

Modulating Heparanase Activity: Tuning Sulfation Pattern and Glycosidic Linkage of Oligosaccharides

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1. General Information

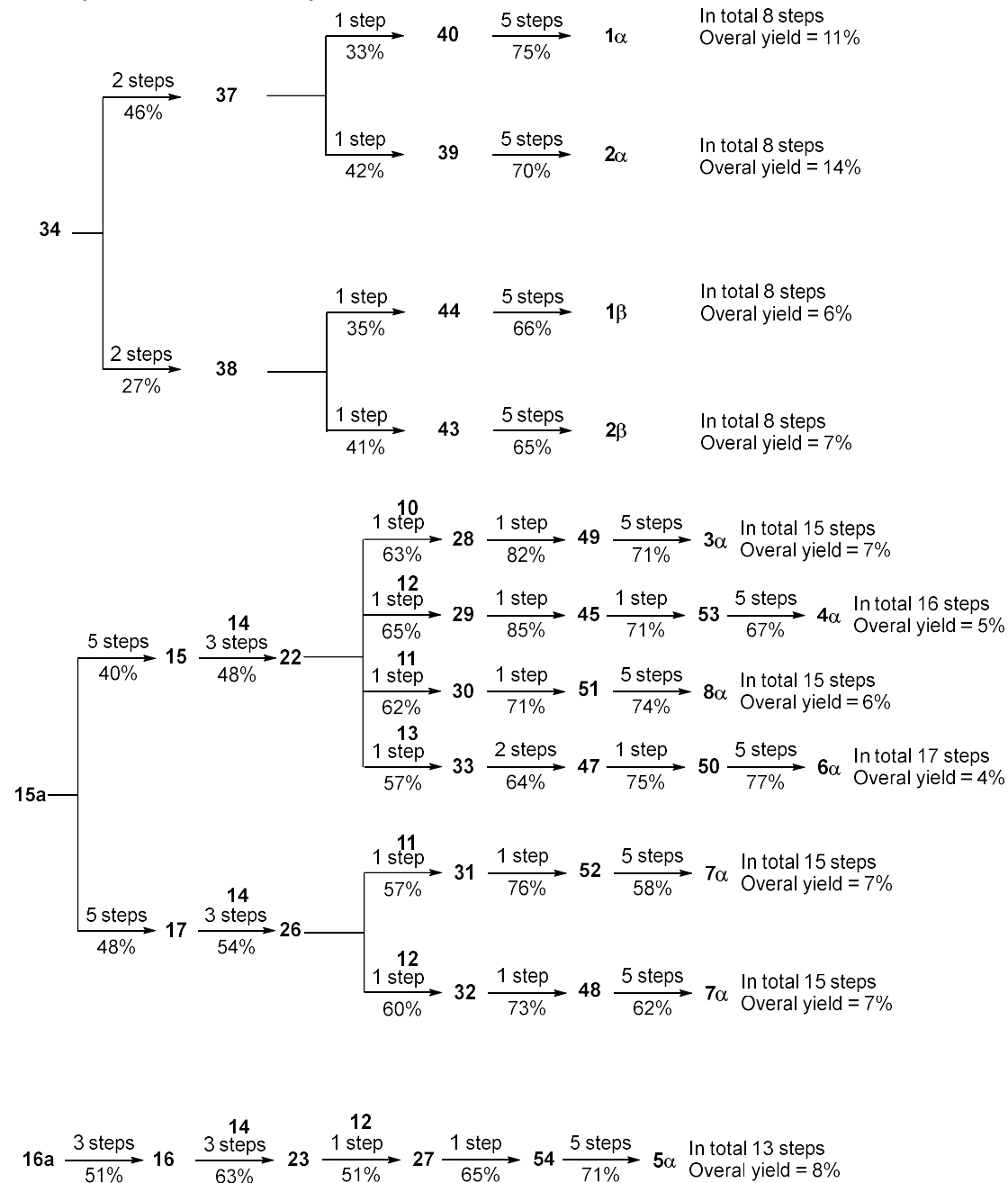
Methods and Reagents. All reactions were performed in oven-dried flasks fitted with septa under a positive pressure of nitrogen atmosphere. Organic solutions were concentrated using a Buchi rotary evaporator below 40 °C at 25 torr. Analytical thin-layer chromatography was routinely utilized to monitor the progress of the reactions and performed using pre-coated glass plates with 230-400 mesh silica gel impregnated with a fluorescent indicator (250 nm). Visualization was then achieved using UV light, iodine, or ceric ammonium molybdate. Flash column chromatography was performed using 40-63 μm silica gel (SiliaFlash F60 from Silicycle). Dry solvents were obtained from a SG Waters solvent system utilizing activated alumina columns under an argon pressure. All other commercial reagents were used as received from Sigma Aldrich, Alfa Aesar, Acros Organics, TCI, and Combi-Blocks, unless otherwise noted.

Instrumentation. All new compounds were characterized by Nuclear Magnetic Resonance (NMR) spectroscopy and High-Resolution Mass spectrometry (HRMS). All ^1H NMR spectra were recorded on either Agilent 400 or 600 MHz spectrometers. All ^{13}C NMR spectra were recorded on either Agilent 100 or 150 MHz spectrometer. Chemical shifts are expressed in parts per million (δ scale) referenced to the residual proton in the NMR solvent (CDCl_3 : δ 7.26 ppm, δ 77.16 ppm). Data are presented as follows: chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, m = multiplet, and bs = broad singlet), integration, and coupling constant in hertz (Hz).

High resolution mass spectra (HRMS) were recorded using a Micromass LCT Premier XE instrument (Waters) and were determined by electrospray ionization (ESI).

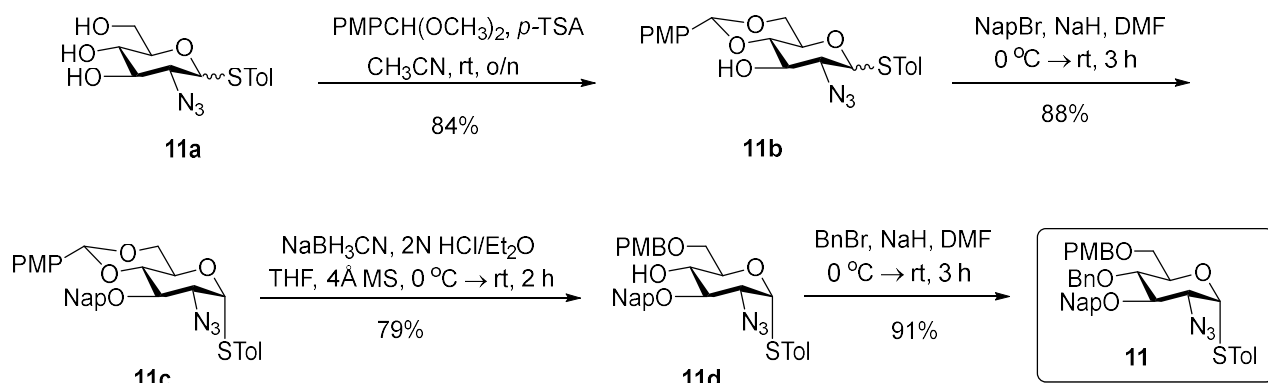
2. Modular Synthetic Scheme of Trisaccharides and Monosaccharide Building Blocks

2.1. Synthetic summary

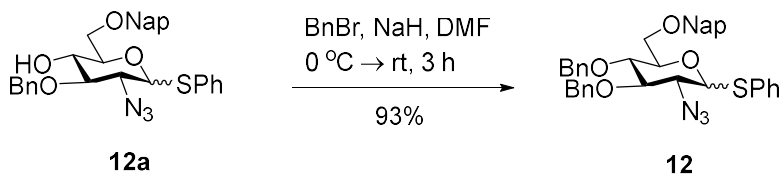


2.2. General Synthetic Schemes for Monosaccharide Building Blocks Preparation

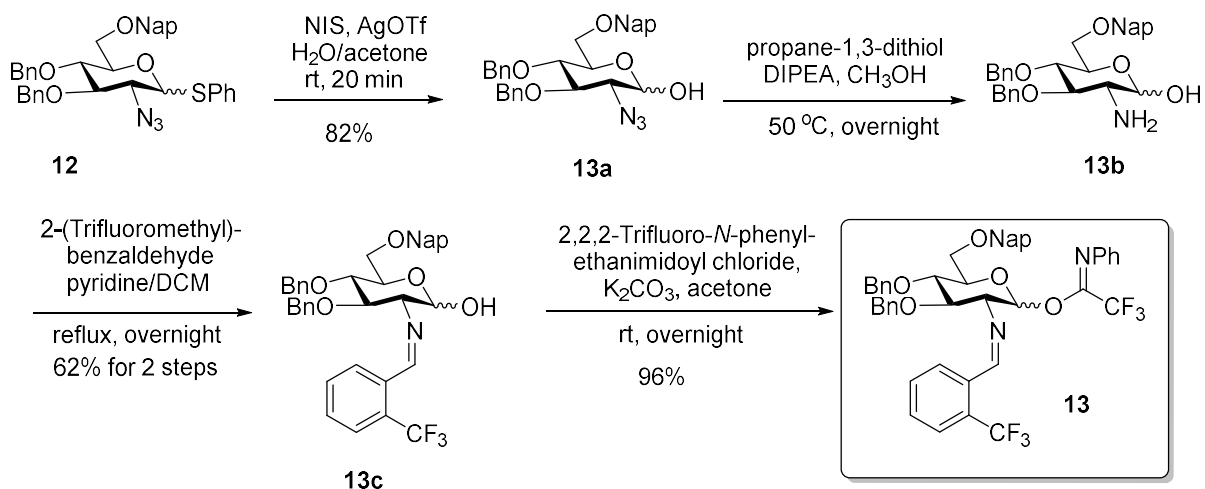
p-Tolyl 2-azido-2-deoxy-3-*O*-(2-naphthylmethyl)-4-*O*-benzyl-6-*O*-(*p*-methoxybenzyl)-1-thio- α -D-glucopyranoside (11):



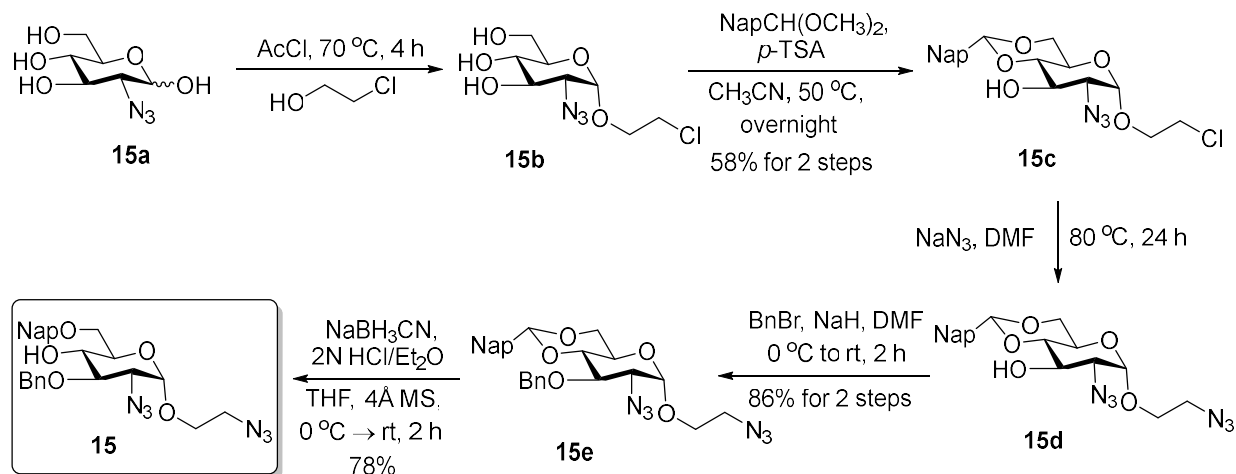
Phenyl 2-azido-2-deoxy-3,4-di-*O*-benzyl-6-*O*-(2-naphthylmethyl)-1-thio-D-glucopyranoside (12):



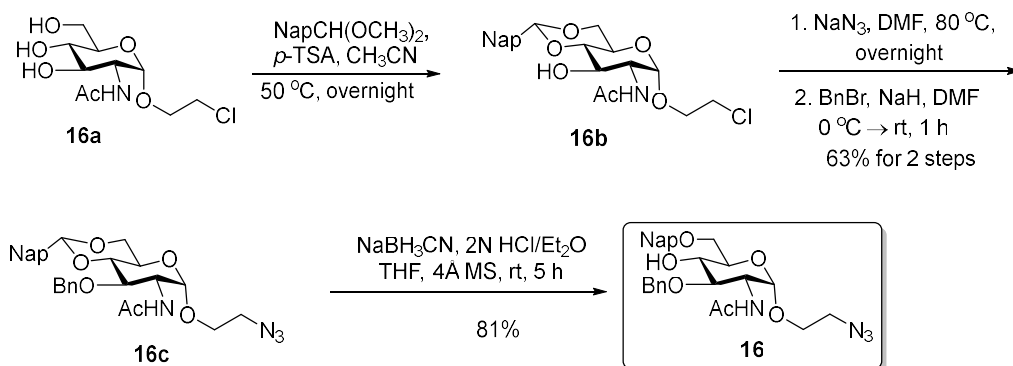
2-*N*-[(2-trifluoromethyl)benzylidene]-2-deoxy-3,4-di-*O*-benzyl-6-*O*-(2-naphthylmethyl)-D-glucopyranosyl *N*-phenyl-trifluoroacetimidate (13):



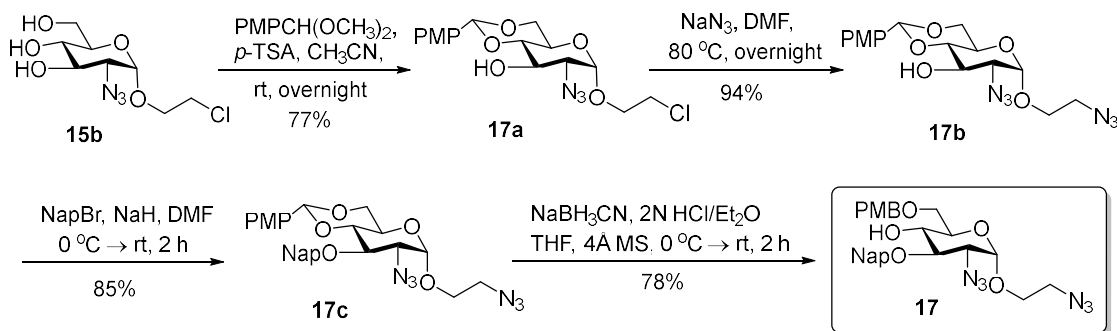
2-Azidoethyl 2-azido-2-deoxy-3-*O*-benzyl-6-*O*-(2-naphthylmethyl)- α -D-glucopyranoside (15):



2-Azidoethyl 2-acetamido-2-deoxy-3-*O*-benzyl-6-*O*-(2-naphthylmethyl)- α -D-glucopyranoside (16):

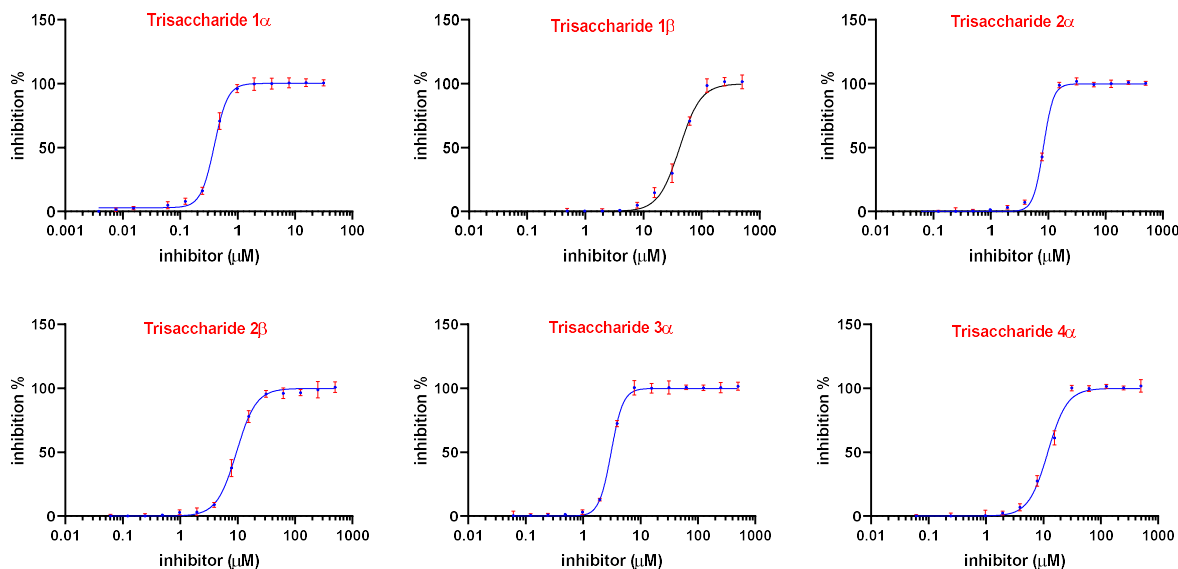


2-Azidoethyl 2-azido-2-deoxy-3-*O*-(2-naphthylmethyl)-6-*O*-(*p*-methoxybenzyl)- α -D-glucopyranoside (17):



3. TR-FRET Heparanase Inhibition Assay¹

42 μL of HS trisaccharide solution in Milli-Q water (0.0038-500 μM) or just Milli-Q water (as a control), and 42 μL of heparanase (5.3 nM, R&D Systems) solution in pH 7.5 triz buffer (consisting of 20 mM TrisHCl, 0.15 M NaCl and 0.1% CHAPS) or just buffer as blank were added into microtubes and pre-incubated at 37 $^{\circ}\text{C}$ for 10 min bringing the [heparanase] to 0.5 nM. Next, 84 μL of biotin-heparan sulfate-Eu cryptate (Cisbio, Cat #: 61BHSKAA) (58.6 ng in pH 5.5 0.2 M NaOAc buffer) was added to the microtubes, and the resulting mixture was incubated for 60 min at 37 $^{\circ}\text{C}$. The reaction mixture was stopped by adding 168 μL of Streptavidin-XLent! (Cisbio, Cat #: 611SAXLA) (1.0 $\mu\text{g}/\text{ml}$) solution in pH 7.5 dilution buffer made of 0.1 M NaH_2PO_4 , 0.8 M KF, 0.1% BSA. After the mixture had been stirring at room temperature for 15 min, 100 μL (per well) of the reaction mixture was transferred to a 96 well microplate (Corning #3693 96 well, white polystyrene, half-area) in triplicates and HTRF emissions at 616 nm and 665 nm were measured by exciting at 340 nm using a SpectraMax iD5 Microplate Reader (Molecular Devices).



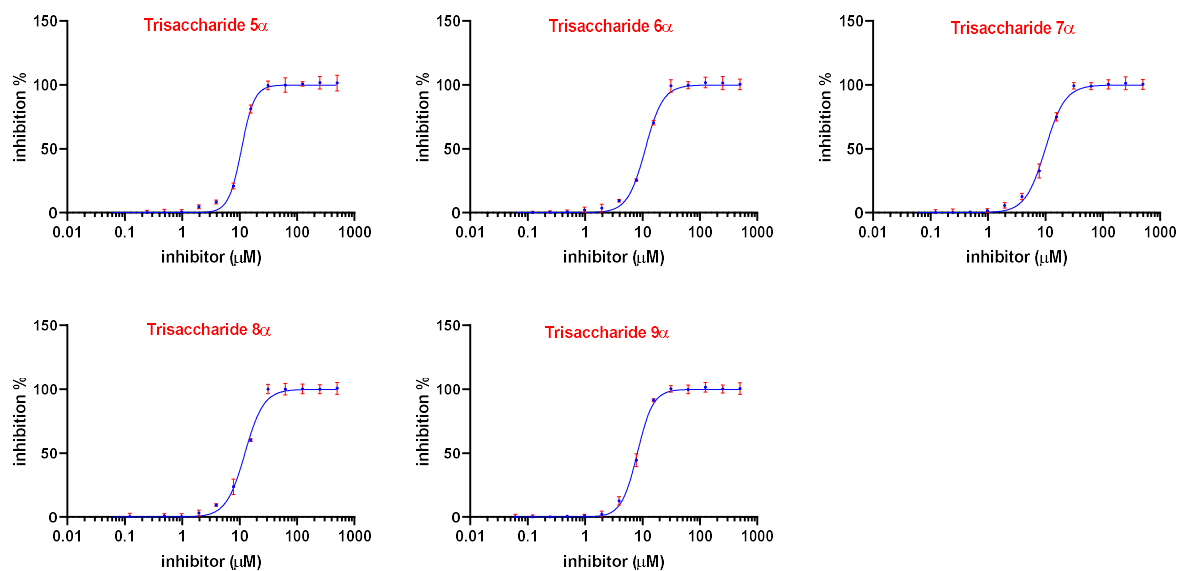


Figure S1. Inhibition of heparanase by different trisaccharide ligands.

4. Trisaccharides Hydrolysis Assay²

Micro centrifuge tubes were pretreated for 2h at 37 °C by using a solution of phosphate buffered saline comprising of 0.05% Tween 20 (PBST) and 4% bovine serum albumin. Tubes were then washed three times with PBST, dried, stored at 4 °C, and used for assay within a week. A 100 μ M solution of fondaparinux or trisaccharide with heparanase enzyme (3 nM) in pH 5.0 sodium acetate buffer (40 mM) were incubated at 37 °C in a microtube. The enzymatic reaction was stopped at different time points by adding equal volumes of reaction mixture and freshly made 1.69 mM WST-1 (Toronto Research Chemicals) in 0.1 M NaOH into a new microtube and developed at 60 °C for 60 min. A 200 μ l (per well) solution of developed reaction solution was transferred to a clear 96-well microplate in triplicates and absorbance was measured at 584 nm with a SpectraMax iD5 Microplate Reader (Molecular Devices). For the controls, exactly the same procedure was followed for a 100 μ M solution of trisaccharides without heparanase enzyme to rationalize non-enzymatic autohydrolysis.

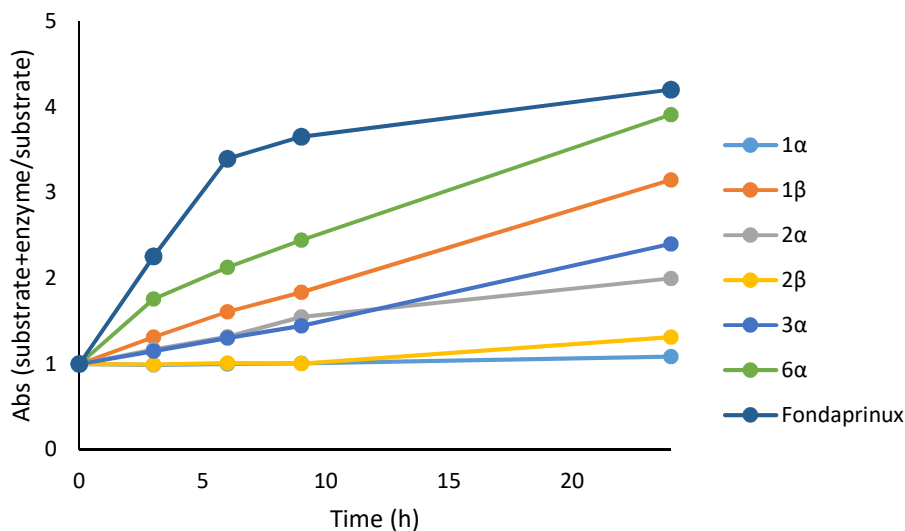


Figure S2. Hydrolytic potential of **1α**, **1β**, **2α**, **2β**, **3α** or **6α** with heparanase over time compared to fondaprinux.

5. Two-Stage Chromogenic Assay to Evaluate Anticoagulant Activity²

BIOPHEN Heparin AntiXa (2 stages) USP/EP (Cat #: A221005-USP) kits from Aniara and BIOPHEN Heparin Anti-IIa (2 stages) USP/EP (Cat #: A220005-USP) were utilized to assess FXa and FIIa activity, respectively.

Factor Xa activity:

All the reagents were reconstituted and prepared according to the manufacturer's instructions and incubated at 37 °C for 15 min. Different concentrations of heparin (0.002-500 nM; 40 μL) or trisaccharide **1α** (3.9-4000 nM; 40 μL) and ATIII (0.04 IU; 40 μL) were added to a deep-well block (Nunc 96 DeepWell 1.0 mL/well, clear), mixed, and incubated at 37 °C for 2 min. To the reaction mixture, FXa (0.32 μg; 40 μL) was added by multichannel pipette and was incubated at 37 °C for another 2 min (stage 1), then FXa specific chromogenic substrate (0.048 mmol; 40 μL) was added. The reaction was stopped by adding citric acid (240 μL; 20 g/L) exactly after 2 min. A 100 μL solution was then transferred to a clear 96-well microplate in triplicate, and absorbance at 405 nm was measured with a SpectraMax iD5 Microplate Reader (Molecular Devices). The sample blank was measured by mixing the reagents in reverse order from that of the test, i.e. citric

acid, FXa substrate, FXa, ATIII, and sample. The sample blank value was deducted from the absorbance measured for the corresponding assay.

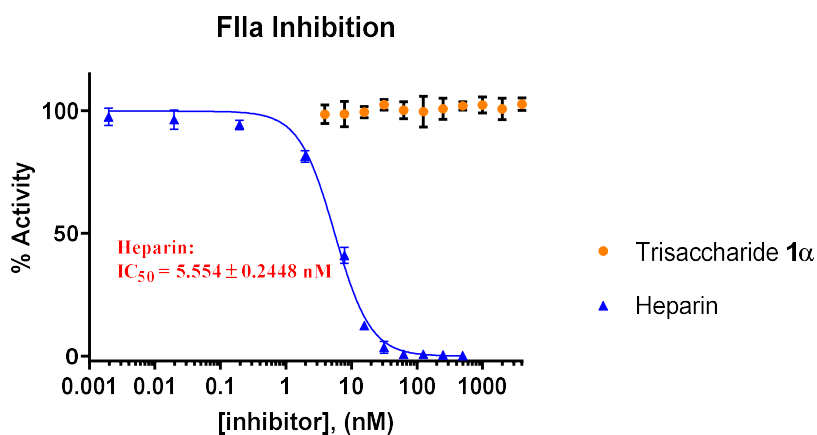


Figure S3. Inhibition of FXa by trisaccharide **1α** in comparison to heparin.

Factor IIa activity

All the reagents were reconstituted and prepared according to the manufacturer's instructions and incubated at 37 °C for 15 min. Different concentrations of heparin (0.002-500 nM; 40 μL) or trisaccharide **1α** (3.9-4000 nM; 40 μL) and ATIII (0.01 IU; 40 μL) were added to a deep-well block (Nunc 96 DeepWell 1.0 mL/well, clear), mixed, and incubated at 37 °C for 2 min. To the reaction mixture, FIIa (1.2 nkat; 40 μL) was added by multichannel pipette and was incubated at 37 °C for another 2 min (stage 1), then FIIa specific chromogenic substrate (0.048 mmol; 40 μL) was added. The reaction was stopped by adding citric acid (240 μL; 20 g/L) exactly after 2min. 100 μL was transferred to a 96-well microplate in triplicate, and absorbance at 405 nm was measured with SpectraMax iD5 Microplate Reader (Molecular Devices). The sample blank was measured by mixing the reagents in reverse order from that of the test, i.e. citric acid, FXa substrate, FXa, ATIII, and sample. The sample blank value was deducted from the absorbance measured for the corresponding assay.

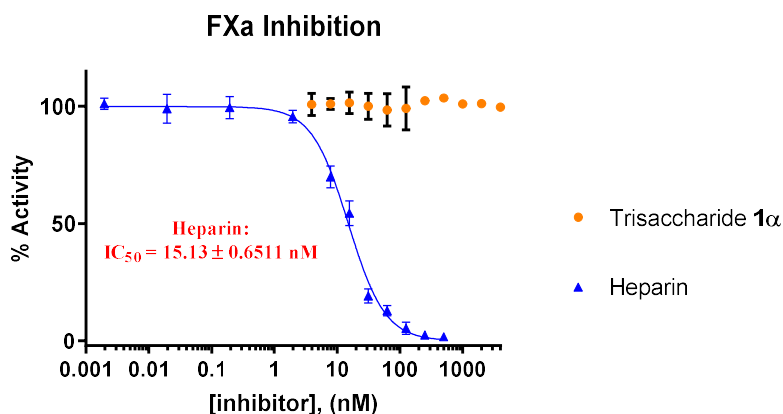
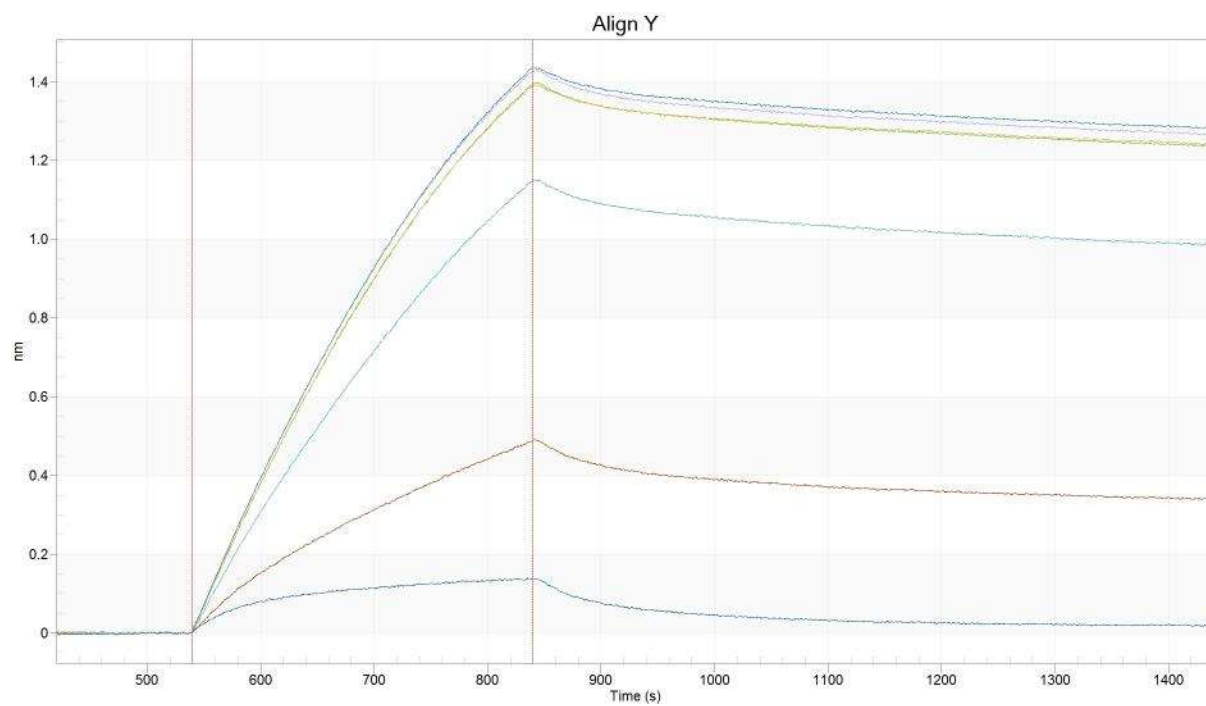
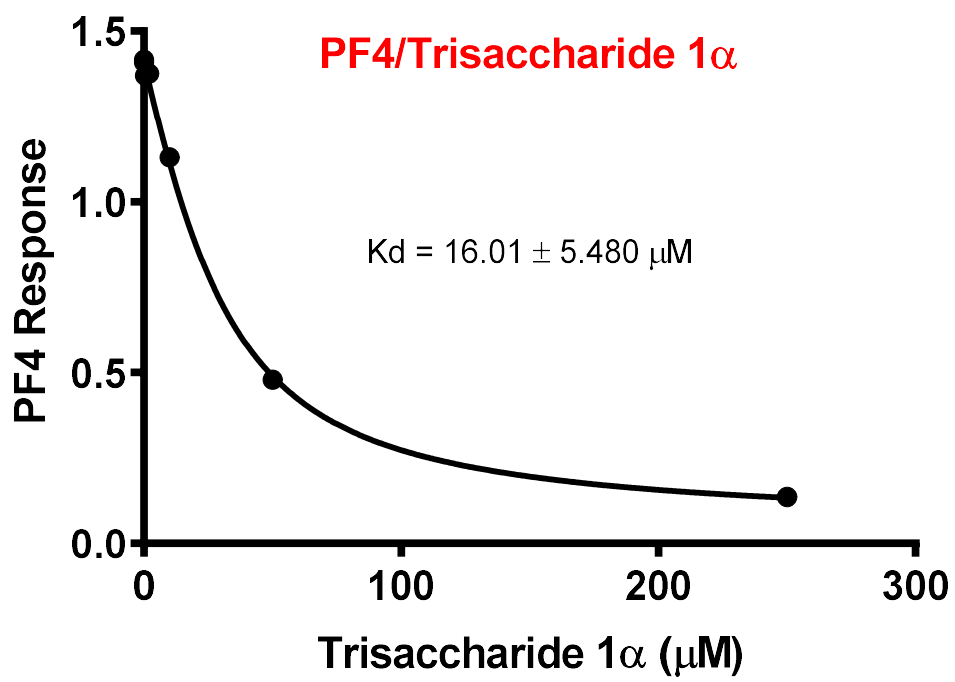


Figure S4. Inhibition of FIIa by trisaccharide **1α** in comparison to heparin.

6. Platelet Factor 4 Binding Test by Biolayer Interferometry (BLI) Assay¹

BLI assays were performed on an Octet Red Instrument (fortéBIO) at 25 °C. Immobilization and binding analysis were carried out at 1000 rpm using HBS-EP buffer [10 mM HEPES, pH 7.4, 150 mM NaCl, 3.0 mM EDTA, and 0.005% (v/v) surfactant tween20]. A solution affinity assay, used to determine affinities of ligands by SPR analysis was adopted to BLI.³ In this method PF 4 (100 nM; 100 μL) was mixed with various concentrations of trisaccharide **1α** (0.08-250 μM; 100 μL) or heparin (0.4-400 nM; 100 μL). Free protein in this equilibrium mixture is tested for binding against immobilized heparin (all proteins are carrier-free and purchased from R&D Systems). Heparin-biotin (Creative PEGworks, 18 kDa, 1 biotin per HP polymer), 5 μg /mL was immobilized on to streptavidin biosensors (fortéBio) for 5 min. Binding experiments were carried under conditions of mass transport. Binding was fitted to equation 1 of ref 10 using Graphpad Prism. BLI response was used in place of F and ligand (heparin / trisaccharide **1α**) concentration was used in place of [metal].



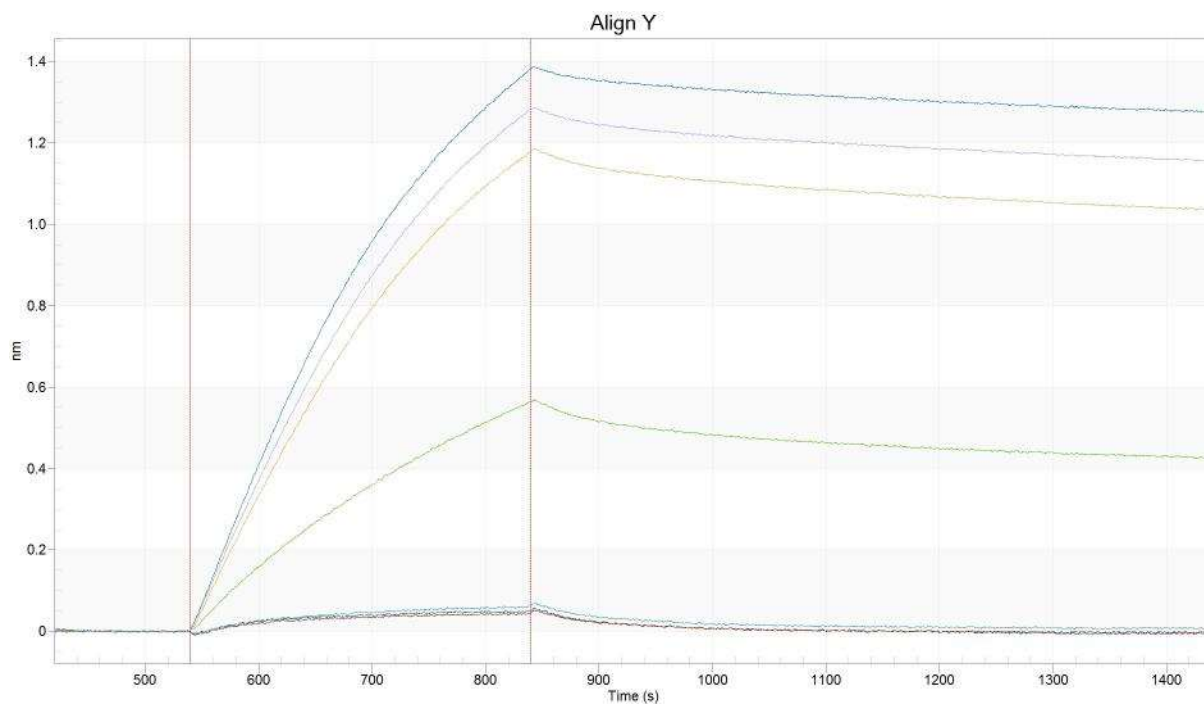
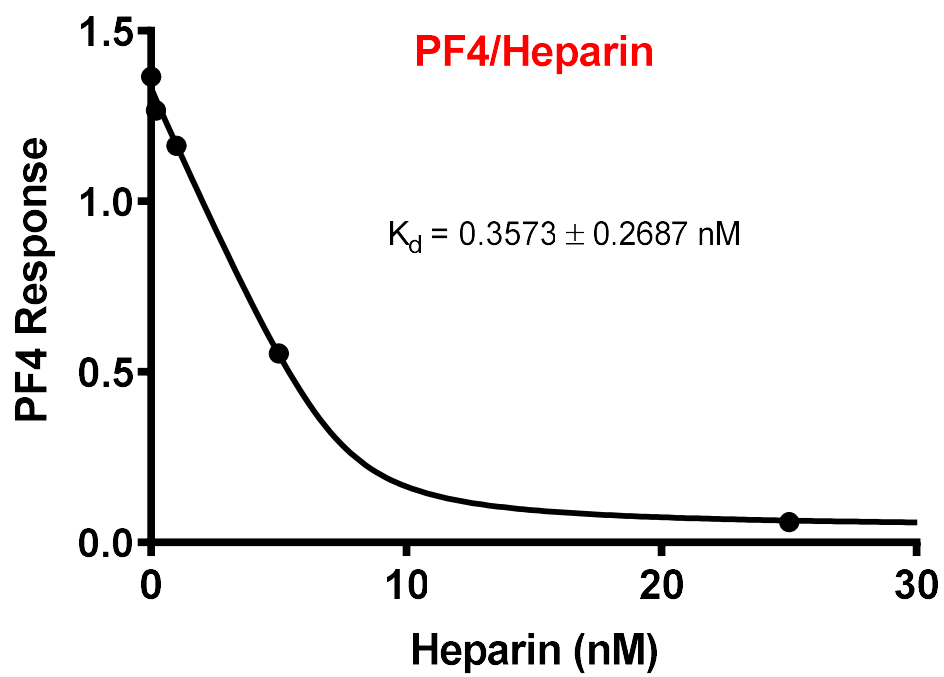


Figure S5. BLI assay to test binding affinity of PF4 and trisaccharide **1a** / heparin.

7. Inhibition of ECM Degradation Assay

Briefly, sulfate [³⁵S] labeled ECM coating the surface of 35 mm tissue culture dishes,¹² is incubated (5 h, 37°C, pH 6.0, 1 ml final volume) with recombinant human heparanase (0.5 ng/ml) in the absence and presence of trisaccharide **1α**. The reaction mixture contains: 50 mM NaCl, 1 mM DTT, 1 mM CaCl₂, and 10 mM buffer Phosphate-Citrate, pH 6.0. To evaluate the occurrence of proteoglycan degradation, the incubation medium is collected and applied for gel filtration on Sepharose 6B columns (0.9 x 30 cm). Fractions (0.2 ml) are eluted with PBS and counted for radioactivity. The excluded volume (V₀) is marked by blue dextran and the total included volume (V_t) by phenol red. Degradation fragments of HS side chains, characterized as described,¹³ are eluted from Sepharose 6B at 0.5 < Kav < 0.8 (fractions 20-35). Results are best represented by the actual gel filtration pattern.¹⁴⁻¹⁶ Each experiment was performed at least three times and the variation of elution positions (Kav values) did not exceed ±15%.

8. Inhibition of Heparanase in Pancreatic β Cells

Culture of mouse pancreatic β cell line MIN6 and detection of cellular mitochondrial ROS using mitochondrial ROS trackers. Mouse pancreatic β cell line (insulinoma) MIN6 was cultured as we previously described.¹⁷ Specifically, MIN6 cells were cultured with high-glucose DMEM supplemented with 10% fetal bovine serum (FBS), 50μM β-mercaptoethanol, and antibiotics. Before experiments, MIN6 cells were seeded in 4-well slide-chambers for immunofluorescence analyses. When the cells reached approximately 50% confluency, they were cultured in the conditioned medium from heparanase-producing CHO cells or control CHO cells. Heparanase-producing CHO cells were provided by Dr. Israel Vlodaysky (Technion, Israel). Meanwhile, the cells were treated with vehicle (PBS) or the trisaccharide **1α** inhibitor for 24 h. The cells were then stained with mitochondrial ROS tracker probe using the concentration of 100 nM according to the manufacturer's instruction (Molecular Probes, Invitrogen). Mitochondrial ROS in the MIN6 cells were visualized by fluorescence microscopy, and the extents and intensities of fluorescent activities, which reflect intracellular mitochondrial ROS, were quantified using ImageJ software.

Quantitative real-time PCR (qPCR) - Total RNA from Min-6 cells was extracted using Trizol by following manufacture's instruction and complementary DNA was synthesized from 500 ng of total RNA to with High Capacity cDNA Reverse Transcription Kit (AB applied biosystems). The

abundance of mRNA was measured by q PCR analysis using the SYBR Green PCR Master mix (Applied Biosystems).

The sequences of the primers for SOD1: 5'-GCGGTGAACCAGTTGTGTTGTC-3' and 5'-CAGTCACATTGCCAGGTCTCC-3'; and for ERO1 α : 5'-ATGGACTIONGTGTTGGCTGCTT-3' and 5'-GCTTTCCGGCATATTTGCGA-3'.

9. Computational study

All molecular docking and MD simulations were conducted with the YASARA Structure software package (www.yasara.org). Detail procedures for the computation study were reported in previous article.⁵

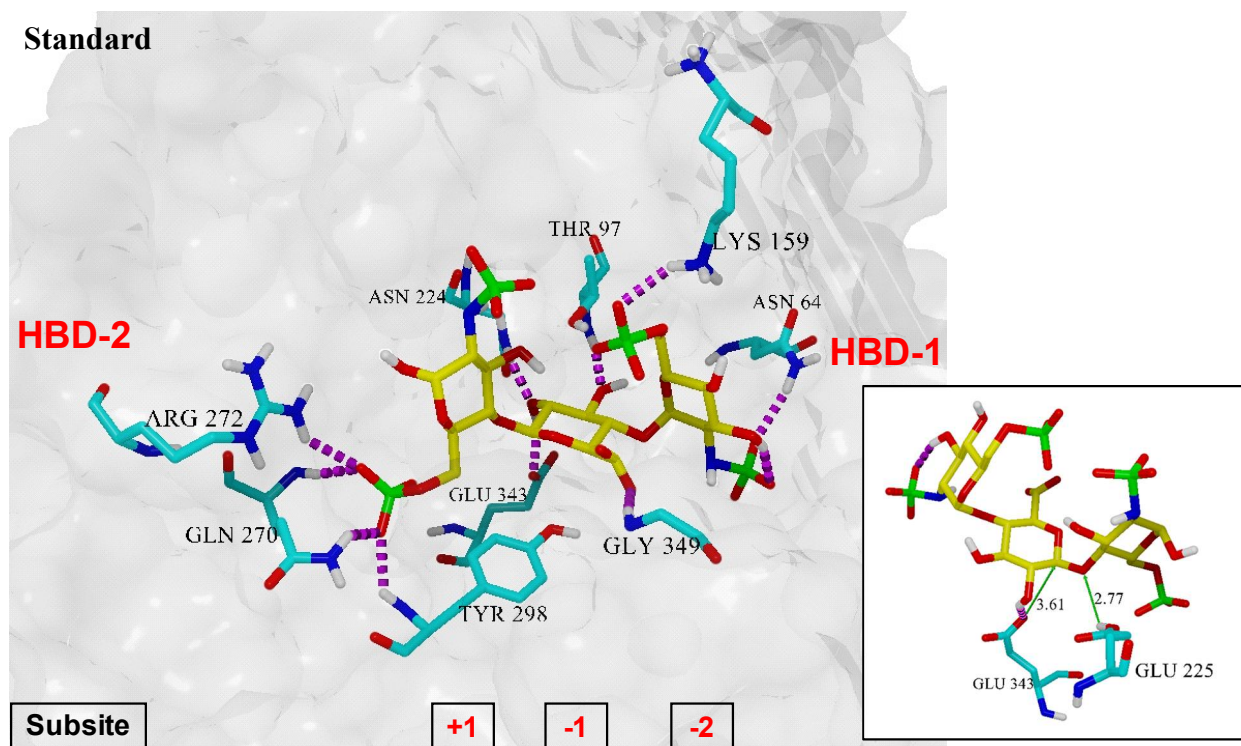
9.1. Computational Docking

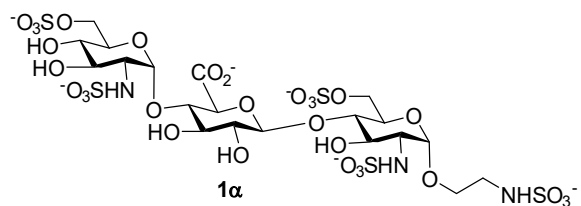
In the docking study, the enzyme structure was inherited from previously modified *apo* heparanase structure (PDB code: 5E8M).^{5,6} The ligand saccharide backbone was obtained from Glycam GAGs builders (www.glycam.com), then the sulfation patterns and aliphatic portion was modified on GaussView 5.0.⁷ The modified ligand pdb files were then subjected to energy minimization in YASARA, and saved in .job format. Each ligand was docked separately into heparanase within the simulation cell (80 x 61 x 76 Å) using Autodock VINA⁸ default parameters. The ligand and enzyme were subjected to 100 docking runs, where AMBER14 force field⁹ was applied to the protein, and GLYCAM06¹⁰ and GAFF/Am1BCC force field was applied to each ligand. During docking study, the ligands and receptor binding pocket residues were kept flexible. The most populated clusters of the docking runs was subjected to MD simulation.

