Supplemental Information

Bump-and-Hole Engineering

Identifies Specific Substrates

of Glycosyltransferases in Living Cells

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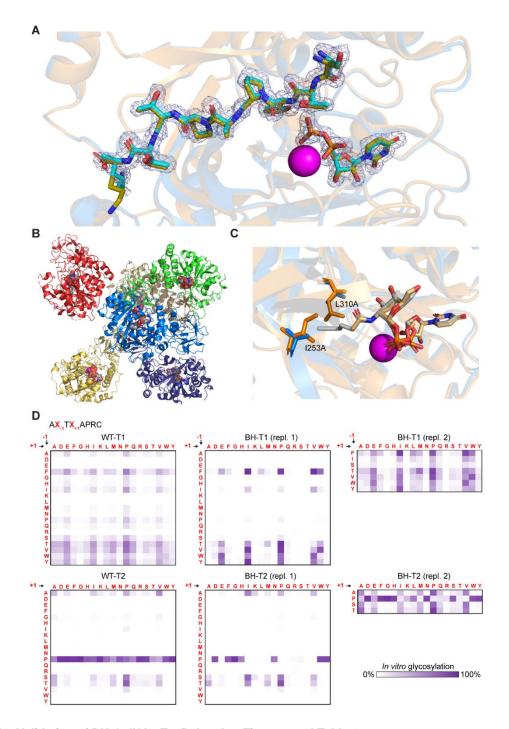


Figure S1. Validation of BH-GalNAc-Ts, Related to Figure 2 and Table 1.

- (A) Overlay of ligands bound in BH-T2/EA2/UDP/Mn2+ (ligands cyan) and a published crystal structure of WT-T2/EA2/UDP/Mn2+ (ligands olive, PDB 2FFU), with electron density (map rendered at 1 σ and carved at 1.6 Å) taken from the BH-T2 co-crystal structure. Mn2+ ions are colored in magenta and overlay completely.
- (B) Crystal structure of BH-T2/1/Mn2+ in the hexameric unit cell. UDP-GalNAc analog **1** is rendered in sphere representation.
- (C) Superposition of the active sites of WT-T2 (PDB 4D0T, orange) with UDP-GalNAc (light brown) and BH-T2 (blue) with UDP-GalNAc analog 1 (grey). Gatekeeper residues are rendered in stick representation. Mn²⁺ ions are magenta and overlay completely.
- (D) Substrate specificities of BH-T1 and BH-T2 and comparison with WT enzymes as determined in an *in vitro* glycosylation assay with detection by SAMDI-MS. WT data corresponds with reported substrate specificities, and two replicates are shown for BH enzymes with the full library or a focused sub-library.

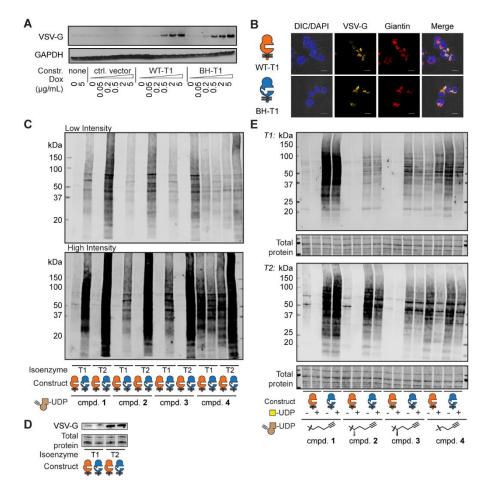


Figure S2. Localization of BH-GalNAc-T1 to the Golgi compartment and glycosylation of proteins, Related to Figure 3.

- (A) WT-T1 and BH-T1 are expressed by stably transfected HepG2 cells in a Dox-inducible fashion.
- (B) Fluorescence microscopy of HepG2 cells stably transfected with T1 constructs, induced with 2 μ g/mL Dox and subsequently stained. Inset: magnification of a single cell. Scale bar, 10 μ m.
- (C) Streptavidin blot from Figure 3C depicted in two different intensities.
- (D) Expression of GalNAc-Ts in lysates used in (C).
- (E) In vitro glycosylation was repeated with a membrane fraction from untransfected HepG2 cells, using soluble GalNAc-Ts to perform glycosylations (Choi et al., 2019). Reactions were performed with or without a two-fold excess of UDP-GalNAc over UDP-sugars 1, 2, 3 and 4.

