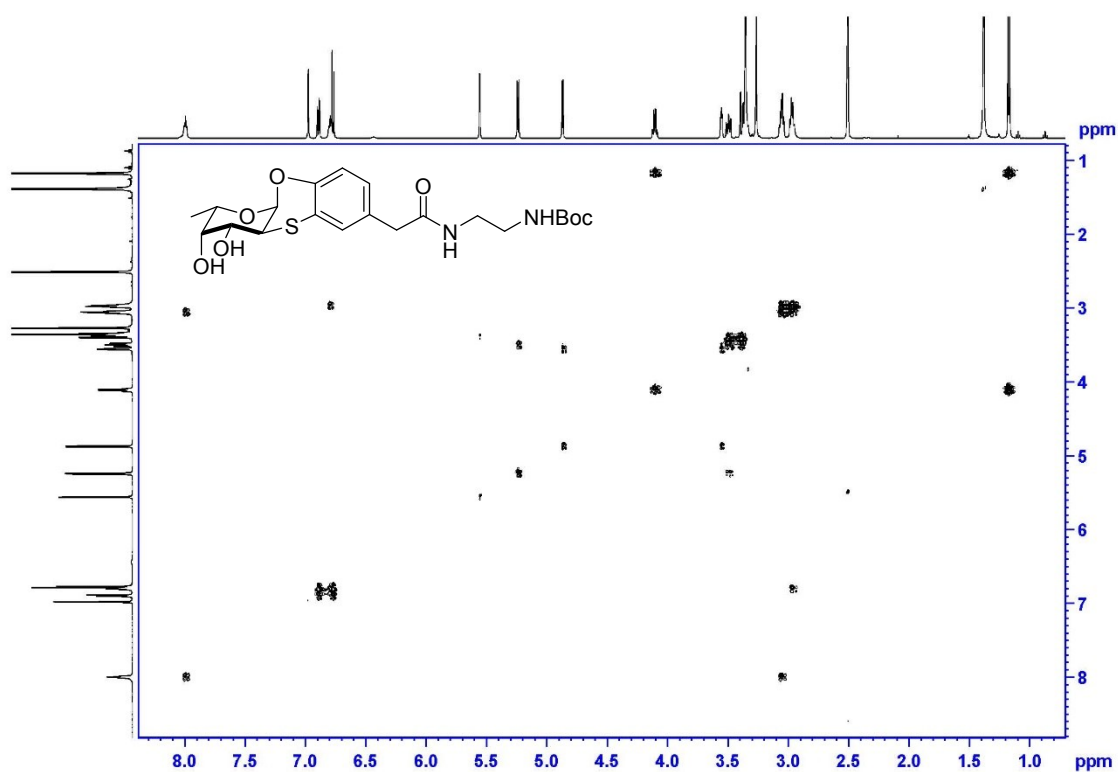


^{13}C NMR at 125 MHz in DMSO- d_6 at 25 $^\circ\text{C}$

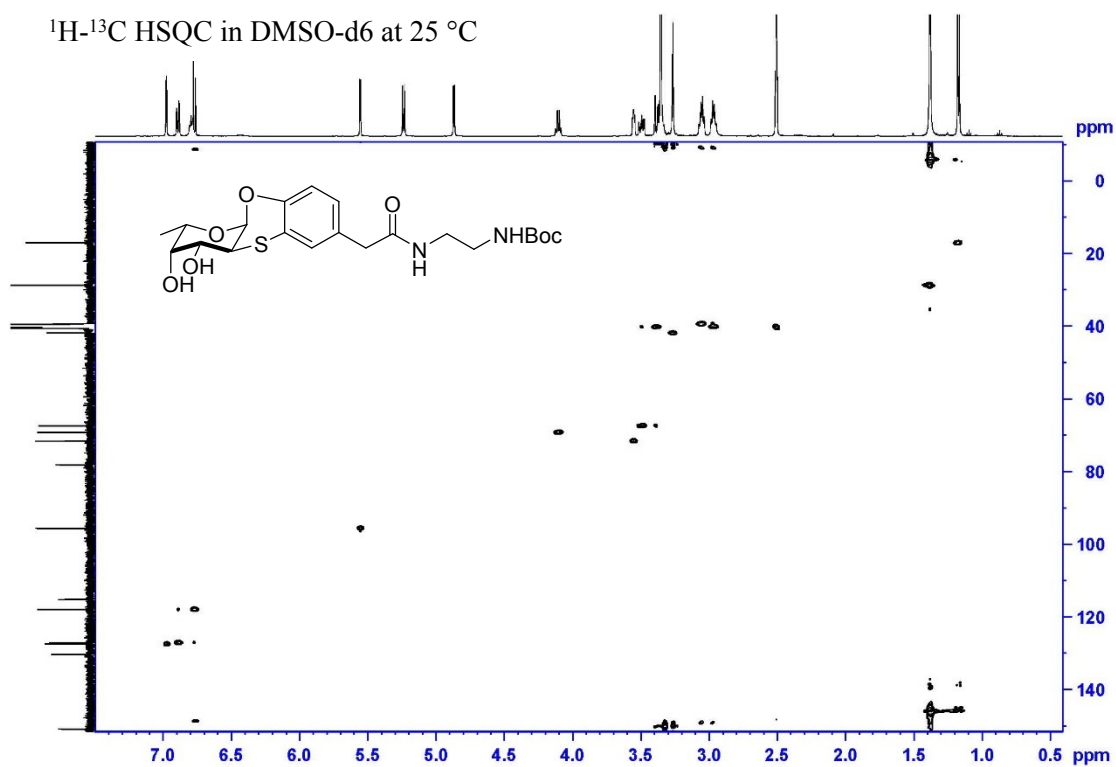


NMR of compound 10:

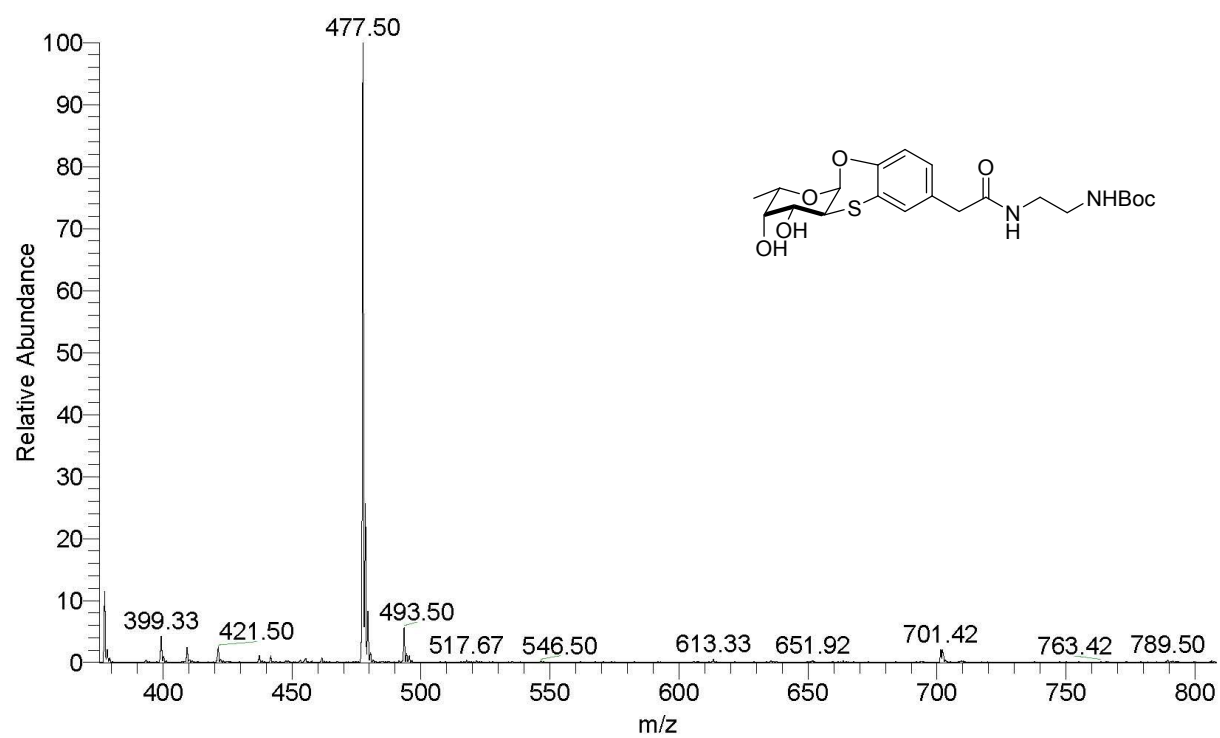
^1H - ^1H COSY in DMSO- d_6 at 25 °C



^1H - ^{13}C HSQC in DMSO- d_6 at 25 °C

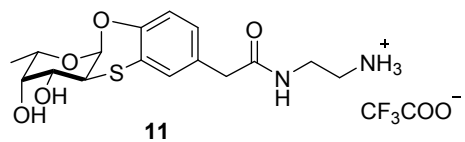
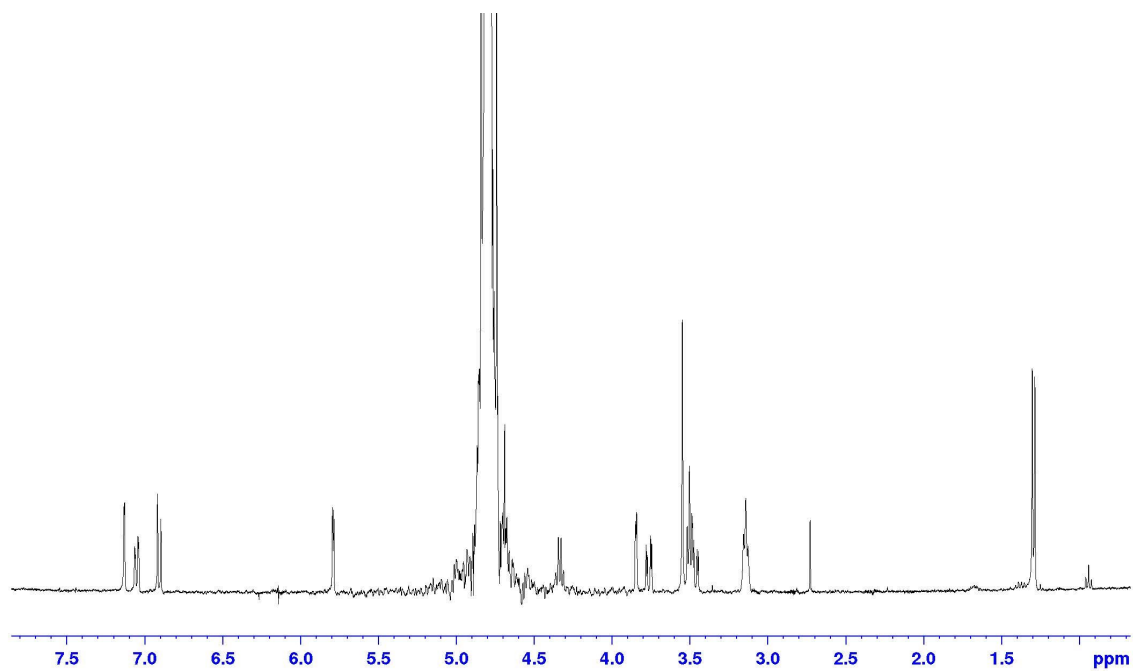


ESI-MS of compound 10:

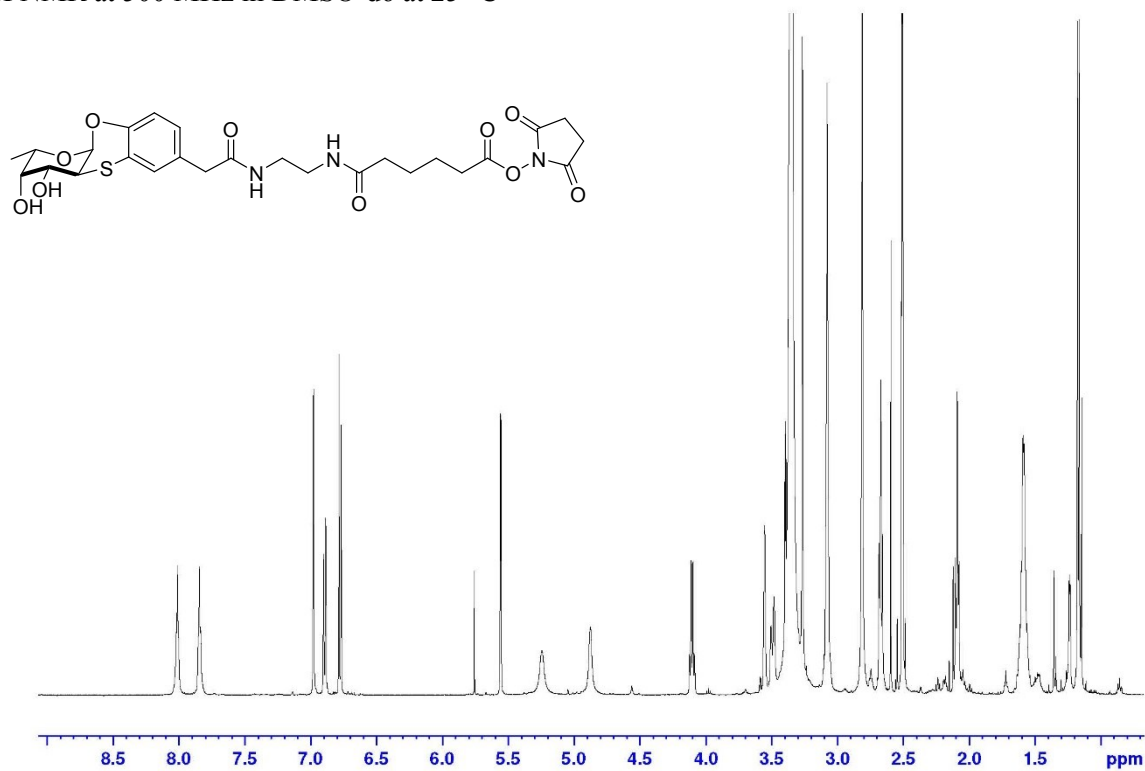


NMR of compound 11:

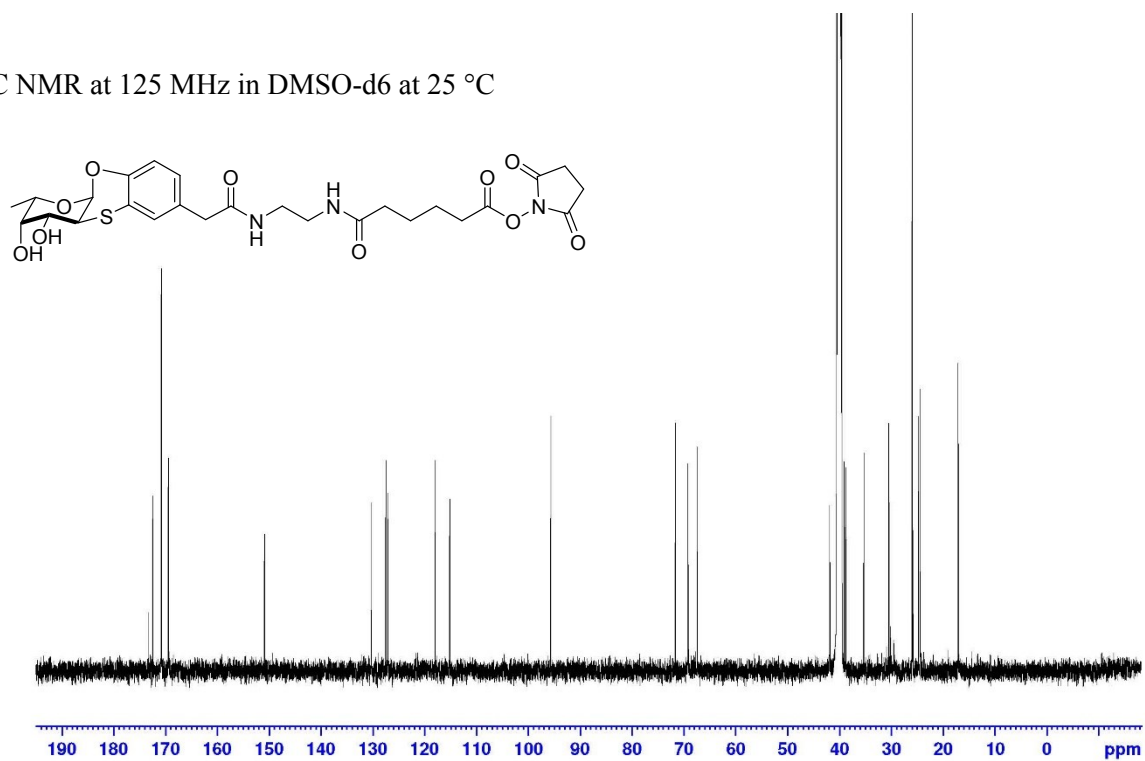
^1H NMR at 500 MHz in D_2O at 25 °C



^1H NMR at 500 MHz in DMSO- d_6 at 25 °C

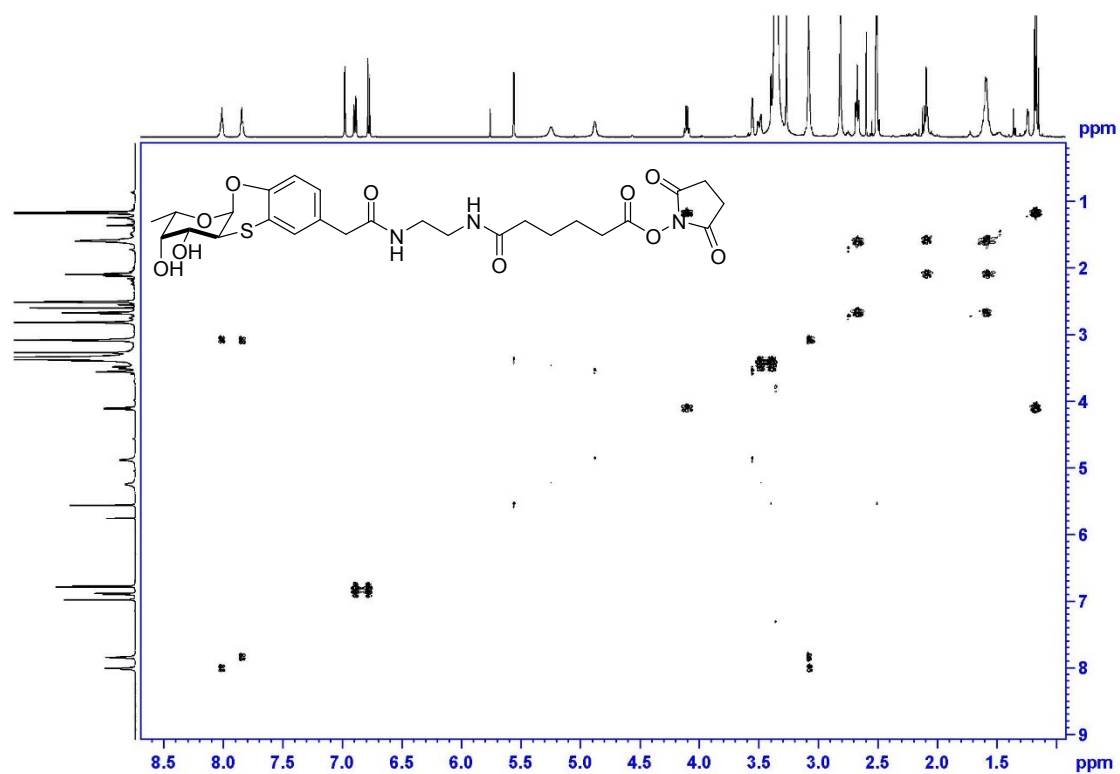


^{13}C NMR at 125 MHz in DMSO- d_6 at 25 °C

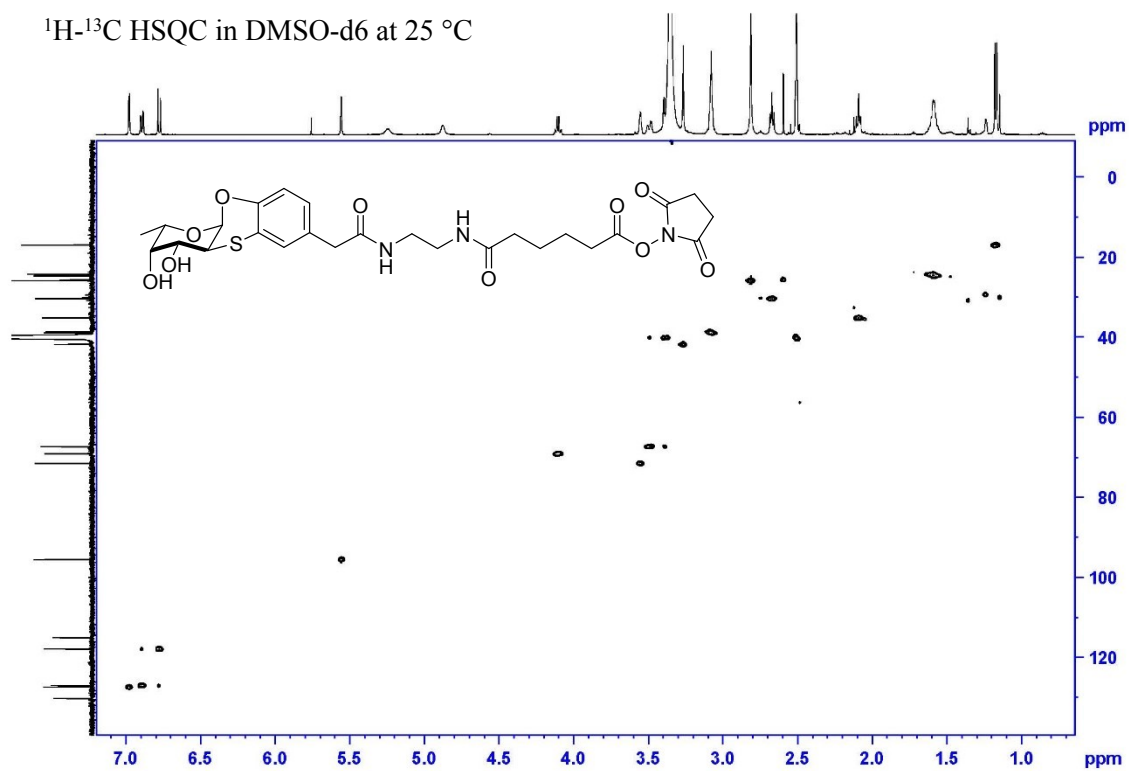


NMR of compound 7:

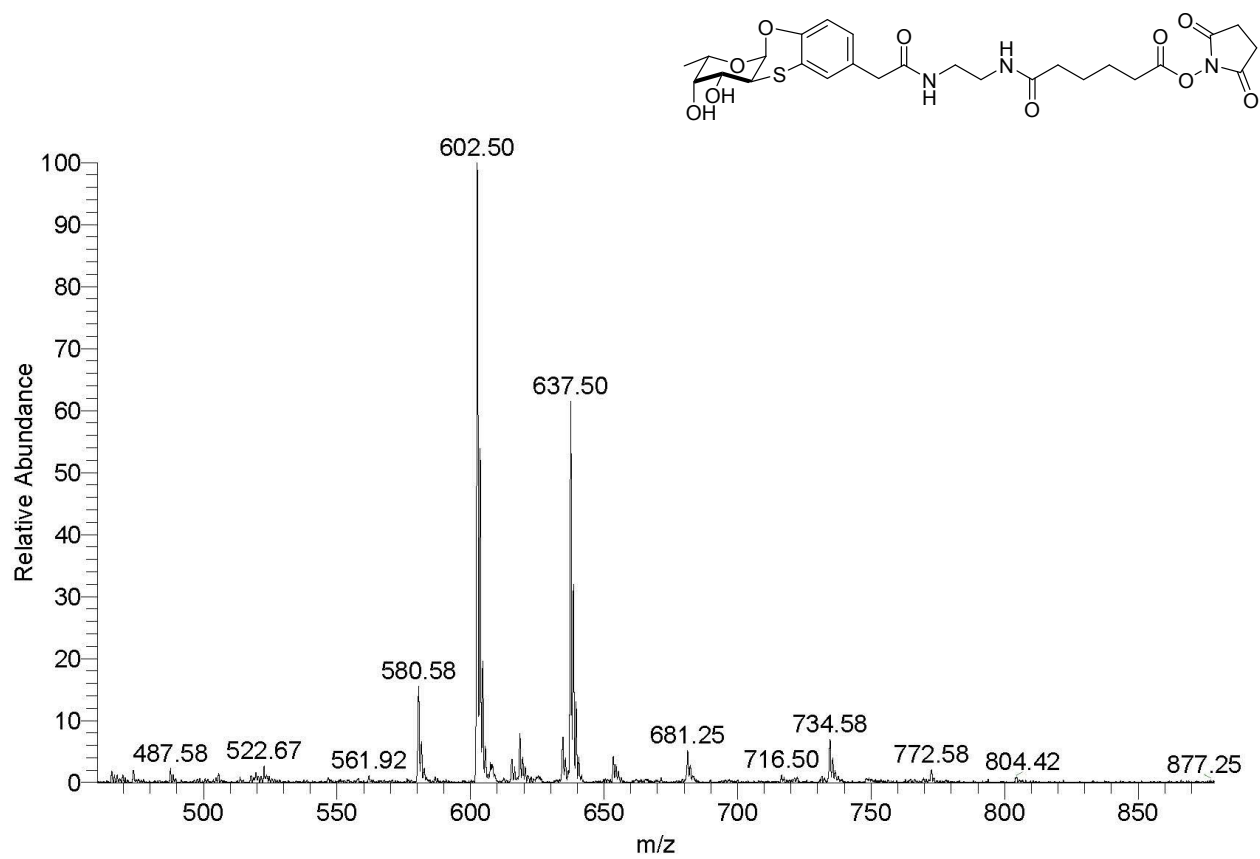
^1H - ^1H COSY in DMSO- d_6 at 25 °C



^1H - ^{13}C HSQC in DMSO- d_6 at 25 °C