9.2. Docking Results for HS Trisaccharides

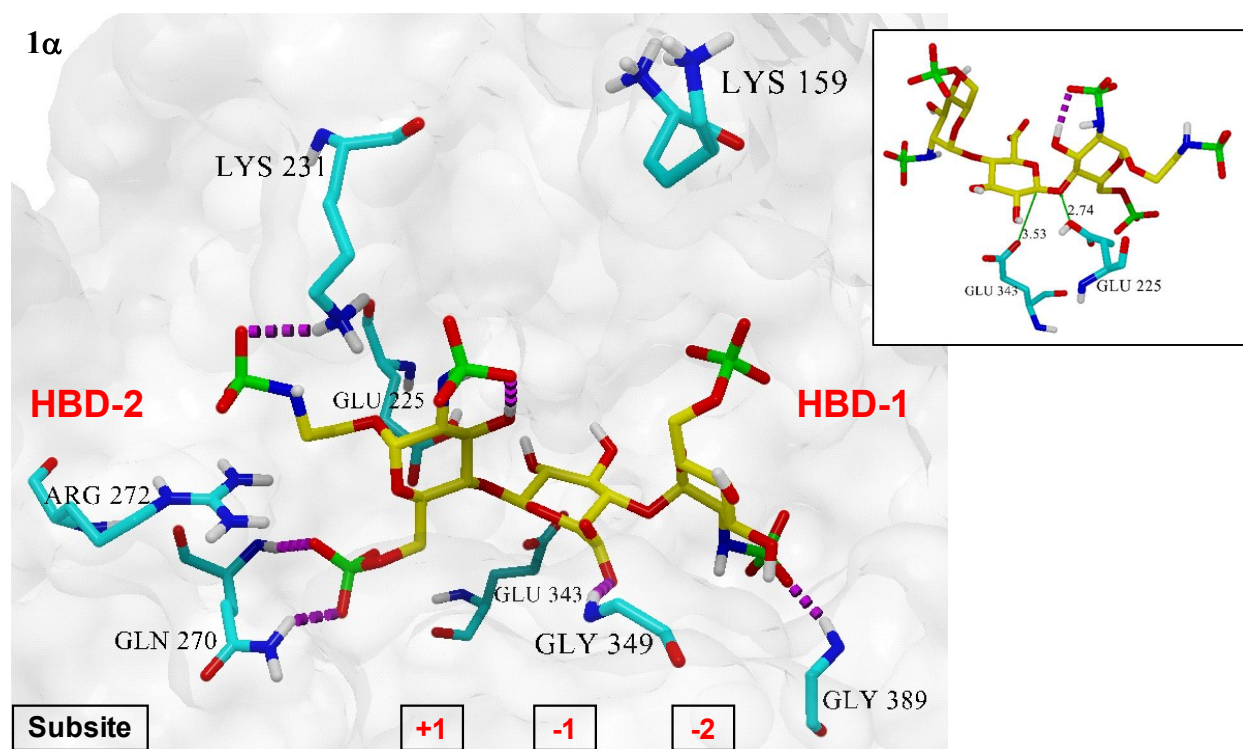
Figure S6: Snapshots of the first cluster when ligands docked into human heparanase and the distance between the catalytic residues and the scissile bond

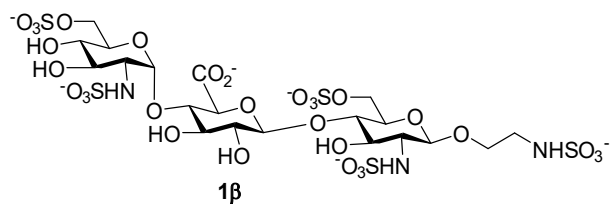
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003	002	000008.8185+-000000.0695	00000000343552.2965



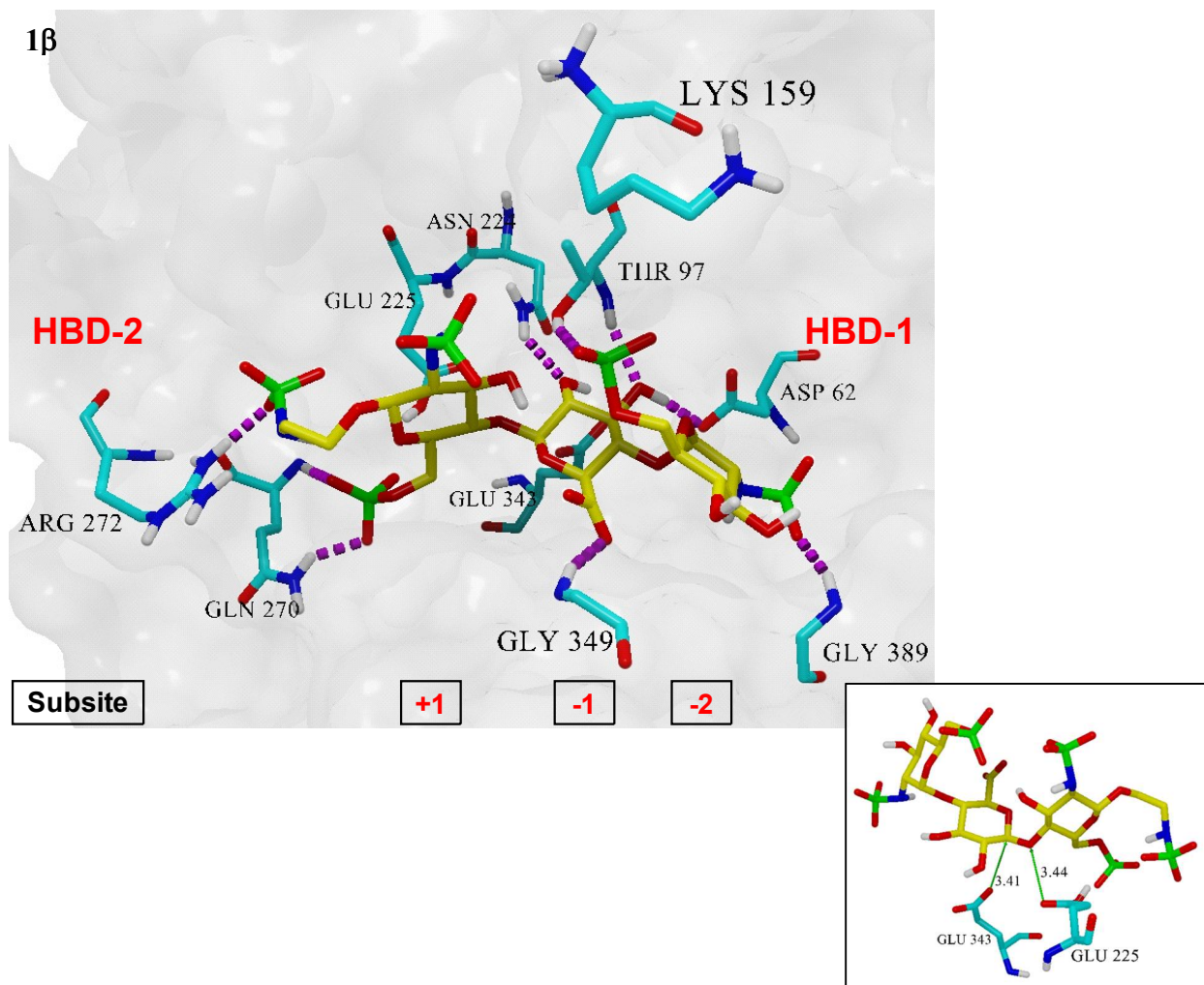


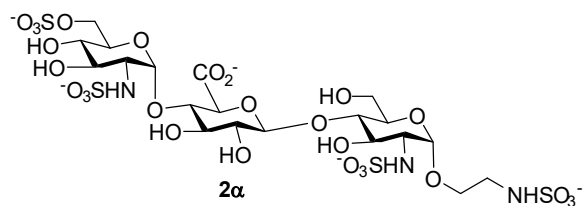
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003	001	000009.3710+-000000.0000	00000000135209.3990
004	004	000008.6332+-000000.3046	00000000469658.2439
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006	001	000007.6410+-000000.0000	00000002506723.6529





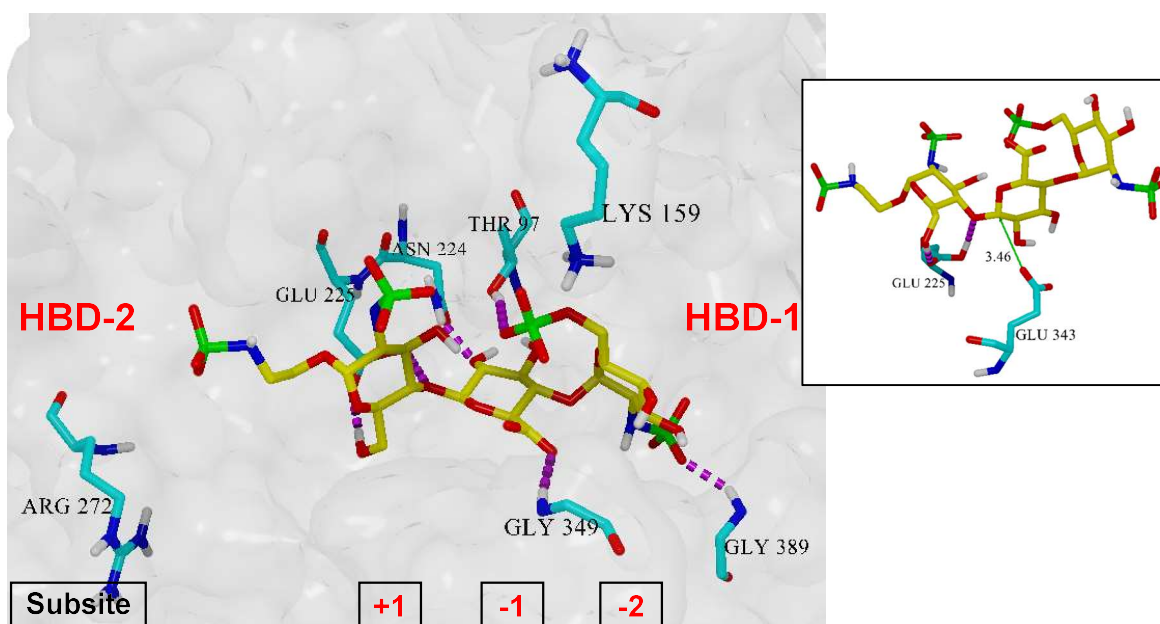
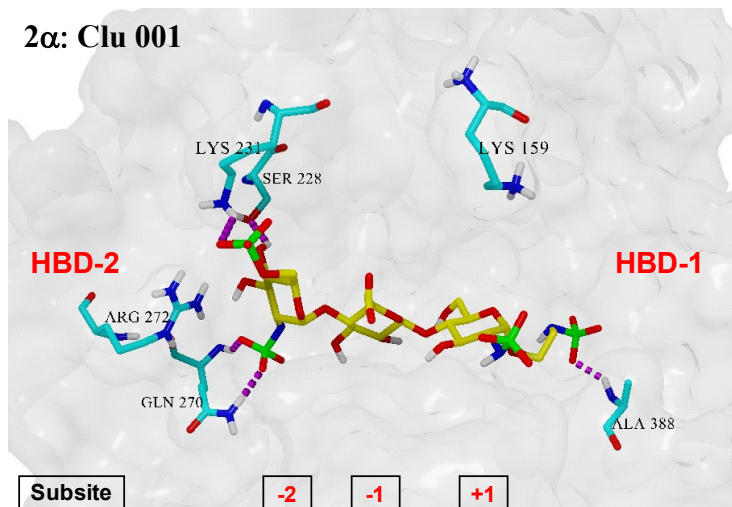
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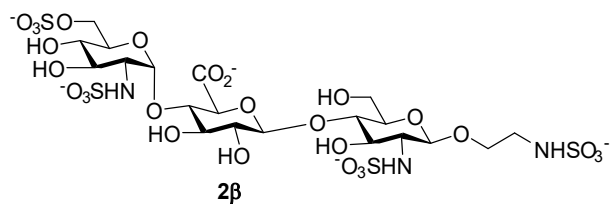




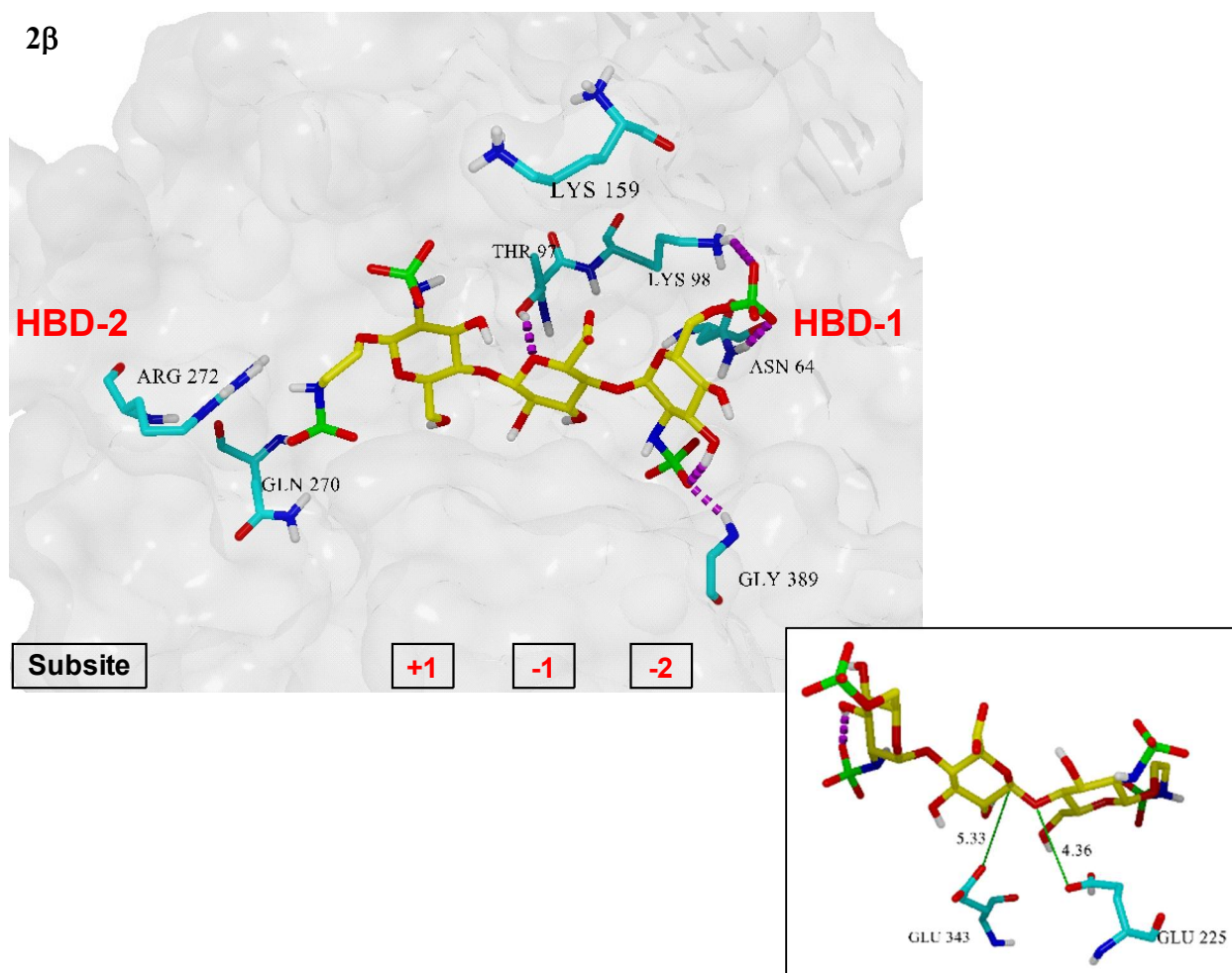
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004	002	000007.7145+-000000.1695	00000002214269.3720
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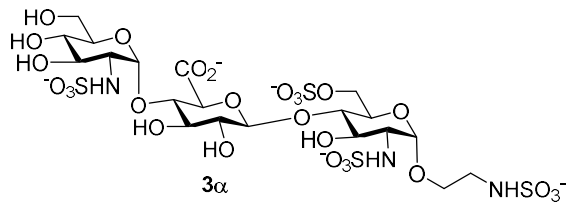
2α: Clu 001



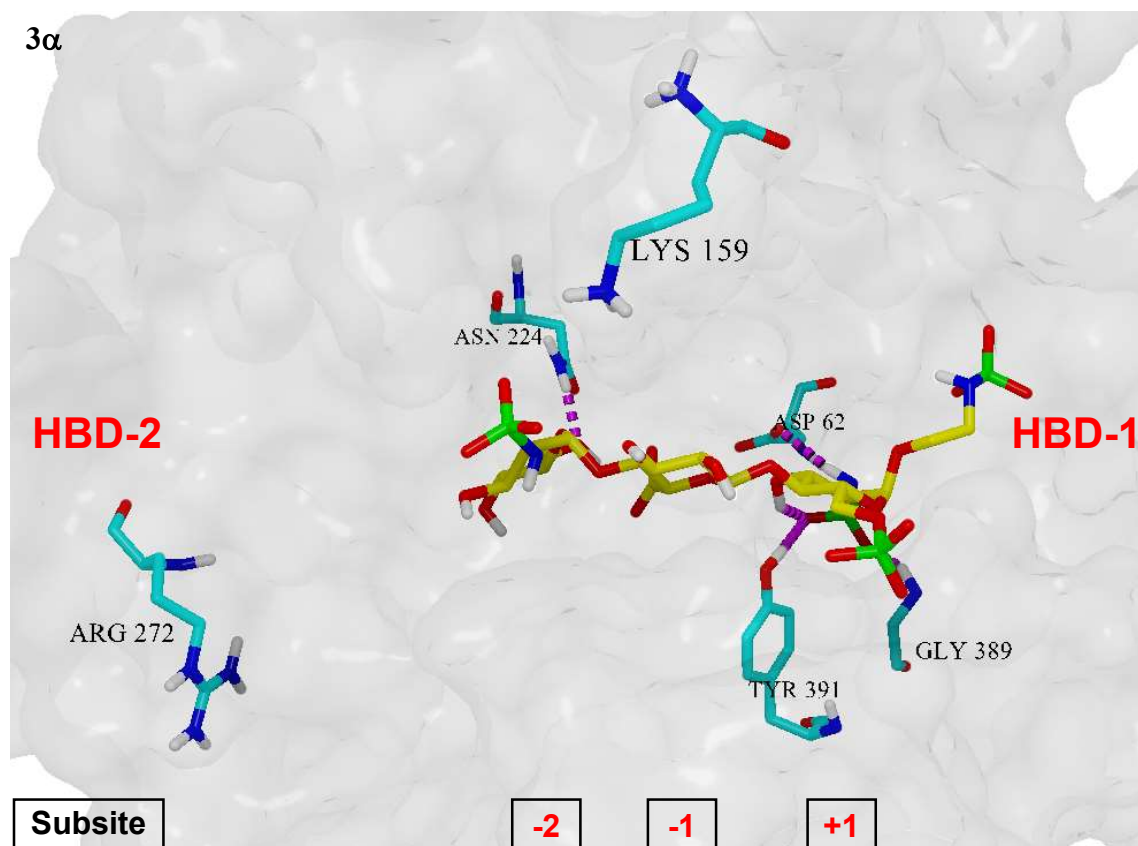


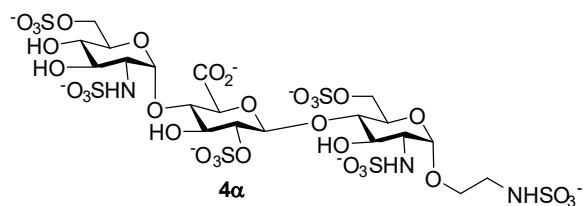
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006	001	000006.8340+-000000.0000	00000009786818.2811
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009	001	000006.6810+-000000.0000	00000012670426.9642
010	001	000006.6700+-000000.0000	00000012907865.2525
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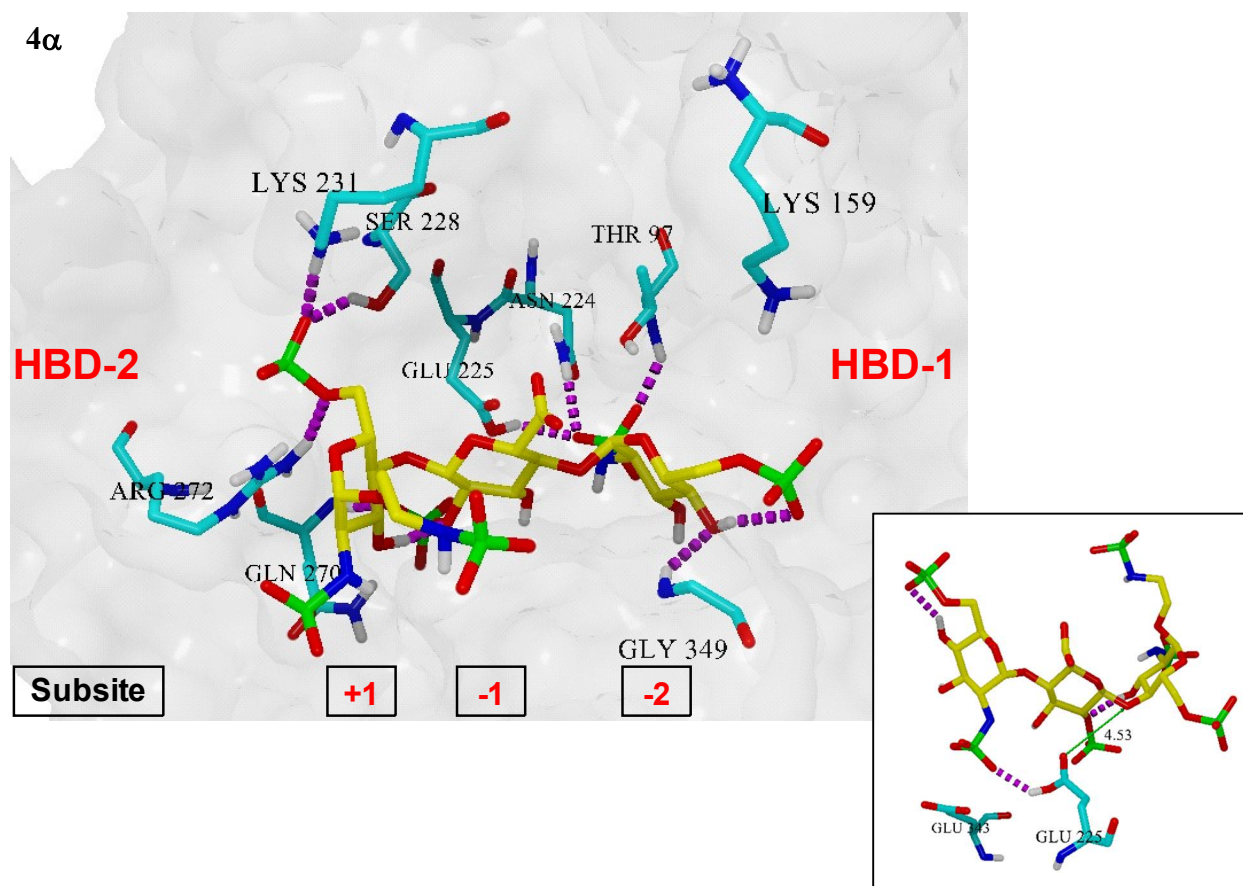


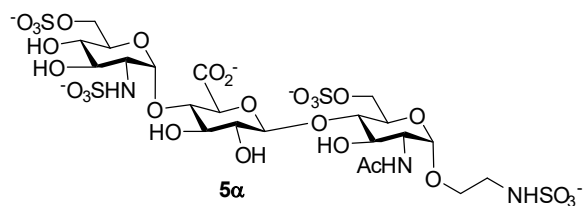
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005	001	000007.0270+-000000.0000	00000007065967.1517
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007	001	000006.8680+-000000.0000	00000009241009.1910
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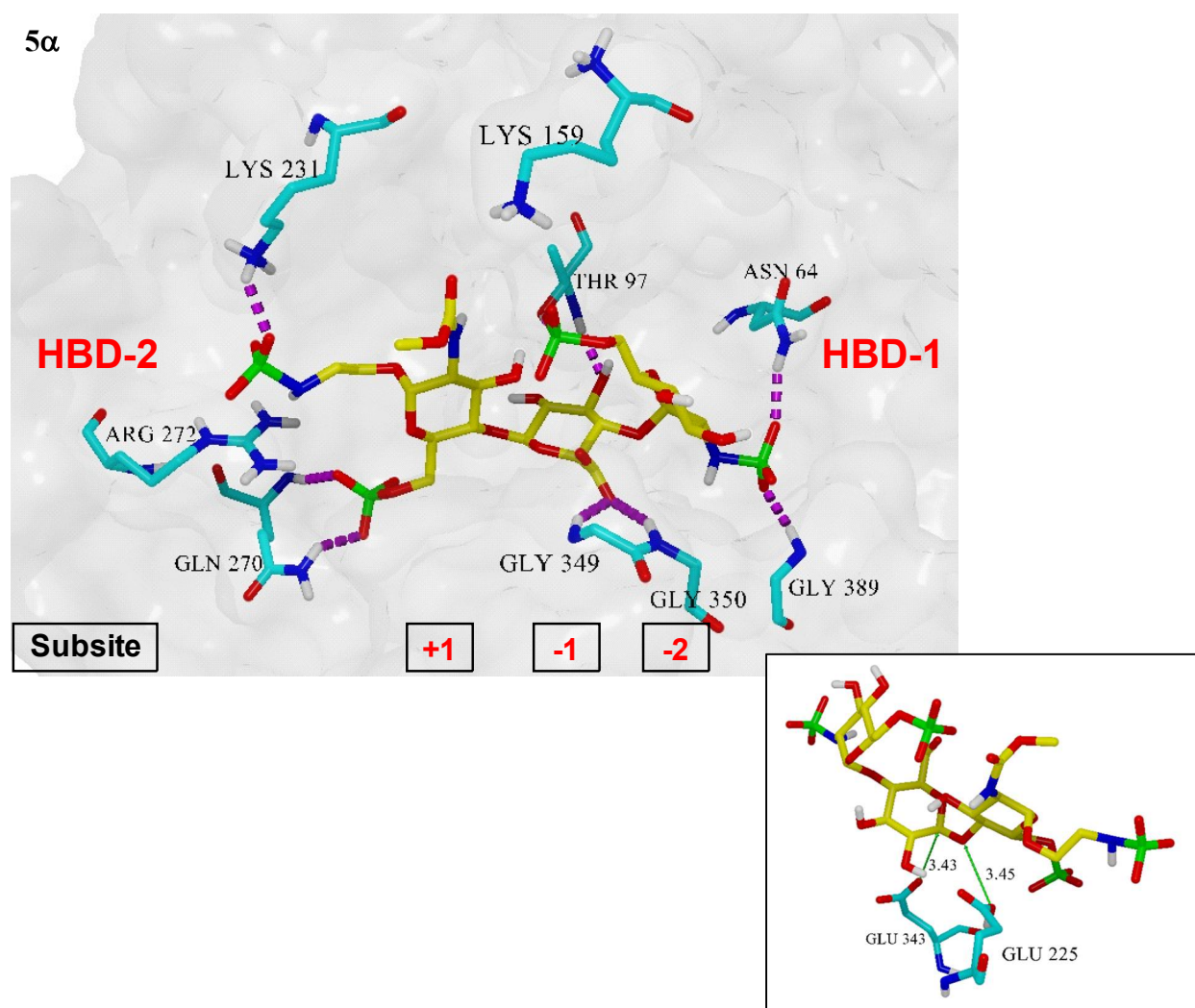


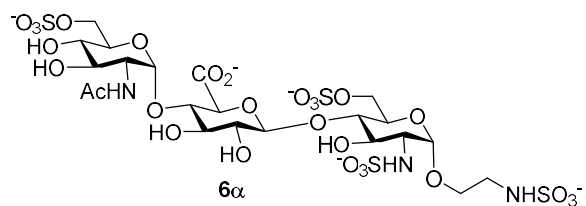
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005	001	000007.6750+-000000.0000	000000002366922.2220
006	001	000007.5600+-000000.0000	000000002873953.7925
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008	001	000007.5130+-000000.0000	000000003111221.8575



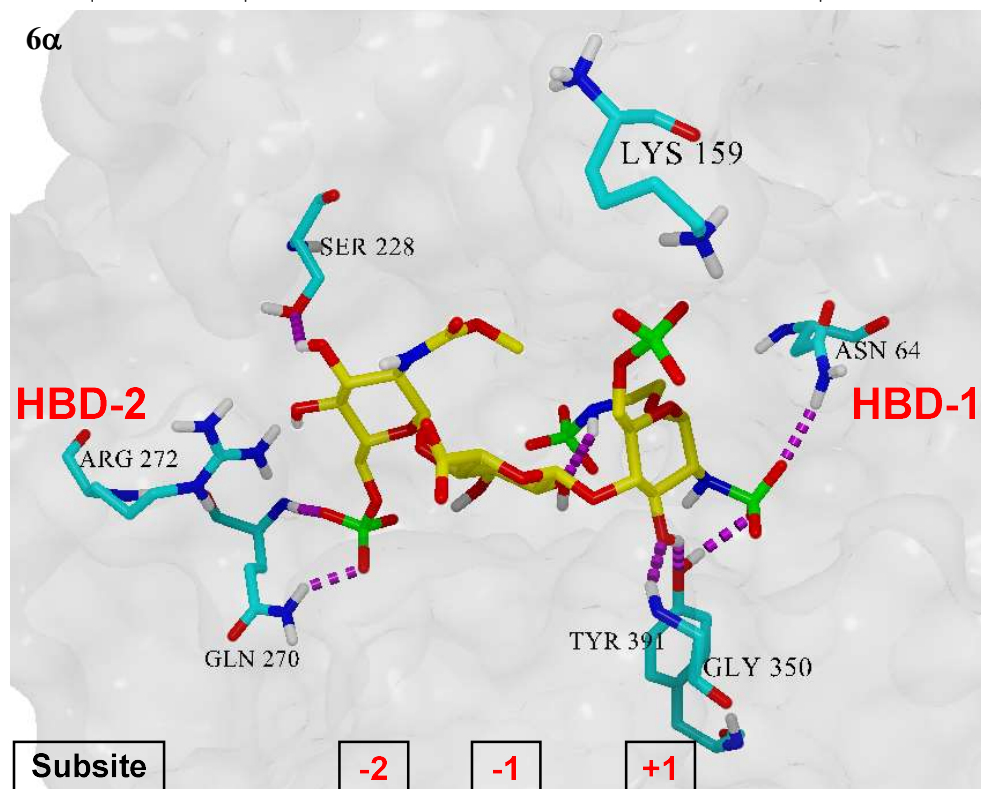


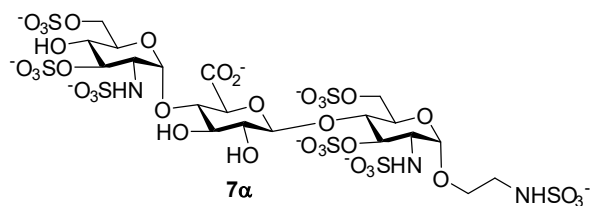
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002	003	000008.9677+-000000.1176	00000000267086.7681
003	003	000008.4820+-000000.4666	00000000606246.0493
004	005	000008.0832+-000000.2766	00000001188423.8783
005	001	000008.1730+-000000.0000	00000001021285.6477
006	002	000007.8135+-000000.0845	00000001873539.8824



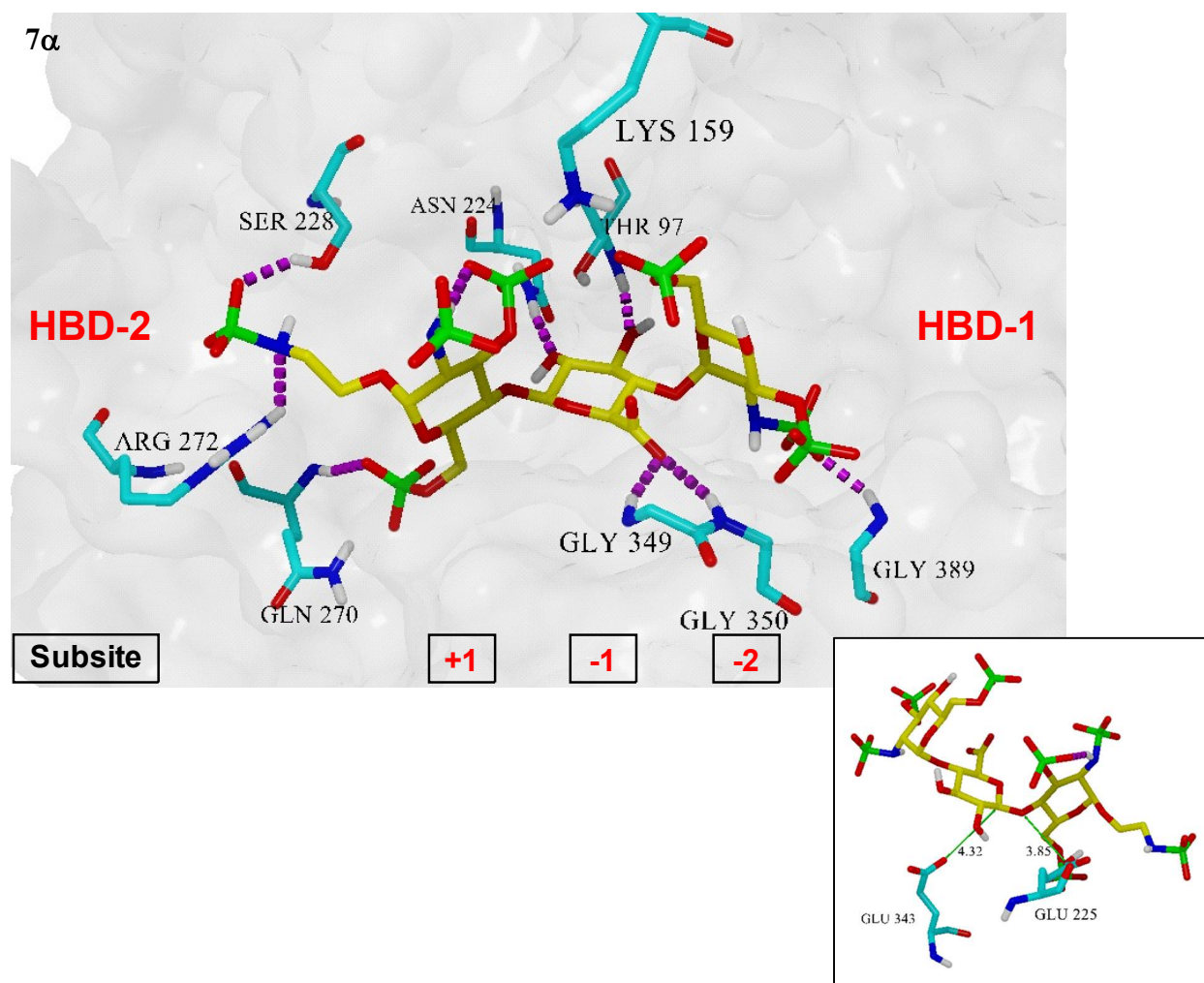


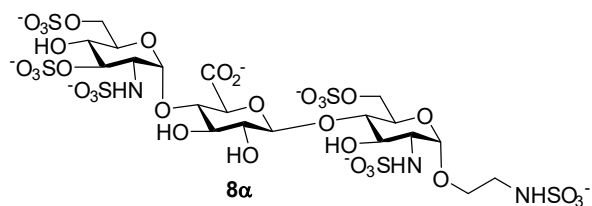
Clu	Members	Bind.energy spread [kcal/mol]	Dissoc. constant [pM]
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002	001	000008.5070+-000000.0000	00000000581197.4745
003	001	000008.4690+-000000.0000	00000000619695.0101
004	001	000008.3330+-000000.0000	00000000779590.4108
005	001	000008.2310+-000000.0000	00000000926047.3751
006	001	000008.2140+-000000.0000	00000000953003.3801
007	001	000008.0510+-000000.0000	00000001254799.6455
008	003	000007.6833+-000000.1532	00000002333864.8466
009	003	000007.2710+-000000.1149	00000004680781.2506
010	004	000006.9325+-000000.1604	00000008287826.7693
011	001	000006.8150+-000000.0000	00000010105752.6661
012	001	000006.7300+-000000.0000	00000011664715.3546
013	001	000006.6450+-000000.0000	00000013464171.2299



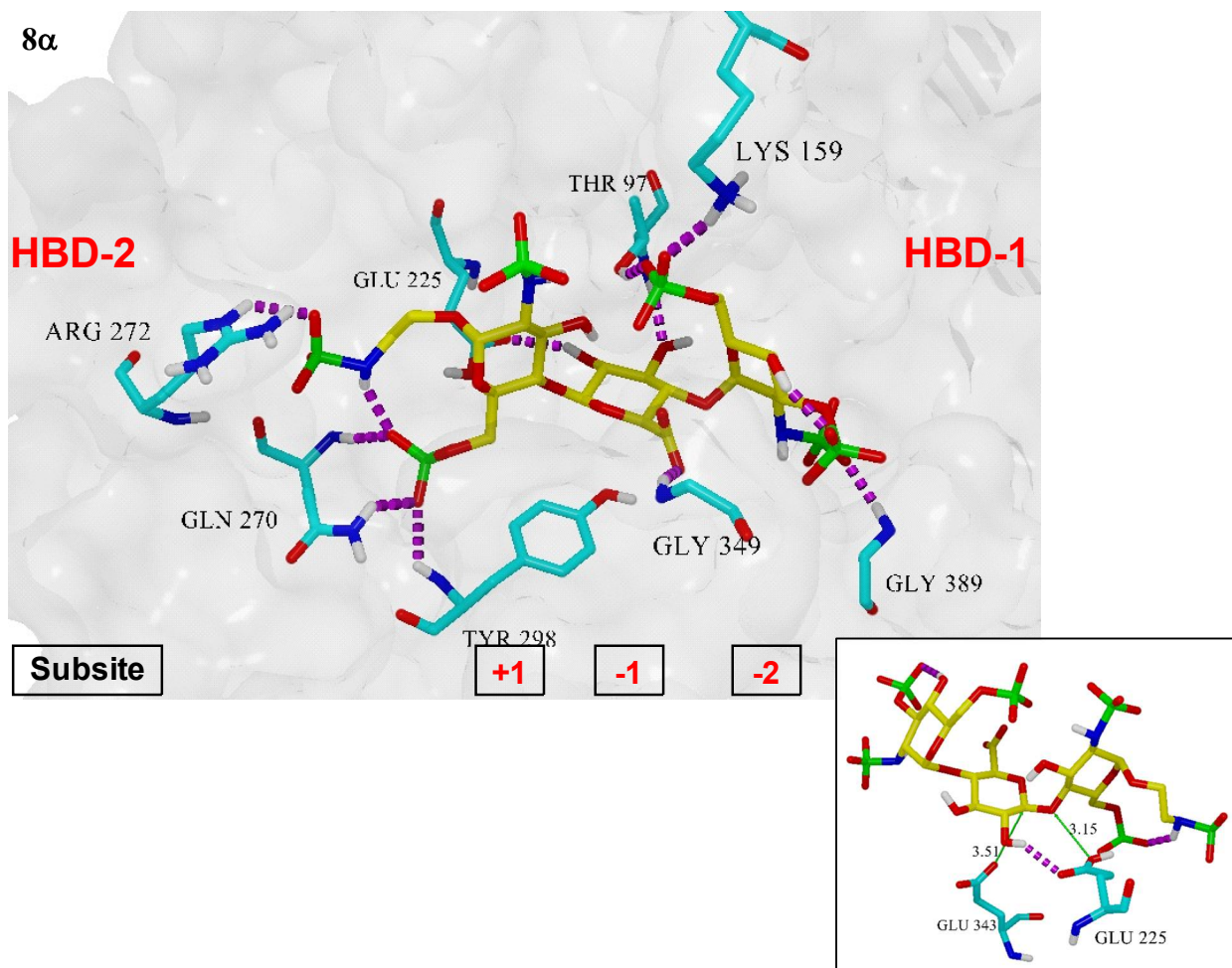


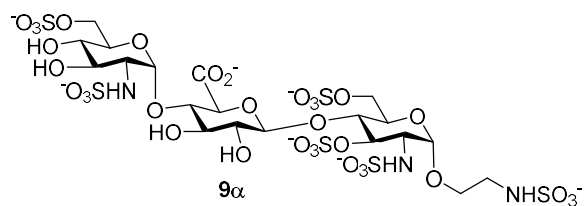
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003	002	000008.5505+-000000.1175	00000000540055.0431
004	002	000007.8640+-000000.0630	00000001720465.8644
005	002	000007.6770+-000000.0990	00000002358946.4528
006	004	000007.2752+-000000.1354	00000004647324.9099
007	001	000007.3750+-000000.0000	00000003927224.4646
008	001	000007.3030+-000000.0000	00000004434678.3692
009	001	000007.2370+-000000.0000	00000004957245.9638
010	001	000007.1370+-000000.0000	00000005868686.7699



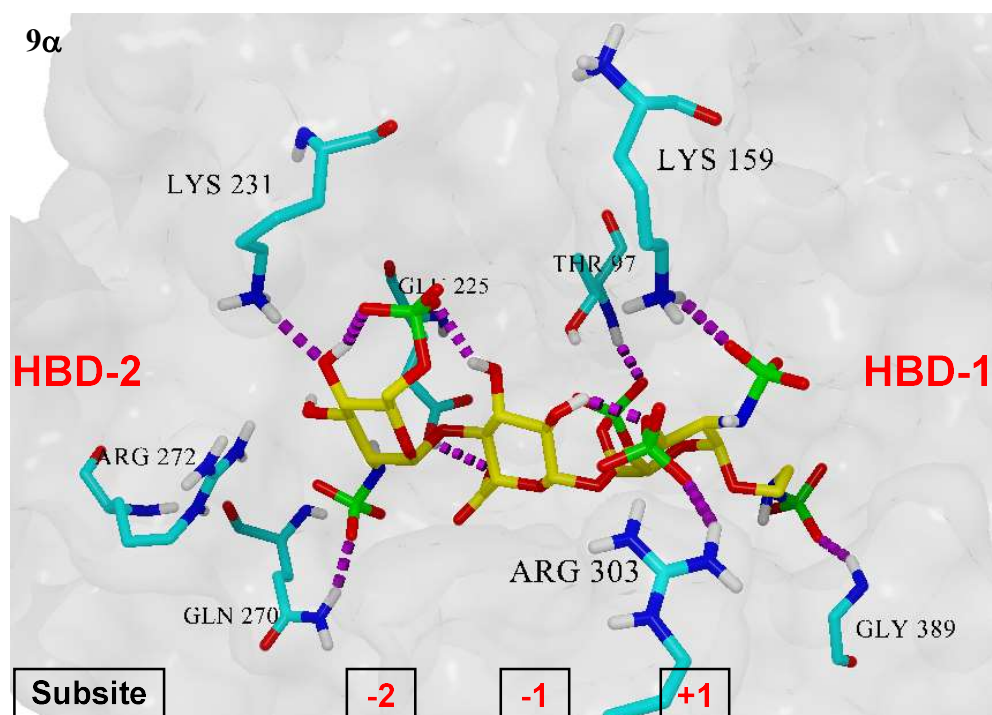


Clu	Members	Bind.energy spread [kcal/mol]	Dissoc. constant [pM]
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002	003	000009.9593+-000000.2828	00000000050090.5229
003	004	000009.7858+-000000.1594	00000000067141.8071
004	001	000009.7630+-000000.0000	00000000069770.1005
005	004	000009.5748+-000000.1096	00000000095864.3483
006	001	000009.5040+-000000.0000	00000000108023.3395





Clu	Members	Bind.energy spread [kcal/mol]	Dissoc. constant [pM]
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002	001	000009.2050+-000000.0000	00000000178931.1836
003	001	000008.6190+-000000.0000	00000000481090.4998
004	001	000008.1180+-000000.0000	00000001120631.2920
005	001	000007.9030+-000000.0000	00000001610864.4683
006	002	000007.6850+-000000.0140	00000002327309.3568
007	002	000007.4250+-000000.0720	00000003609402.5303
008	003	000007.3183+-000000.0573	00000004321382.5274
009	002	000007.2120+-000000.0790	00000005170894.4260
010	001	000007.2650+-000000.0000	00000004728423.9477
011	001	000007.2530+-000000.0000	00000004825169.0517
012	002	000007.1125+-000000.1095	00000006116453.2049
013	001	000007.1910+-000000.0000	00000005357457.2666
014	001	000007.0480+-000000.0000	00000006819908.8375



9.3. Molecular Dynamic Simulations

The most populated clusters (heparanase-ligand complexes) from the each docking run were subjected to MD simulation. Each enzyme-ligand complex was imported into YASARA and energy minimized in *vacuo*. Meanwhile, a simulation cell was formulated with at least 10 Å from all three sides of the enzyme-ligand complex (86 x 61x 59 Å for **1α** complex and 67 x 89 x 61 Å for **1β** complex). AMBER14 force field was applied with periodic boundary conditions. The force field parameters were assigned using YASARA's "AutoSMILES" feature. The simulations were run in a default physiological solution (pH 7.4, 0.9% m/v NaCl solution with TIP3P water,¹¹ water density set at 0.997 g/mL) at 298 K. The pK_a of titratable side chains was predicted and assigned to respective groups before running MD and Glu 225 was manually protonated.