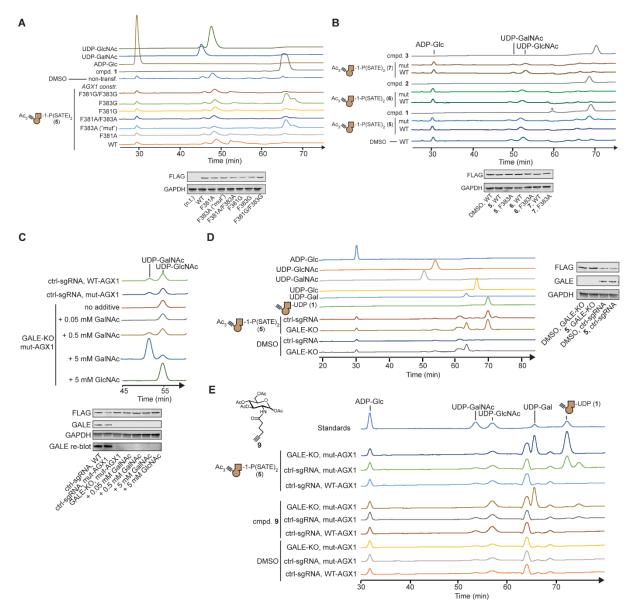


Figure S3. Biosynthesis of UDP-GalNAc analog 1 by mut-AGX1 and epimerization by GALE, Related to Figure 4.

- (A) HPAEC-PAD traces of extracts from HEK293T cells transiently expressing AGX1 constructs, and fed with GalNAc-1-phosphate analog 5 or DMSO. All traces are normalized to the retention time of ADP-Glc as an external standard. Data is of a single experiment.
- (B) Full traces of the data displayed in Fig. 4B. Asterisk indicates an artefact from solvent filling.
- (C) HPAEC-PAD traces of GALE-KO or control sgRNA-transduced K-562 cells stably transfected with the indicated FLAG-tagged AGX1 constructs and fed with different concentrations of GalNAc or GlcNAc. Expression of AGX1 (FLAG) and GALE were analyzed by Western blot. Samples were re-blotted with a higher concentration of GALE antibody to assure absence of GALE in KO cells. Data are from one experiment.
- (D) Cells were fed with DMSO or compound **5**, and UDP-sugar production was measured by HPAEC-PAD. GALE-KO contain elevated levels of UDP-Gal as cells are supplemented with galactose to maintain viability and UDP-Gal cannot be epimerized to UDP-Glc. Expression levels of AGX1 (FLAG) and GALE are analyzed by Western blot. Data are of one representative out of two independent experiments.
- (E) GALE-KO or control sgRNA-transduced
- (F) K-562 cells stably transfected with the indicated AGX1 constructs were fed with the indicated compounds, and UDP-sugar production was measured by HPAEC-PAD. Data are from one experiment.

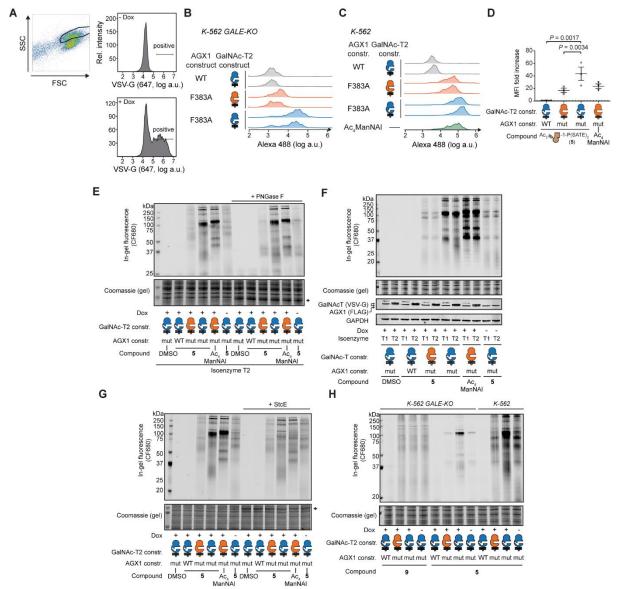


Figure S4. Bioorthogonal, GalNAc-T-selective cell surface labeling, Related to Figure 5.