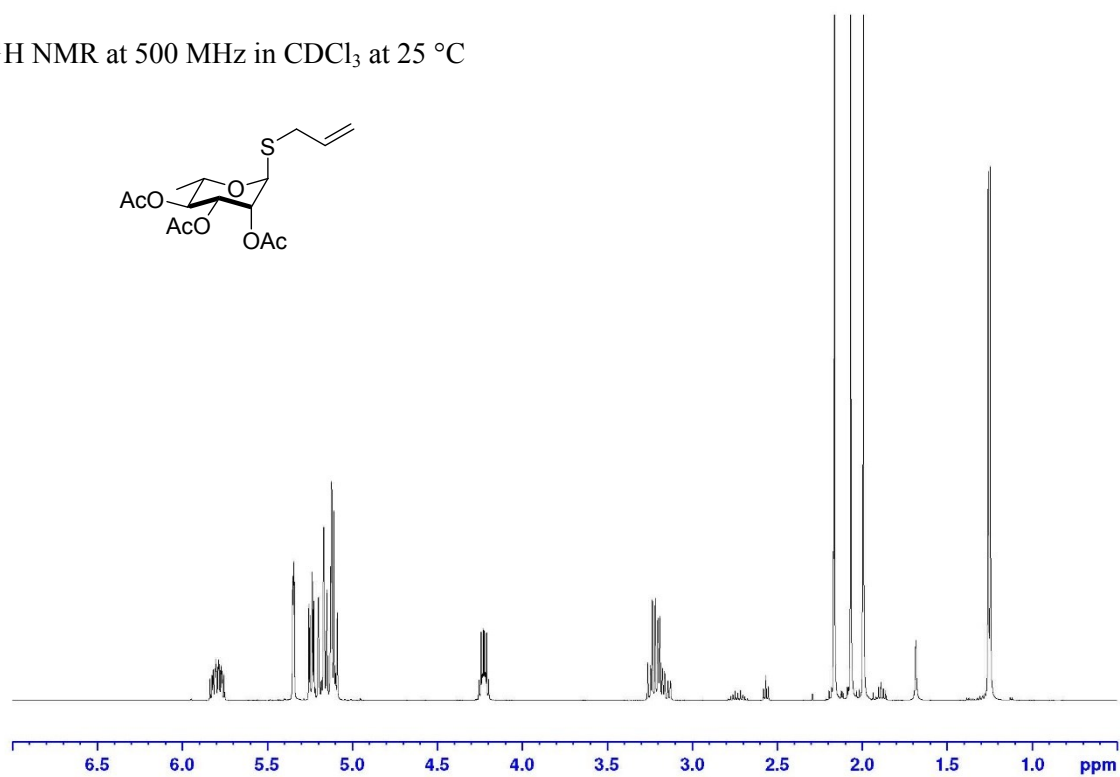


ESI-MS of compound 7:

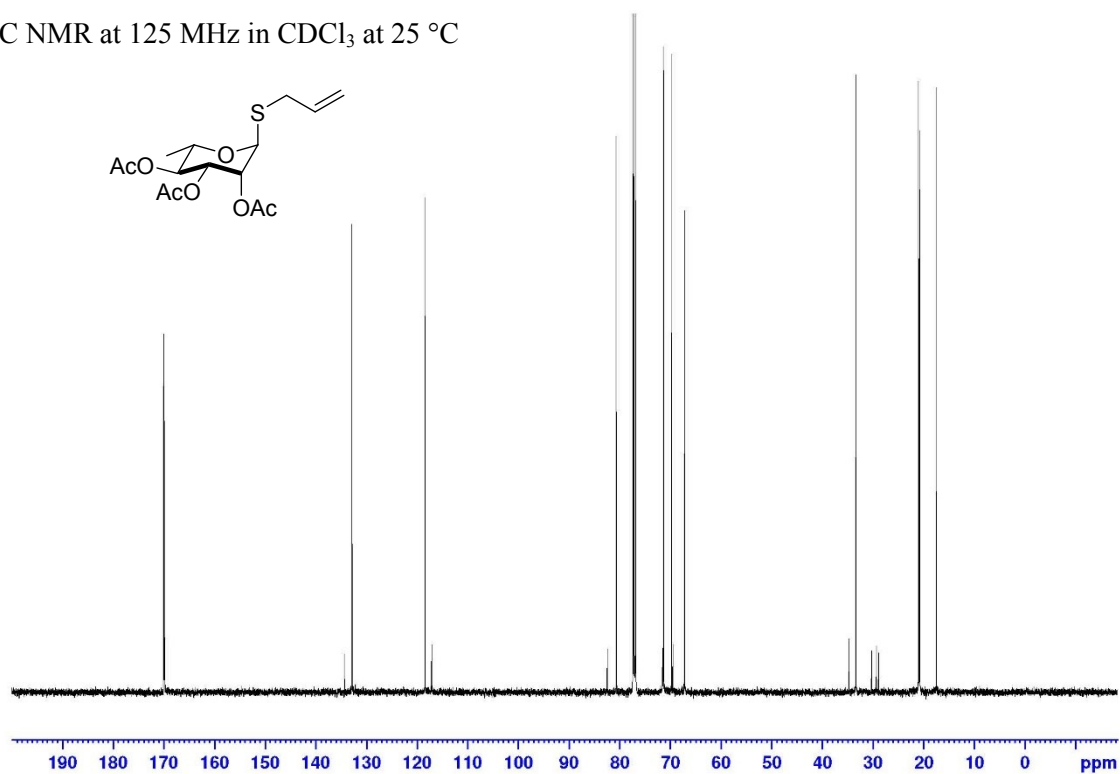


NMR of compound 14:

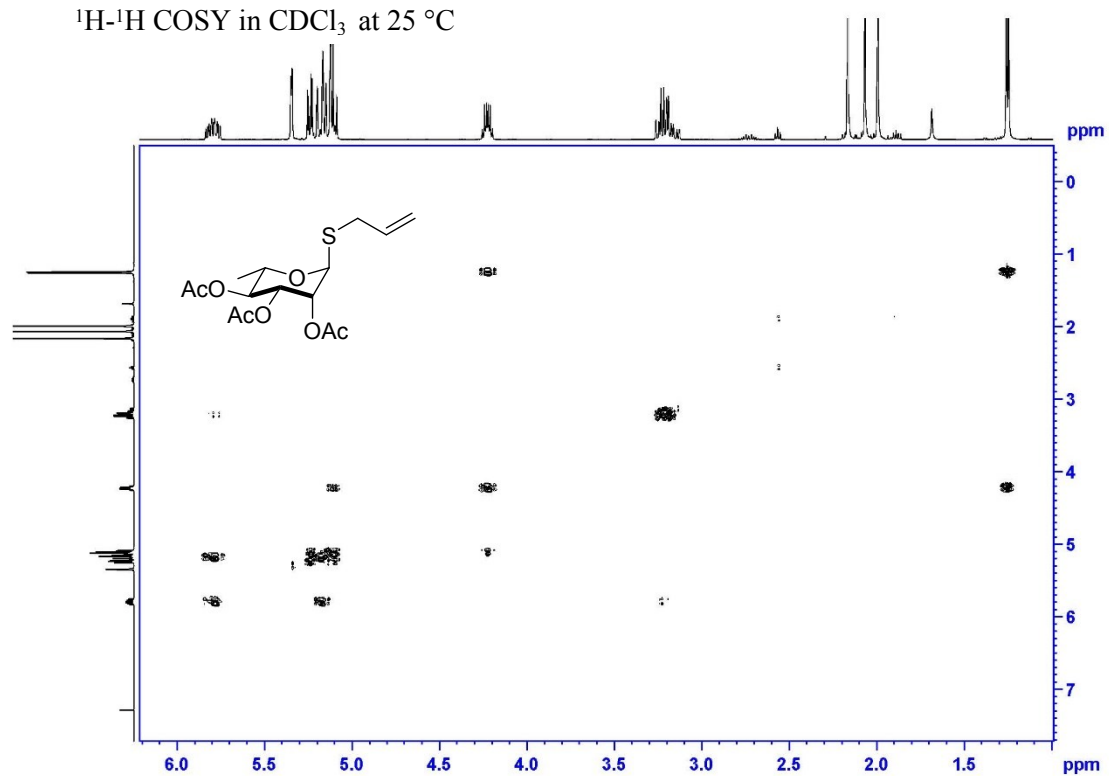
^1H NMR at 500 MHz in CDCl_3 at 25 °C



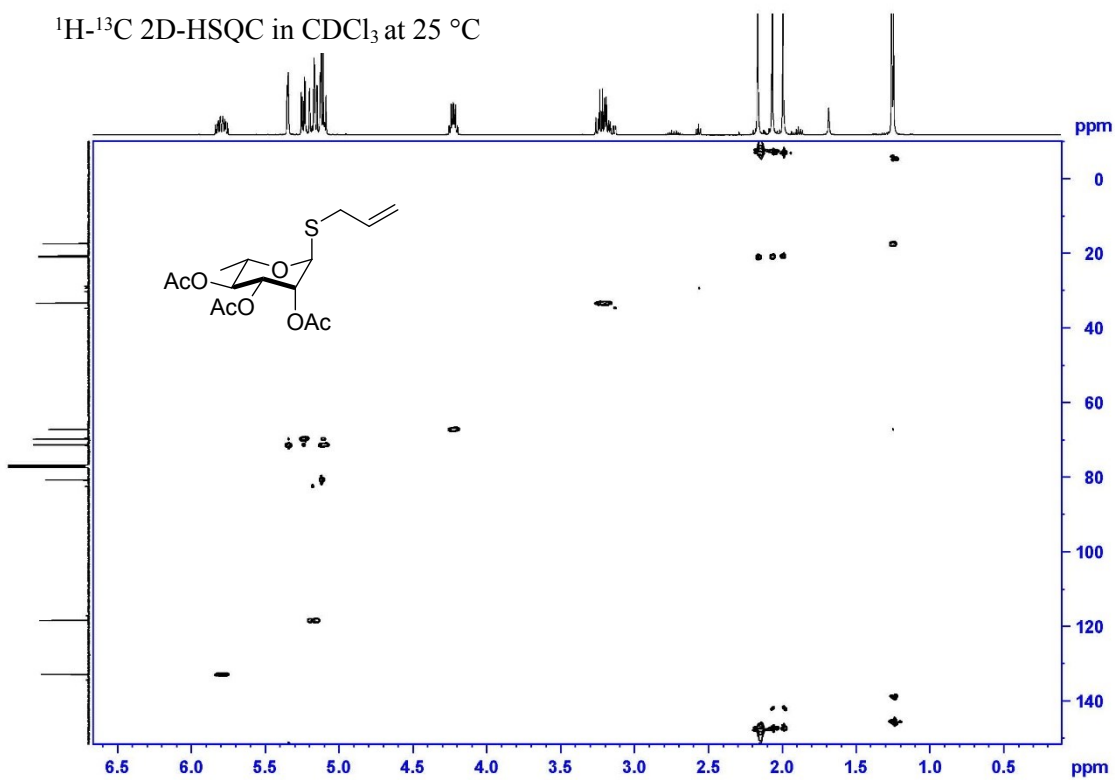
^{13}C NMR at 125 MHz in CDCl_3 at 25 °C