MD simulations were performed for 25000 ps for both **1α** and **1β** complexes initially. As suspicious movements were found in **1α** complex at the end of the simulation, an extra 5000 ps were added to the duration for **1α** complex. The cutoff radius for long-range electrostatics was set to 8 Å. The snapshots were saved every 25 ps for the whole simulation duration, which were then analyzed for the RMSD of the C α and heavy atoms of ligand-protein complex, as well as the distance between the side chain carboxylic carbons of catalytic residues and the scissile bond (Glu225-O1, Glu343-C1).

Figure S7. RMSD of the C α and heavy atoms of (A) **1 α** and (B) **1 β** complex

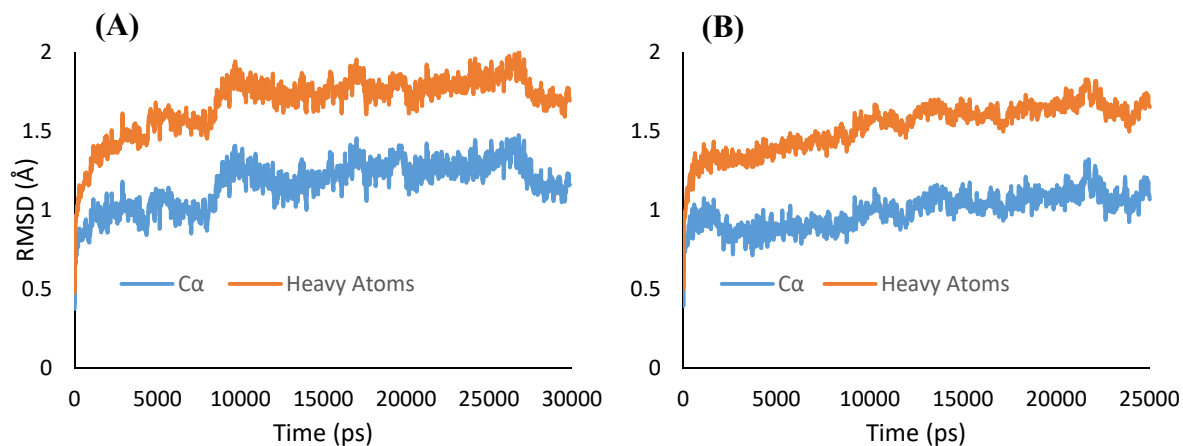


Figure S8. Evolution of distances between catalytic residues and the scissile bond during the simulation in (A) **1 α** and (B) **1 β** complex

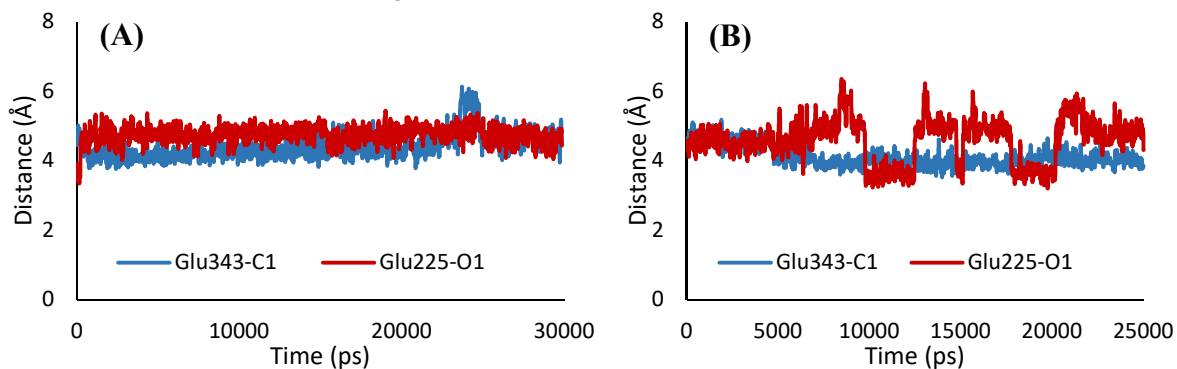
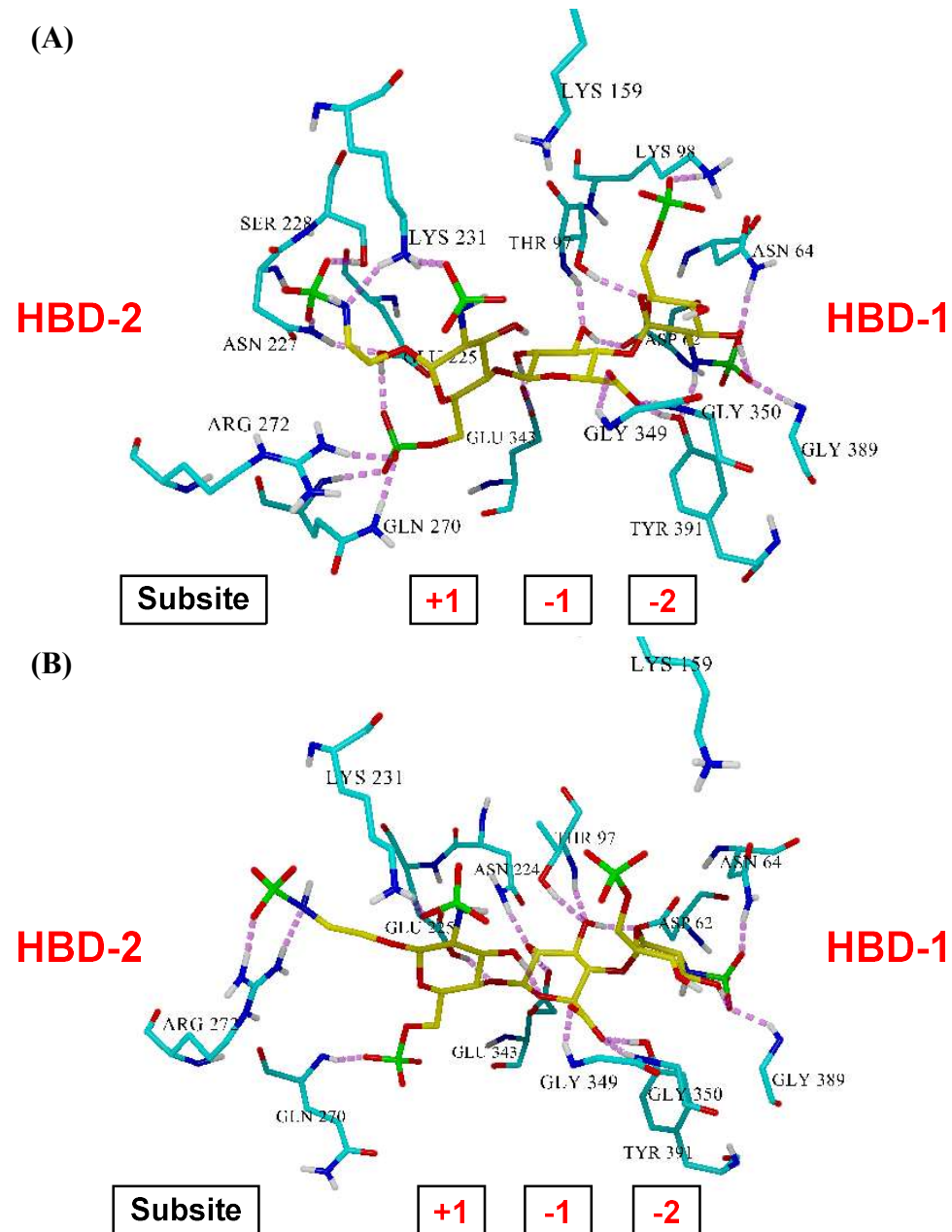


Figure S9. Example snapshots of hydrogen bonding pattern of (A) 1α and (B) 1β complex during MD simulation



10. Reference

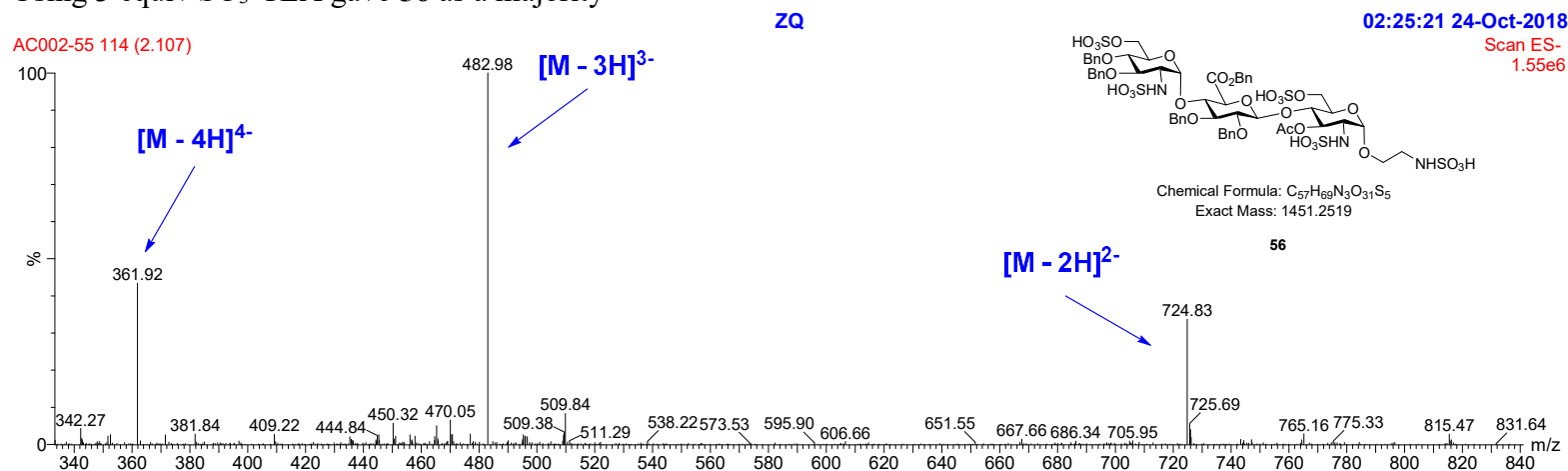
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11. Mass Spectra

11.1. Detection for Microwave-Assisted Sulfonation Reaction

Using 3 equiv $\text{SO}_3 \cdot \text{TEA}$ gave **56** as a majority



Using 5 equiv $\text{SO}_3 \cdot \text{TEA}$ produced more **57** as side-product

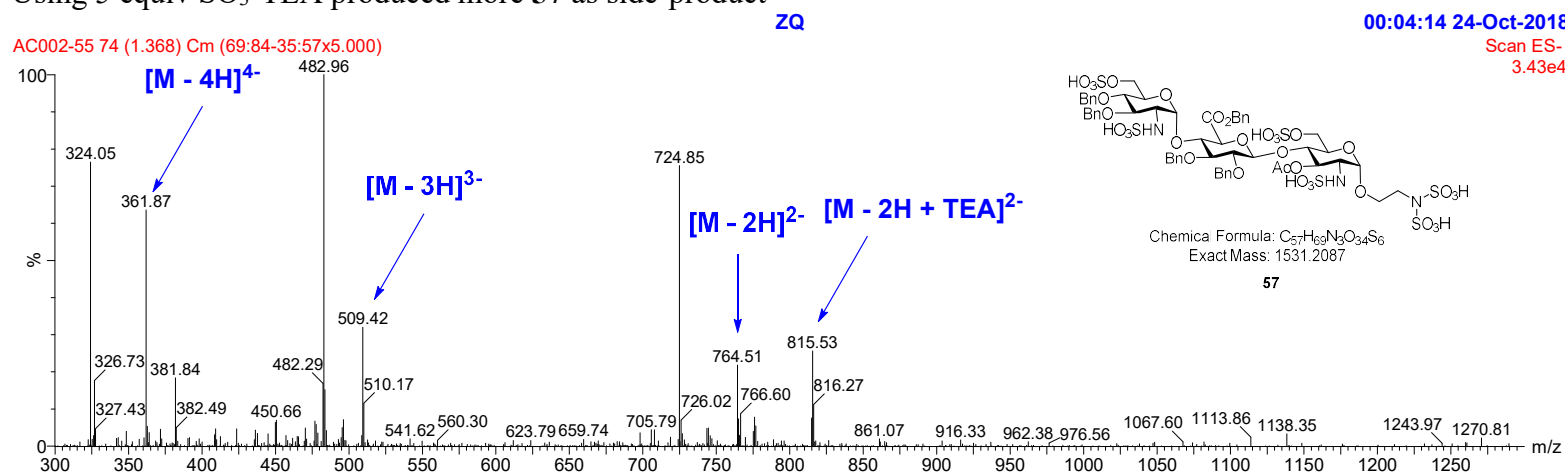


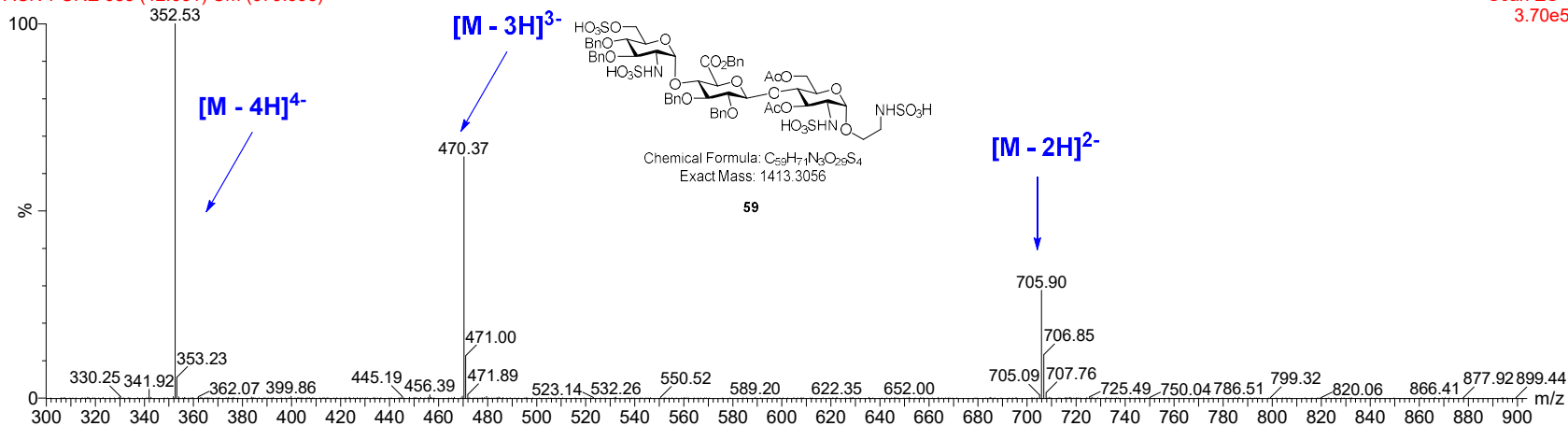
Figure S6. Microwave assisted sulfonation monitored by negative-mode mass, indicating 3 equiv $\text{SO}_3 \cdot \text{TEA}$ was good.

ACN-PURE 685 (12.661) Cm (679:693)

ZQ

11:55:15 06-Nov-2018

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3.70e5

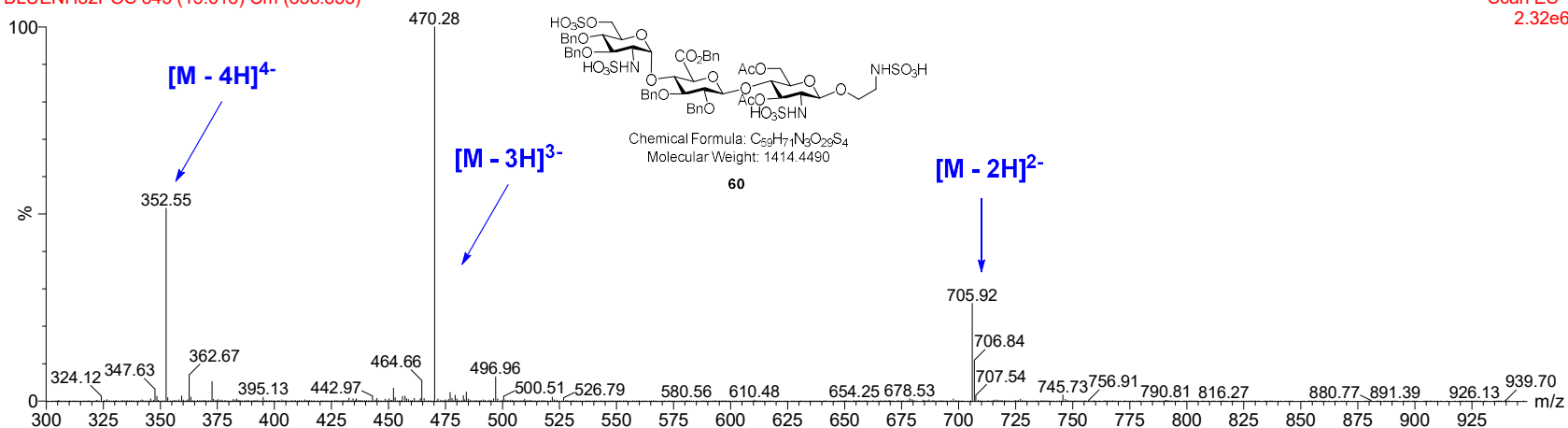


BLUENH32POS 845 (15.618) Cm (838:855)

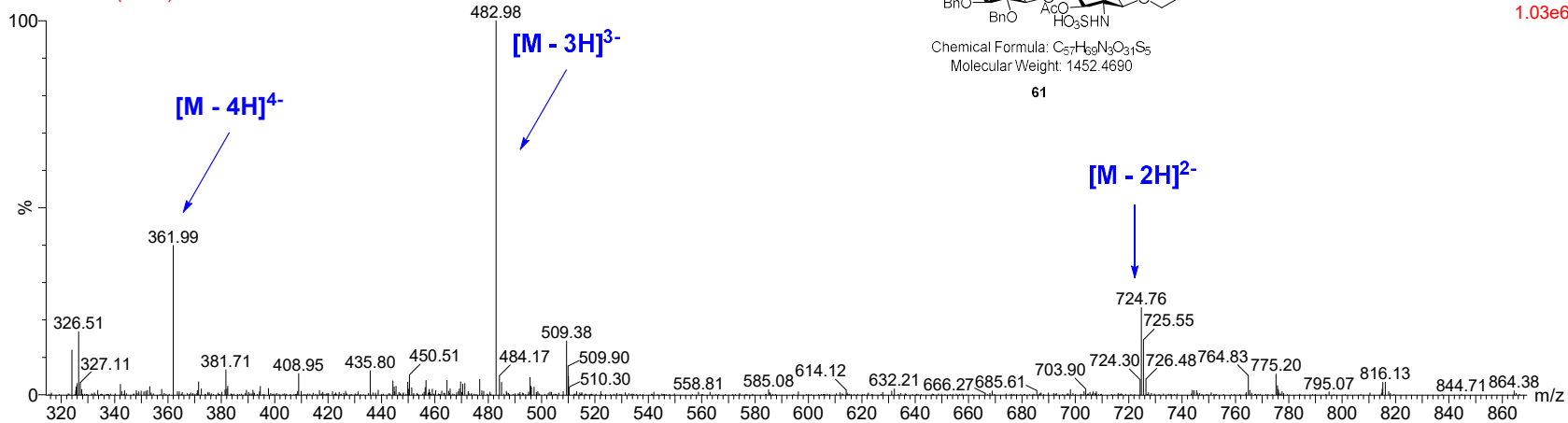
ZQ

18:17:48 19-Sep-2018

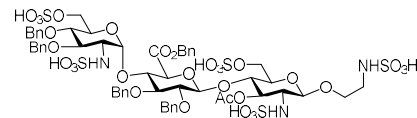
Scan ES-
2.32e6



AC002-55 73 (1.349)



ZQ



Chemical Formula: C₂₇H₃₉N₃O₃₁S₅
Molecular Weight: 1452.4690

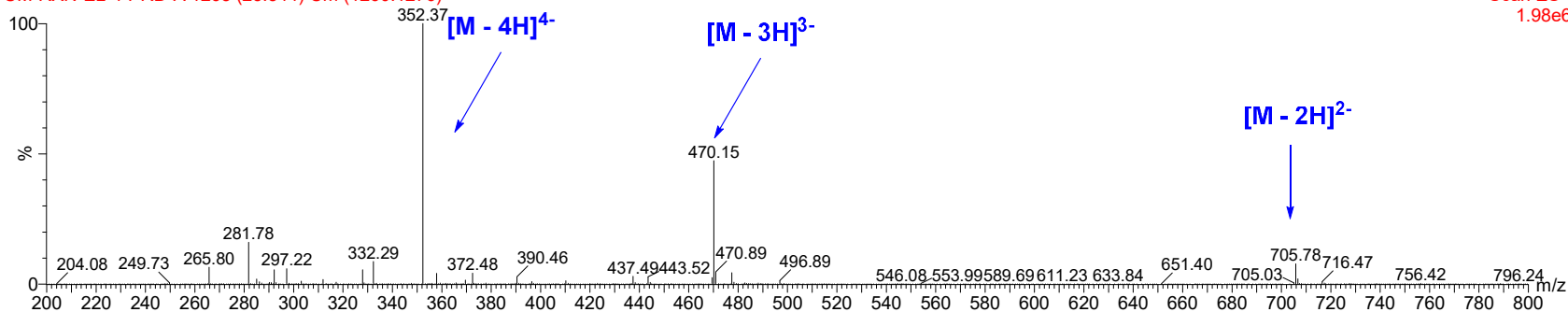
61

04:11:13 24-Oct-2018

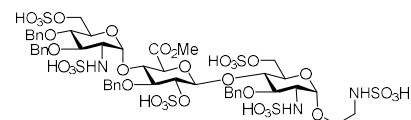
Scan ES-

1.03e6

UM-RXN-EL-4-PRD-A 1263 (23.344) Cm (1260:1276)



ZQ



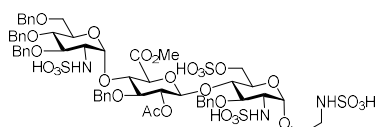
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62

13:41:43 23-Jul-2019

Scan ES-

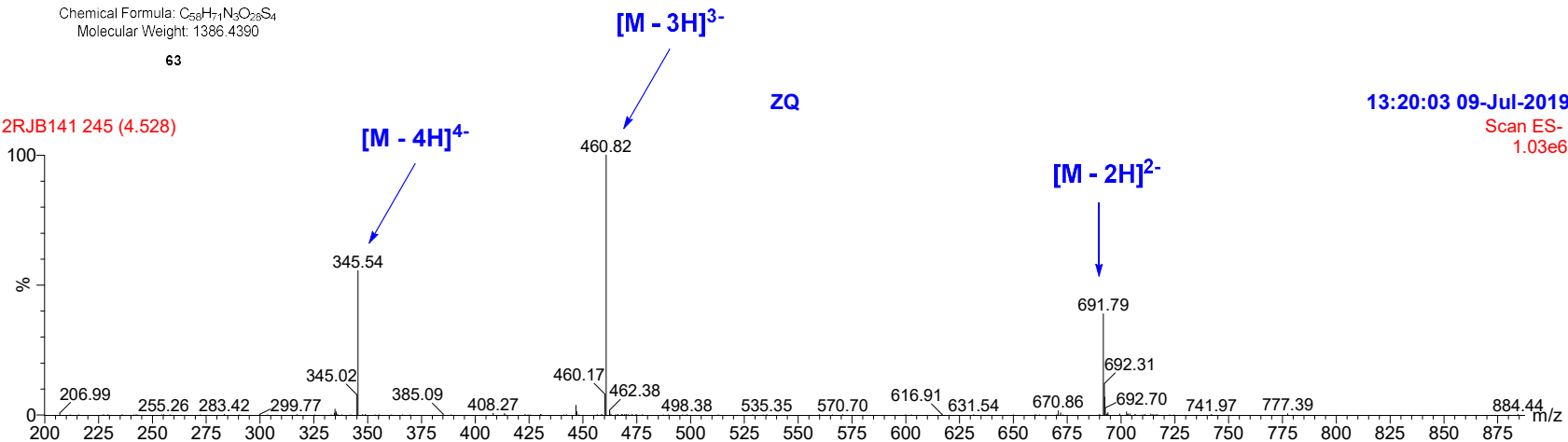
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Molecular Weight: 1386.4390

63

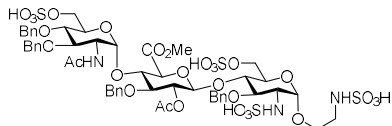
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ZQ

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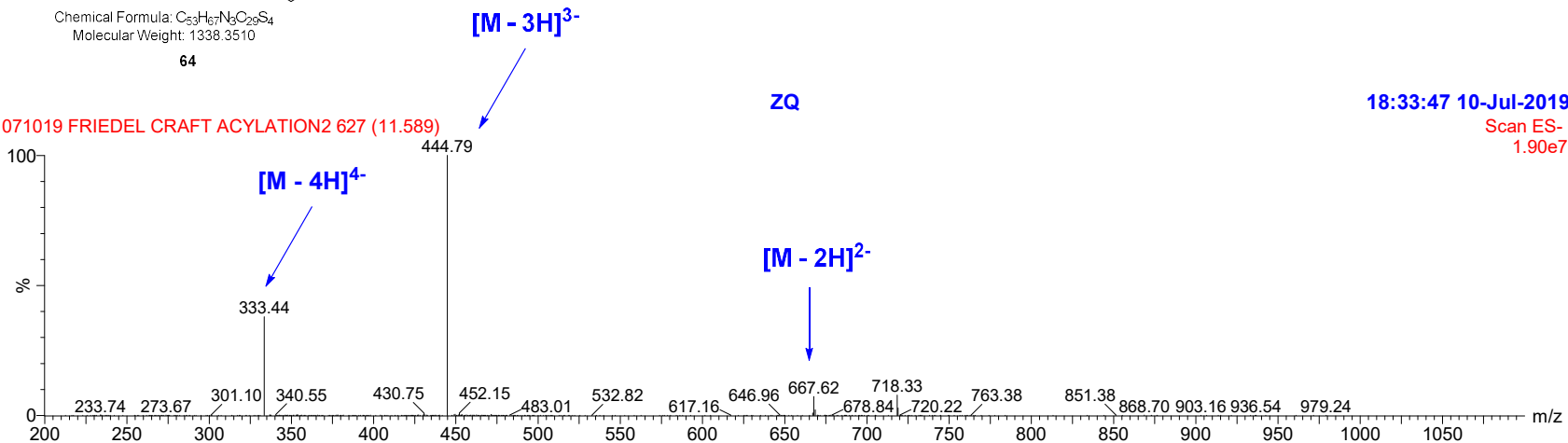
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Chemical Formula: $C_{53}H_{67}N_3O_{29}S_4$
Molecular Weight: 1338.3510

64

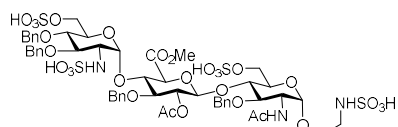
071019 FRIEDEL CRAFT ACYLATION2 627 (11.589)



ZQ

18:33:47 10-Jul-2019

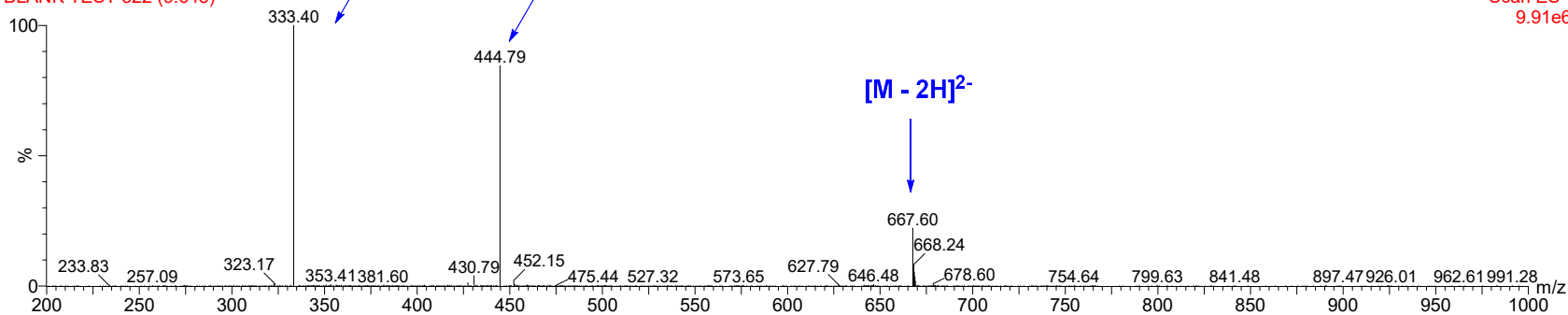
Scan ES-
1.90e7



Chemical Formula: $C_{53}H_{67}N_3O_{29}S_4$
Molecular Weight: 1338.3510

65

BLANK TEST 522 (9.648)



$[M - 4H]^{4-}$

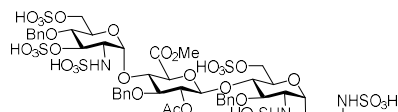
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ZQ

14:04:29 10-Jul-2019

Scan ES-
9.91e6

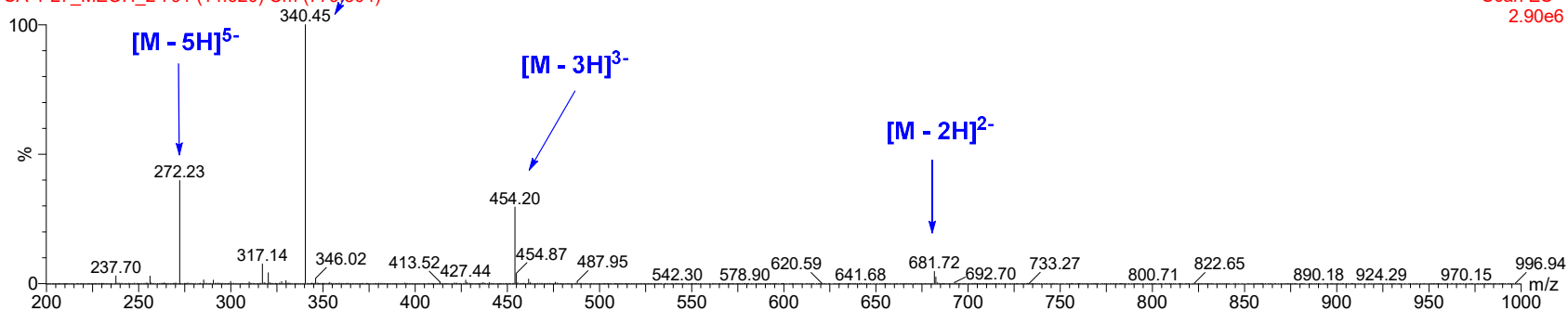
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Chemical Formula: $C_{44}H_{59}N_3O_{34}S_6$
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66

SA-1-27_MEOH_2 791 (14.620) Cm (779:804)



$[M - 4H]^{4-}$

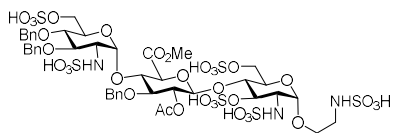
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ZQ

13:58:49 18-Jul-2019

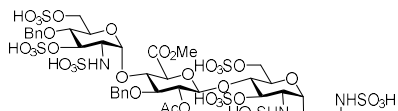
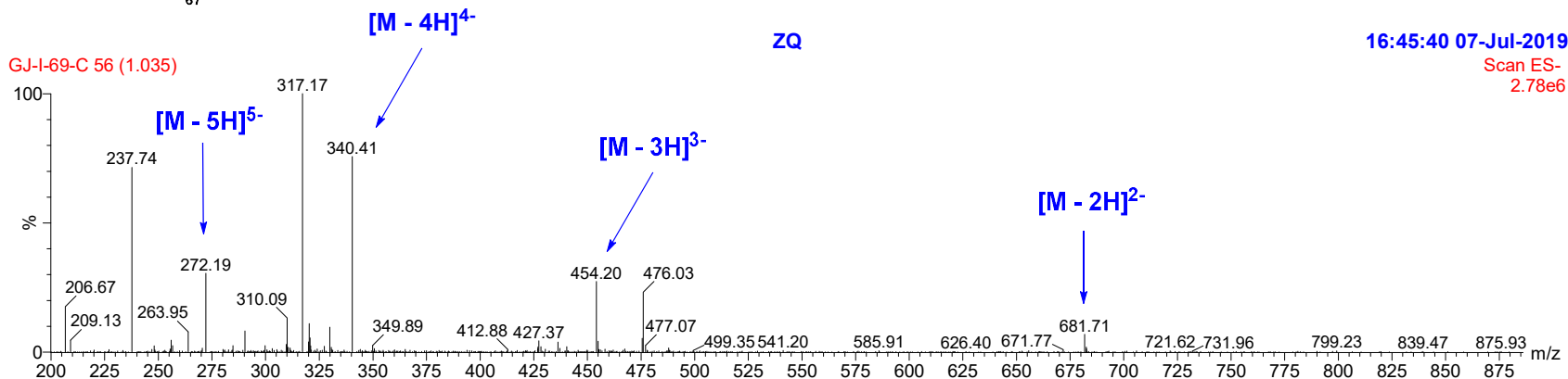
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2.90e6

$[M - 2H]^{2-}$



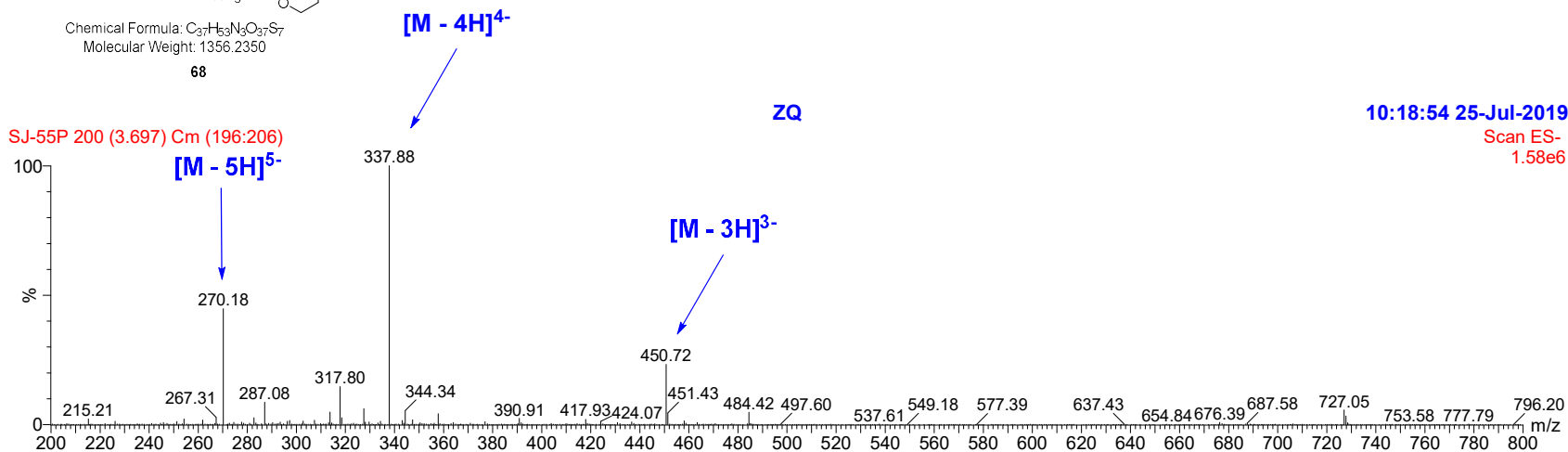
Chemical Formula: $C_{44}H_{69}N_3C_{34}S_6$
Molecular Weight: 1366.3030

67

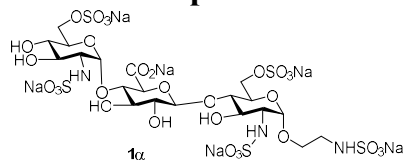


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Molecular Weight: 1356.2350

68

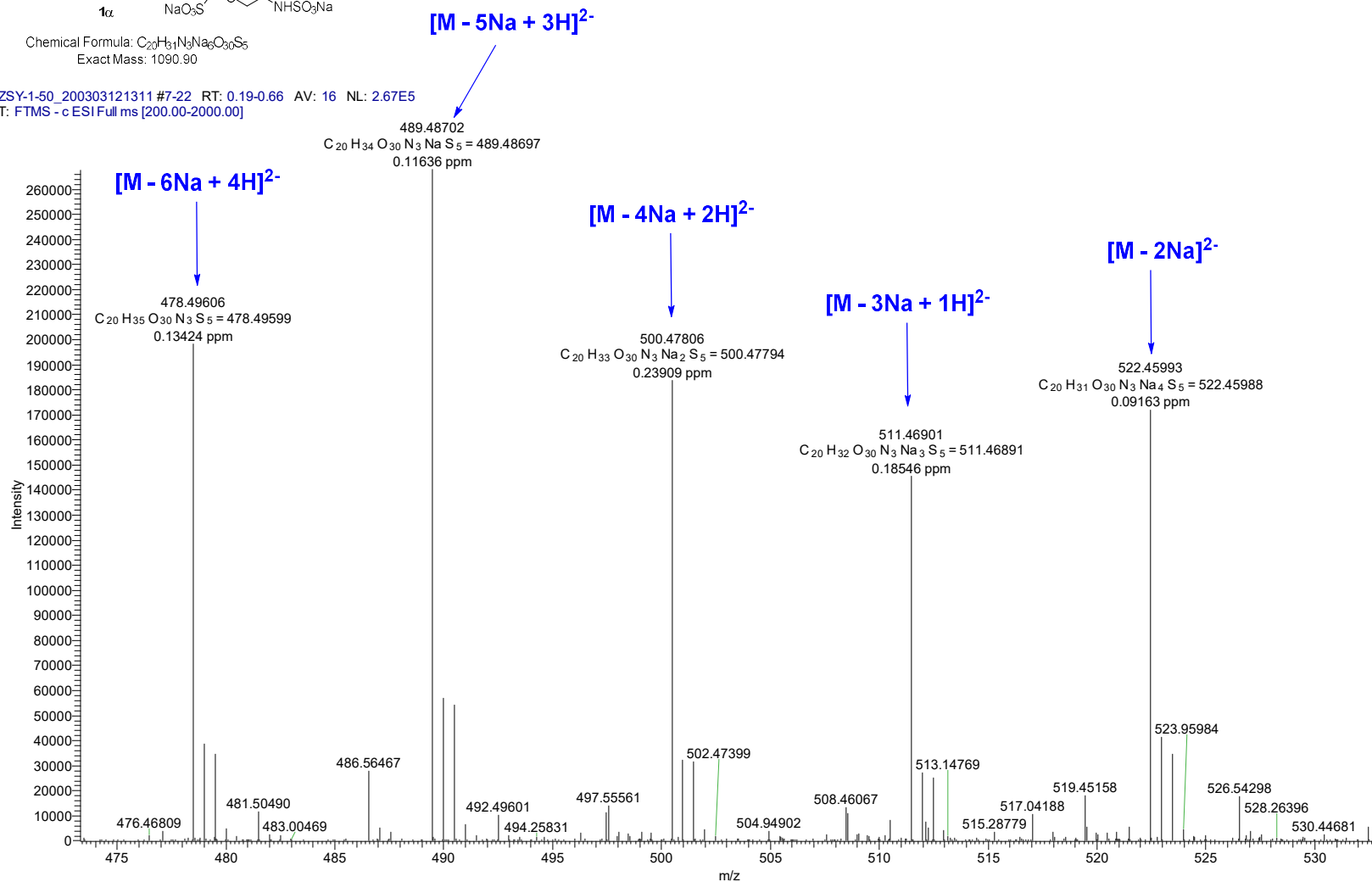


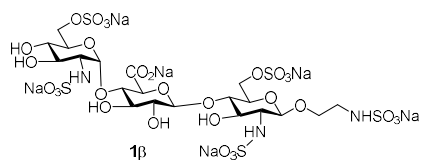
11.2. Mass Spectra for the Final HS Trisaccharides



Chemical Formula: C₂₀H₃₁N₃Na₆O₃₀S₅
Exact Mass: 1090.90

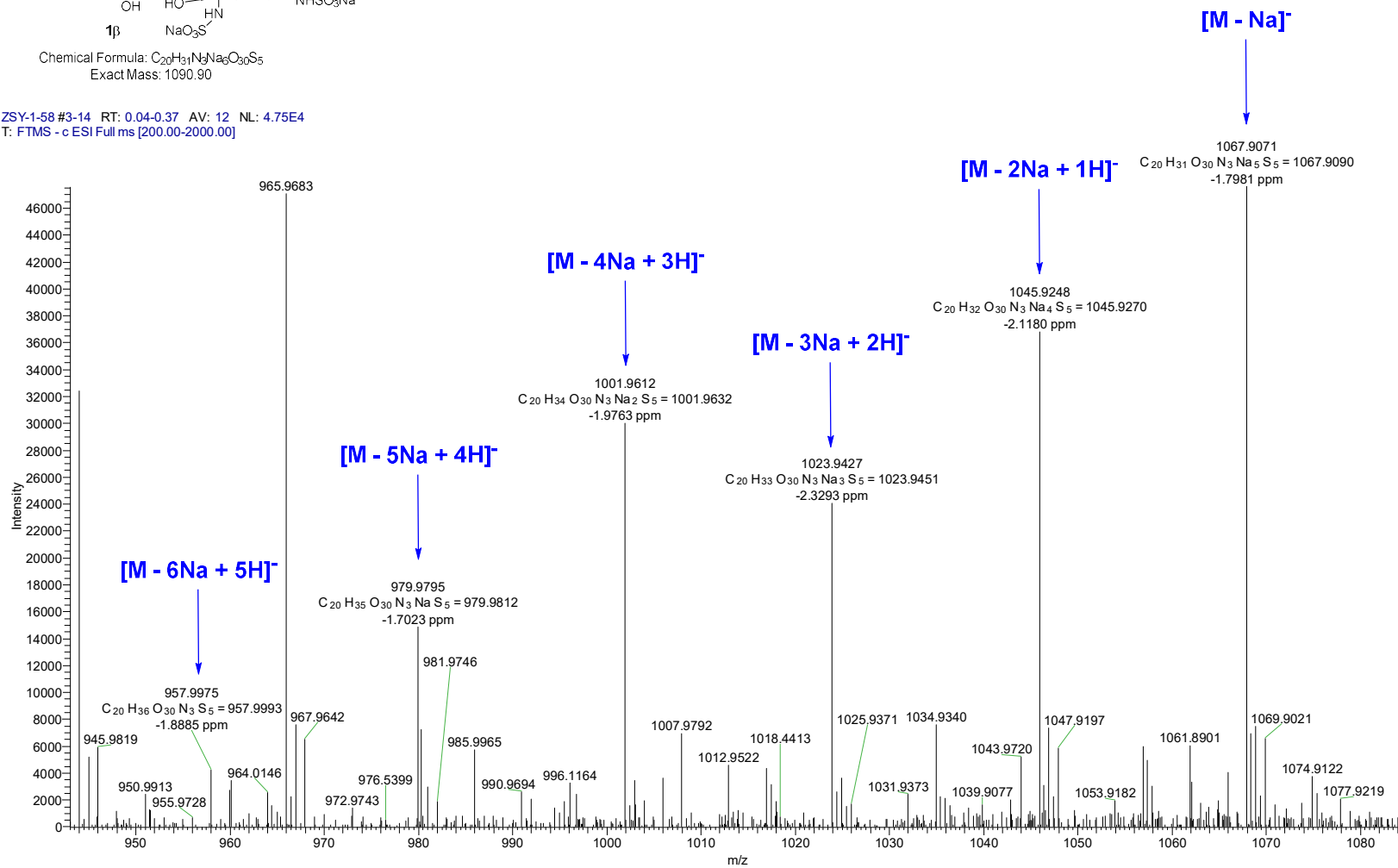
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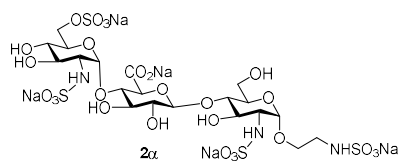