- (A) Gating scheme for flow cytometry experiments, and in-gel fluorescence experiments.
- (B) Primary flow cytometry data of the experiment in Figure 5C. Two technical replicates are shown.
- (C) Primary flow cytometry data of K-562 cells after induction with 0.5 μg/mL Dox and gating on VSV-G-positive cells. Two technical replicates are shown for cells treated with compound **5**.
- (D) Statistical analysis of the experiment in (C). Data are represented as individual values from three independent experiments, mean ± SEM of MB488 median fluorescence intensity of VSV-G positive cells. Statistical analysis was performed by two-tailed ratio paired t-test.
- (E) Cells expressing AGX1 and GalNAc-T2 constructs were labeled as in Figure 5C and analyzed by in-gel fluorescence. Treatment of lysates with PNGase F significantly shifts certain background bands to lower molecular weight. Arrow indicates PNGase F band in Coomassie stain.
- (F) Full gel of the experiment depicted in Figure 5C. The sialic acid precursor Ac₄ManNAI was used as a positive control, and the effect of omitting Dox was investigated. In-gel fluorescence and Coomassie staining are from one gel and expression analyses are from one separate Western Blot.
- (G) Treatment of lysates prepared as in (A) with the glycoprotease StcE. Arrow indicates StcE band in Coomassie stain.
- (H) Dissecting GlcNAc vs. GalNAc labeling by using probes 5 and 9. K-562 GALE-KO cells expressing AGX1 and GalNAc-T2 constructs were treated with Dox or left untreated, and fed with compounds 5 or 9. Labeling was performed as in Figure 5C. K-562 cells prepared as in (A) were used to compare labeling patterns. Data are from one representative out of three independent experiments.

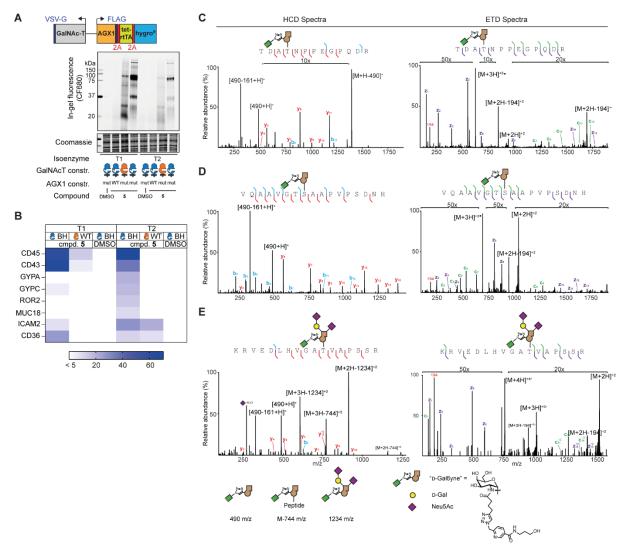


Figure S5. GalNAc-T bump-and-hole pairs selectively label O-glycosylated proteins, Related to Figure 5.