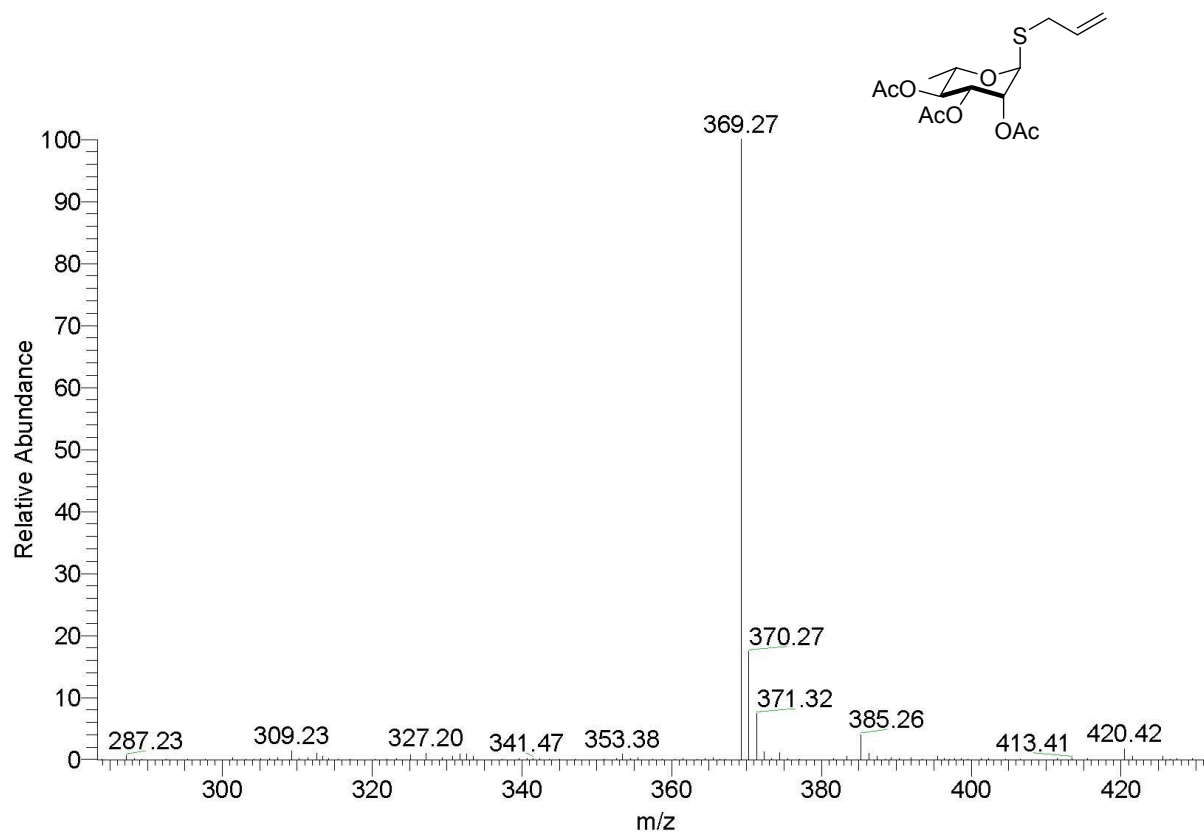
^1H - ^1H COSY in CDCl_3 at 25 °C



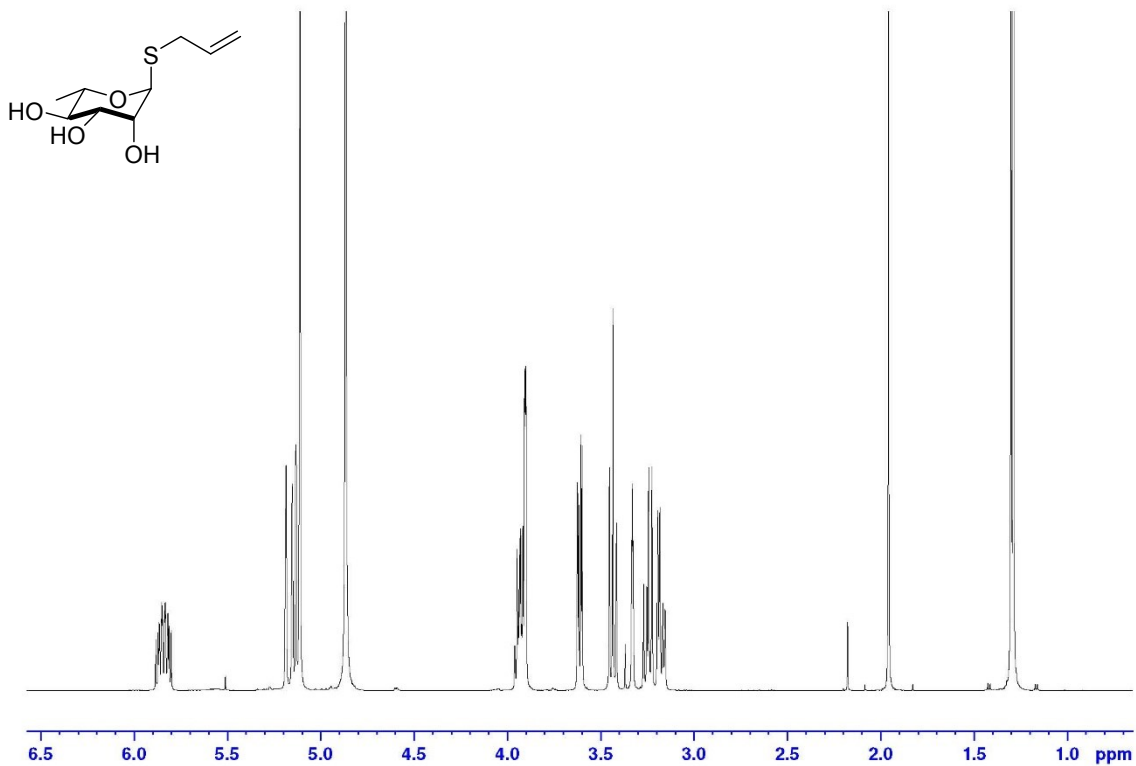
^1H - ^{13}C 2D-HSQC in CDCl_3 at 25 °C



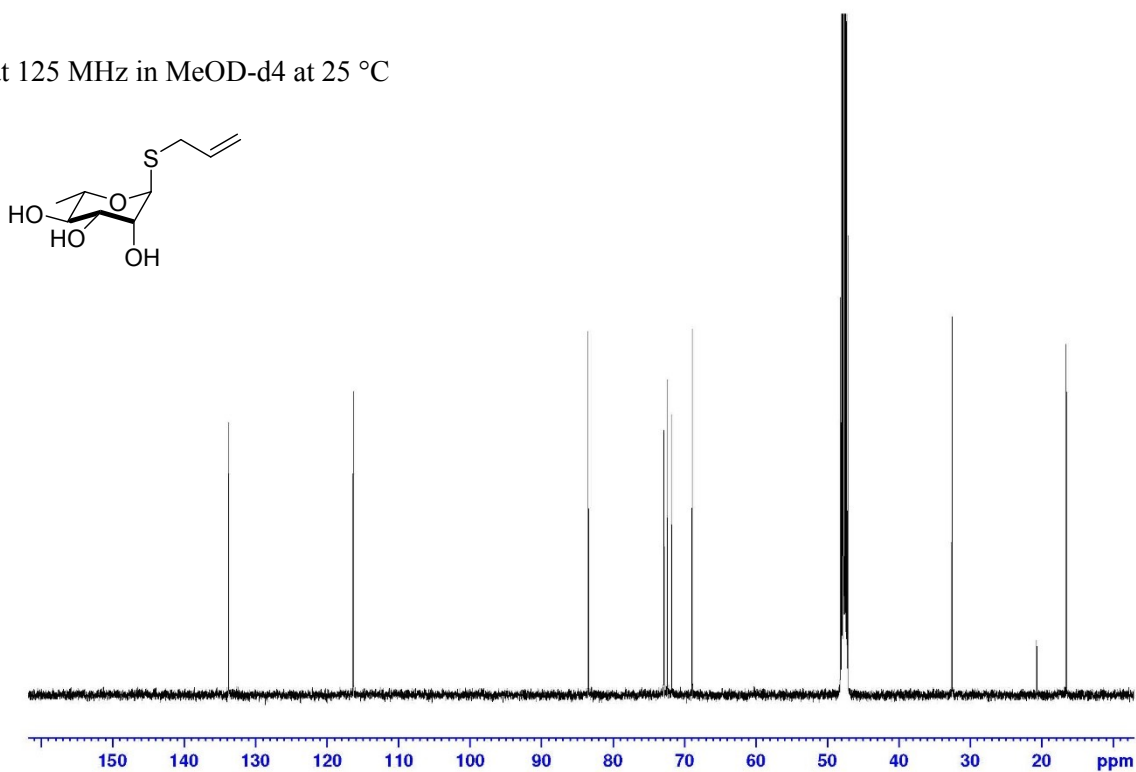
ESI-MS of compound 14:



^1H NMR at 500 MHz in MeOD- d_4 at 25 °C

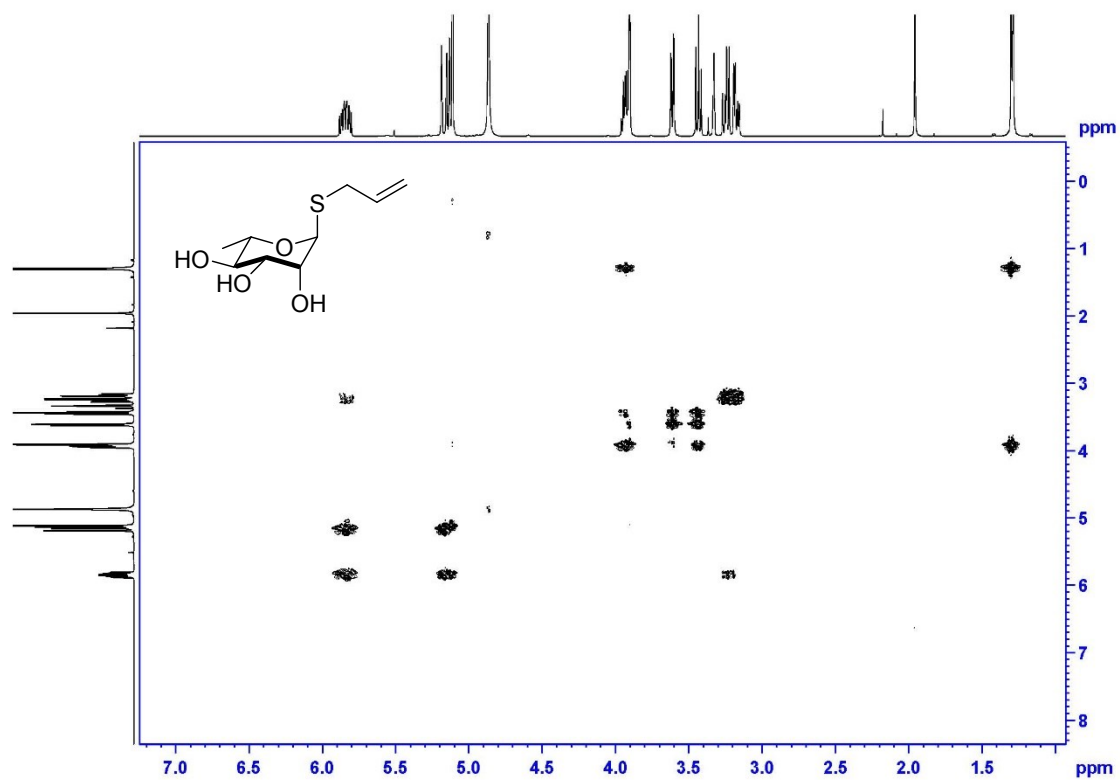


^{13}C NMR at 125 MHz in MeOD- d_4 at 25 °C

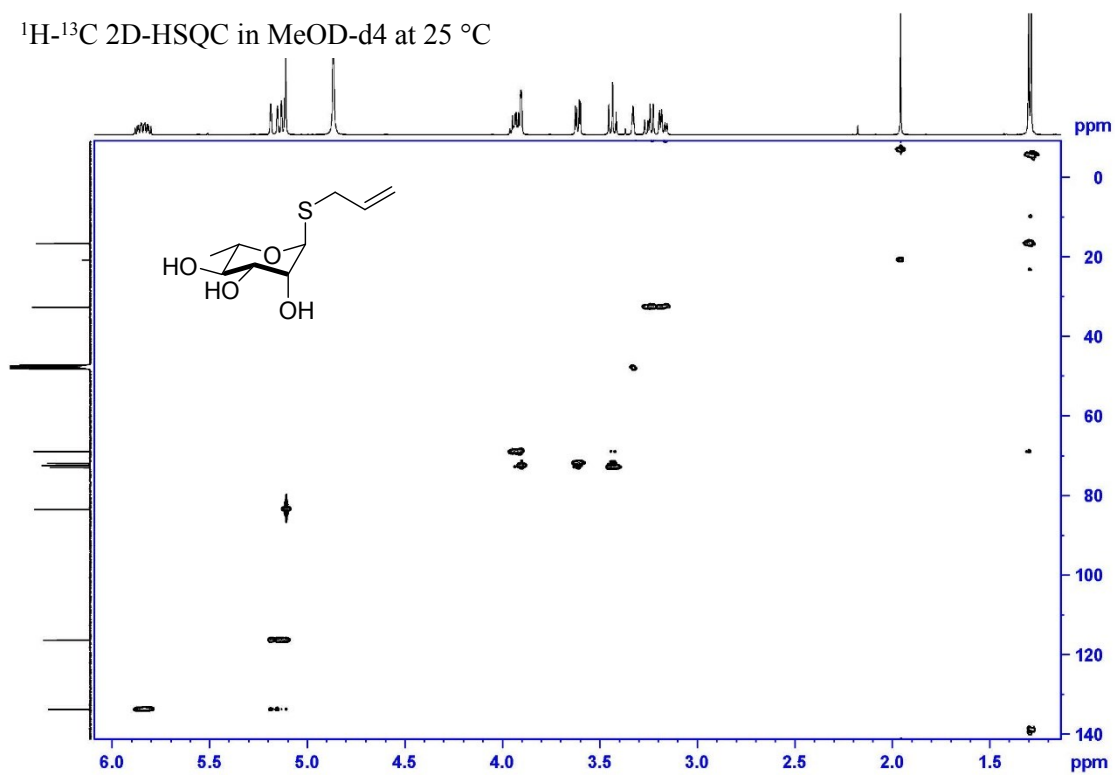


NMR compound 13:

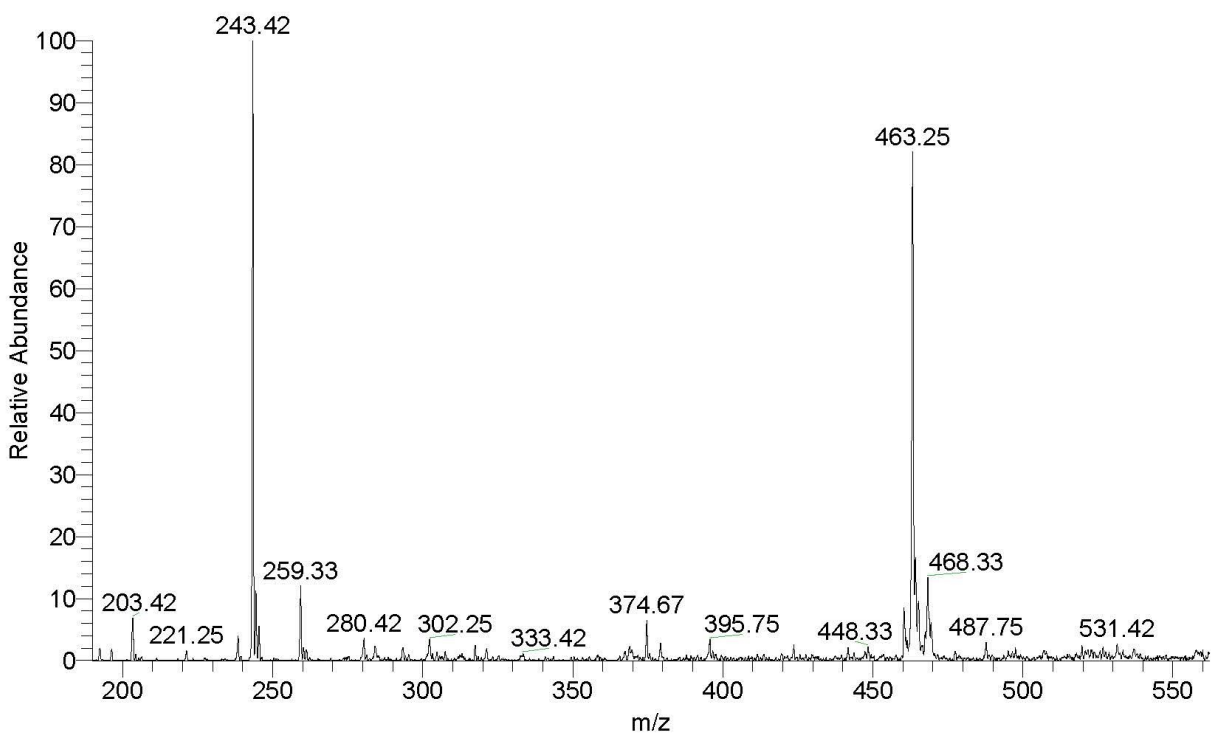
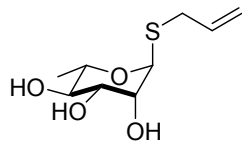
^1H - ^1H COSY in MeOD- d_4 at 25 °C



^1H - ^{13}C 2D-HSQC in MeOD- d_4 at 25 °C



ESI-MS of compound 13:



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