Chemical Formula: $C_{20}H_{31}N_3Na_5O_{30}S_5$
 Exact Mass: 1090.90

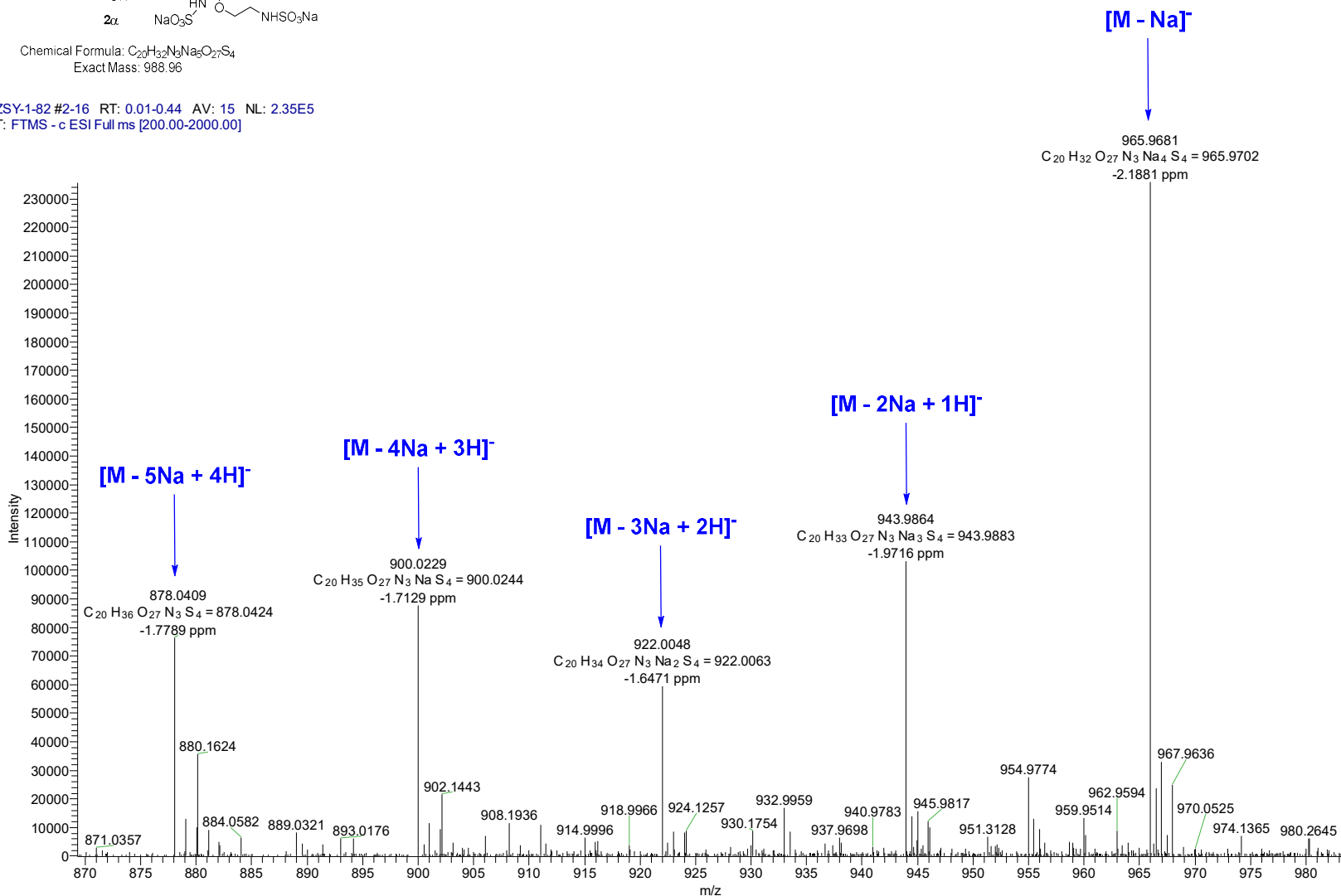
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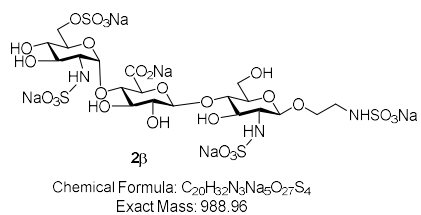




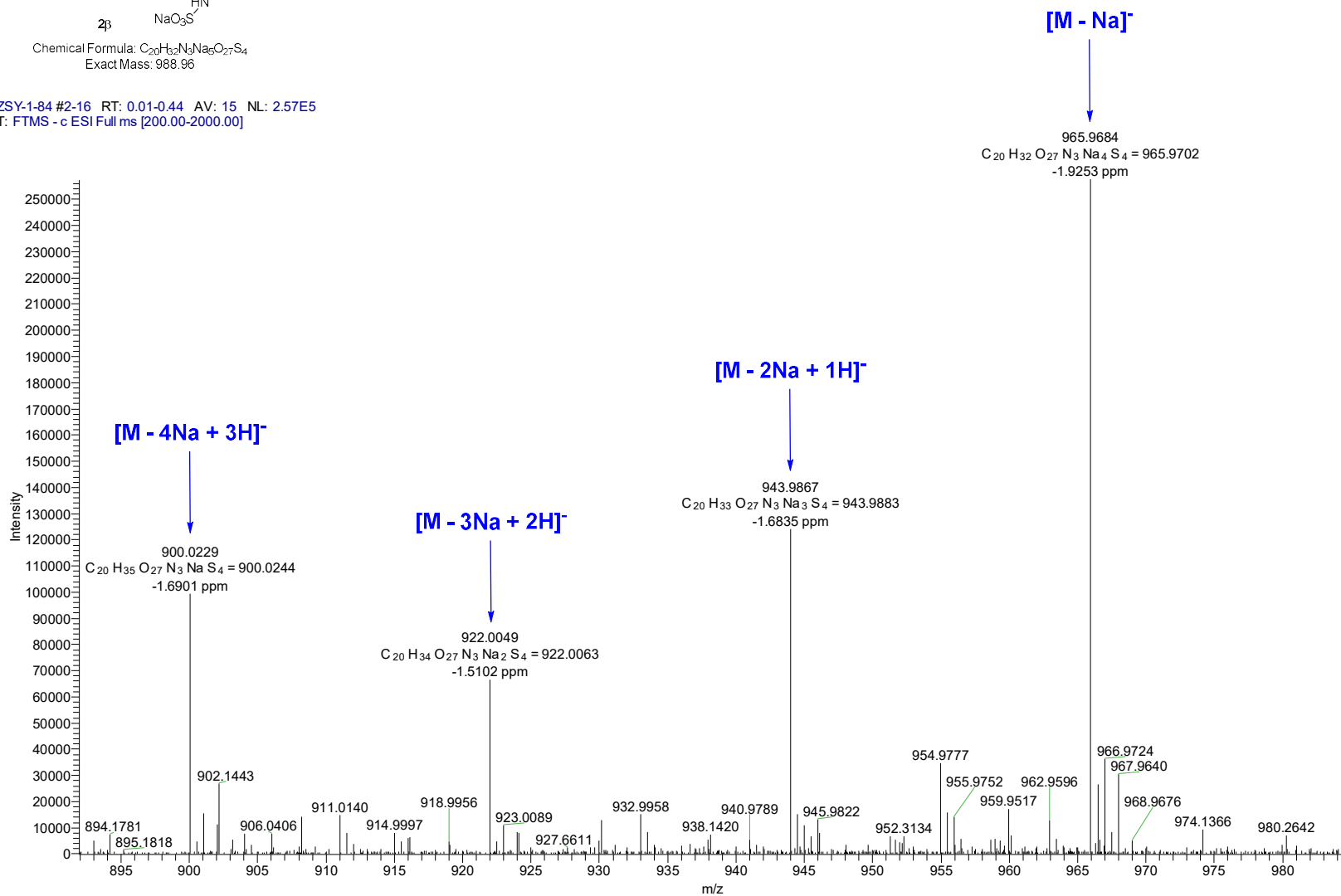
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 Exact Mass: 988.96

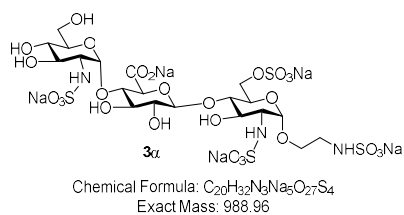
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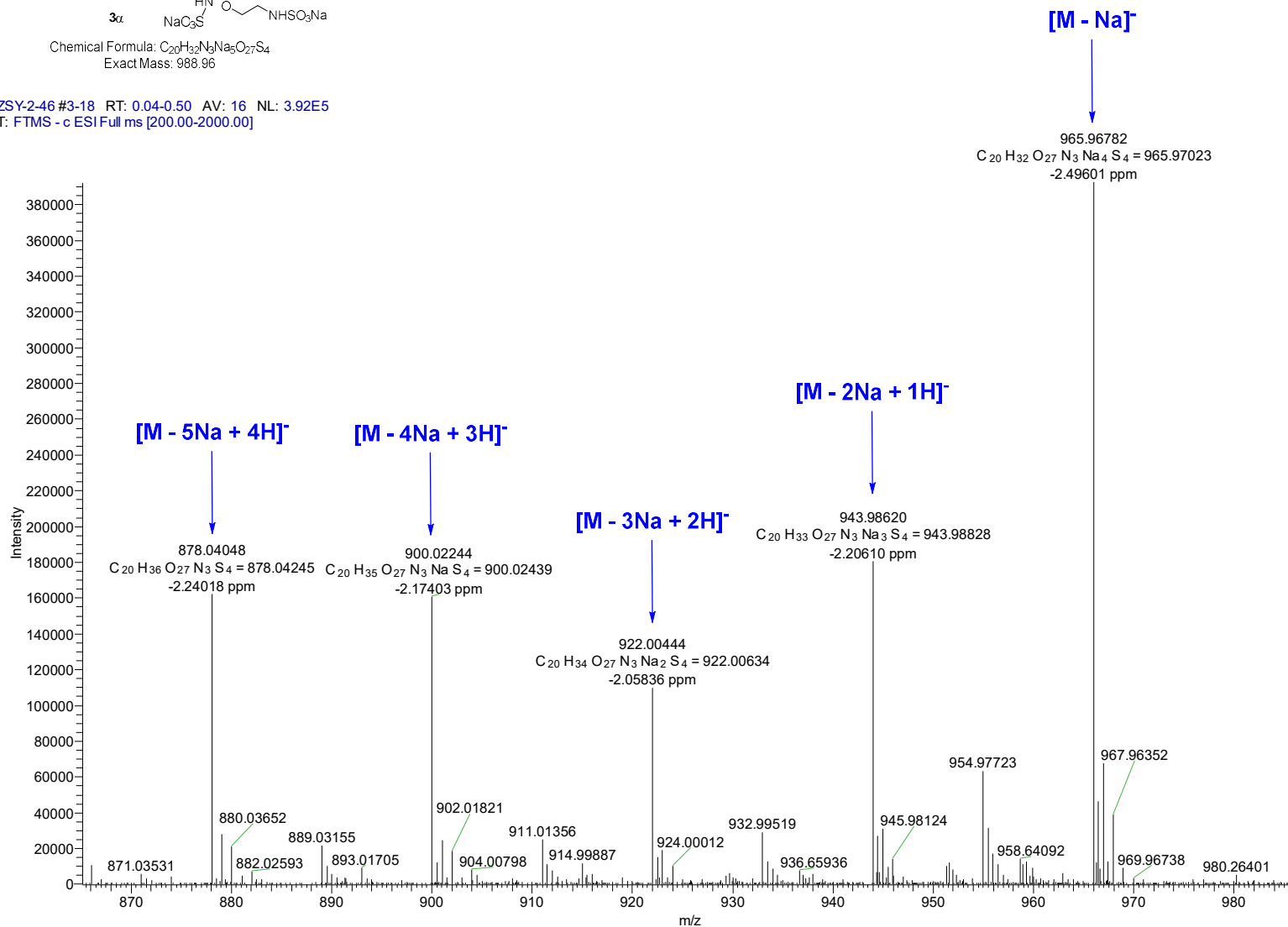


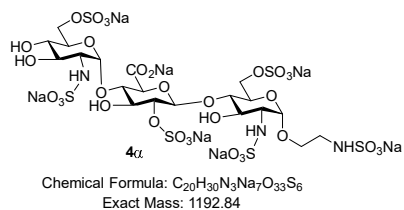
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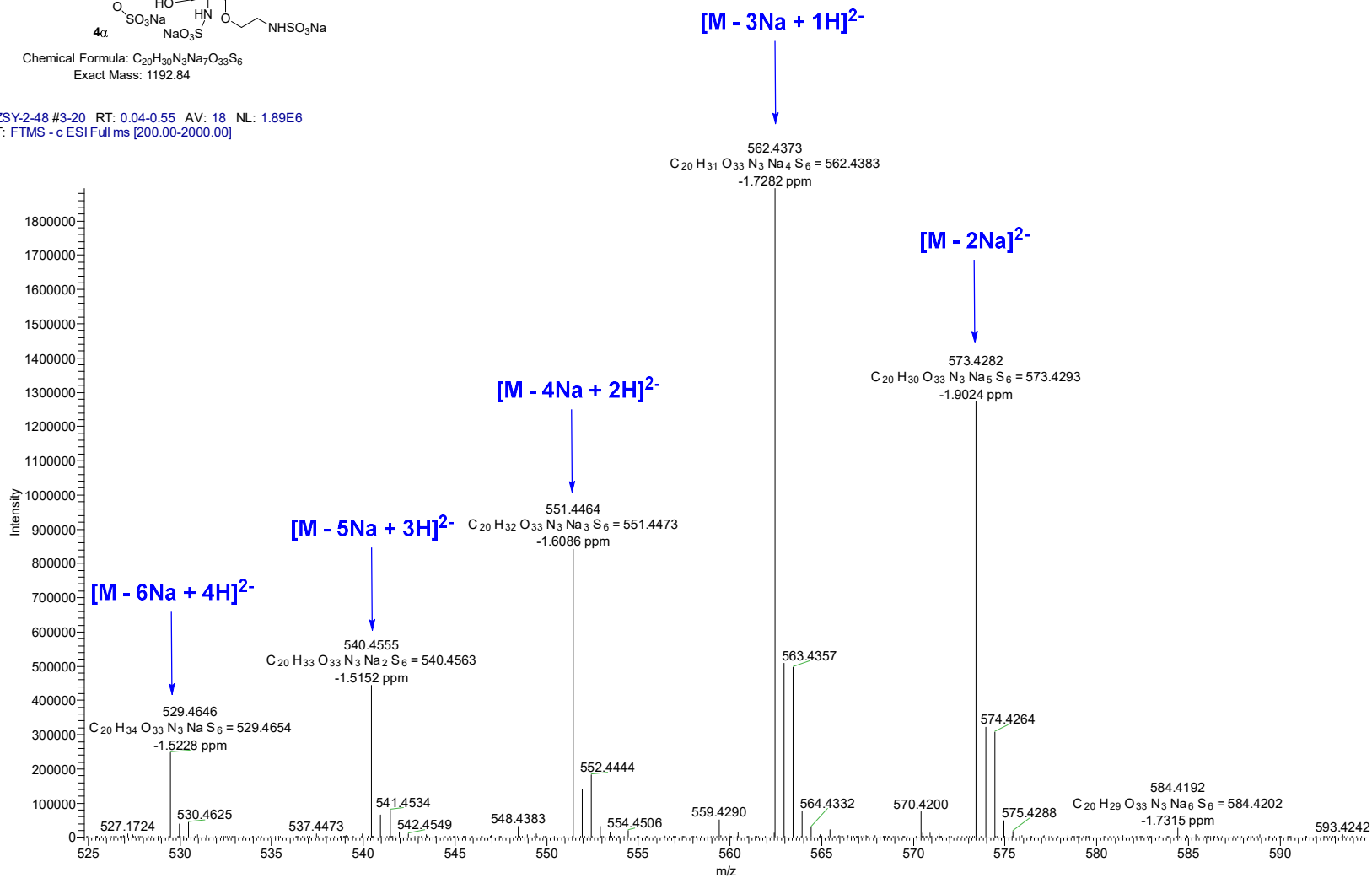


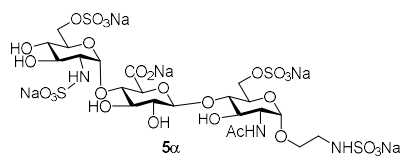
ZSY-2-46 #3-18 RT: 0.04-0.50 AV: 16 NL: 3.92E5
T: FTMS - c ESI Full ms [200.00-2000.00]





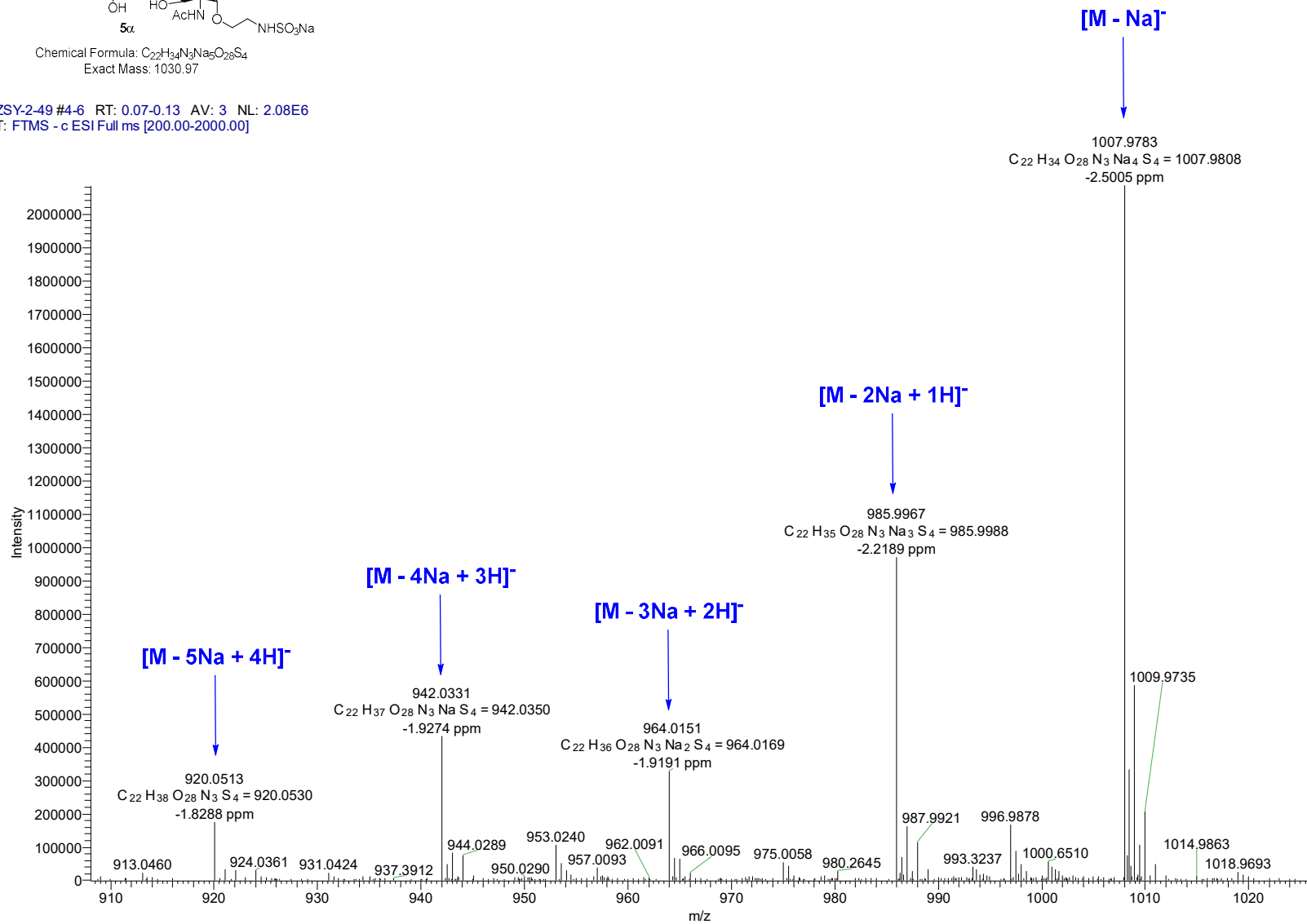
ZSY-2-48 #3-20 RT: 0.04-0.55 AV: 18 NL: 1.89E6
T: FTMS - c ESI Full ms [200.00-2000.00]

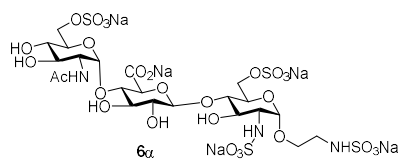




Chemical Formula: C₂₂H₃₄N₃Na₅O₂₈S₄
 Exact Mass: 1030.97

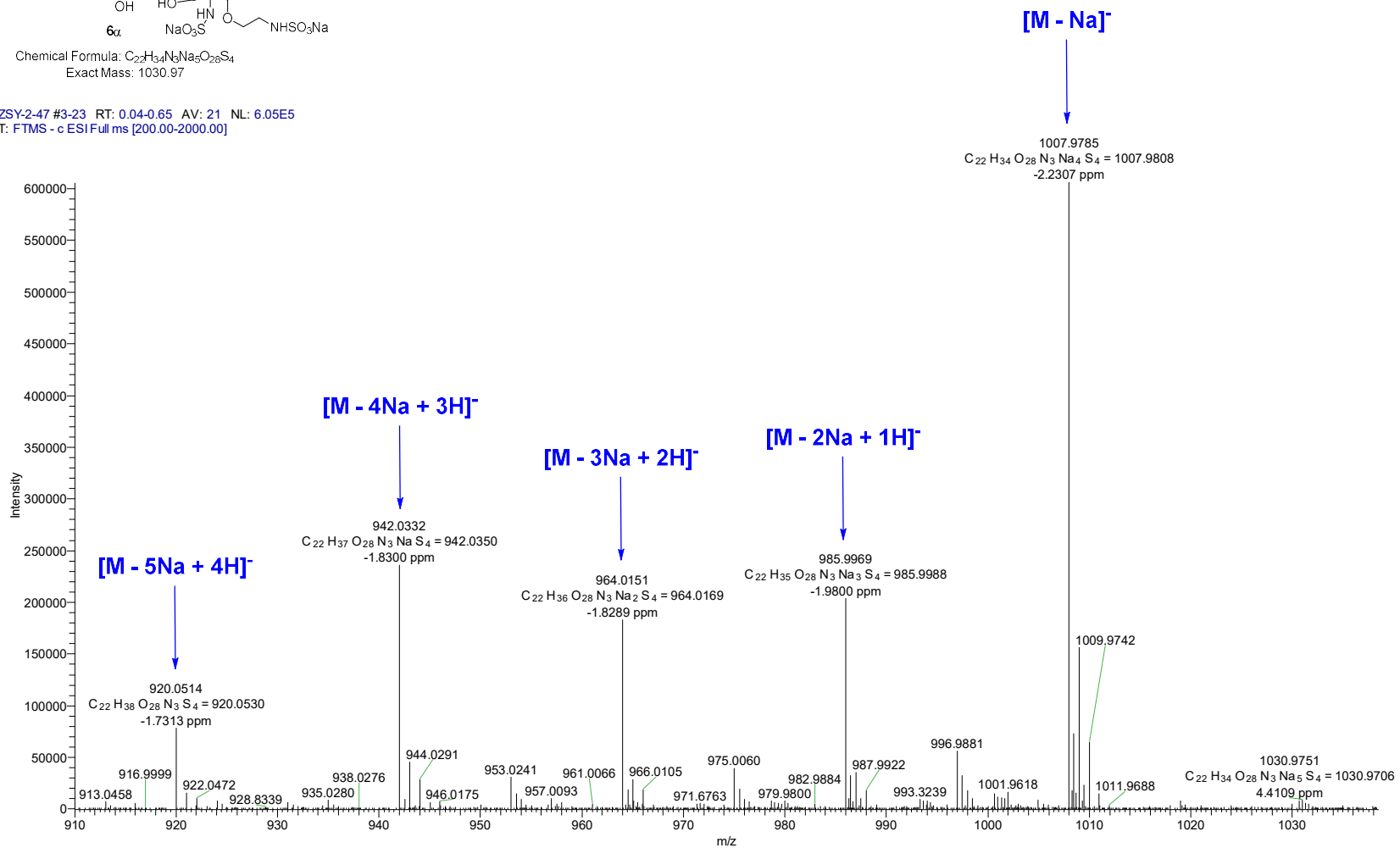
ZSY-2-49 #4-6 RT: 0.07-0.13 AV: 3 NL: 2.08E6
 T: FTMS - c ESI Full ms [200.00-2000.00]

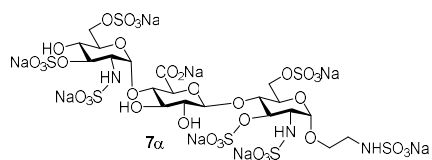




Chemical Formula: C₂₂H₃₄N₃Na₅O₂₈S₄
 Exact Mass: 1030.97

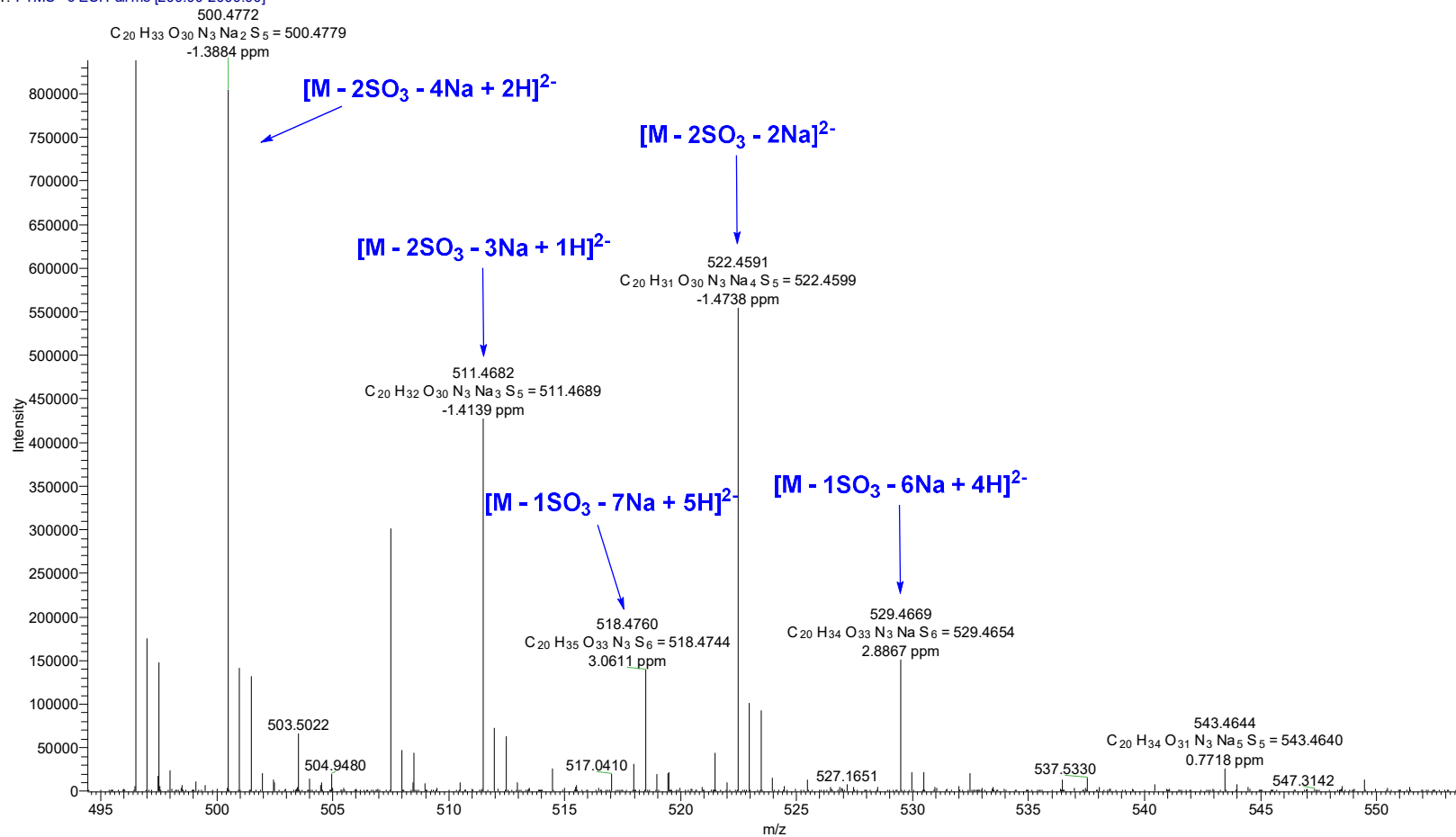
ZSY-2-47 #3-23 RT: 0.04-0.65 AV: 21 NL: 6.05E5
 T: FTMS - c ESI Full ms [200.00-2000.00]

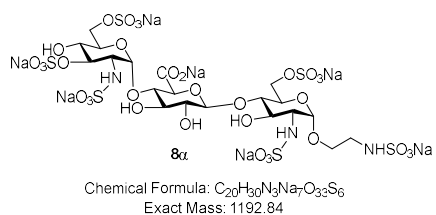




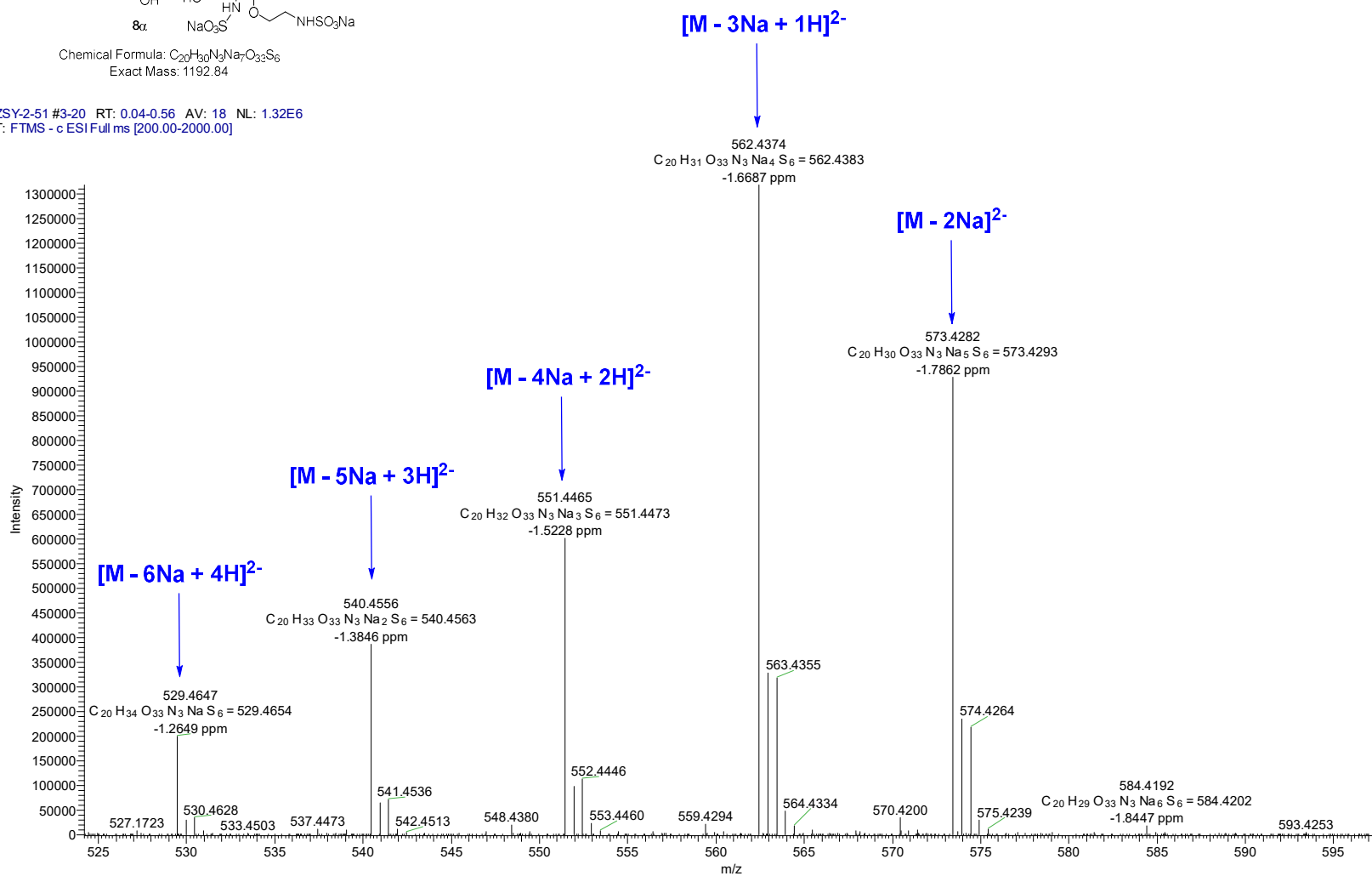
Chemical Formula: C₂₀H₂₉N₃Na₆O₃₆S₇
 Exact Mass: 1294.78

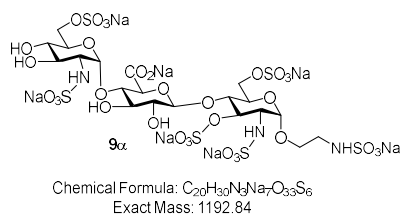
ZSY-2-50 #4-15 RT: 0.07-0.40 AV: 12 NL: 8.37E5
 T: FTMS - c ESI Full ms [200.00-2000.00]



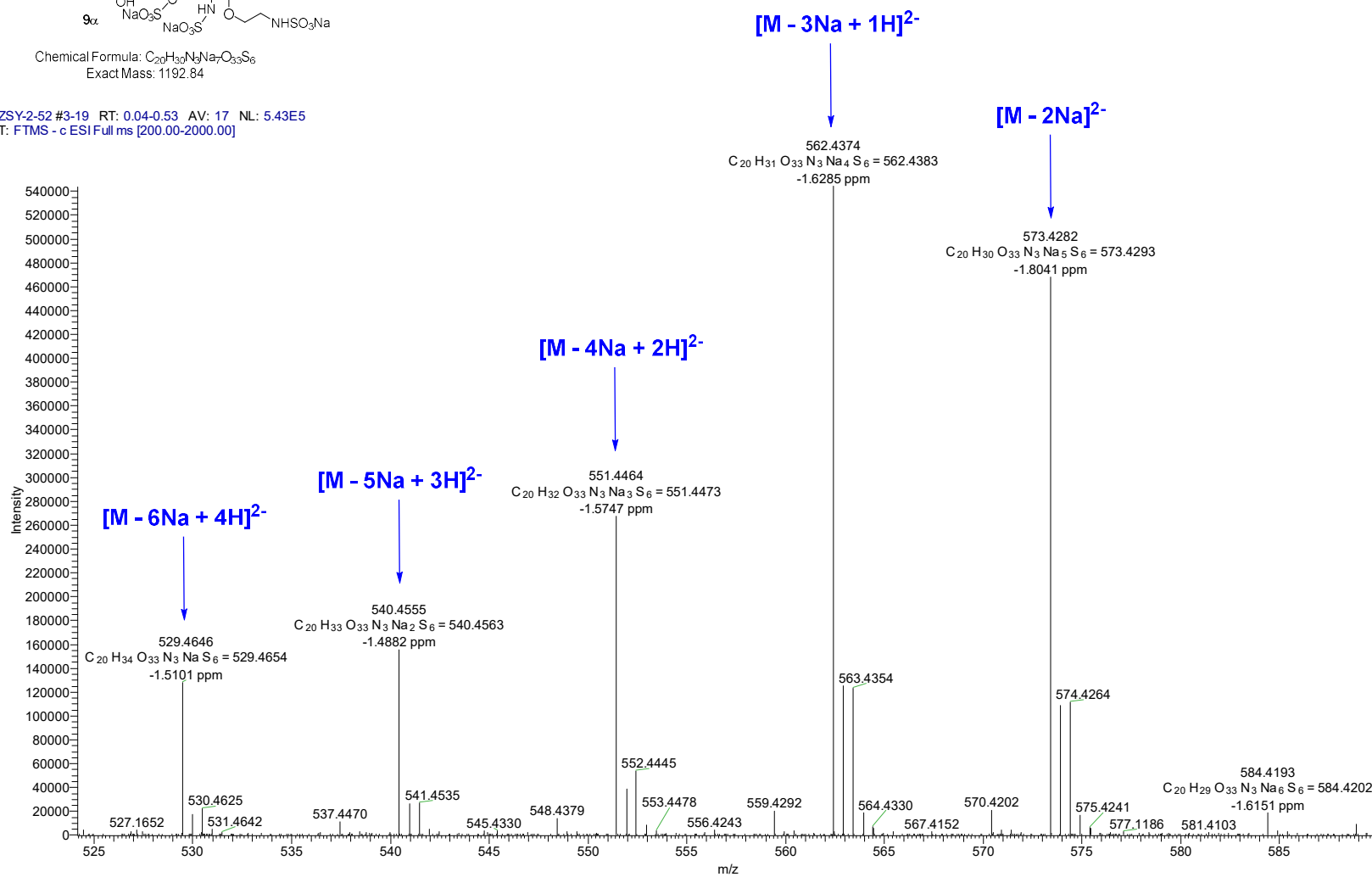


ZSY-2-51 #3-20 RT: 0.04-0.56 AV: 18 NL: 1.32E6
T: FTMS - c ESI Full ms [200.00-2000.00]

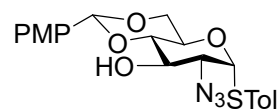




ZSY-2-52 #3-19 RT: 0.04-0.53 AV: 17 NL: 5.43E5
T: FTMS - c ESI Full ms [200.00-2000.00]