- (A) In-gel fluorescence of cell surface proteins in K-562 cells stably expressing GalNAc-T and AGX1 constructs. Cells and samples were treated as in Figure 5C.
- (B) Mass spectrometry proteomics. Heat map represents log prob of detected proteins after enrichment of cell surface proteins of K-562 cells expressing mut-AGX1 and indicated GalNAc-T constructs and fed with the indicated compounds.
- (C-E) Exemplary mass spectra from glycopeptides after modification by BH-T2. HCD (mainly glycan fragmentation) and ETD (mainly peptide fragmentation) spectra are shown, and ions are annotated. y and b ions in HCD spectra were devoid of glycan.
- (C) Glycosylation at Thr28 of STC2 as a newly-identified T2-specific modification (Luo et al., 2005).
- (D) Confirmation of Ser308 as a T2-specific modification of ApoE.
- (E) Extension of chemically tagged GalNAc by elaborating glycosyltransferases on T39 of SERPIN5A. Legend depicts tentative structural assignments of neutral loss fragments. Loss of 161 m/z in HCD and 194 m/z peak in ETD likely depicts fragment masses of the triazole-based linker.

Methods S1, Related to STAR Methods. Characterization of synthetic compounds.

Bis(S-acetyl-2-thioethyl) 3,4,6-tri-O-acetyl-2-deoxy-2-(5-hexynoyl)amido- α -D-galactopyranosyl phosphate (5)

 1 H NMR (600 MHz, CDCl₃) δ 6.24 (d, J = 9.2 Hz, 1H), 5.75 (dd, J = 5.6, 3.3 Hz, 1H), 5.44 (dd, J = 3.2, 1.4 Hz, 1H), 5.18 (dd, J = 11.5, 3.2 Hz, 1H), 4.81 – 4.60 (m, 1H), 4.40 (td, J = 6.6, 1.4 Hz, 1H), 4.29 – 3.93 (m, 4H), 3.34 – 3.06 (m, 6H), 2.37 – 2.30 (m, 8H), 2.28 – 2.17 (m, 2H), 2.15 (s, 3H), 2.03 (s, 3H), 1.99 (s, 3H), 1.95 (t, J = 2.6 Hz, 1H), 1.88 – 1.76 (m, 2H); 13 C NMR (150 MHz, CDCl₃) δ 195.3, 194.9, 172.8, 170.7, 170.4, 170.2, 97.3, 97.3, 83.4, 69.5, 69.3, 68.8, 67.4, 67.3, 66.9, 66.8, 66.6, 66.5, 66.5, 66.5, 61.5, 47.6, 47.6, 47.5, 47.4, 34.8, 34.7, 30.8, 30.7, 30.6, 29.2, 29.2, 29.2, 24.1, 24.0, 20.8, 20.7, 20.6, 17.8, 17.7; HRMS (ESI) calcd. for C₂₆H₃₈NO₁₄PS₂Na (M+Na⁺) 706.1369 found 706.1349 m/z.

Bis(S-acetyl-2-thioethyl) 3,4,6-tri-O-acetyl-2-deoxy-2-(2-(S)-methyl-5-hexynoyl)amido- α -D-galactopyranosyl phosphate (6)

 ^1H NMR (400 MHz, acetone-D₆) δ 7.36 (d, J = 8.3 Hz, 1H), 5.78 (dd, J = 6.0, 3.4 Hz, 1H), 5.50 (dd, J = 3.2, 1.4 Hz, 1H), 5.17 (dd, J = 11.8, 3.2 Hz, 1H), 4.71 – 4.44 (m, 2H), 4.31 – 4.03 (m, 6H), 3.22 (t, J = 6.5 Hz, 4H), 2.62 – 2.44 (m, 1H), 2.44 – 2.28 (m, 7H), 2.19 – 2.11 (m, 5H), 2.01 (s, 3H), 1.94 (s, 3H), 1.90 – 1.75 (m, 1H), 1.61 – 1.49 (m, 1H), 1.12 (d, J = 6.9, 1.6 Hz, 3H); ^{13}C NMR (100 MHz, acetone-D₆) δ 195.2, 177.5, 176.5, 170.7, 170.6, 170.4, 97.6, 84.3, 70.2, 69.4, 67.9, 67.7, 66.9, 62.4, 48.1, 40.3, 33.8, 20.7, 20.6, 18.0, 16.8; HRMS (ESI) calcd. for $C_{27}H_{40}NO_{14}PS_2Na$ (M+Na+) 720.1526 found 720.1523 $\emph{m/z}$.

Bis(S-acetyl-2-thioethyl) 3,4,6-tri-O-acetyl-2-deoxy-2-(2-(R)-methyl-5-hexynoyl)amido- α -D-galactopyranosyl phosphate (7)

 1 H NMR (600 MHz, acetone-D₆) δ 7.35 (d, J = 8.2 Hz, 1H), 5.81 (m, 1H), 5.50 (s, 1H), 5.18 (m, 1H), 4.59 – 4.43 (m, 2H), 4.33 – 4.01 (m, 6H), 3.31 – 3.07 (m, 4H), 2.55 – 2.45 (m, 1H), 2.40 – 2.30 (m, 7H), 2.25 – 2.12 (m, 5H), 2.01 (s, 3H), 1.97 – 1.85 (m, 4H), 1.57 – 1.48 (m, 1H), 1.09 (d, J = 7.0 Hz, 3H); 13 C NMR (150 MHz, acetone-D₆) δ 195.2, 176.6, 170.4, 97.6, 97.6, 84.7, 70.1, 69.5, 68.0, 67.8, 67.1, 66.9, 62.4, 48.3, 40.4, 33.4, 30.6, 30.6, 20.3, 20.6, 18.3, 16.9; HRMS (ESI) calcd. for C_{27} H₄₀NO₁₄PS₂Na (M+Na⁺) 720.1526 found 720.1515 m/z.

3-Hydroxypropyl (6-azidomethyl)nicotinate (SI-7)

 R_f (CH₂CI₂/MeOH 20:1) = 0.3. ¹H NMR (400 MHz, CDCI₃) δ 9.28 (d, J = 2.3 Hz, 1H), 8.49 (dd, J = 8.1, 2.3 Hz, 1H), 7.77 (d, J = 8.1 Hz, 1H), 7.44 (br s, 1H), 4.88 (s, 2H), 4.13 (t, J = 5.5 Hz, 2H), 3.99 (q, J = 5.9 Hz, 2H), 2.70 (br s, 1H), 2.25 – 2.11 (m, 2H); ¹³C NMR (100 MHz, CDCI₃) δ 165.9, 158.8, 147.9, 136.4, 129.4, 121.8, 60.8, 55.4, 38.2, 31.7. HRMS (ESI) calcd. for $C_{10}H_{13}N_5O_2Na$ (M+Na⁺) 258.0966 found 258.0968 m/z.

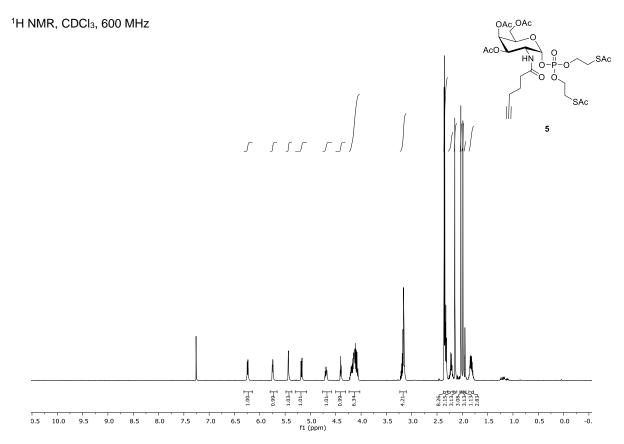
1,3,4,6-Tri-O-acetyl-2-deoxy-2-(5-hexynoyl)amido-αβ-D-glucopyranoside (9)