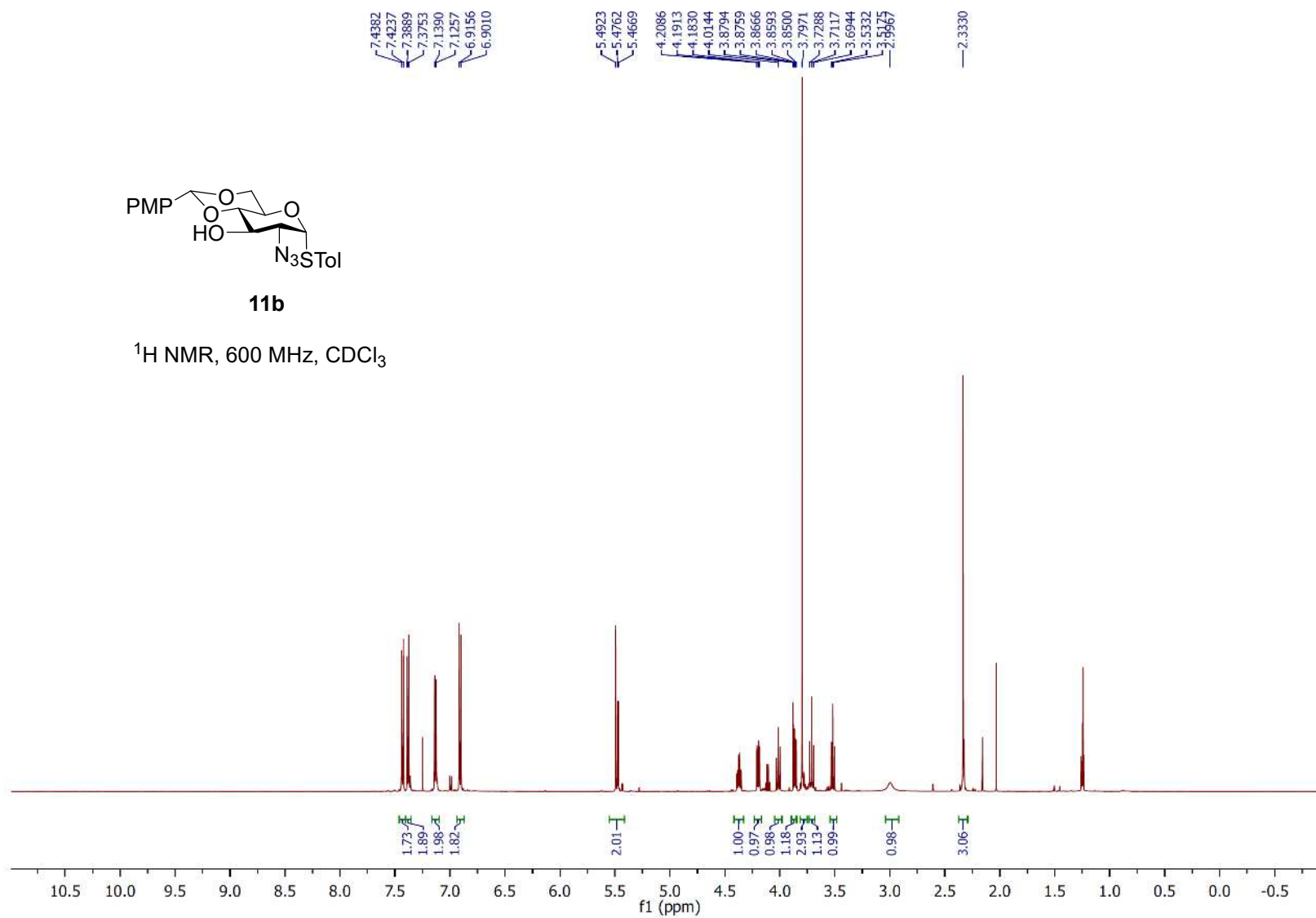


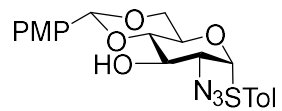
12. NMR Data



11b

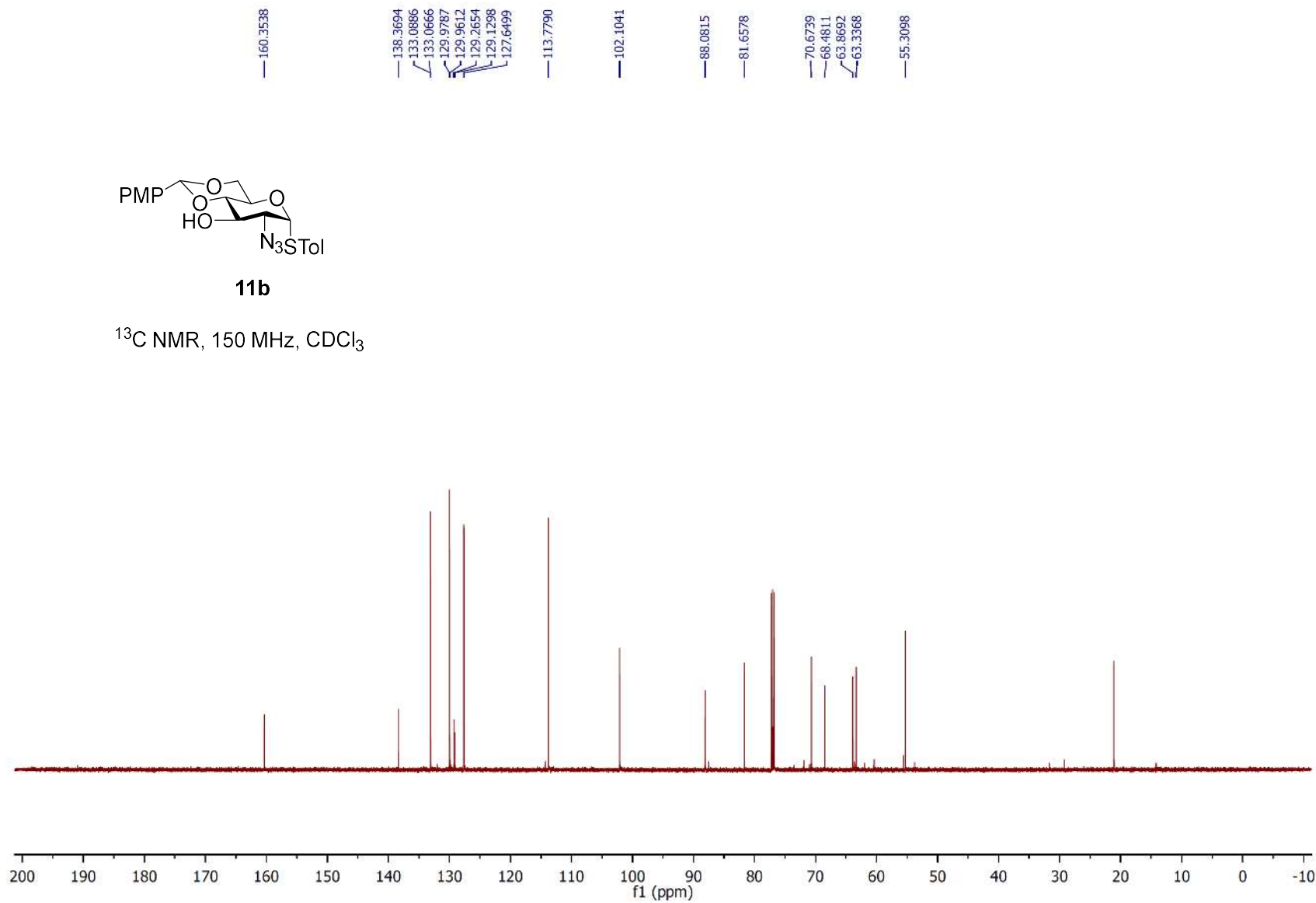
¹H NMR, 600 MHz, CDCl₃

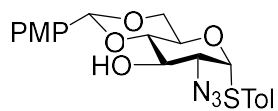




11b

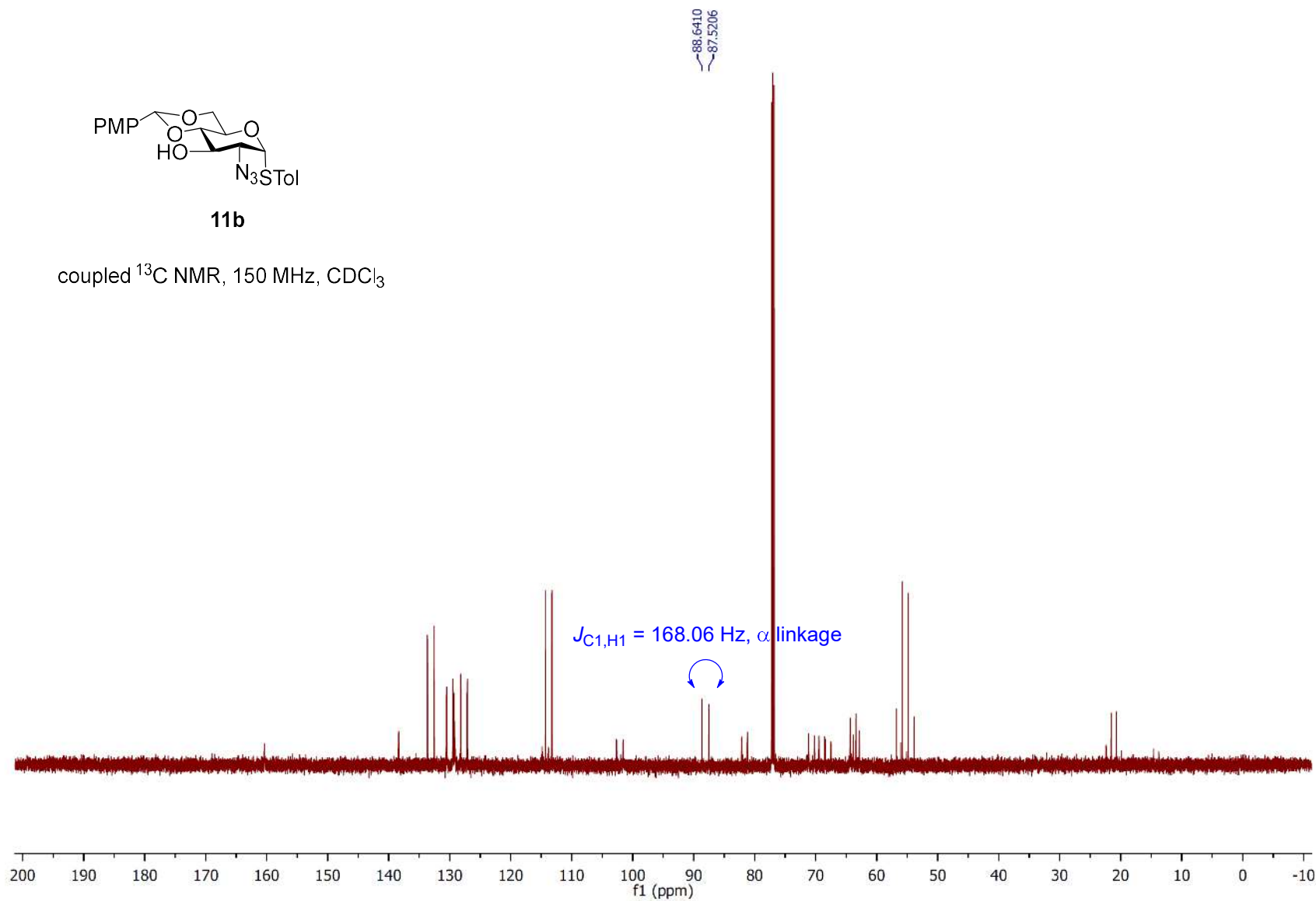
^{13}C NMR, 150 MHz, CDCl_3

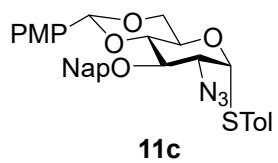




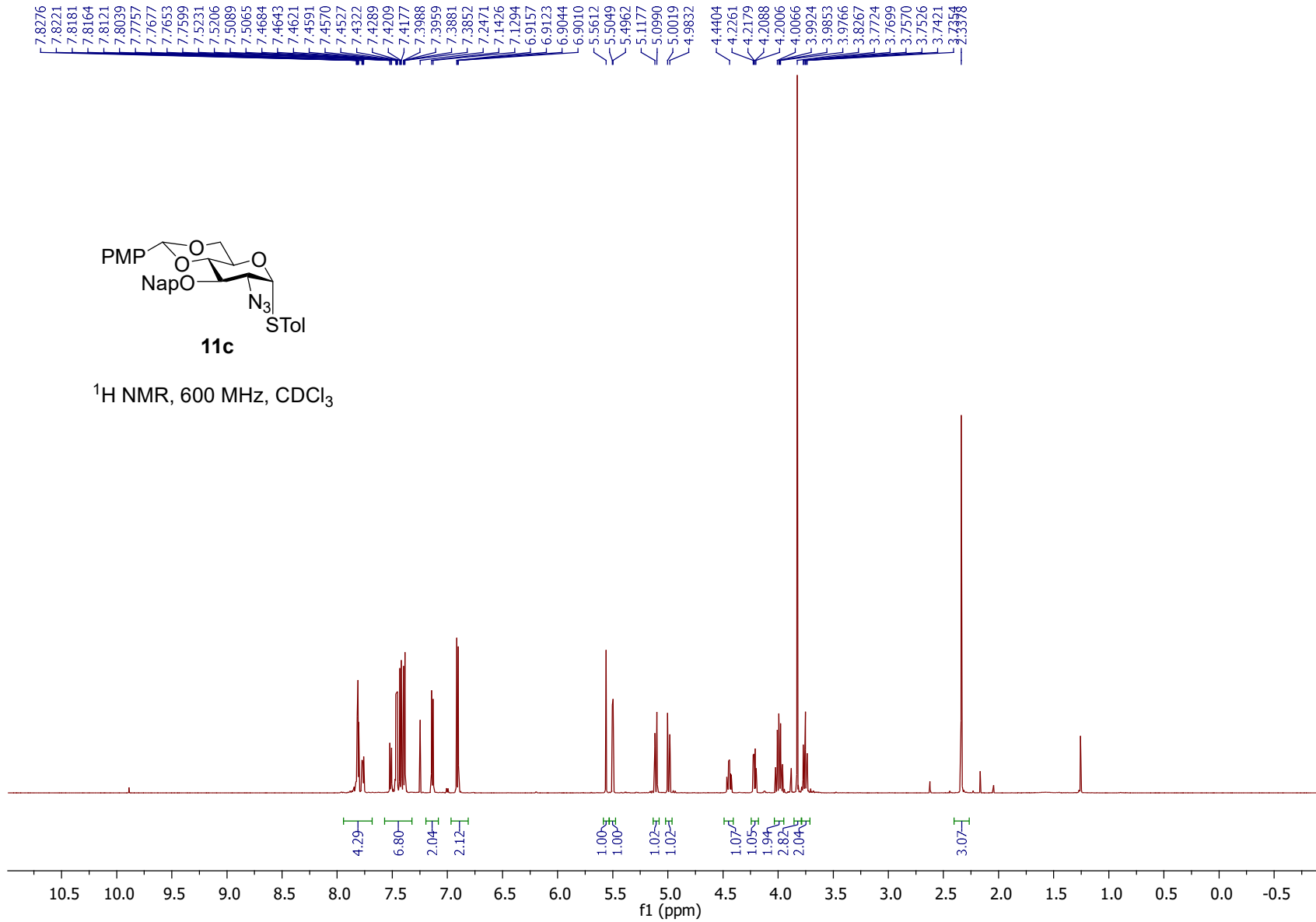
11b

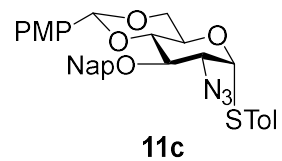
coupled ^{13}C NMR, 150 MHz, CDCl_3



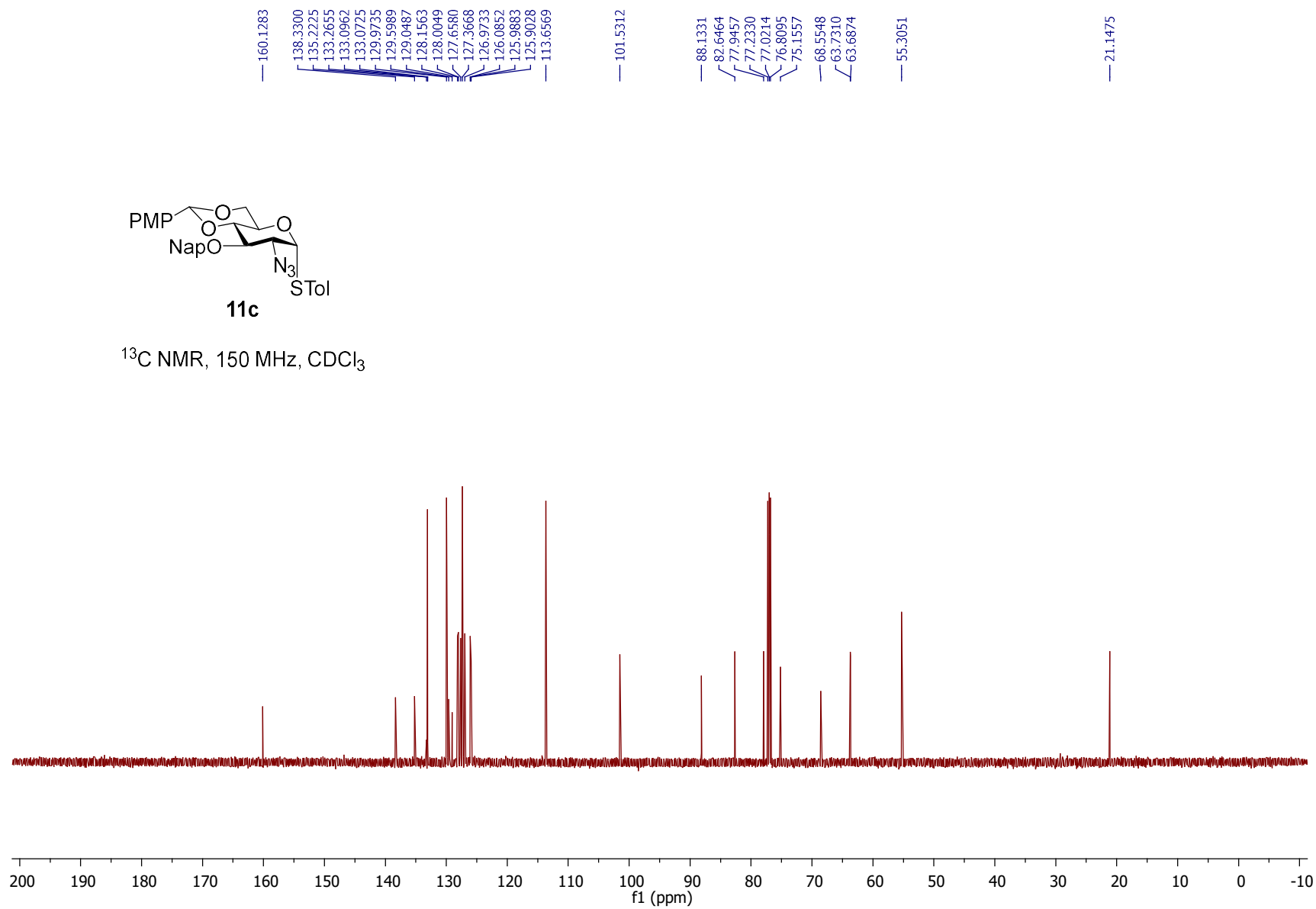


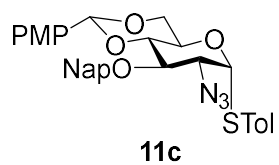
¹H NMR, 600 MHz, CDCl₃



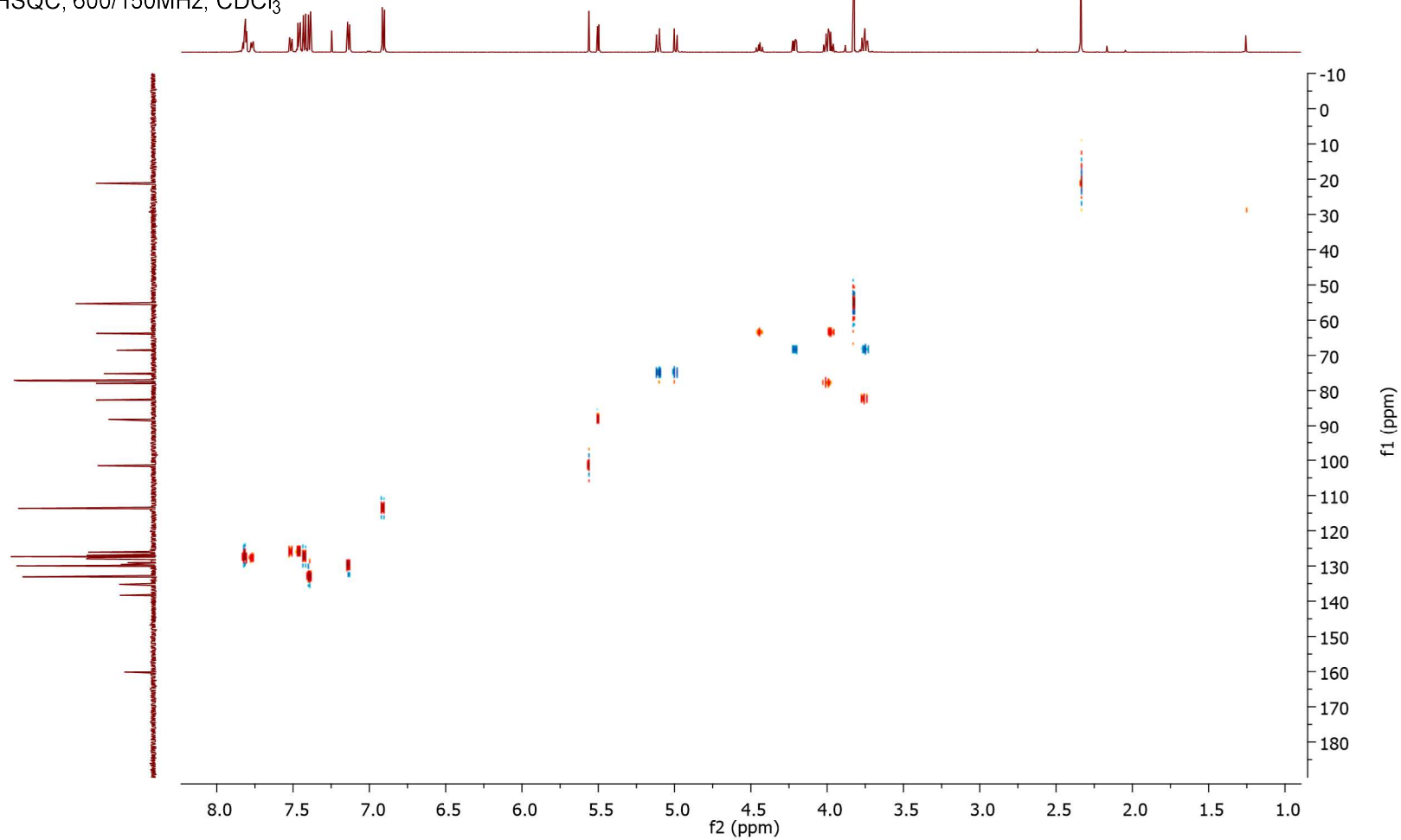


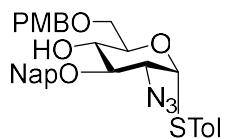
^{13}C NMR, 150 MHz, CDCl_3





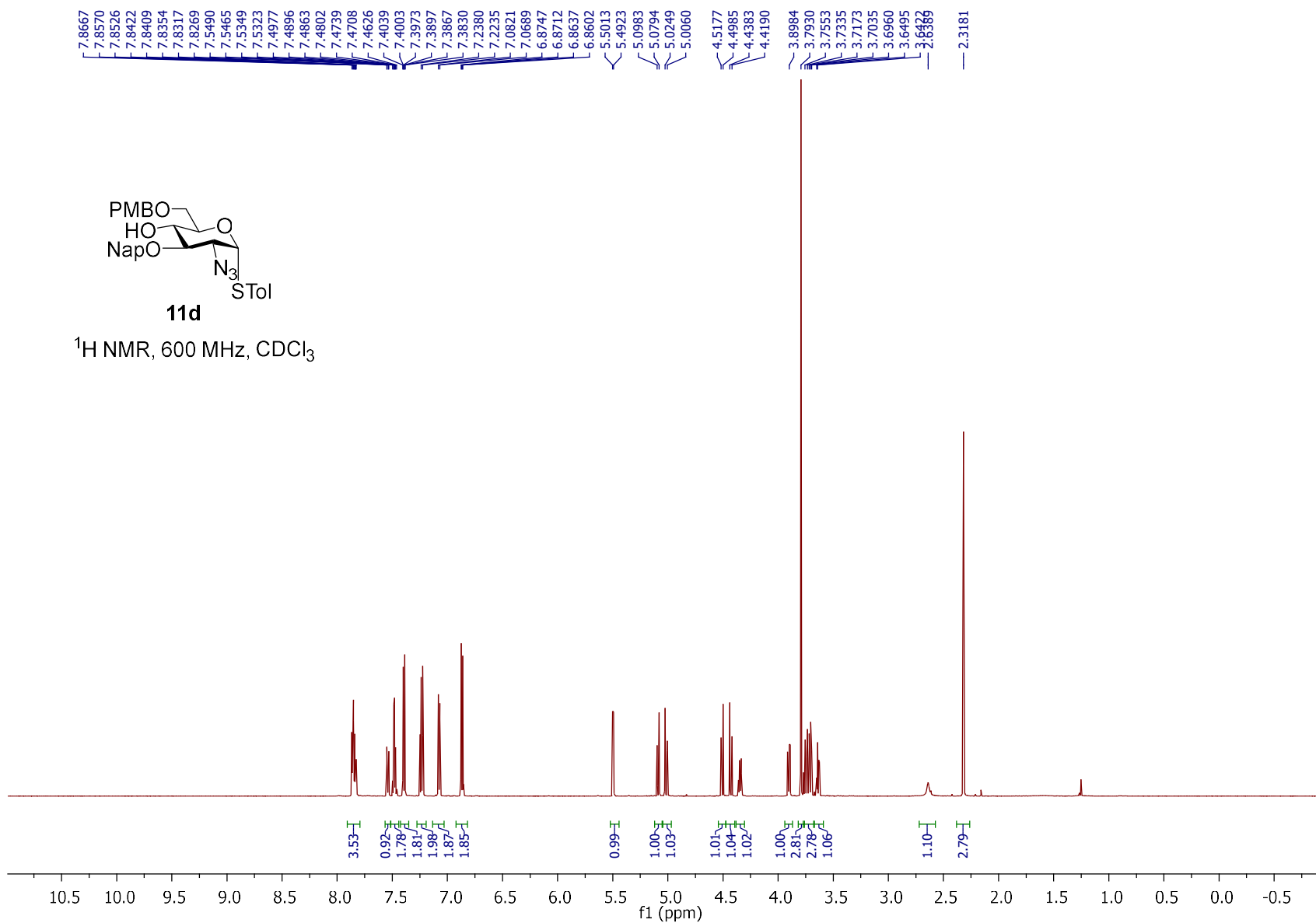
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

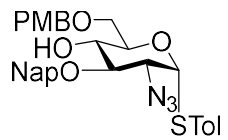




11d

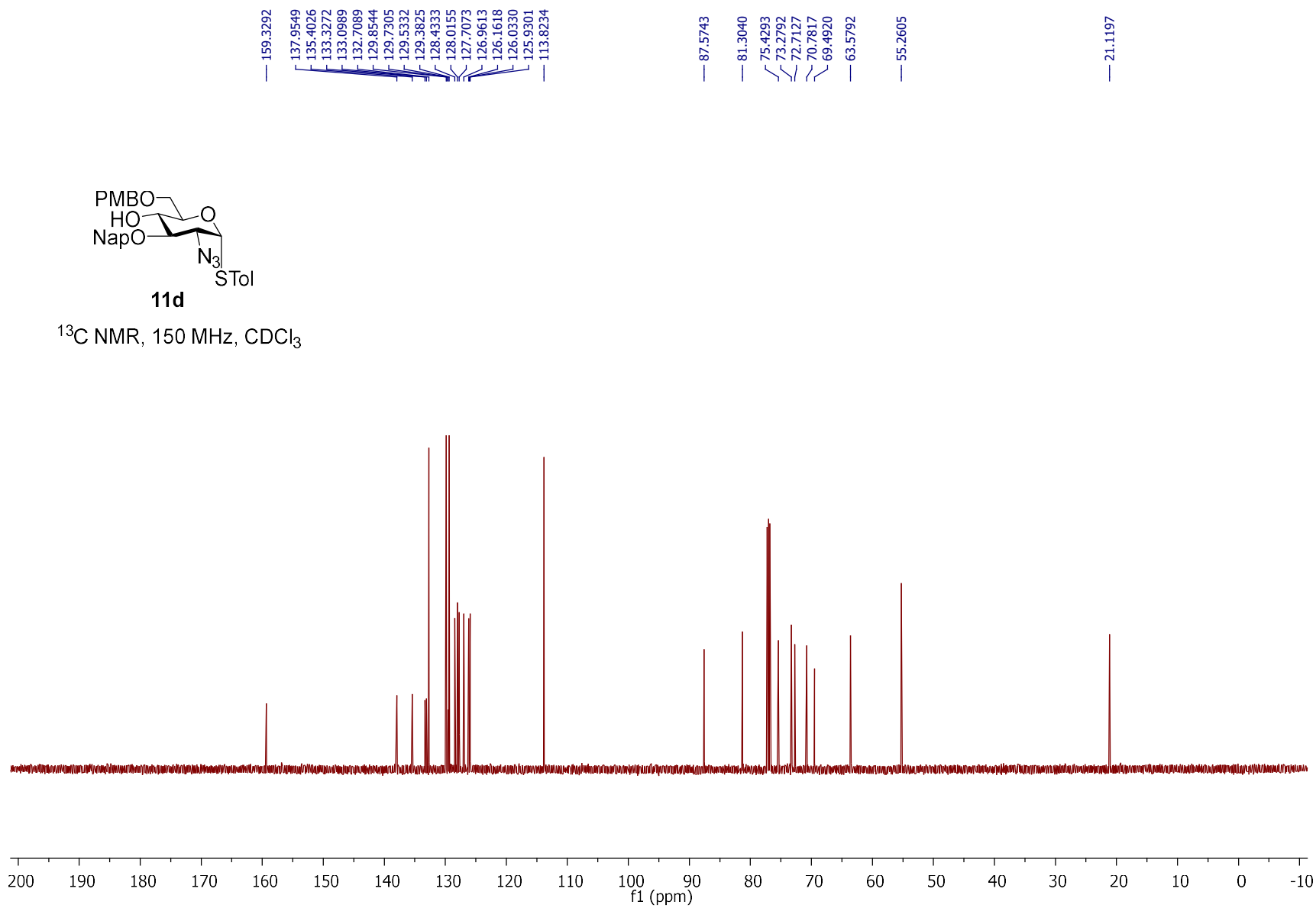
^1H NMR, 600 MHz, CDCl_3

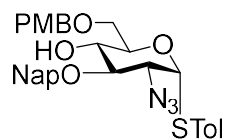




11d

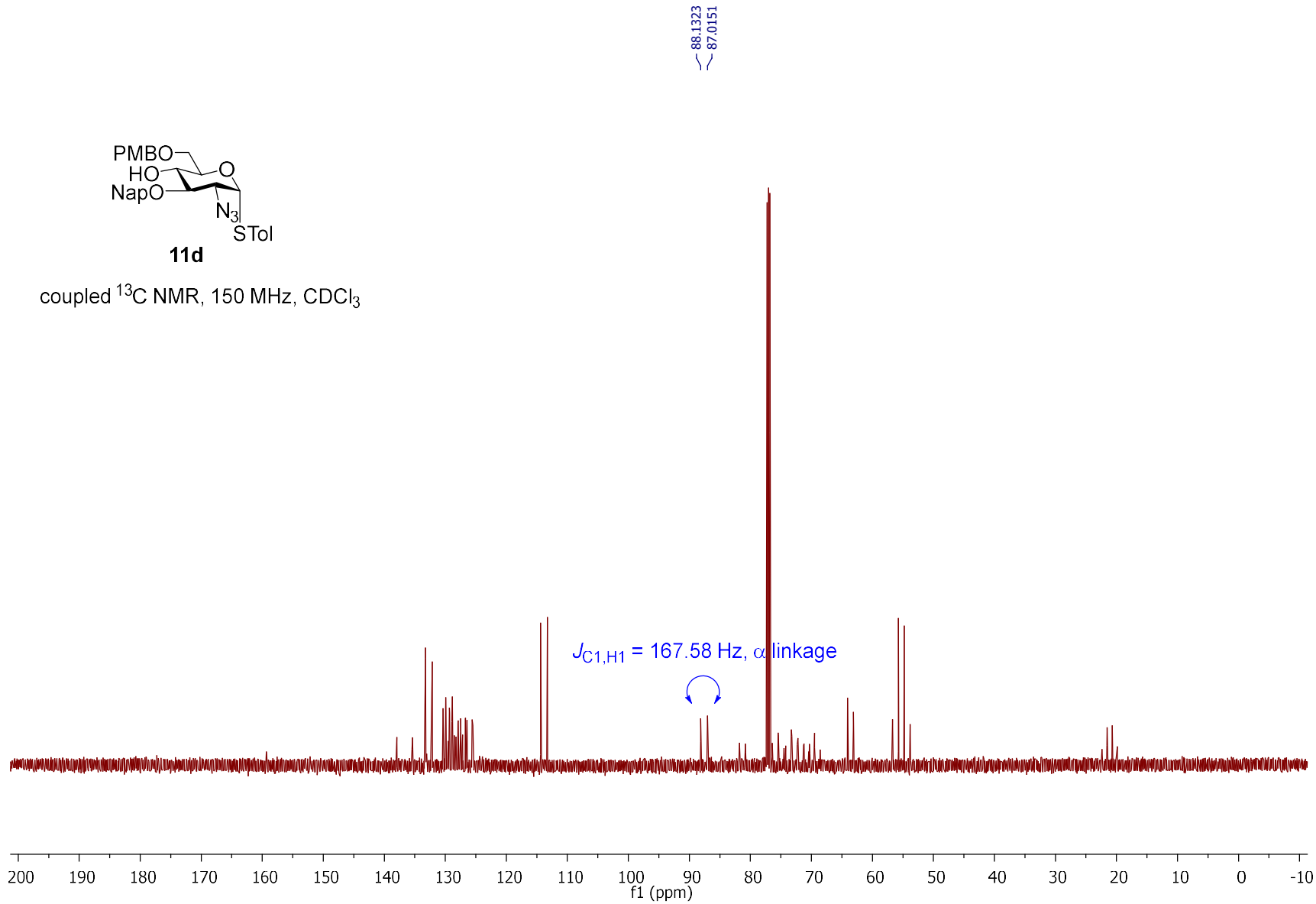
¹³C NMR, 150 MHz, CDCl₃

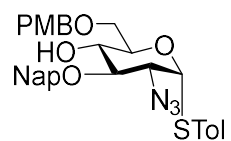




11d

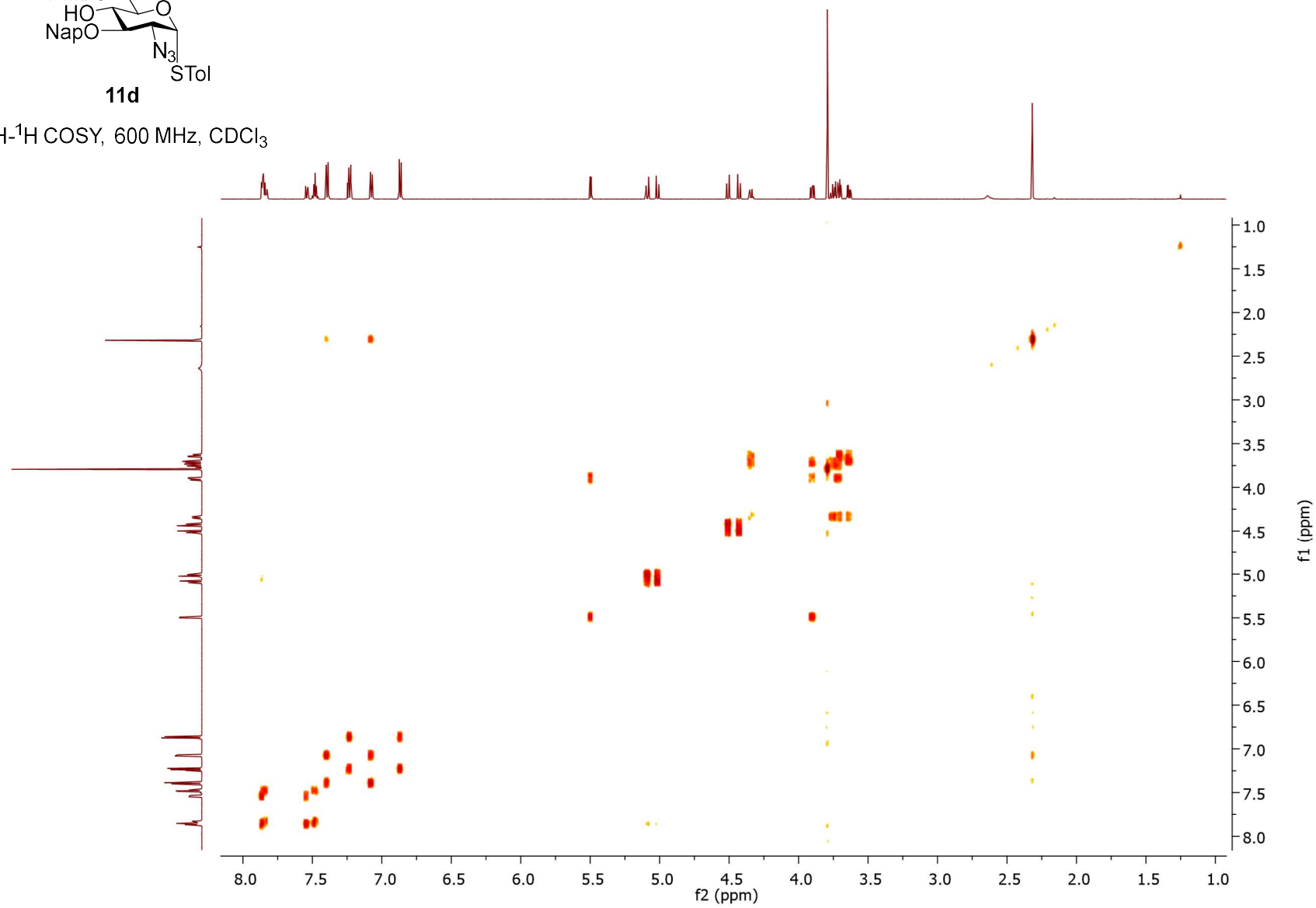
coupled ^{13}C NMR, 150 MHz, CDCl_3

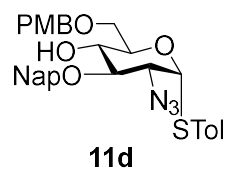




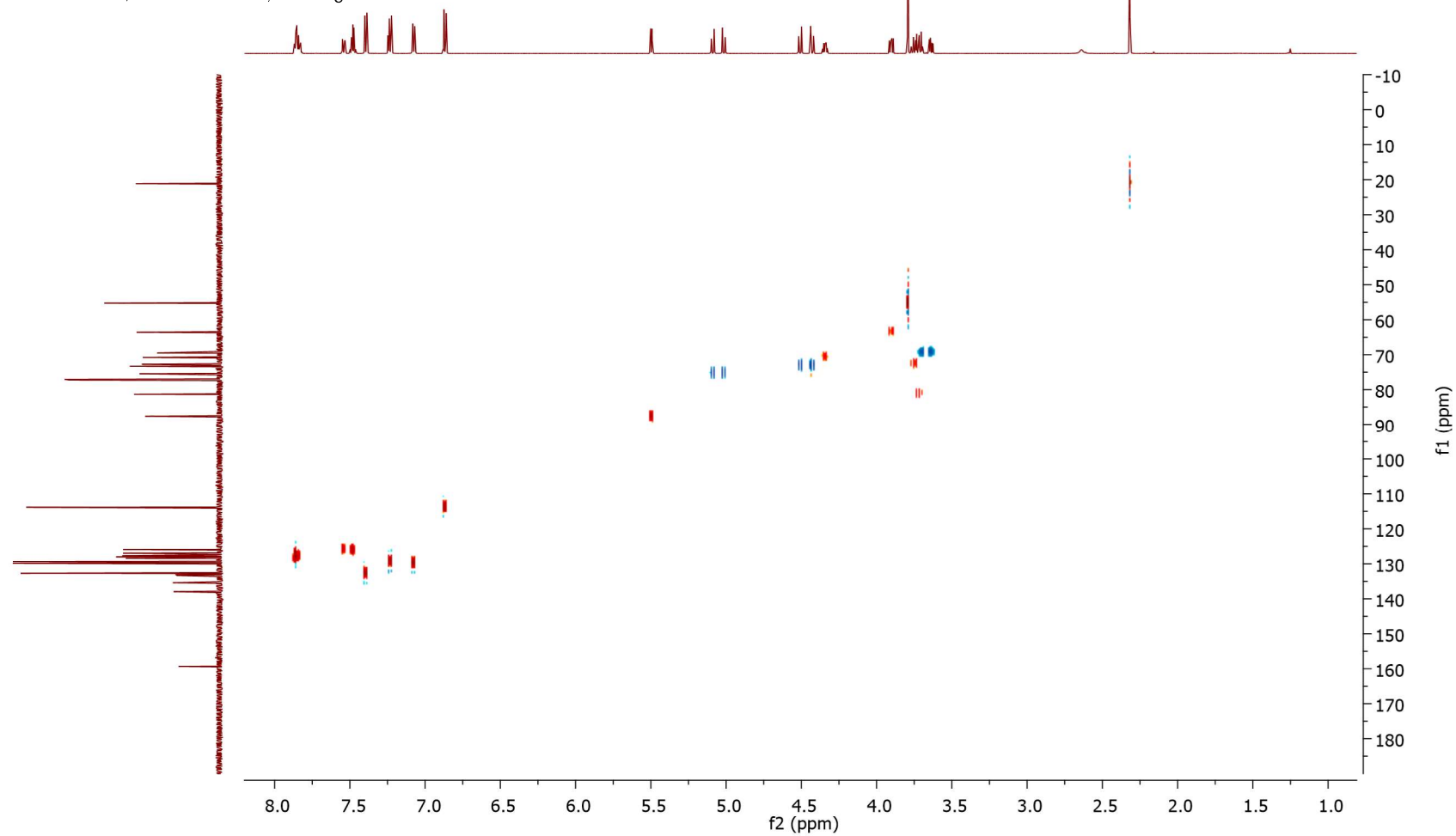
11d

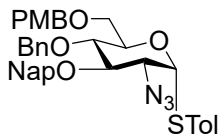
¹H-¹H COSY, 600 MHz, CDCl₃





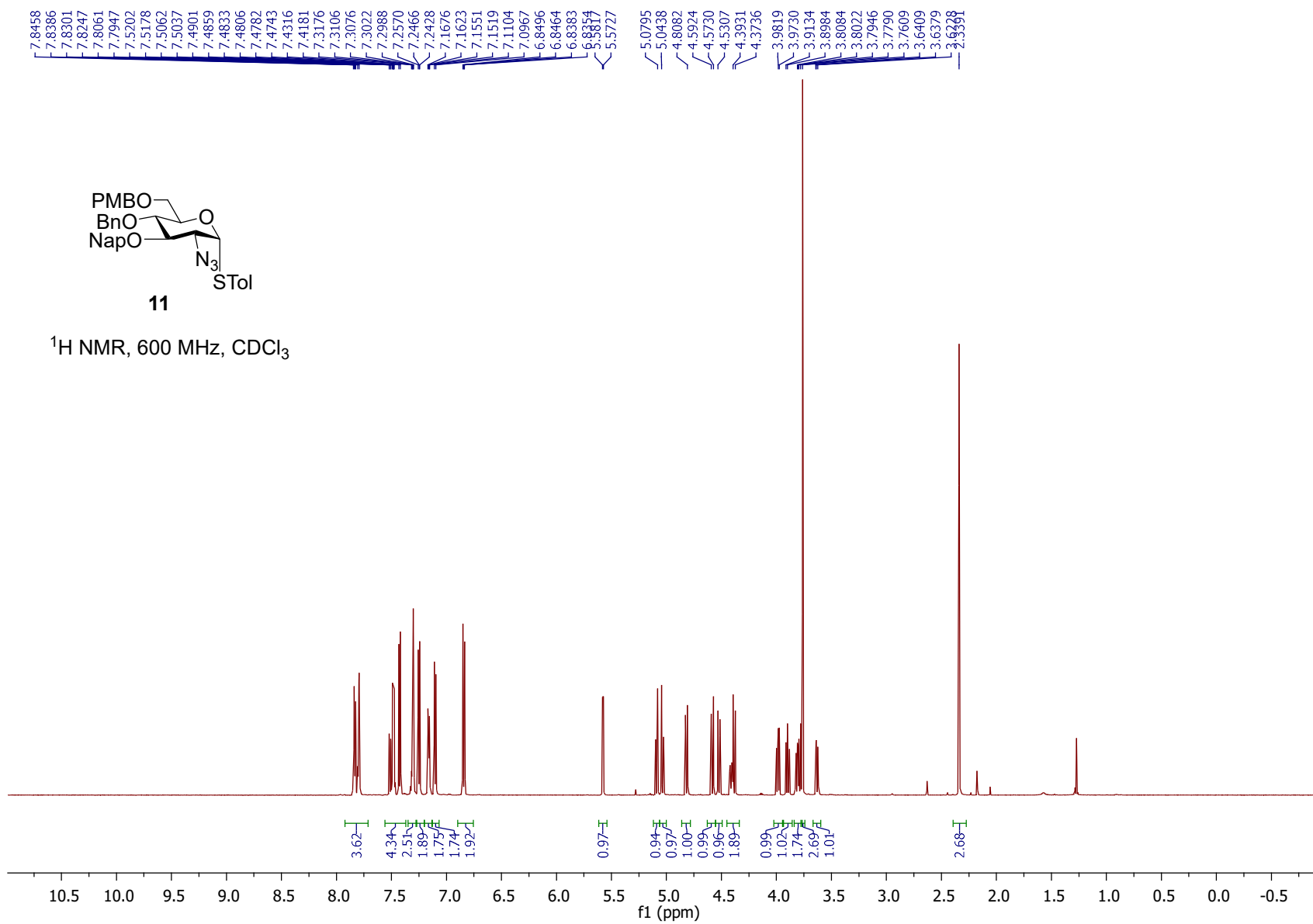
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