 ^{1}H NMR (400 MHz, CDCl₃) δ 5.88 (d, J = 10.2 Hz, 1H), 5.69 (d, J = 8.7 Hz, 1H), 5.30 – 5.01 (m, 2H), 4.43 – 4.20 (m, 2H), 4.11 (dd, J = 12.5, 2.2 Hz, 1H), 3.83 (ddd, J = 9.9, 4.7, 2.2 Hz, 1H), 2.32 – 2.15 (m, 4H), 2.10 (s, 3H), 2.07 (s, 3H), 2.03 (d, J = 1.5 Hz, 6H), 1.95 (t, J = 2.6 Hz, 1H), 1.77 (p, J = 7.0 Hz, 2H). ^{13}C NMR (100 MHz, CDCl₃) δ 172.4, 171.3, 170.8, 169.6, 169.5, 92.6, 83.2, 72.9, 72.6, 69.6, 68.1, 61.8, 52.8, 34.9, 24.0, 21.0, 20.8, 20.8, 20.7, 17.6. HRMS (ESI) calcd. for C₂₀H₂₇NO₁₀Na (M+Na+) 464.1532 found 464.1513 $\emph{m/z}$.

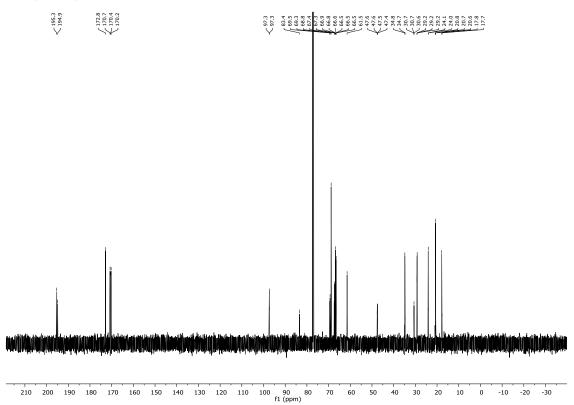
Biotin-PEG₄-dialkoxydiphenylsilane-picolyl azide (10)

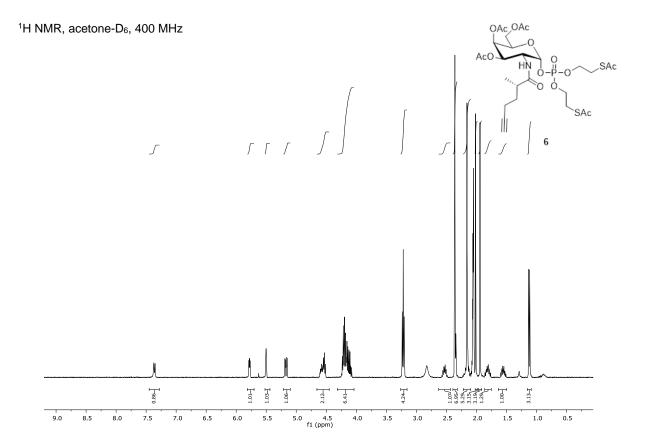
Rf (CH₂Cl₂/MeOH 10:1 with 1% NEt₃) = 0.55. 1 H NMR (600 MHz, CDCl₃) δ 8.93 (d, J = 2.2 Hz, 1H), 8.05 (dd, J = 8.1, 2.3 Hz, 1H), 7.66 – 7.59 (m, 4H), 7.44 – 7.40 (m, 2H), 7.39 – 7.33 (m, 4H), 7.28 (d, J = 7.5 Hz, 1H), 7.24 – 7.20 (m, 1H), 6.68 (s, 1H), 6.58 (s, 1H), 5.55 (s, 1H), 4.68 (s, 1H), 4.52 (s, 2H), 4.49 – 4.43 (m, 1H), 4.32 – 4.25 (m, 1H), 3.90 (t, J = 5.8 Hz, 2H), 3.70 (t, J = 6.1 Hz, 2H), 3.61 – 3.52 (m, 16H), 3.43 – 3.38 (m, 2H), 3.36 (d, J = 6.1 Hz, 2H), 3.13 (td, J = 7.3, 4.5 Hz, 1H), 2.90 (dd, J = 12.8, 5.0 Hz, 1H), 2.69 (d, J = 12.7 Hz, 1H), 2.43 (t, J = 6.0 Hz, 2H), 2.20 (td, J = 7.3, 3.1 Hz, 2H), 1.99 – 1.90 (m, 2H), 1.78 – 1.67 (m, 4H), 1.49 – 1.41 (m, 2H), 1.25 (s, 6H). HRMS (ESI) calcd. for $C_{47}H_{67}N_9O_{10}SSiNa$ (M+Na $^+$) 1000.4399 found 1000.4363 m/z.