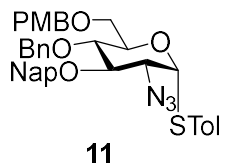




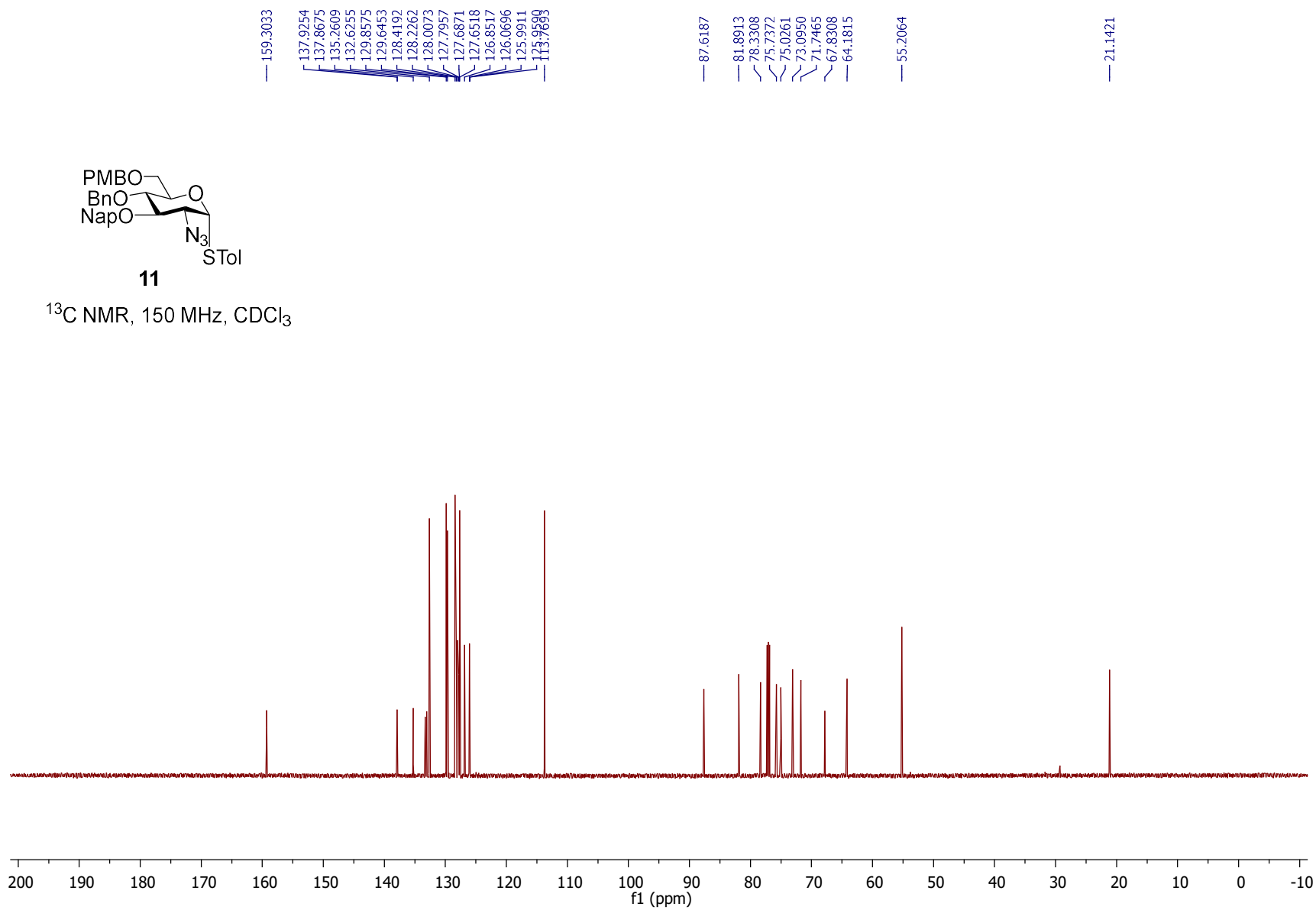
11

¹H NMR, 600 MHz, CDCl₃

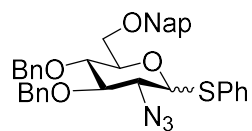




¹³C NMR, 150 MHz, CDCl₃

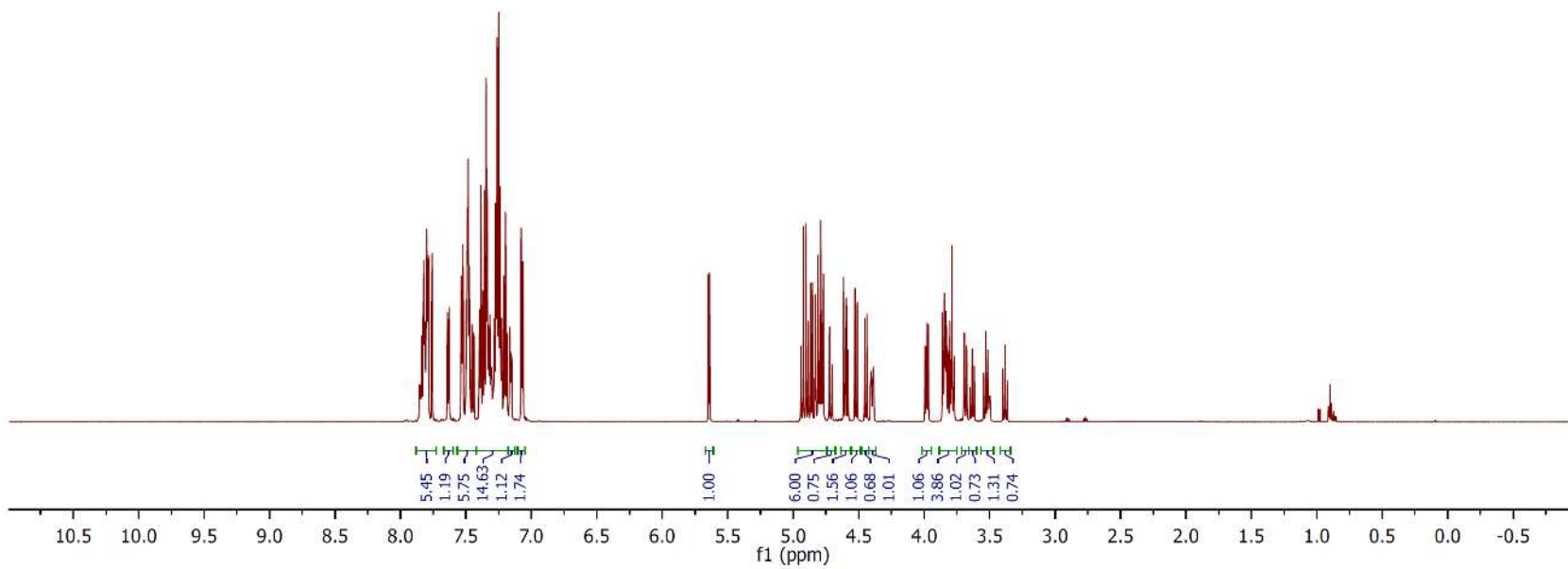


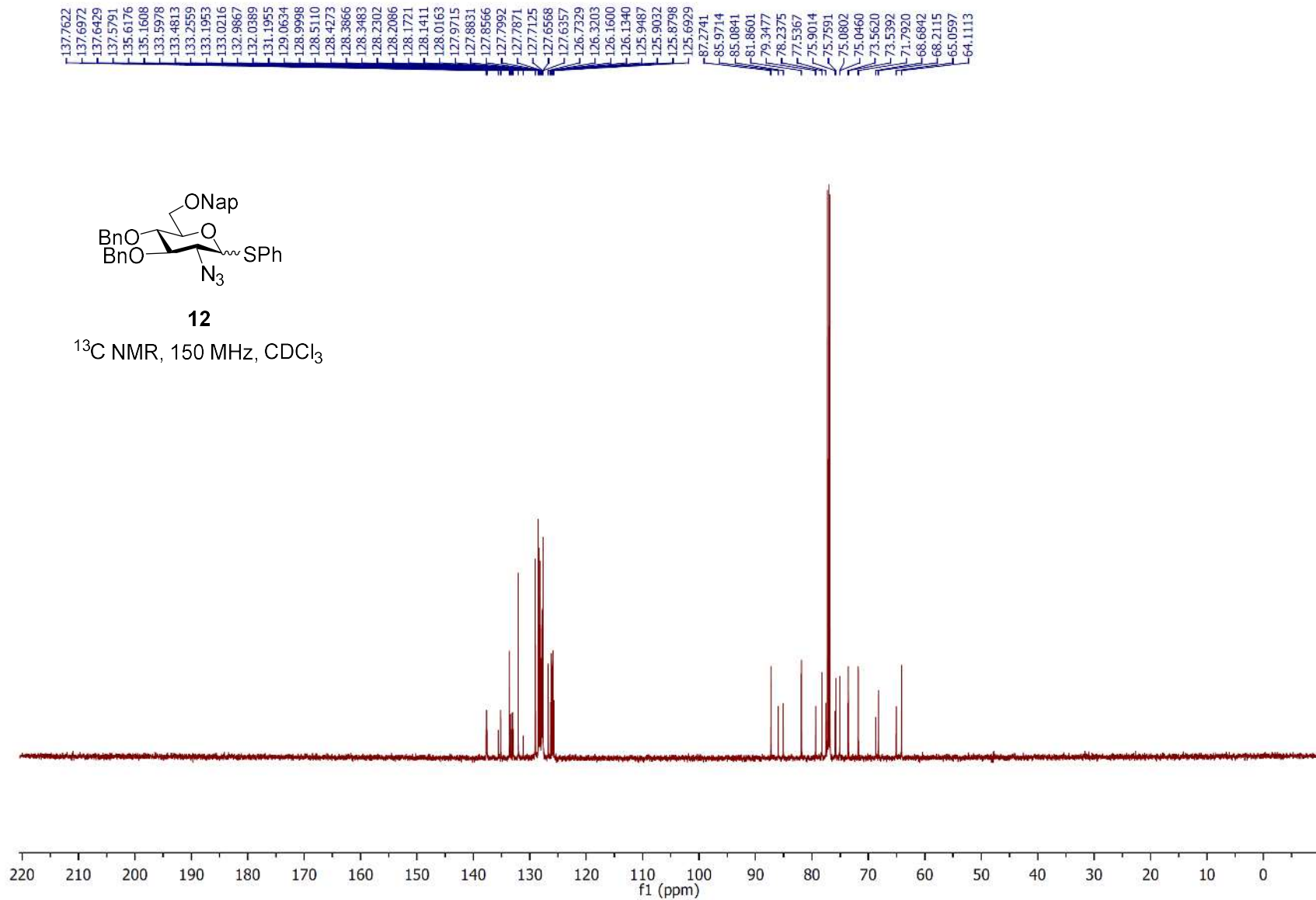
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7.4990
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7.4834
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7.4516
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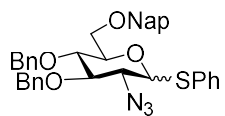


12

¹H NMR, 600 MHz, CDCl₃

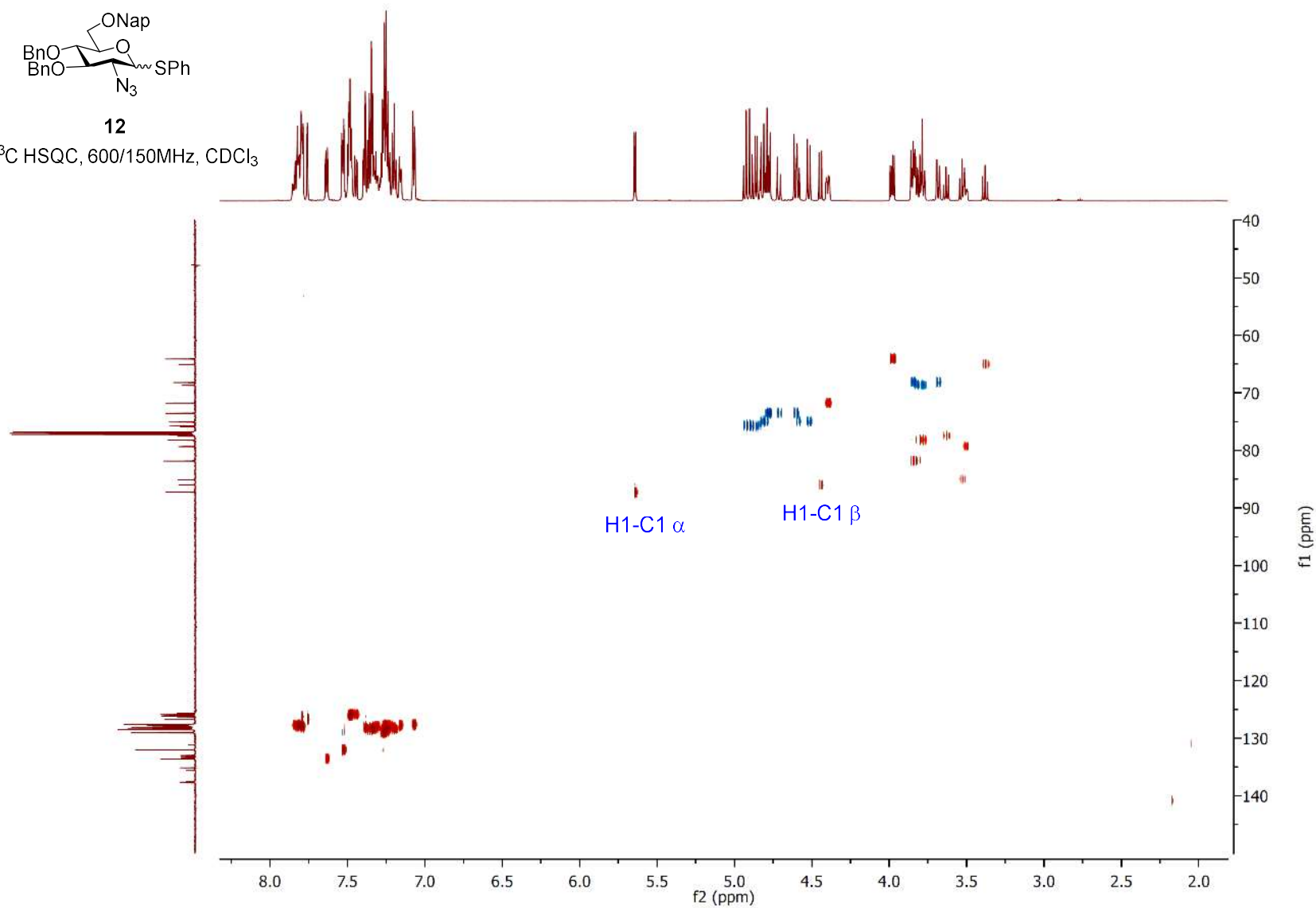


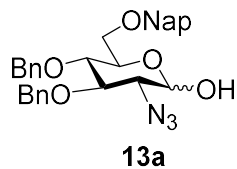




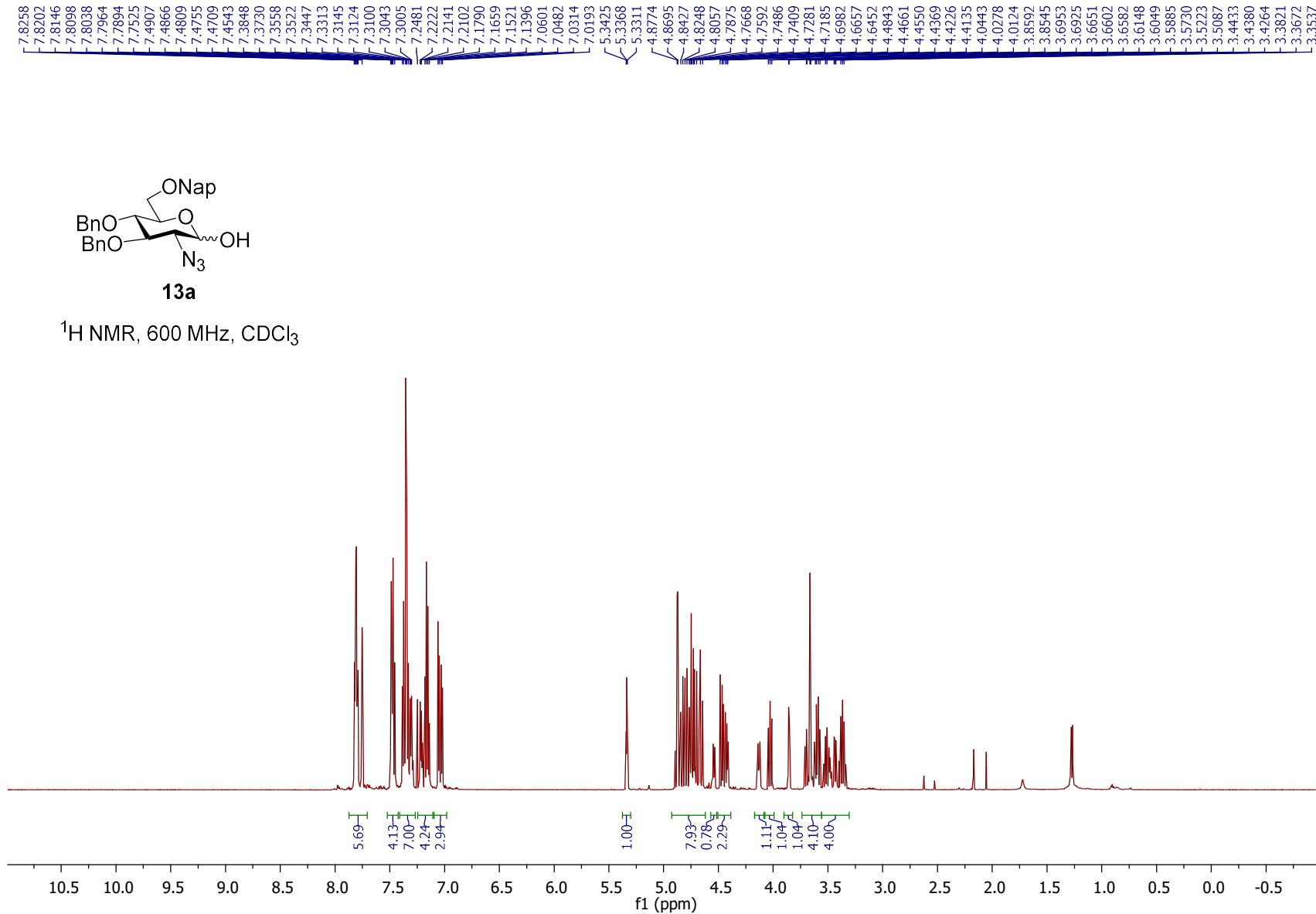
12

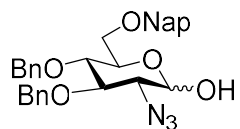
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3





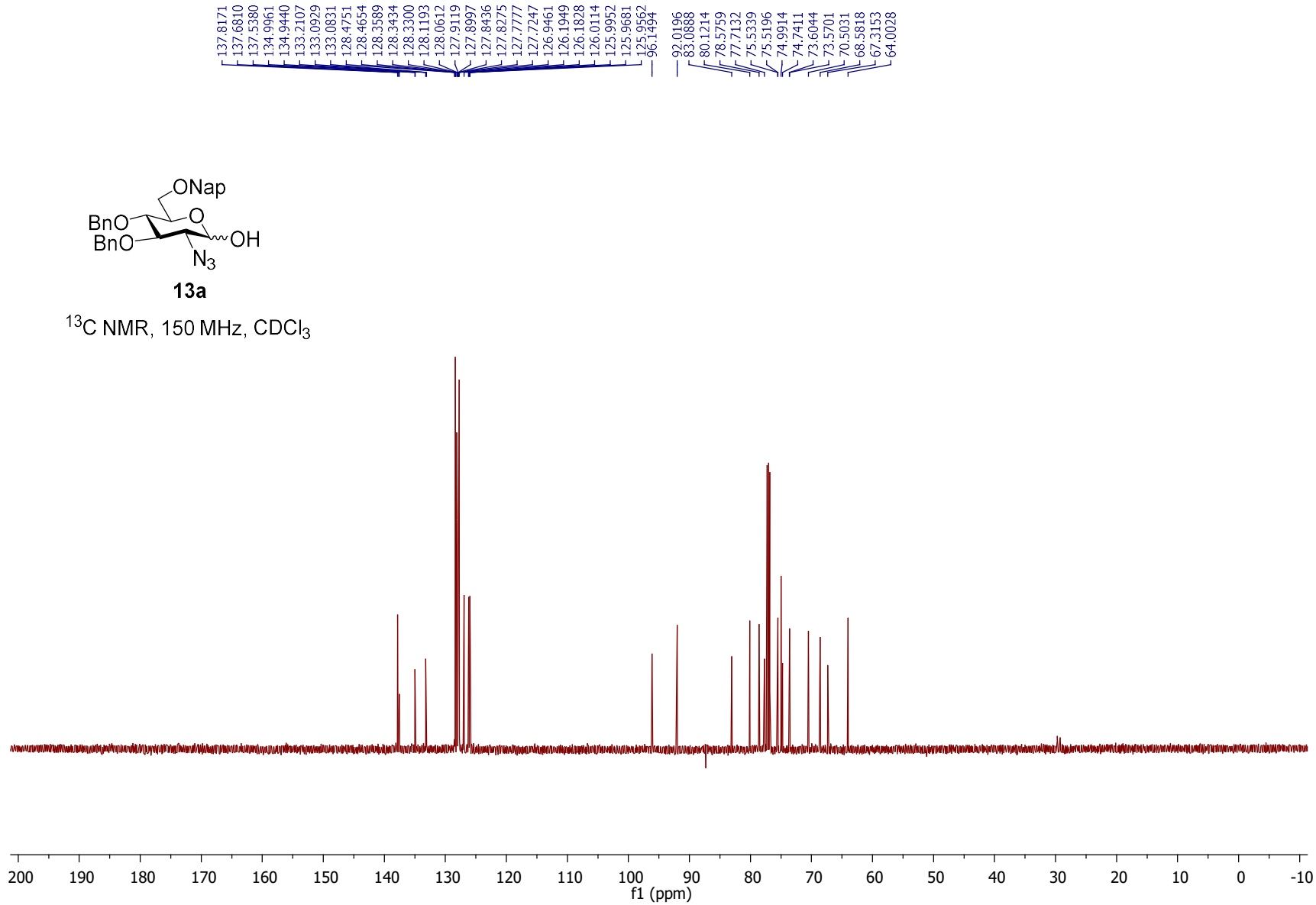
^1H NMR, 600 MHz, CDCl_3

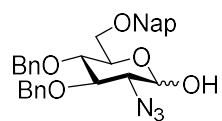




13a

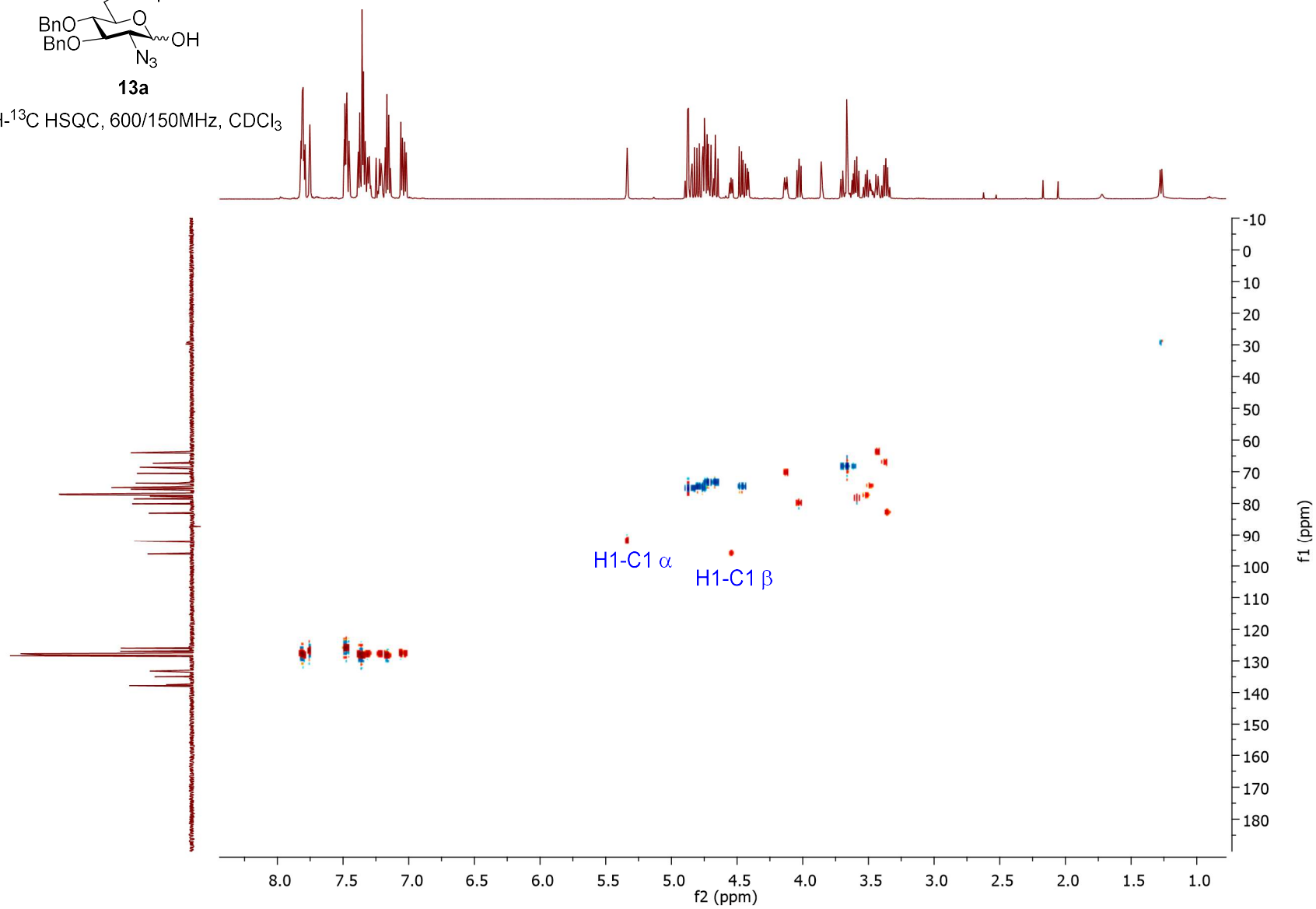
¹³C NMR, 150 MHz, CDCl₃



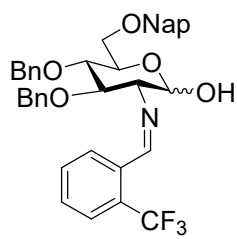


13a

^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

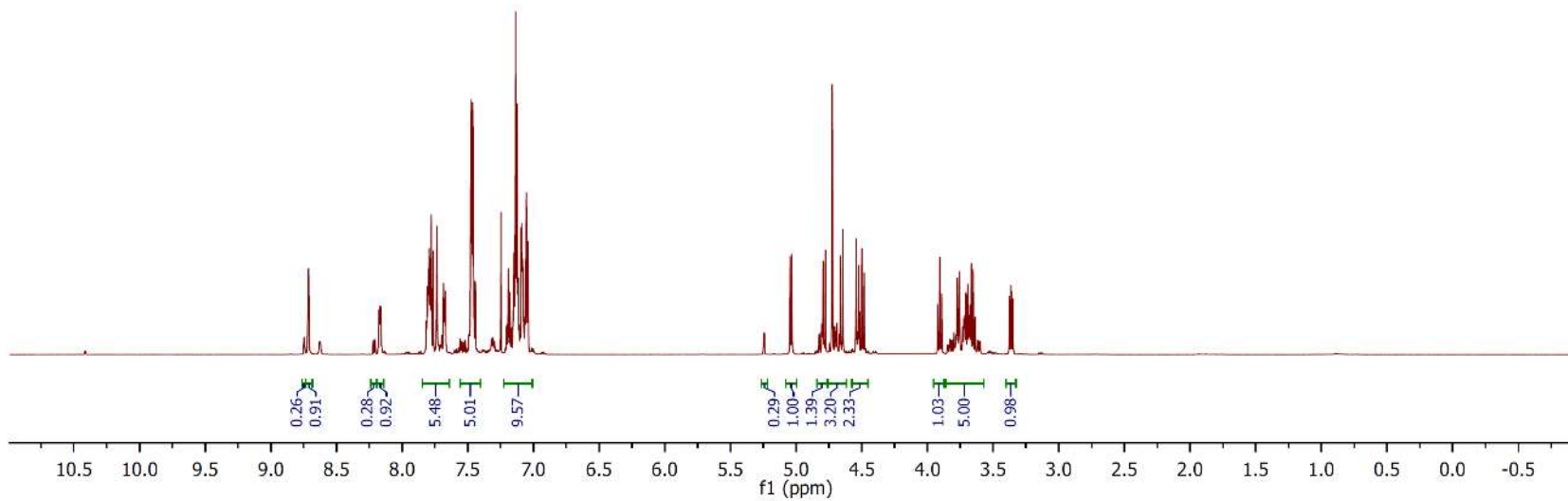


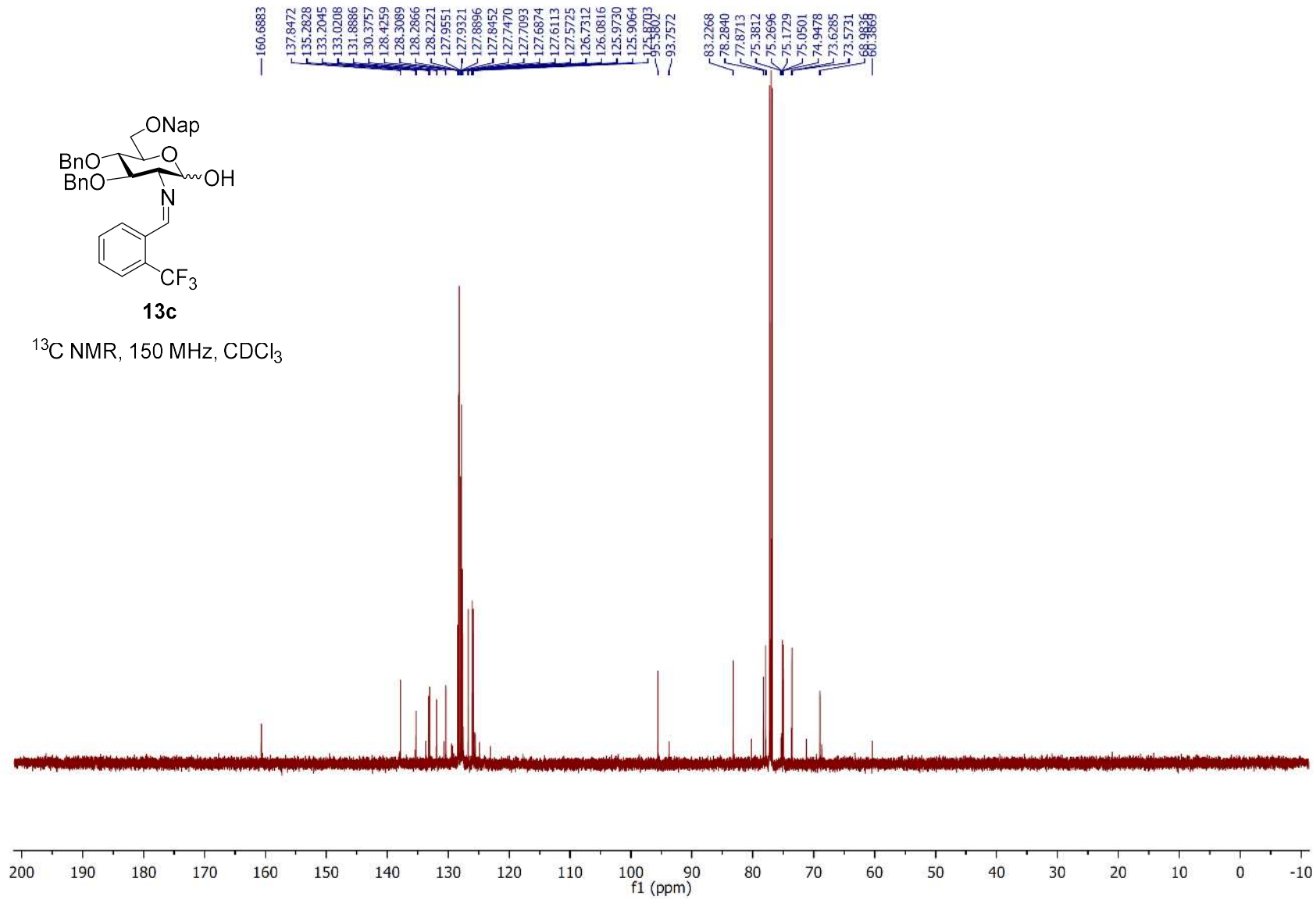
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7.7845
7.7777
7.7631
7.7352
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7.6744
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7.4680
7.4631
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7.4417
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7.1791
7.1550
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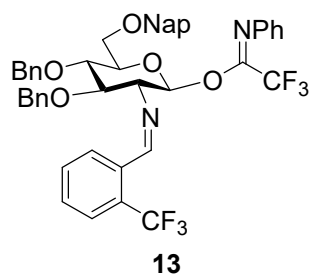


13c

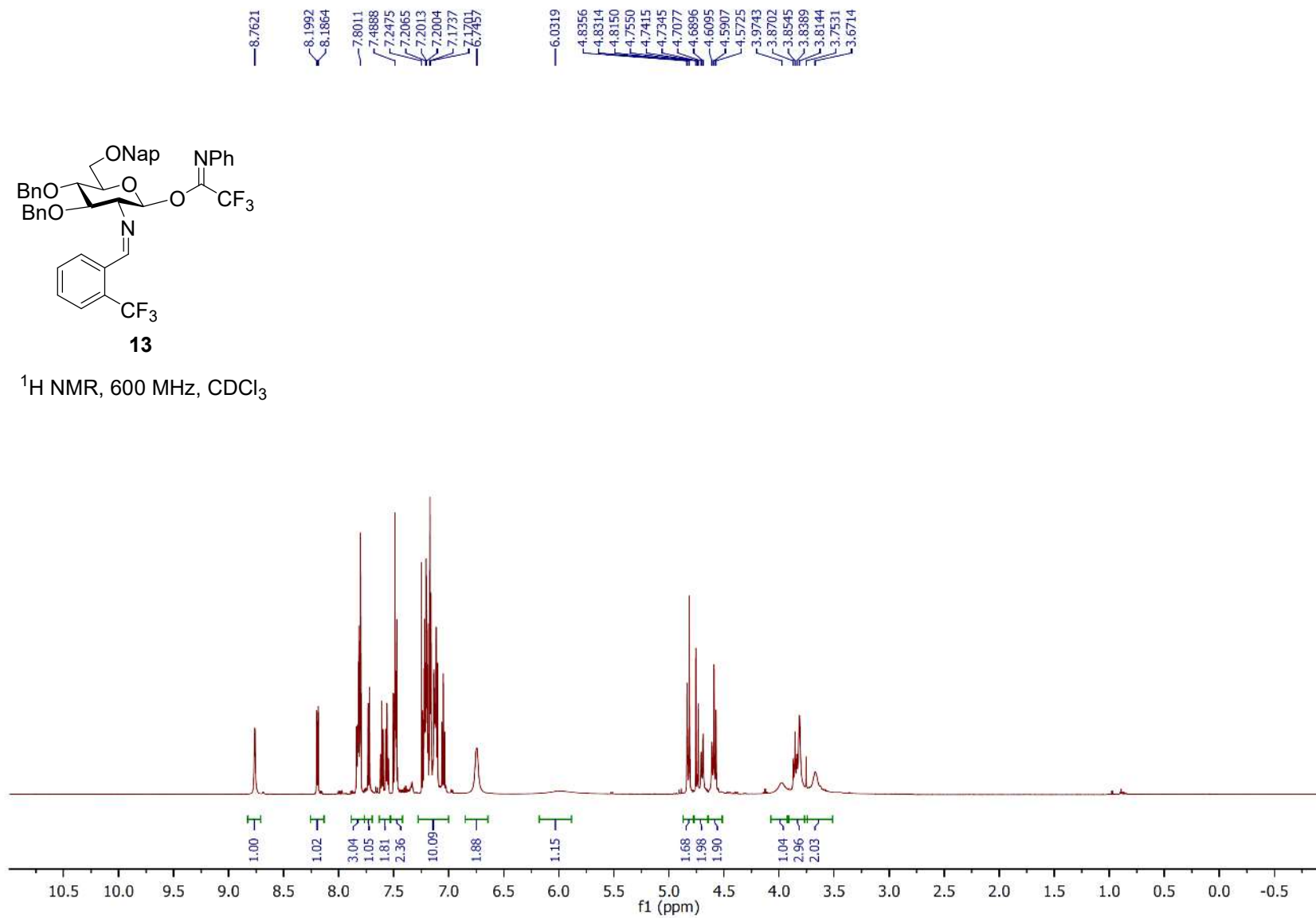
$^1\text{H NMR}$, 600 MHz, CDCl_3

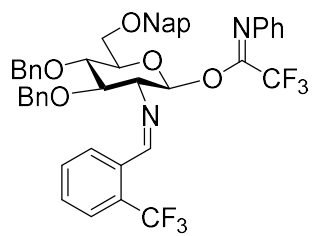






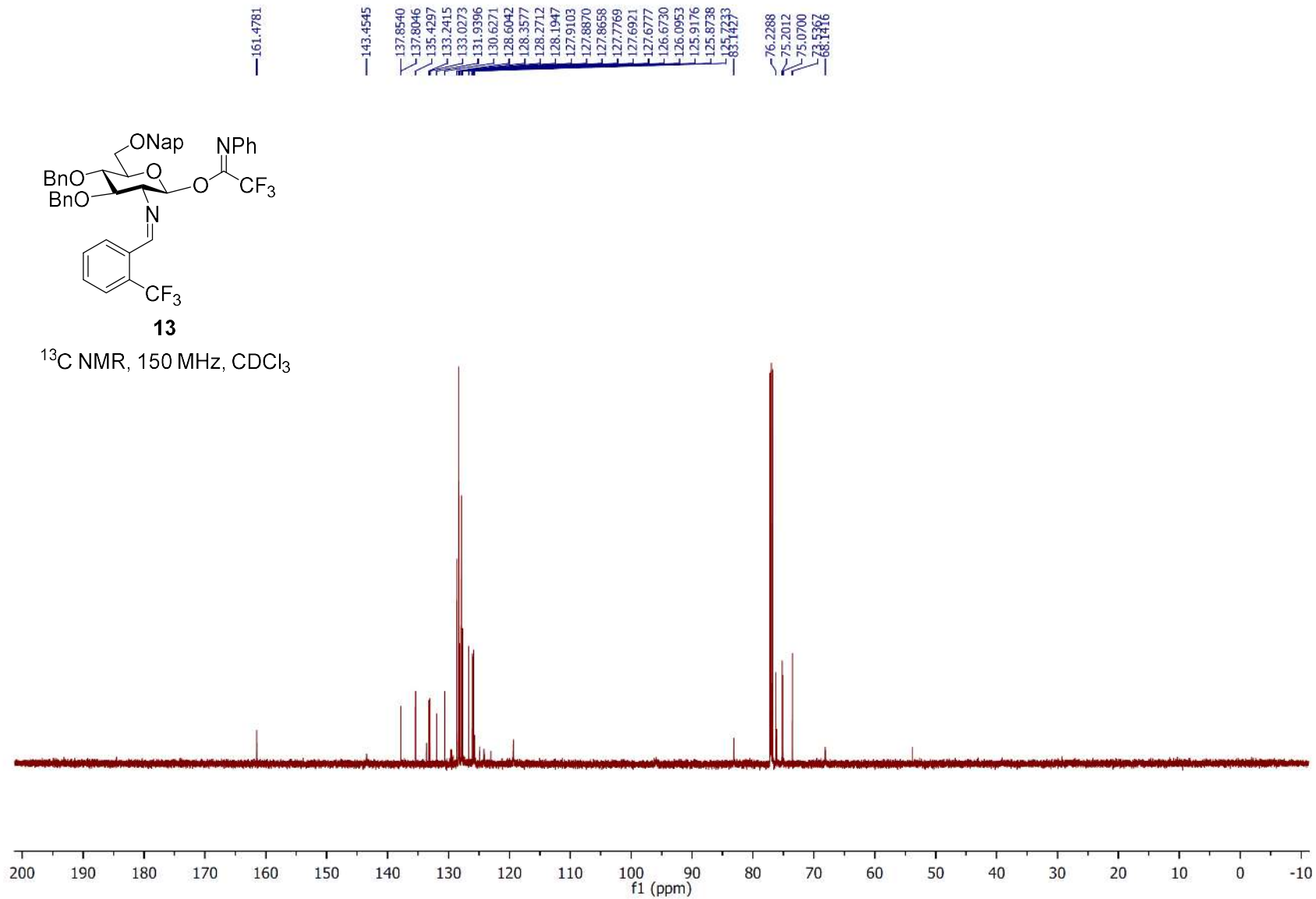
$^1\text{H NMR}$, 600 MHz, CDCl_3

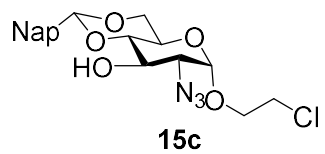




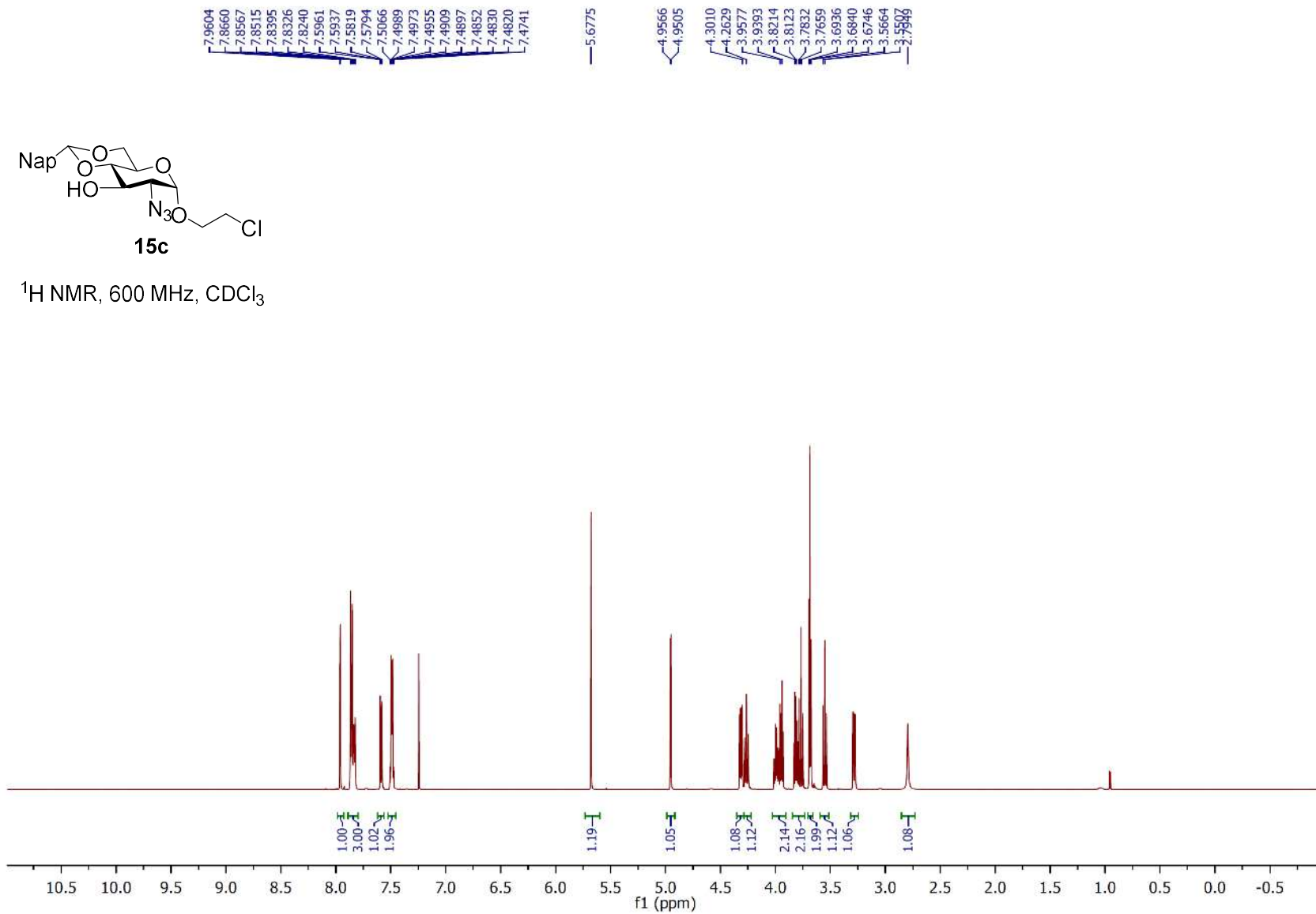
13

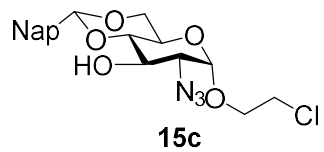
^{13}C NMR, 150 MHz, CDCl_3



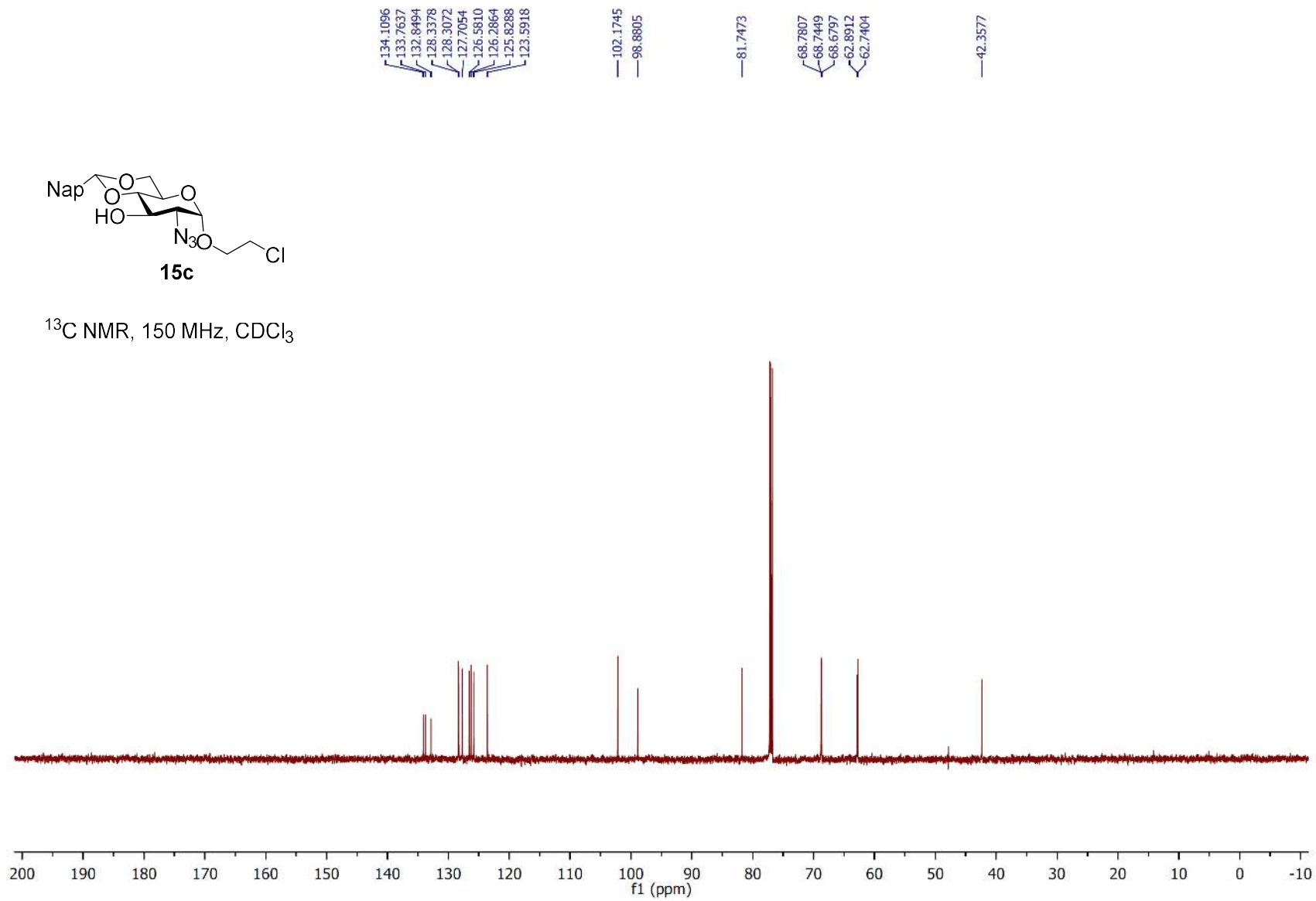


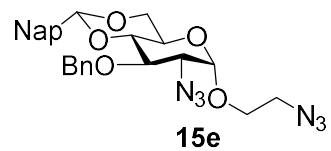
¹H NMR, 600 MHz, CDCl₃



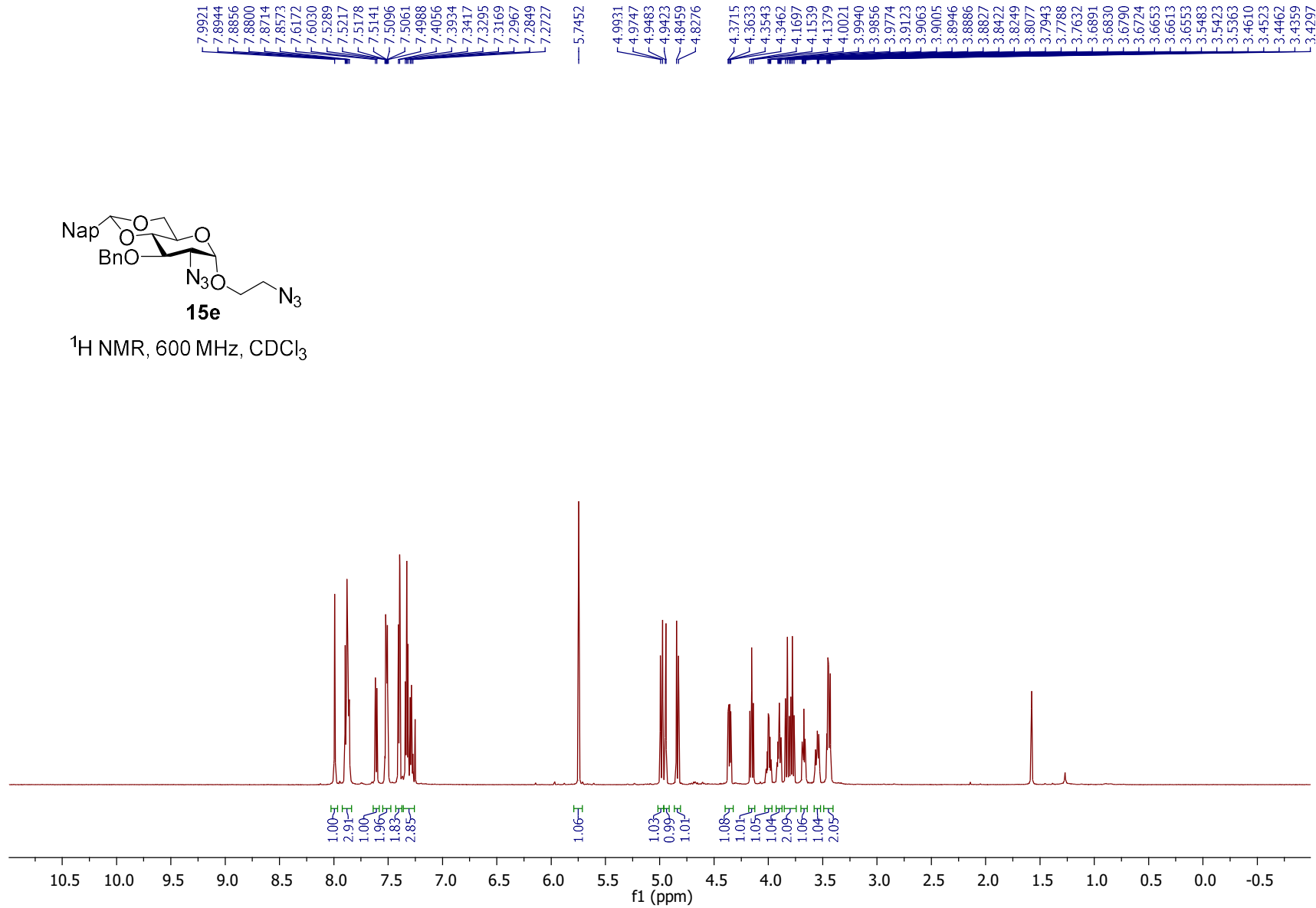


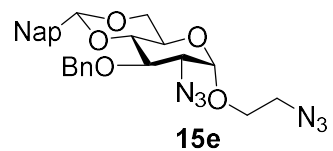
^{13}C NMR, 150 MHz, CDCl_3





$^1\text{H NMR}$, 600 MHz, CDCl_3





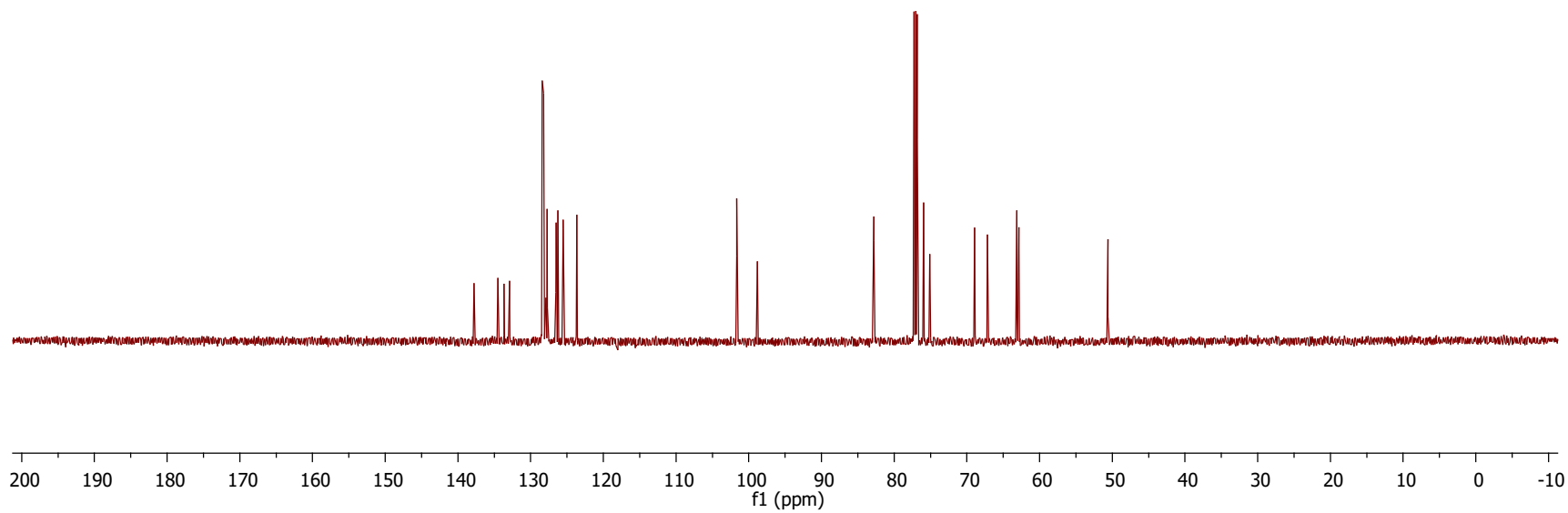
^{13}C NMR, 150 MHz, CDCl_3

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128.2032
128.1597
127.8909
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126.5000
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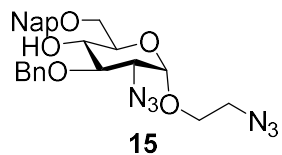
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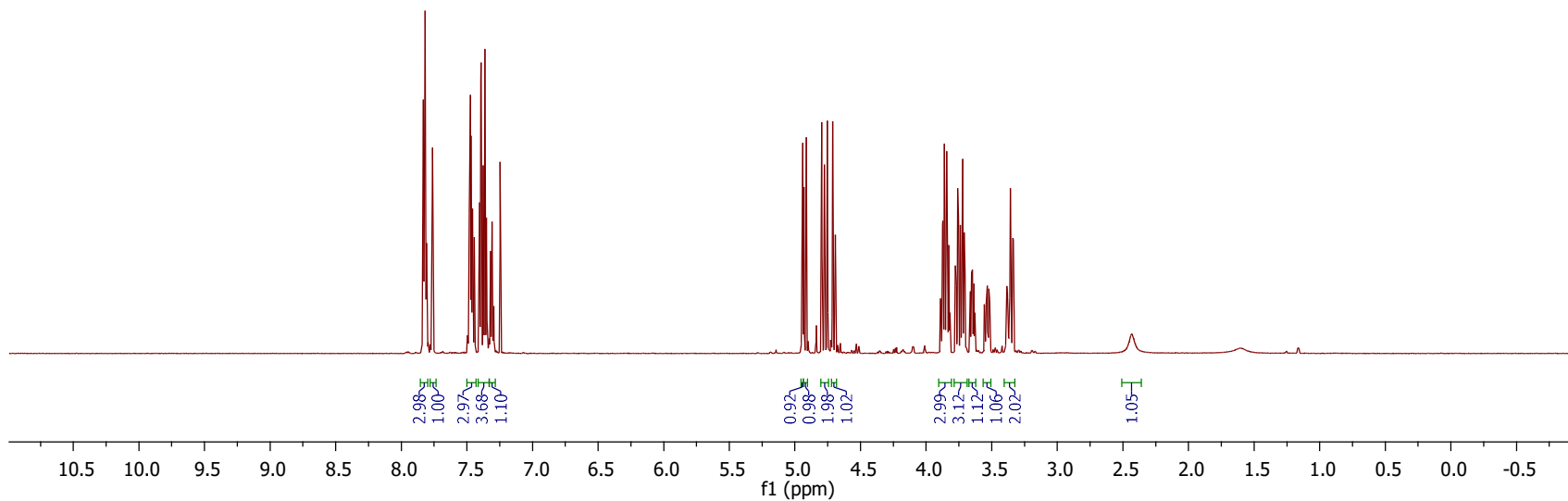
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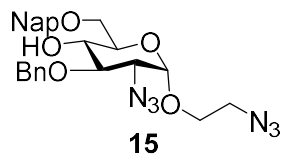


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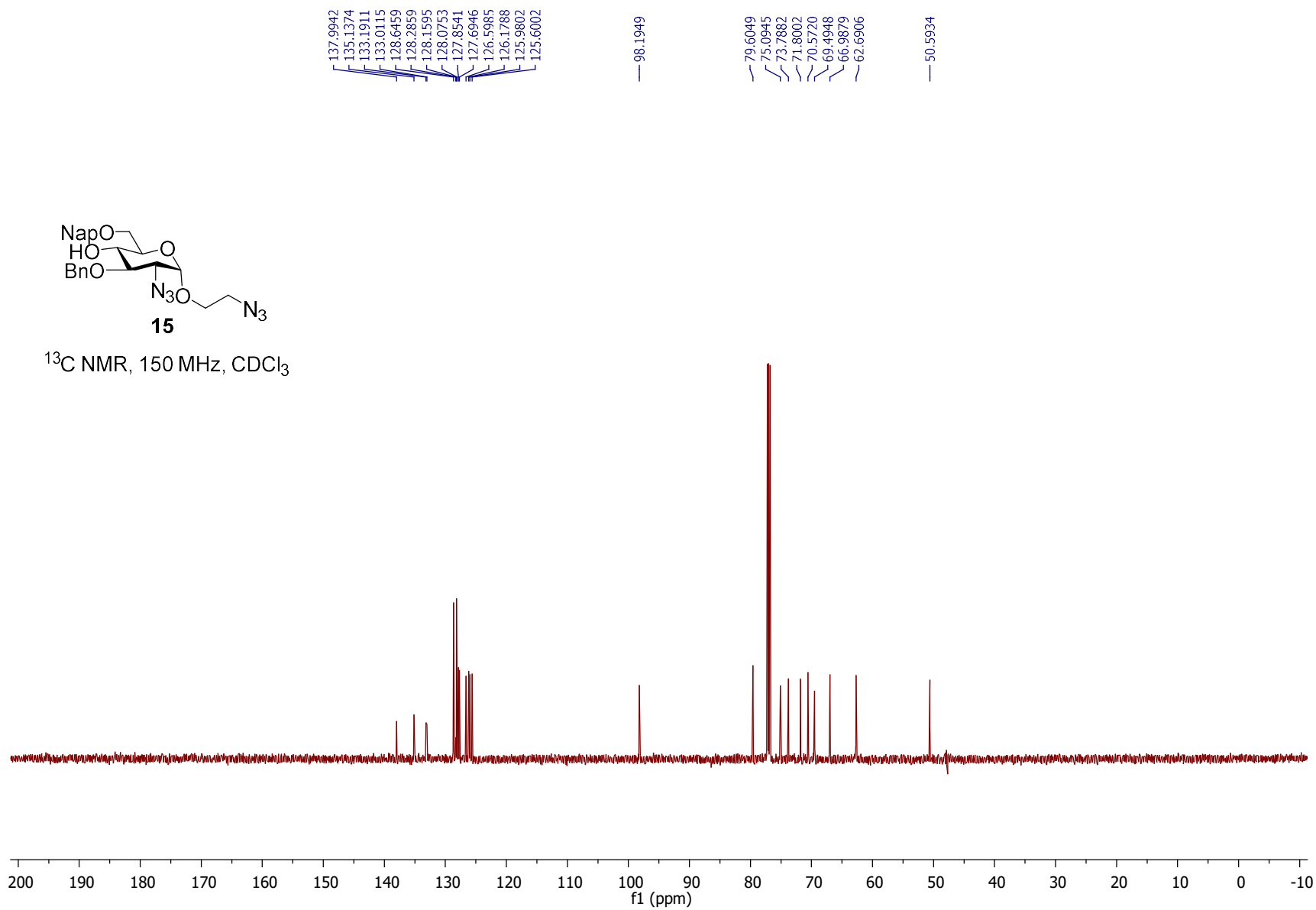


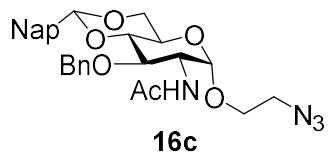
¹H NMR, 600 MHz, CDCl₃



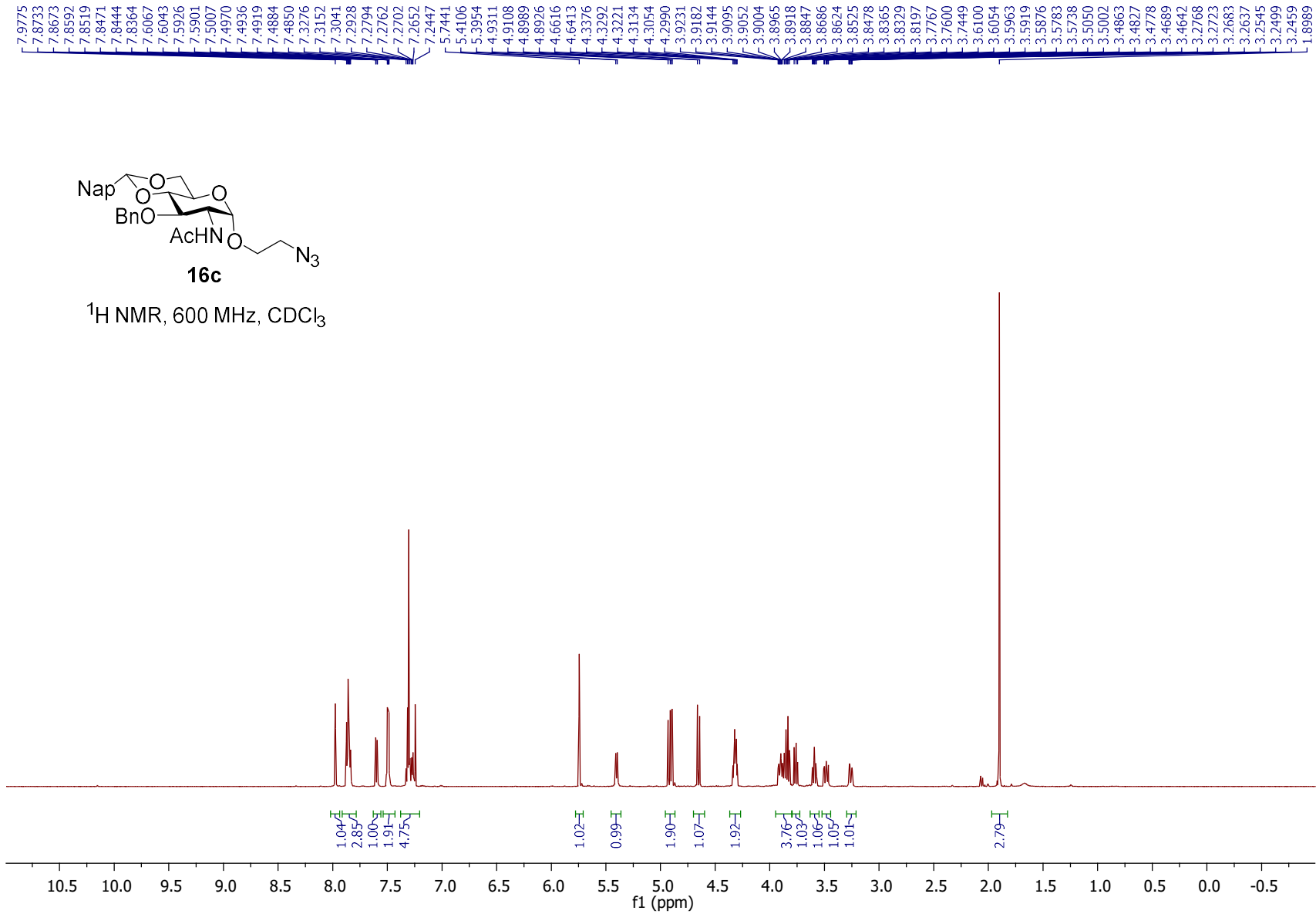


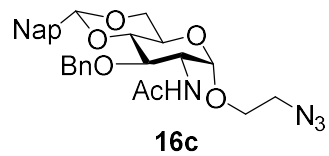
^{13}C NMR, 150 MHz, CDCl_3



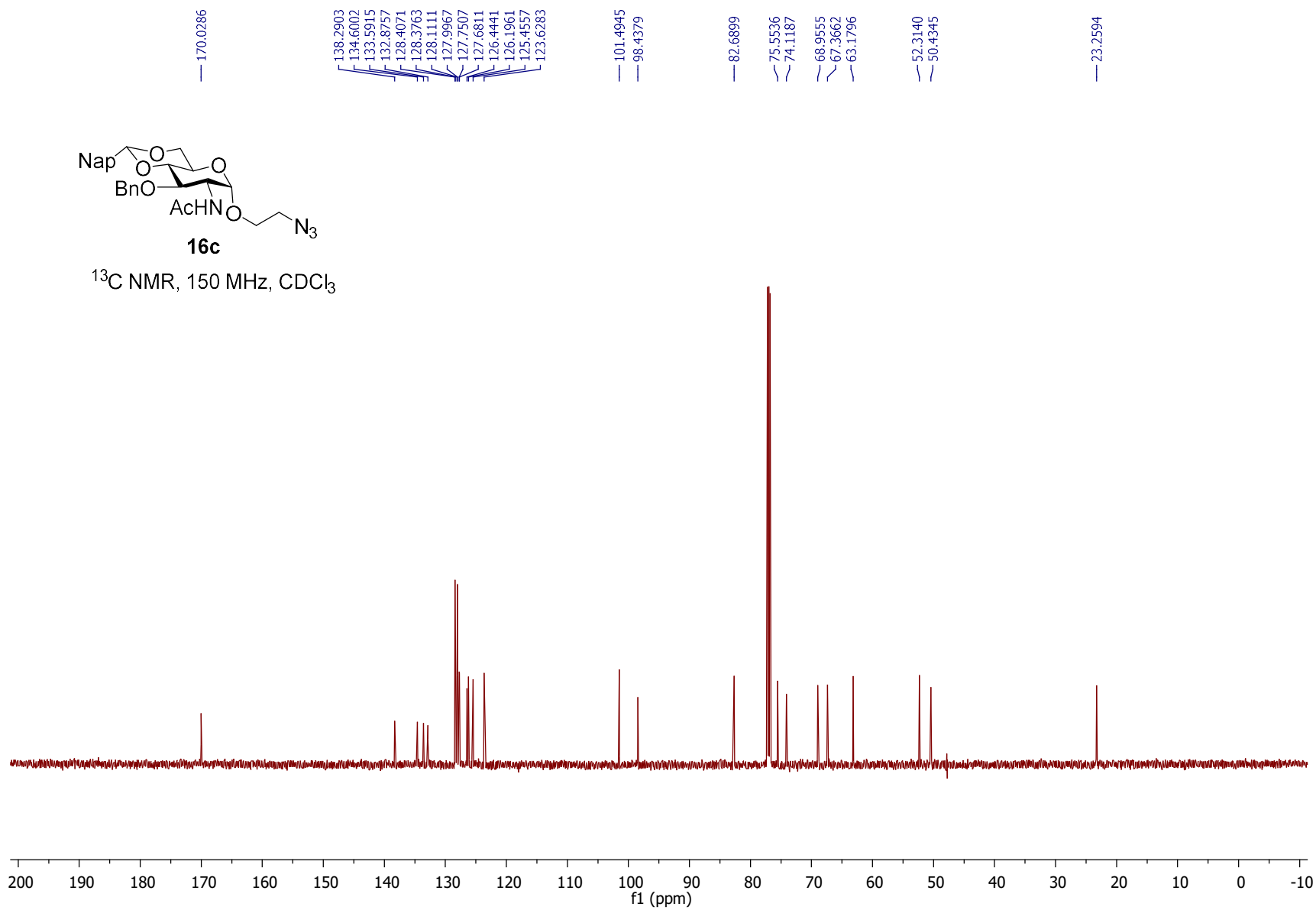


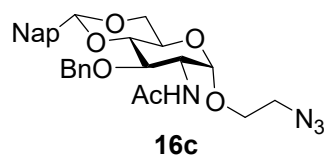
$^1\text{H NMR}$, 600 MHz, CDCl_3



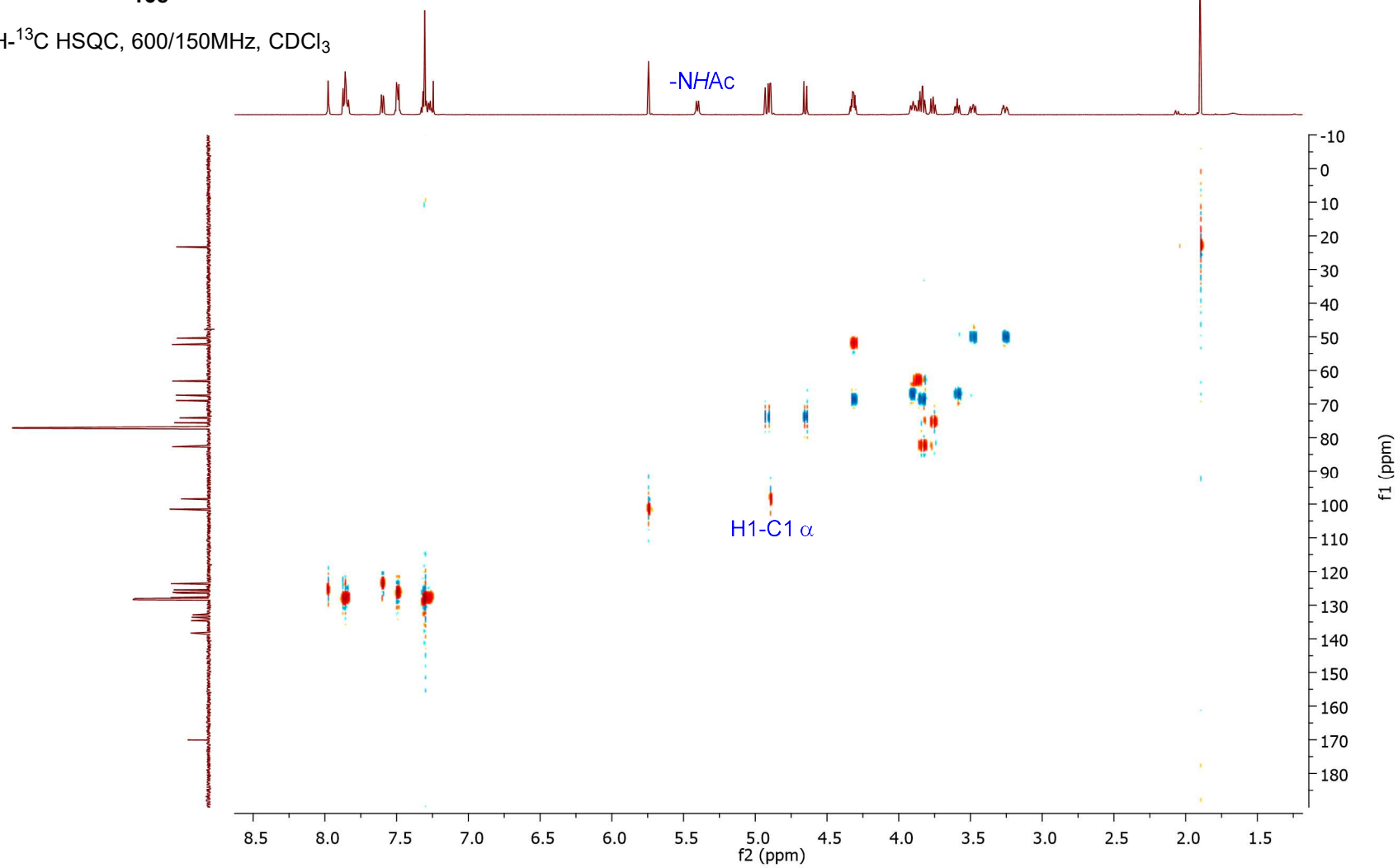


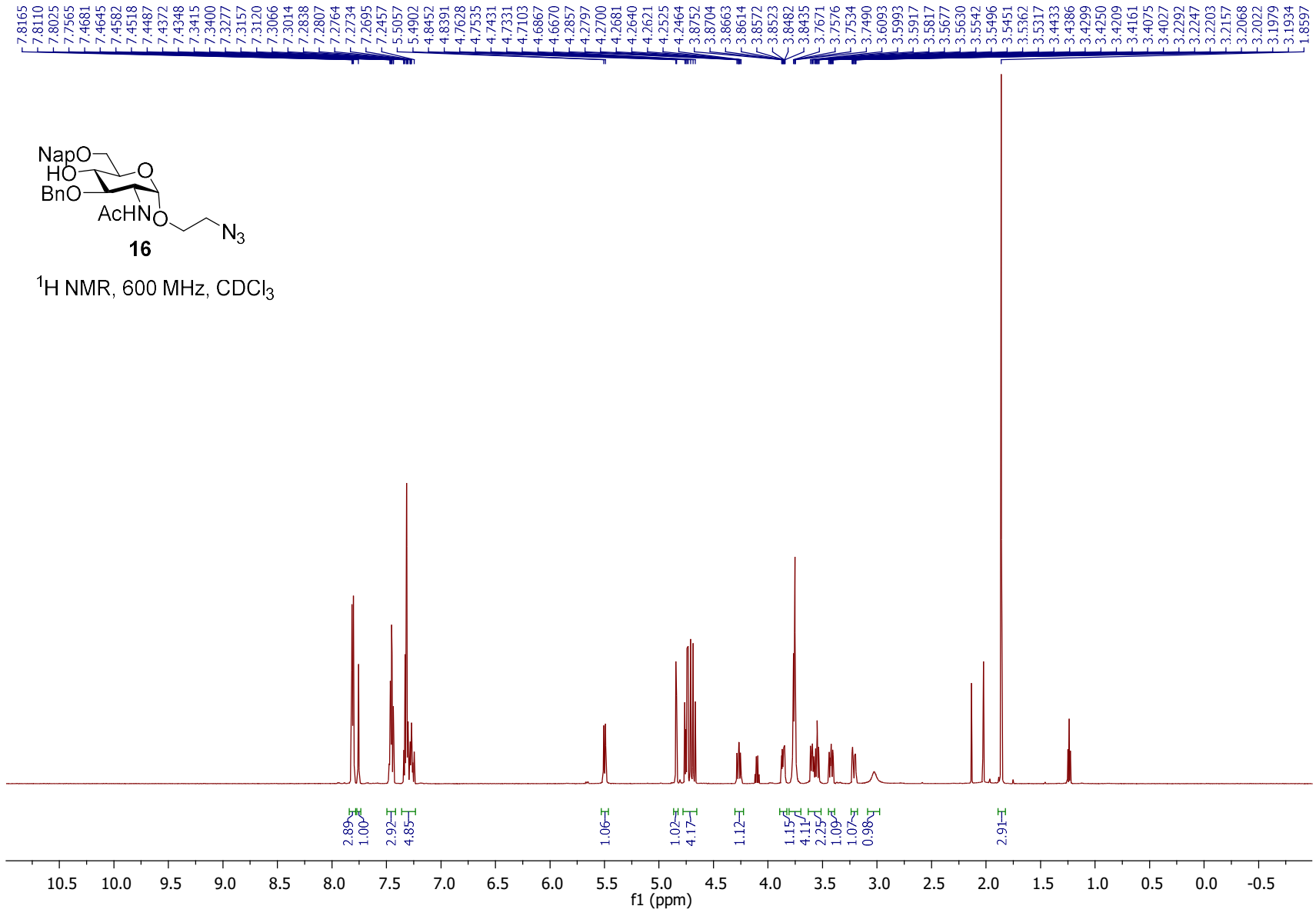
^{13}C NMR, 150 MHz, CDCl_3

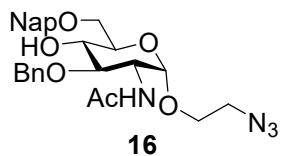




^1H - ^{13}C HSQC, 600/150MHz, CDCl_3







¹³C NMR, 150 MHz, CDCl₃

170.0982

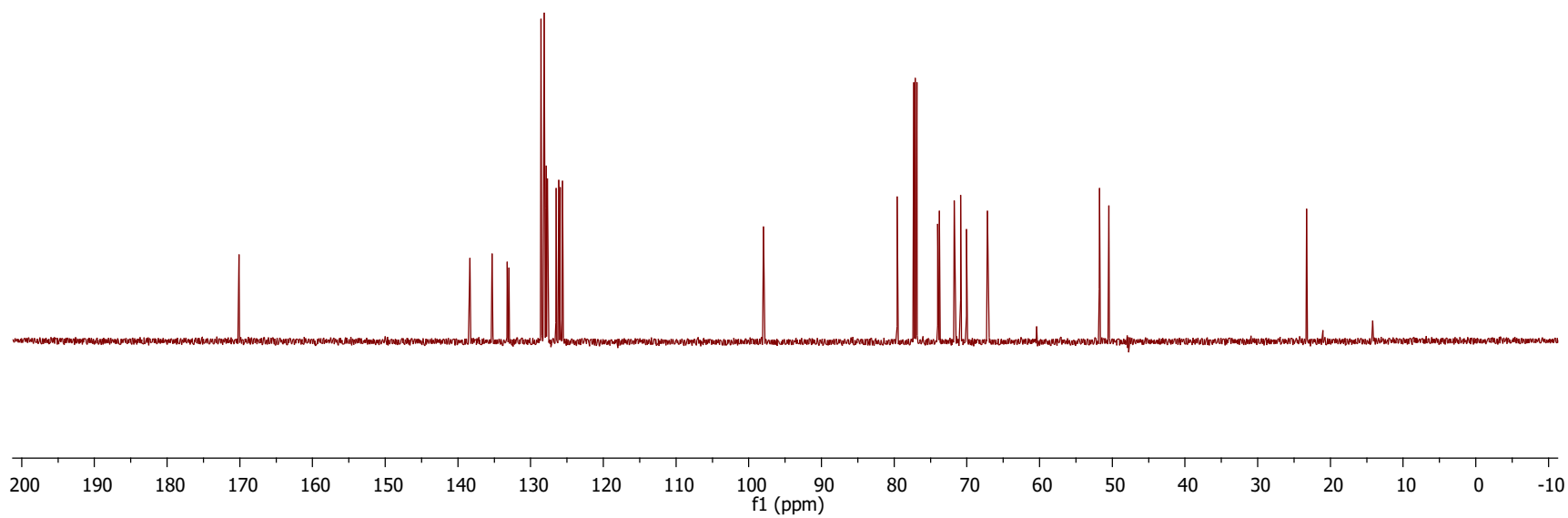
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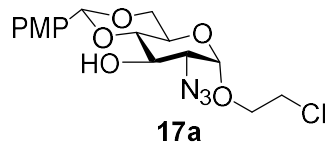
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74.0105
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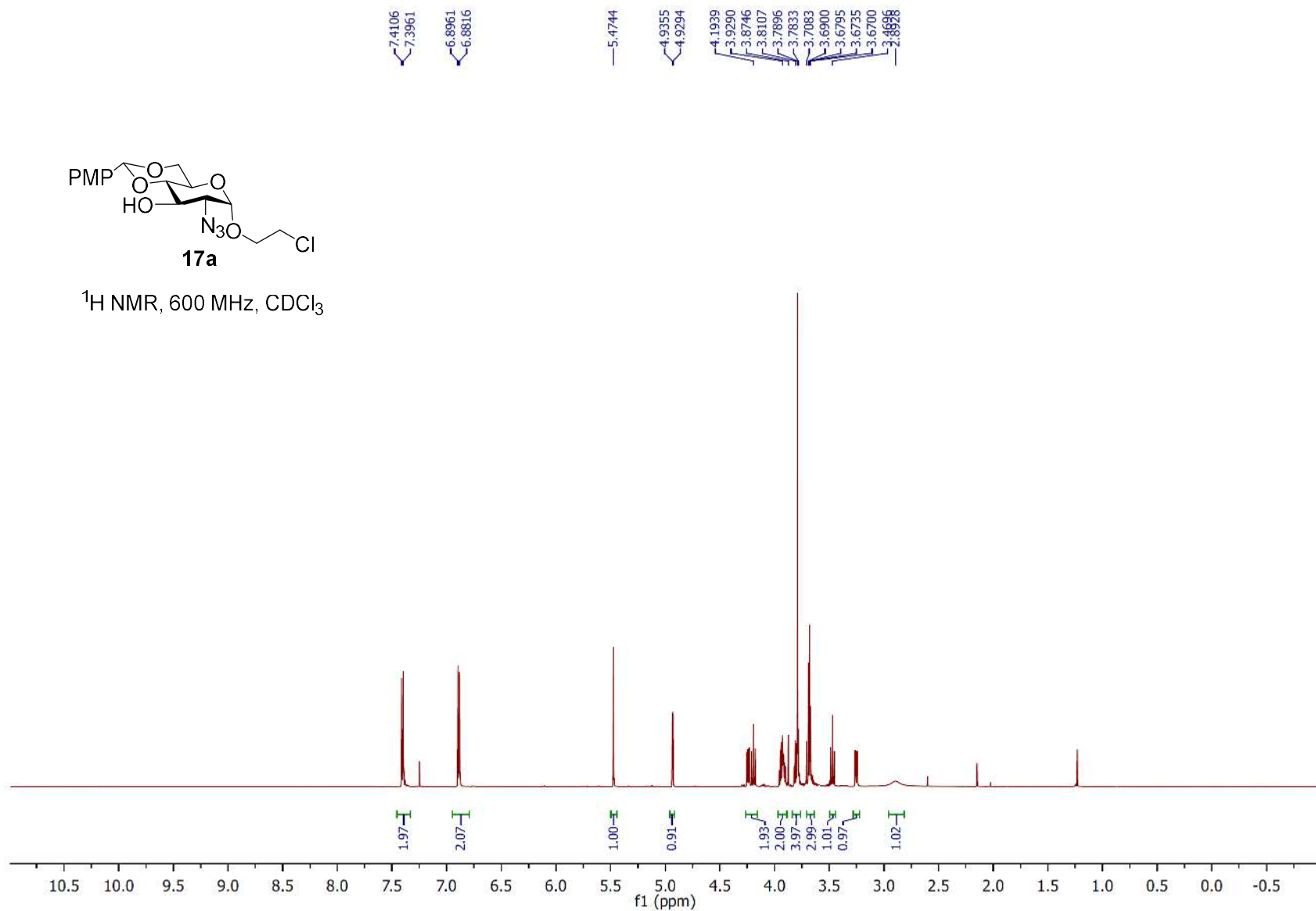
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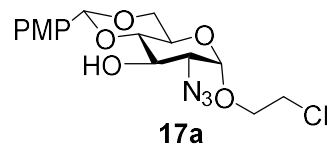
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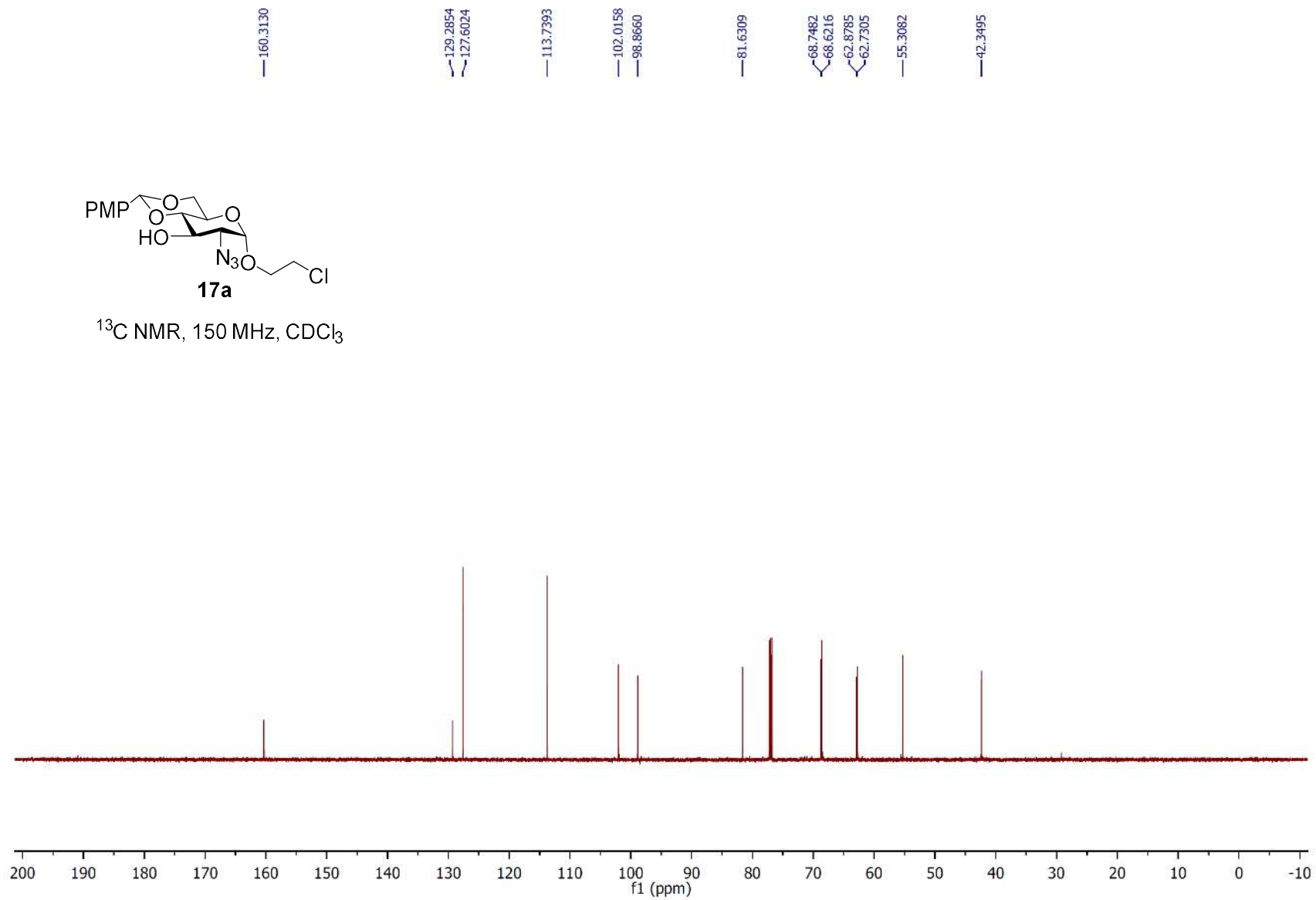