NMR Spectra

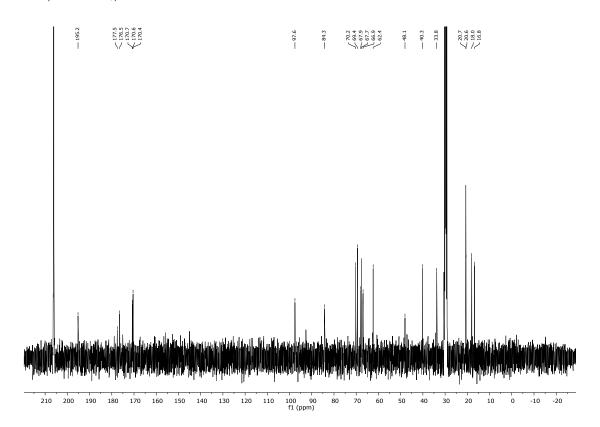


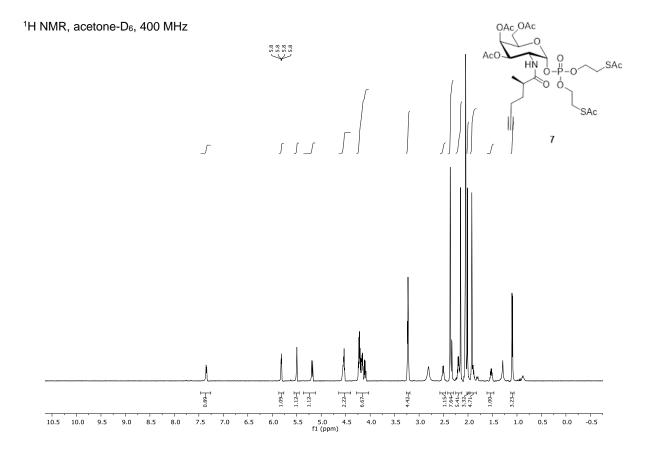


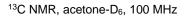


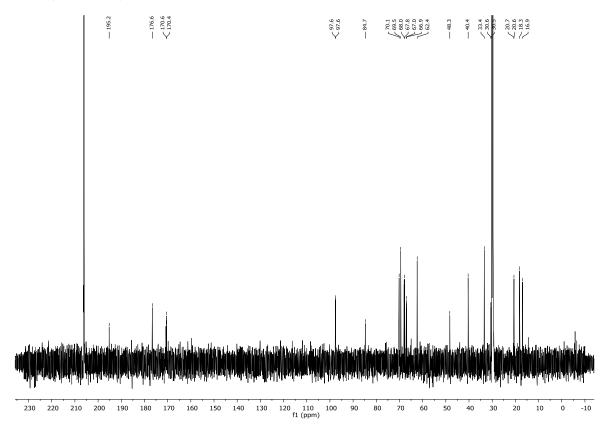


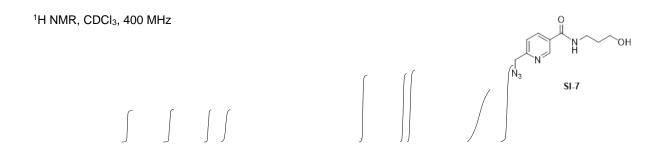
 ^{13}C NMR, acetone-D₆, 100 MHz

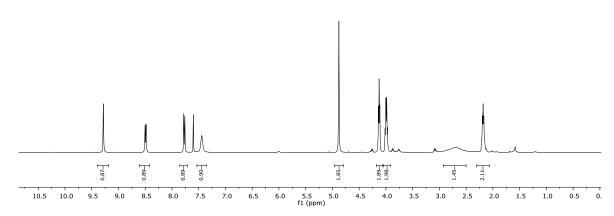












¹H NMR, CDCl₃, 100 MHz