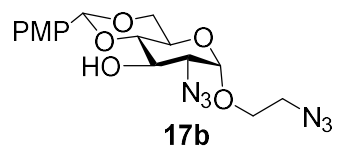
$^1\text{H NMR}$, 600 MHz, CDCl_3



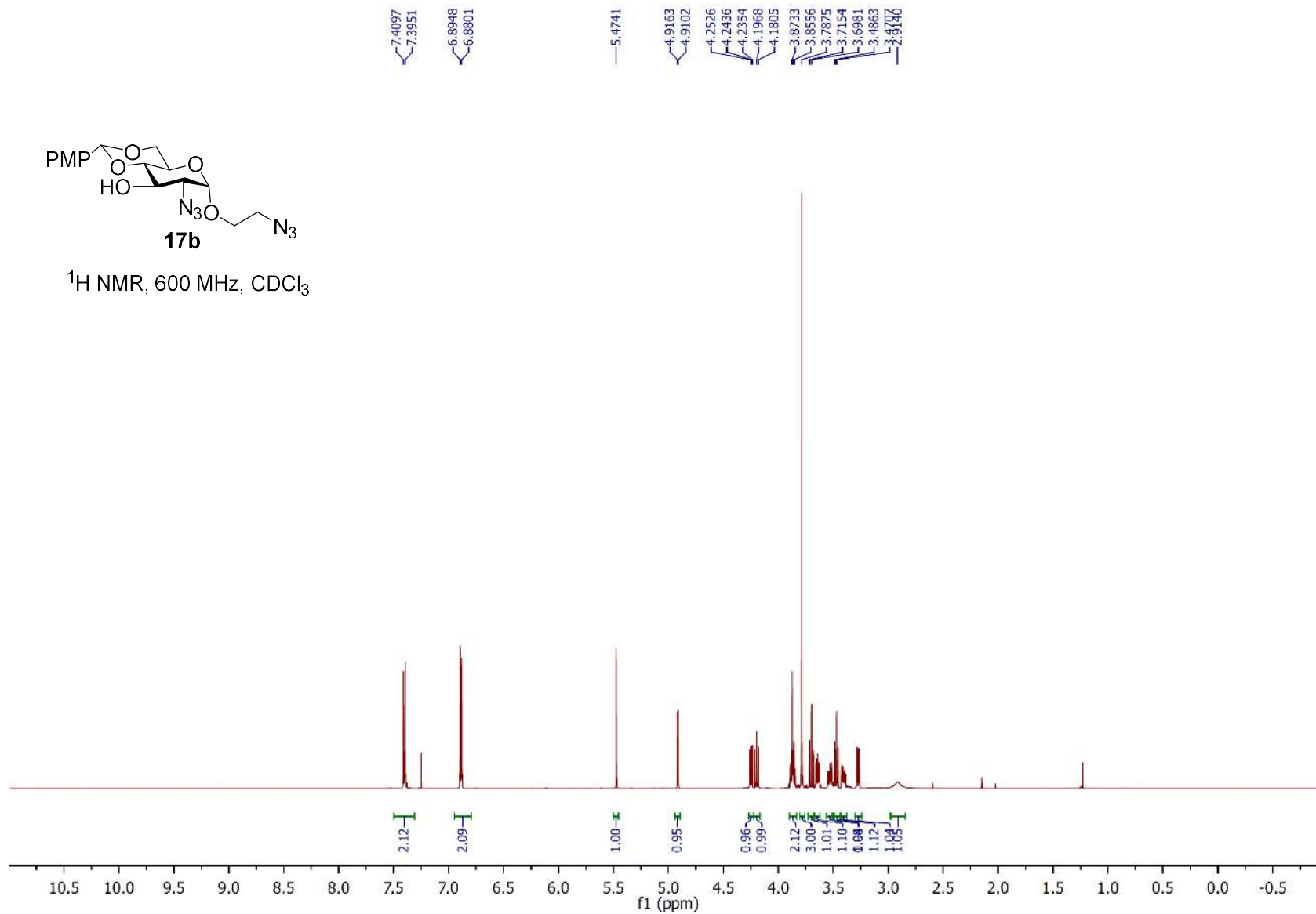


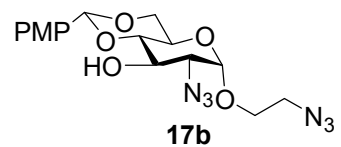
^{13}C NMR, 150 MHz, CDCl_3



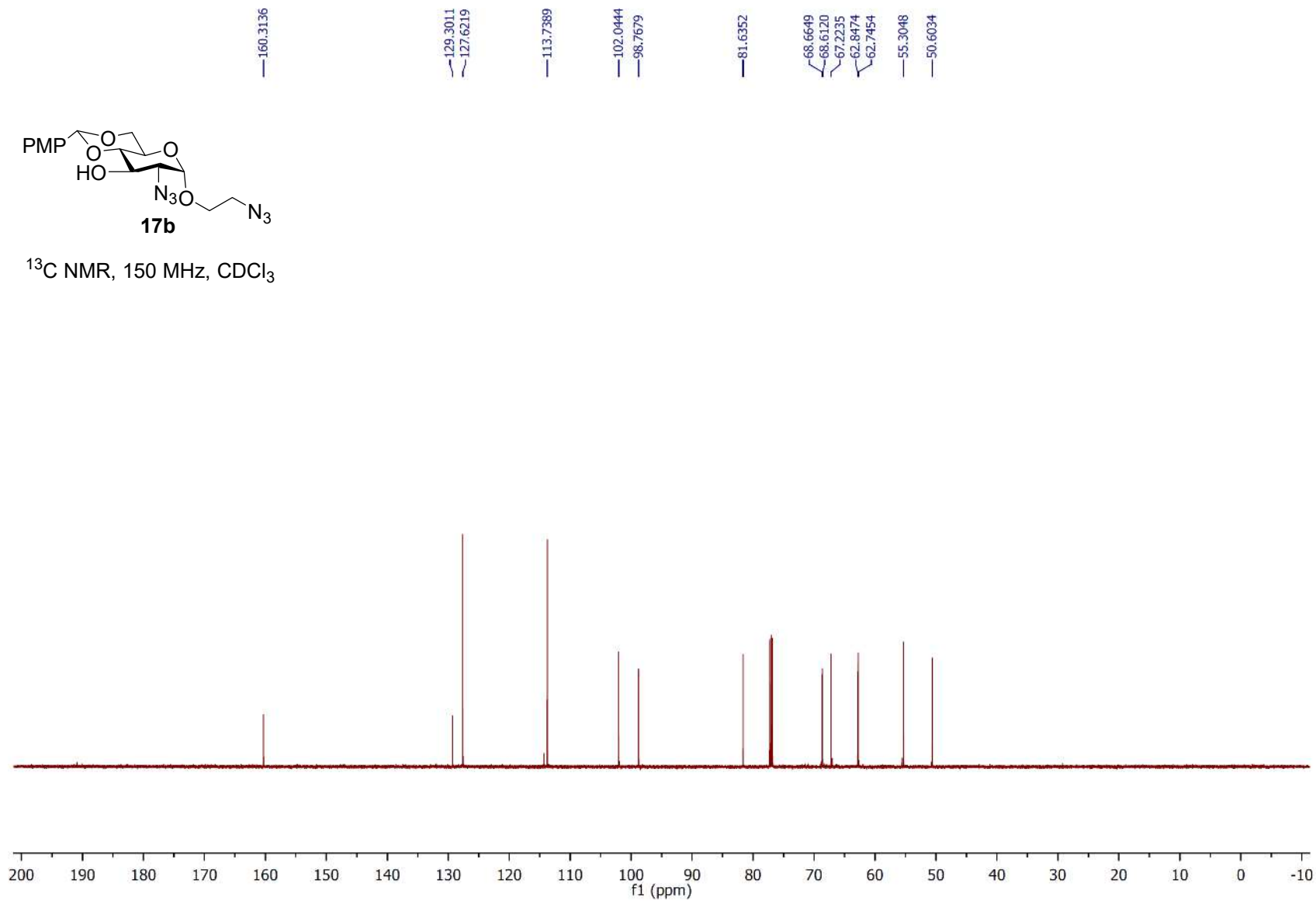


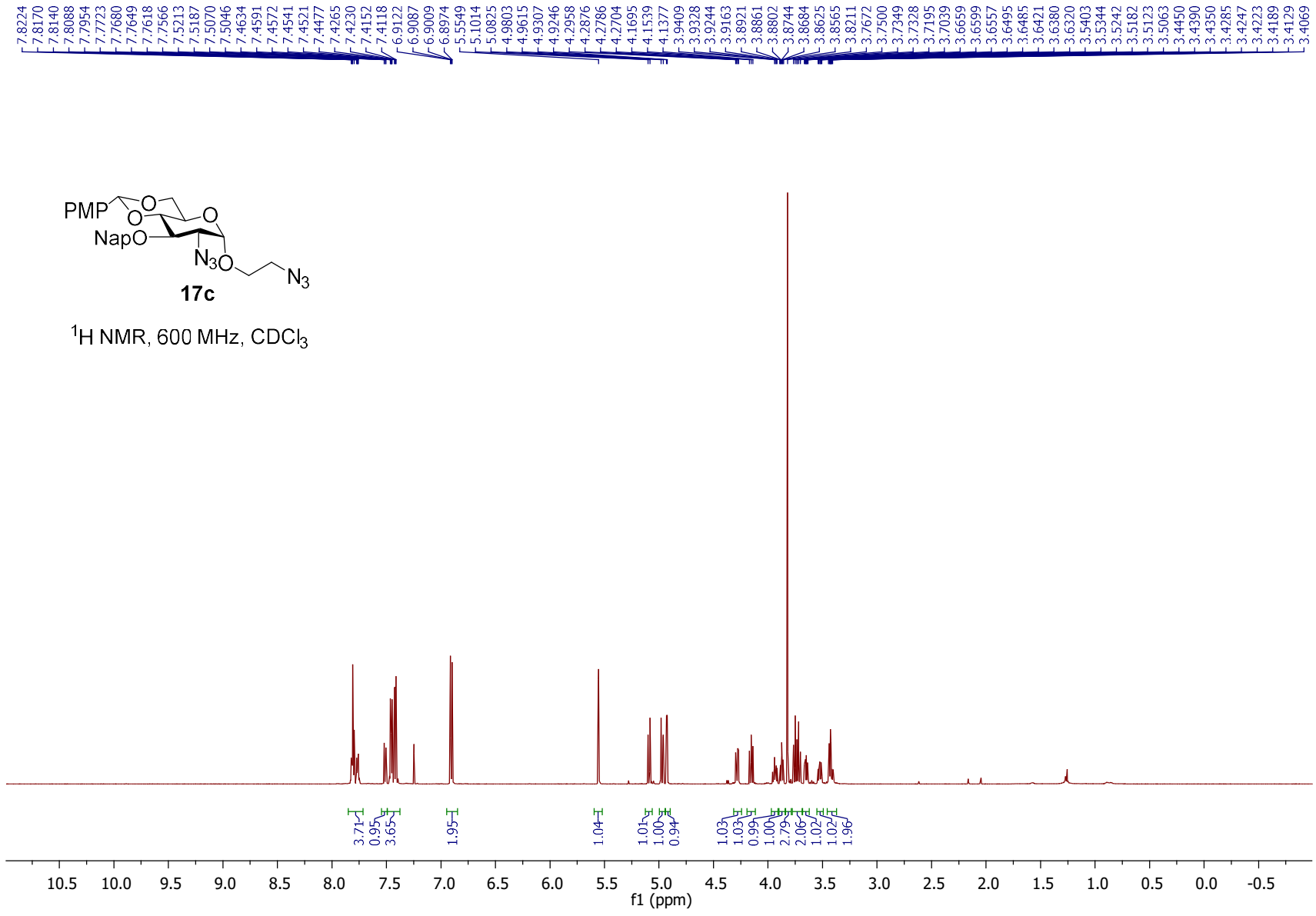
^1H NMR, 600 MHz, CDCl_3

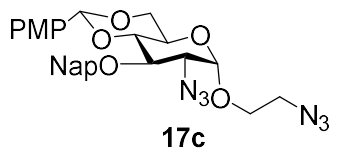




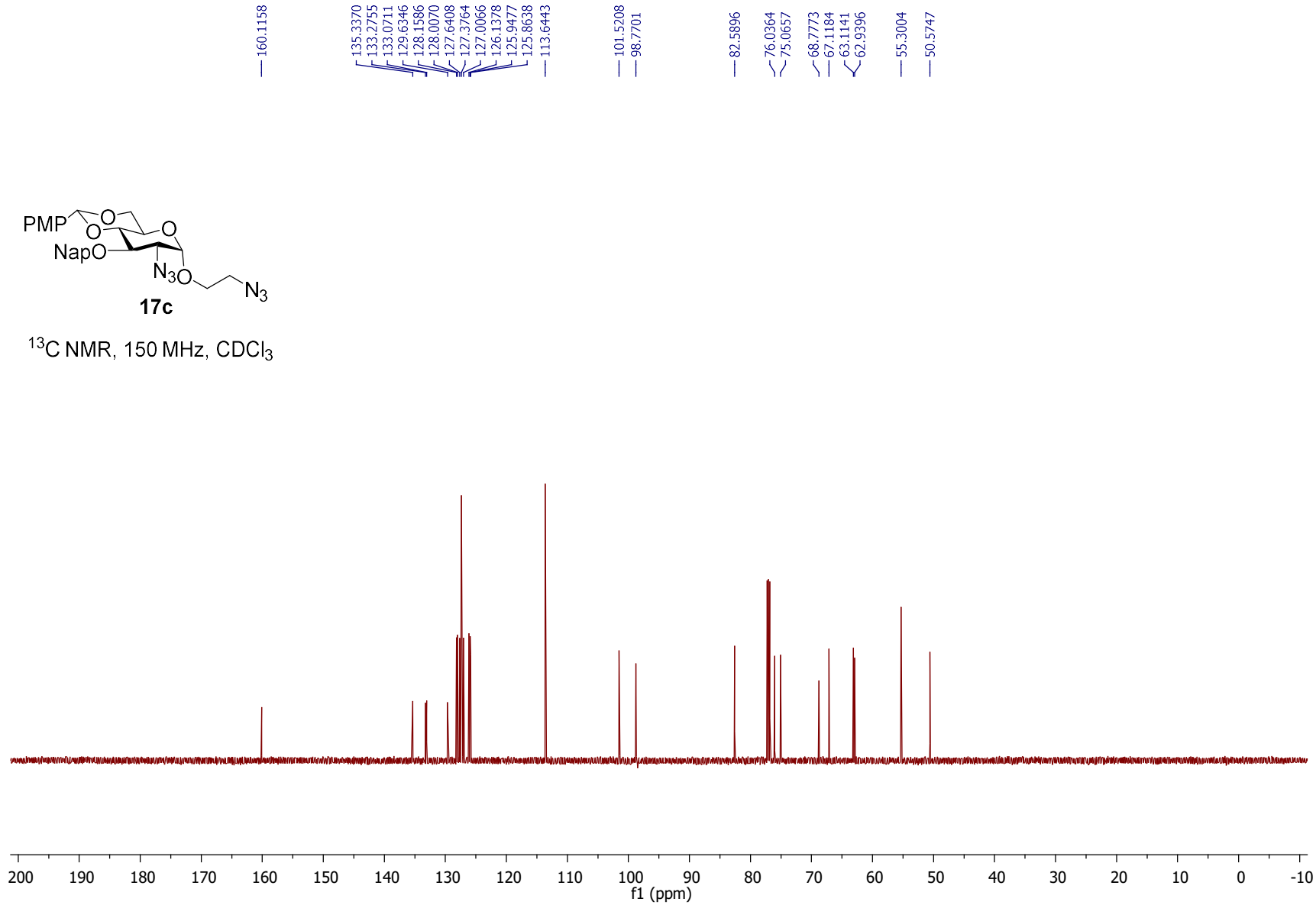
^{13}C NMR, 150 MHz, CDCl_3

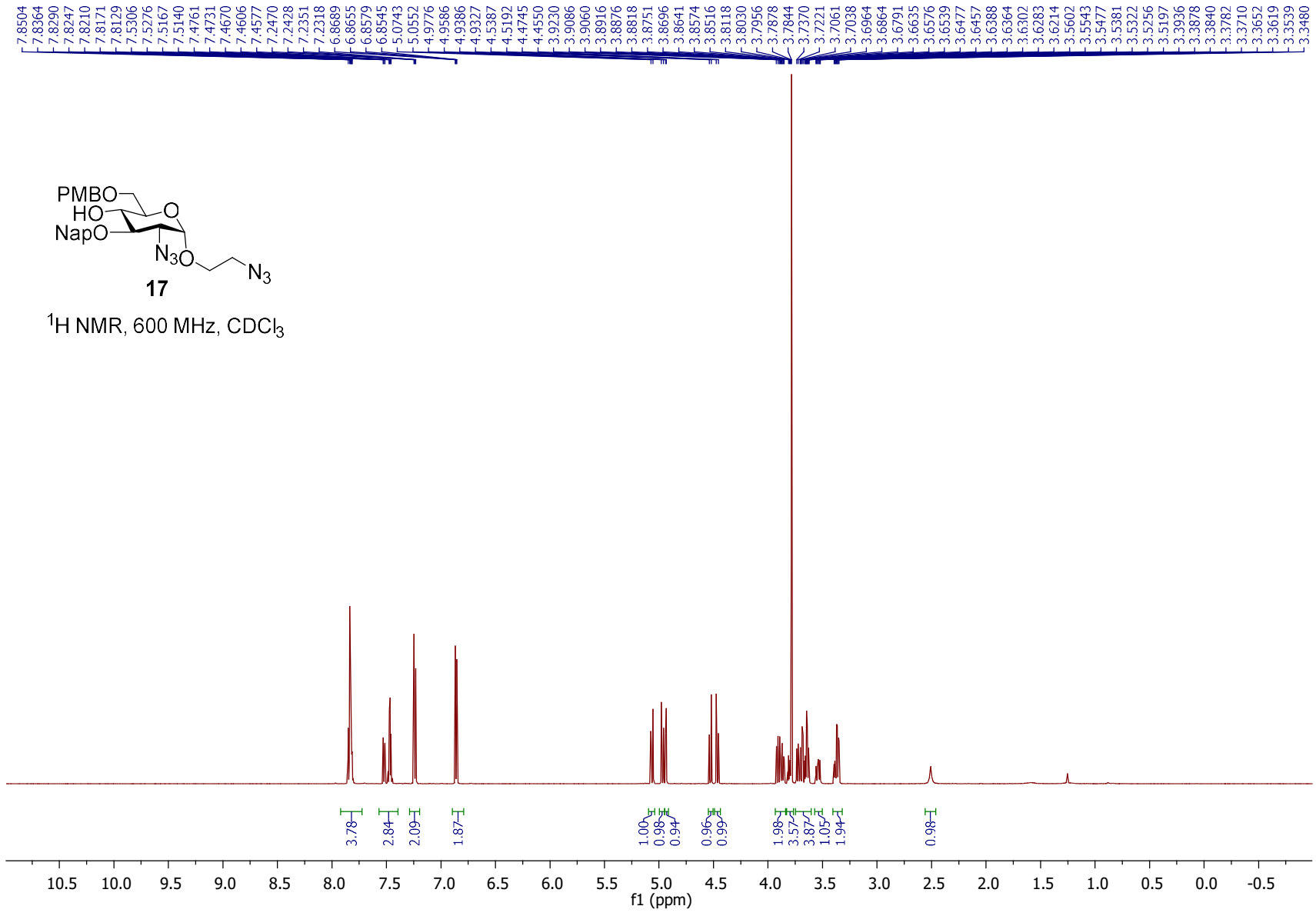


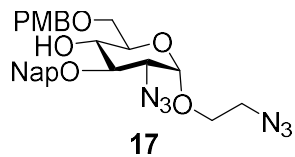




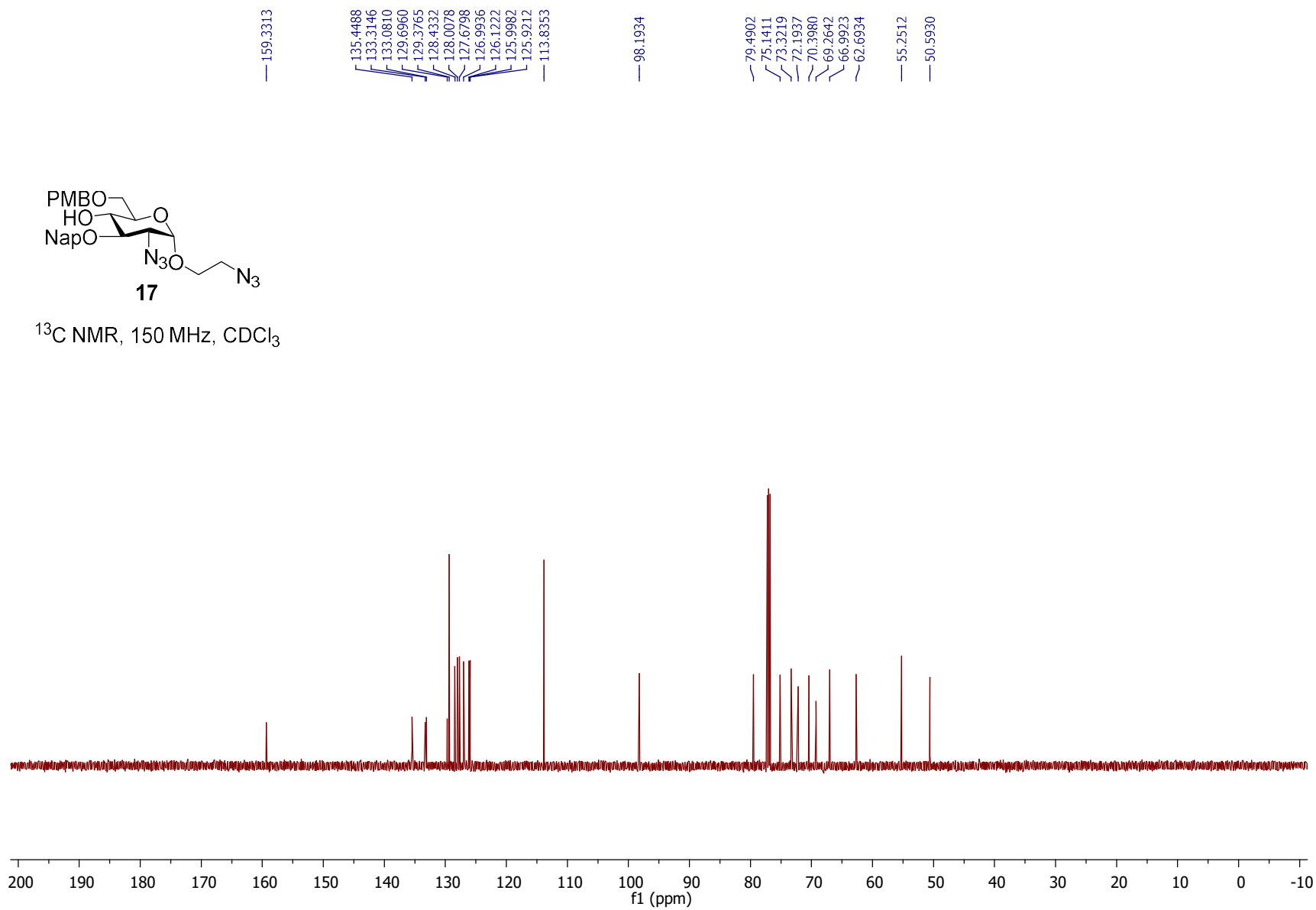
^{13}C NMR, 150 MHz, CDCl_3

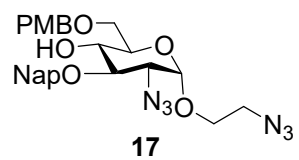




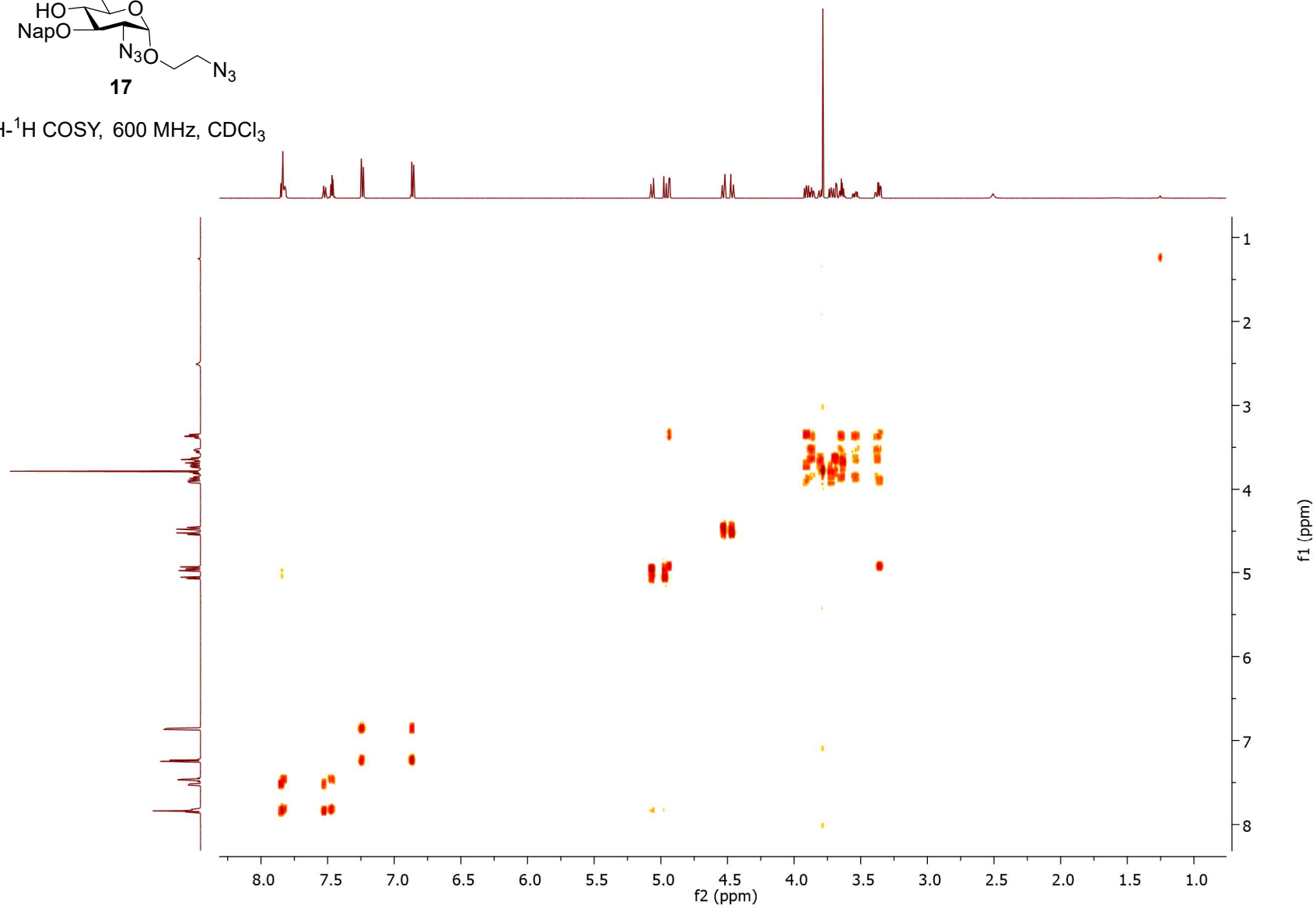


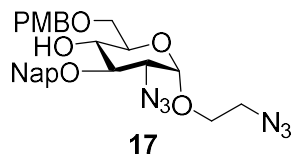
^{13}C NMR, 150 MHz, CDCl_3



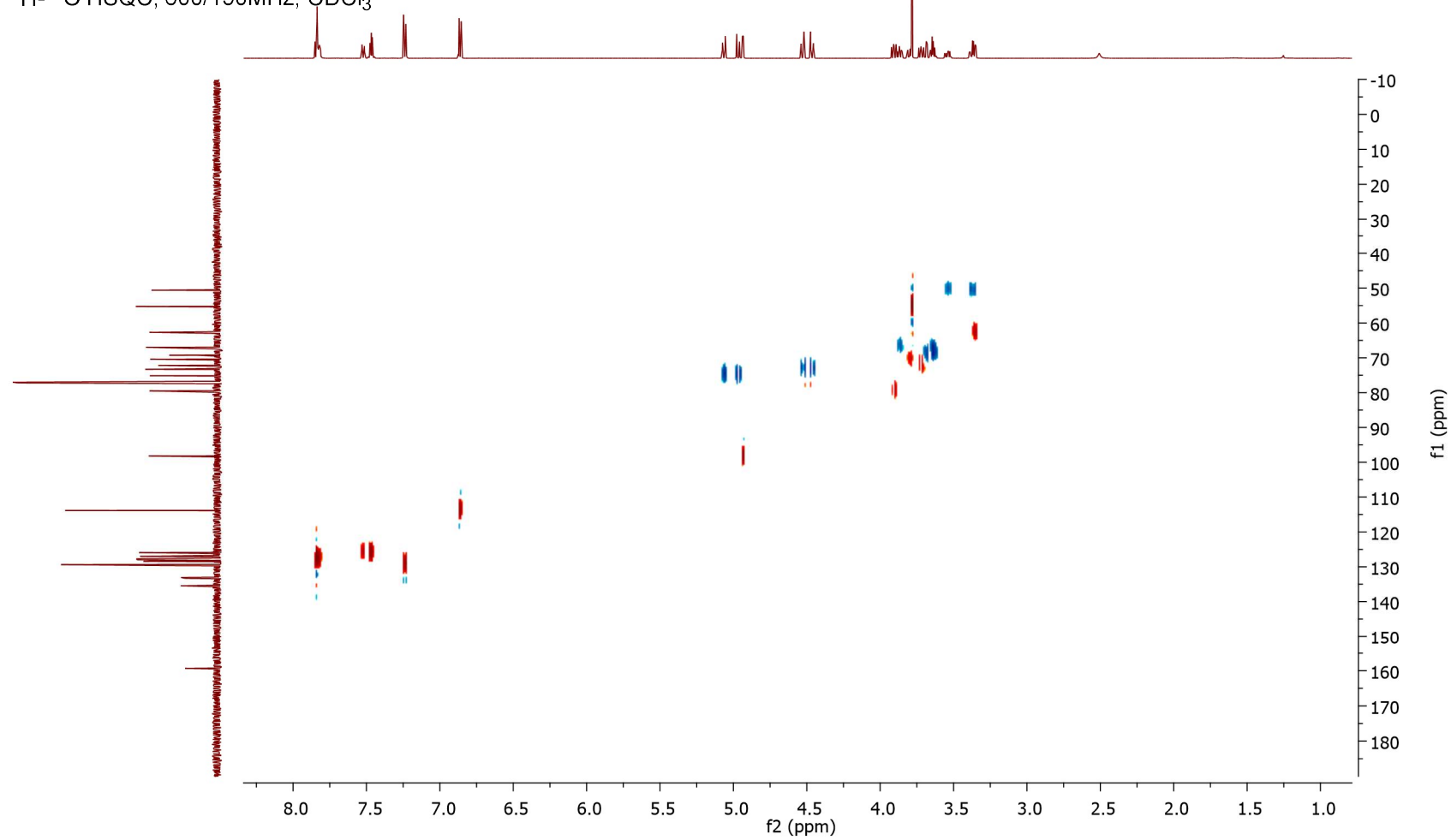


^1H - ^1H COSY, 600 MHz, CDCl_3

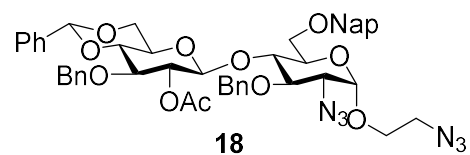




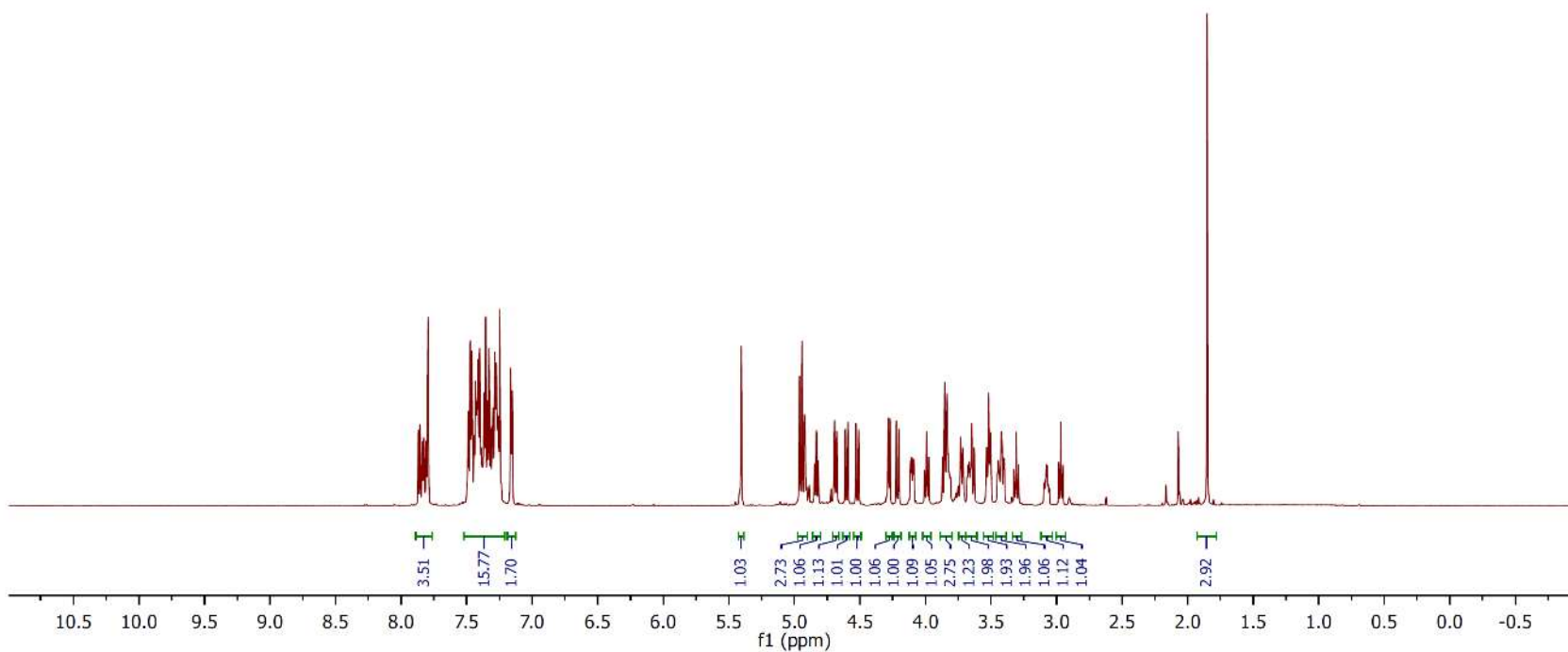
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

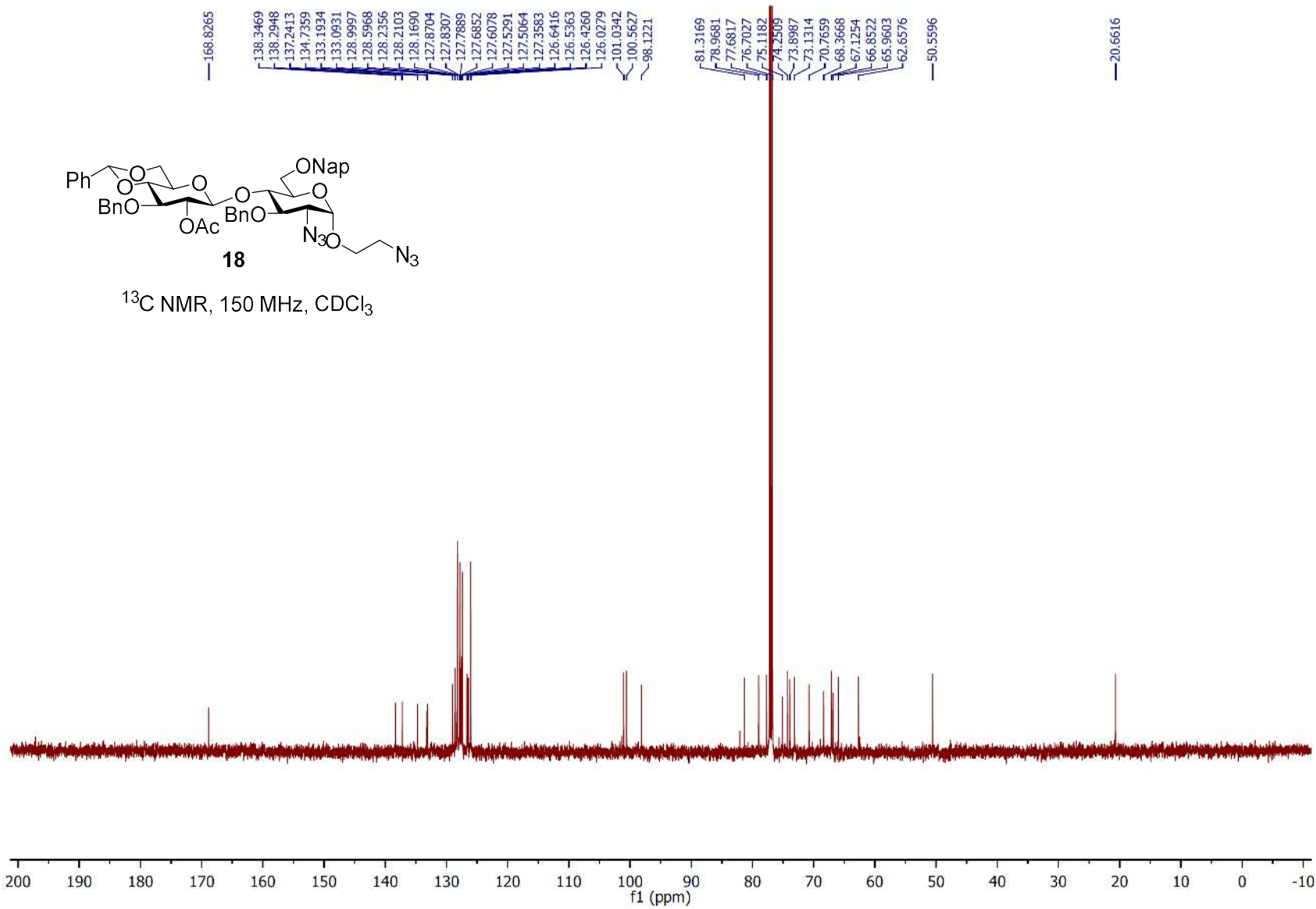


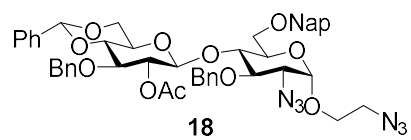
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7.3543
7.3407
7.3287
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7.2860
7.2741
7.2600
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7.1522
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4.9180
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4.1137
4.1057
4.0963
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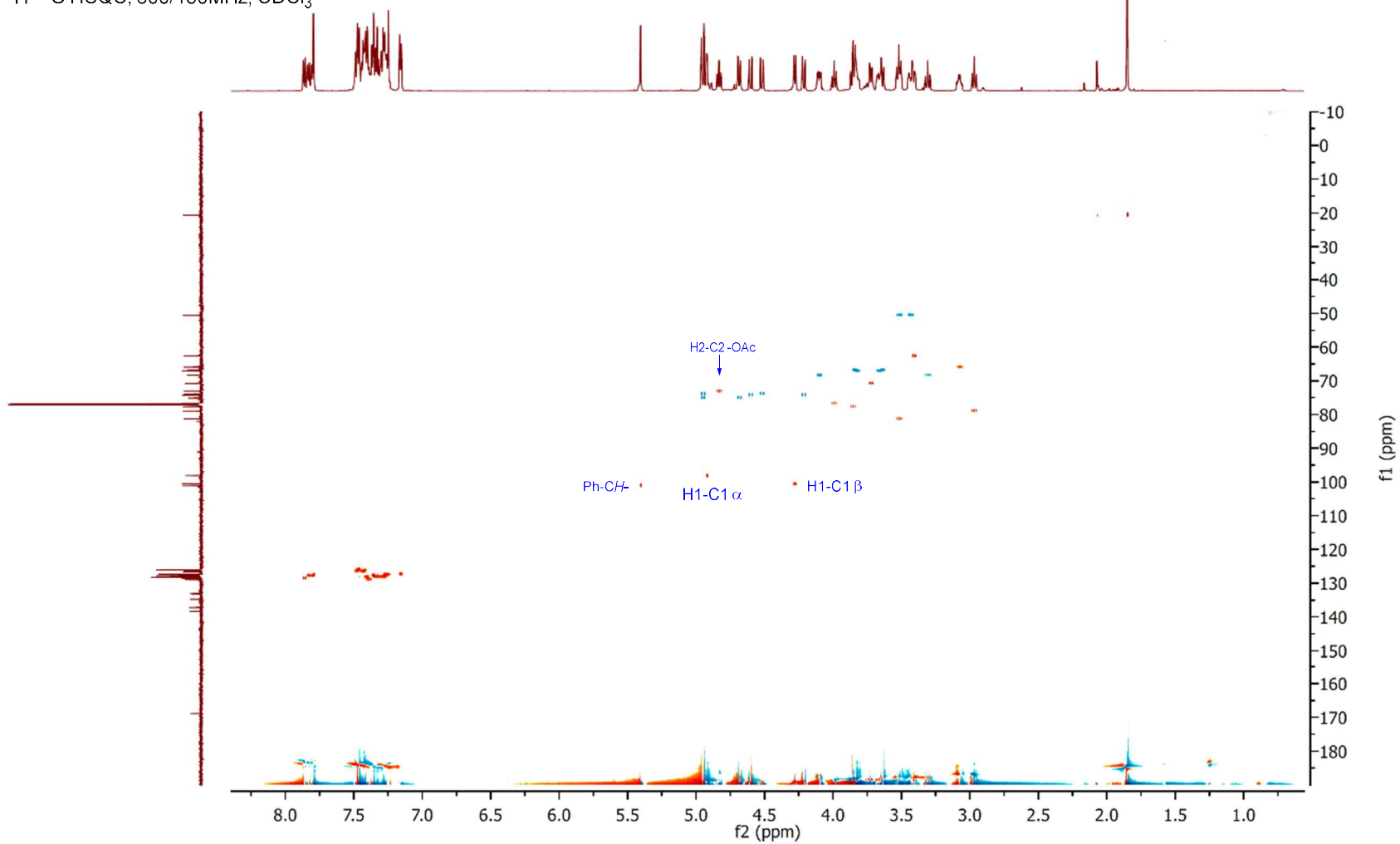
$^1\text{H NMR}$, 600 MHz, CDCl_3



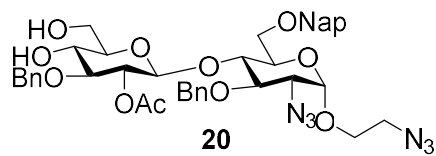




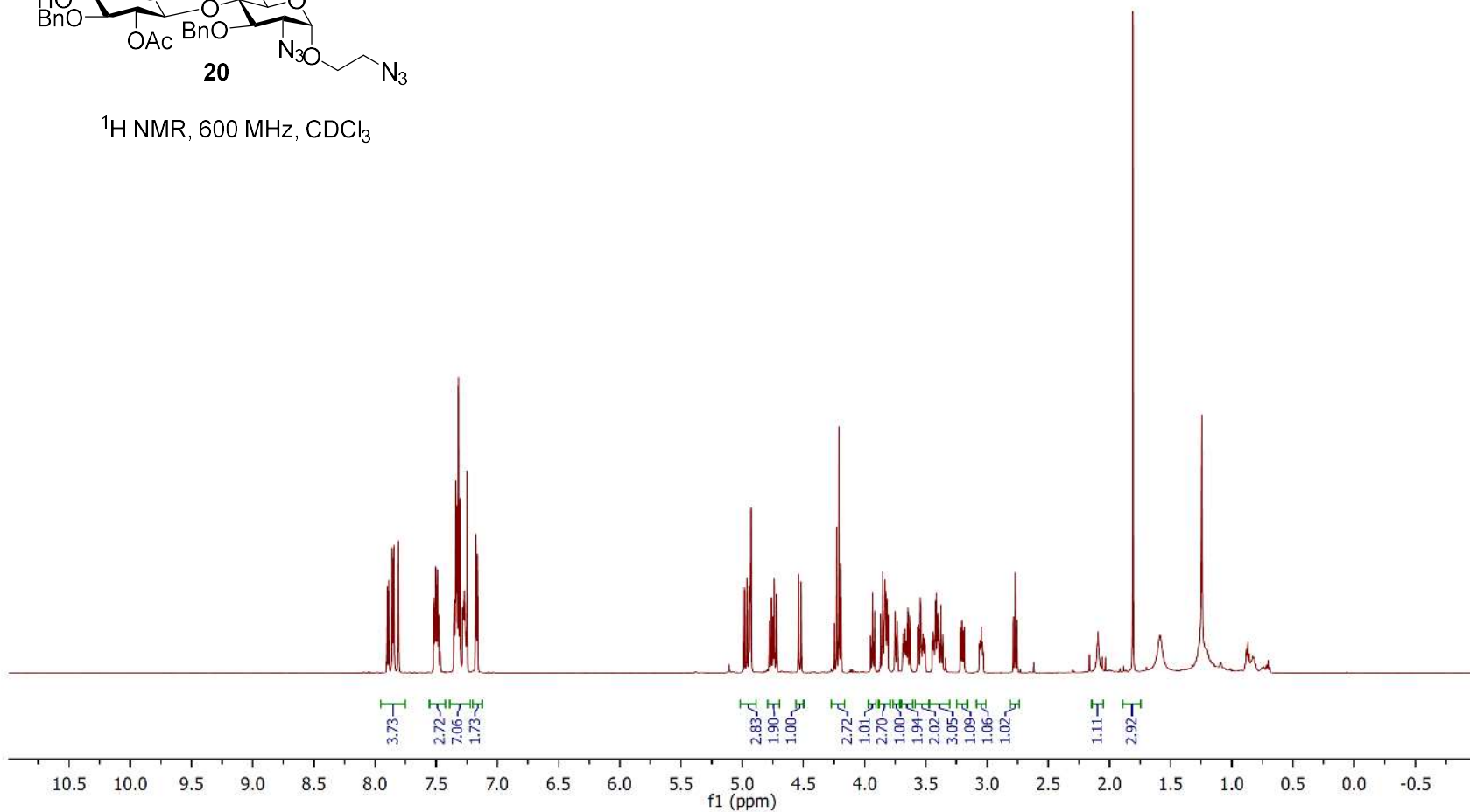
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

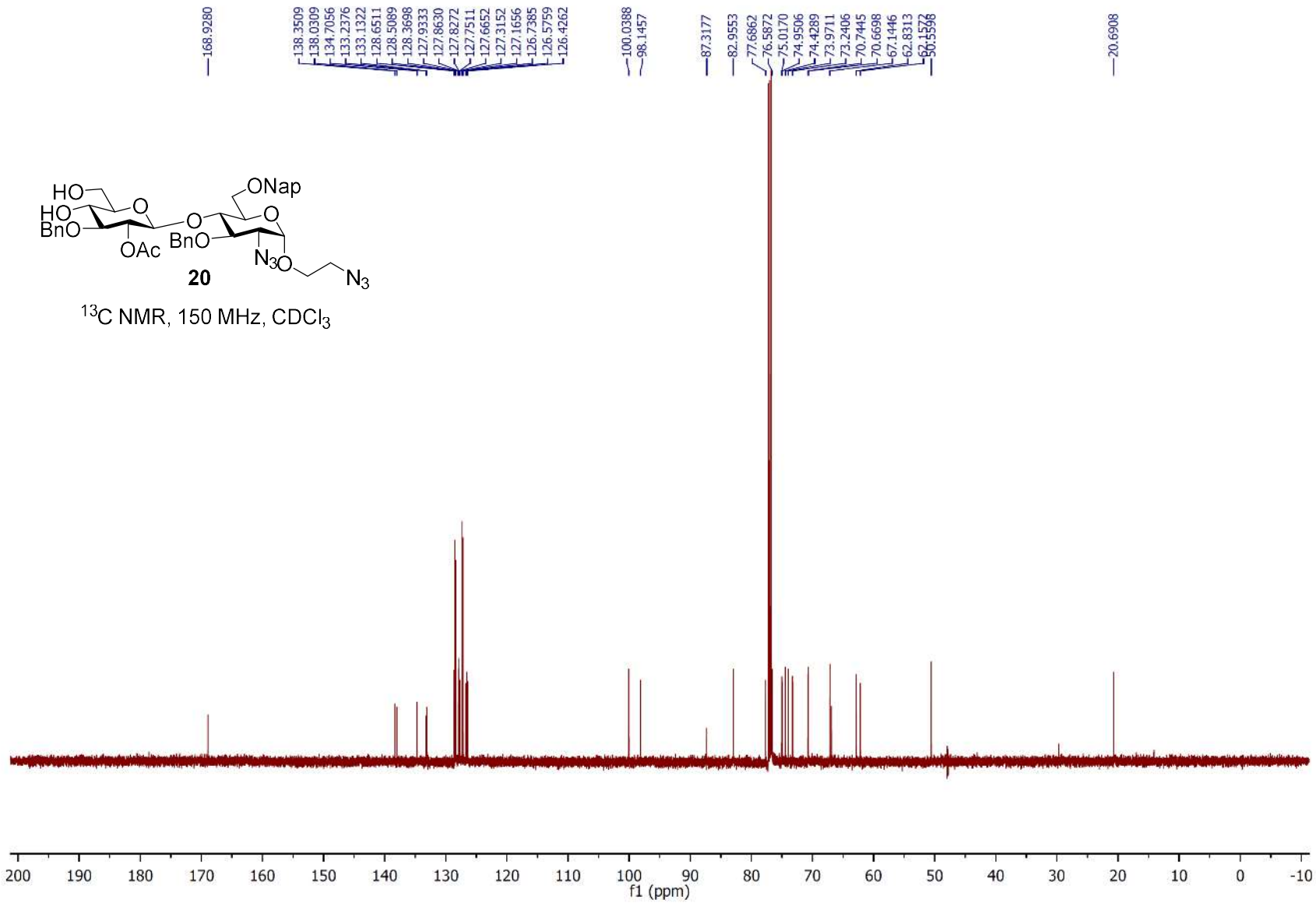


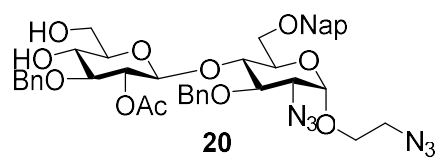
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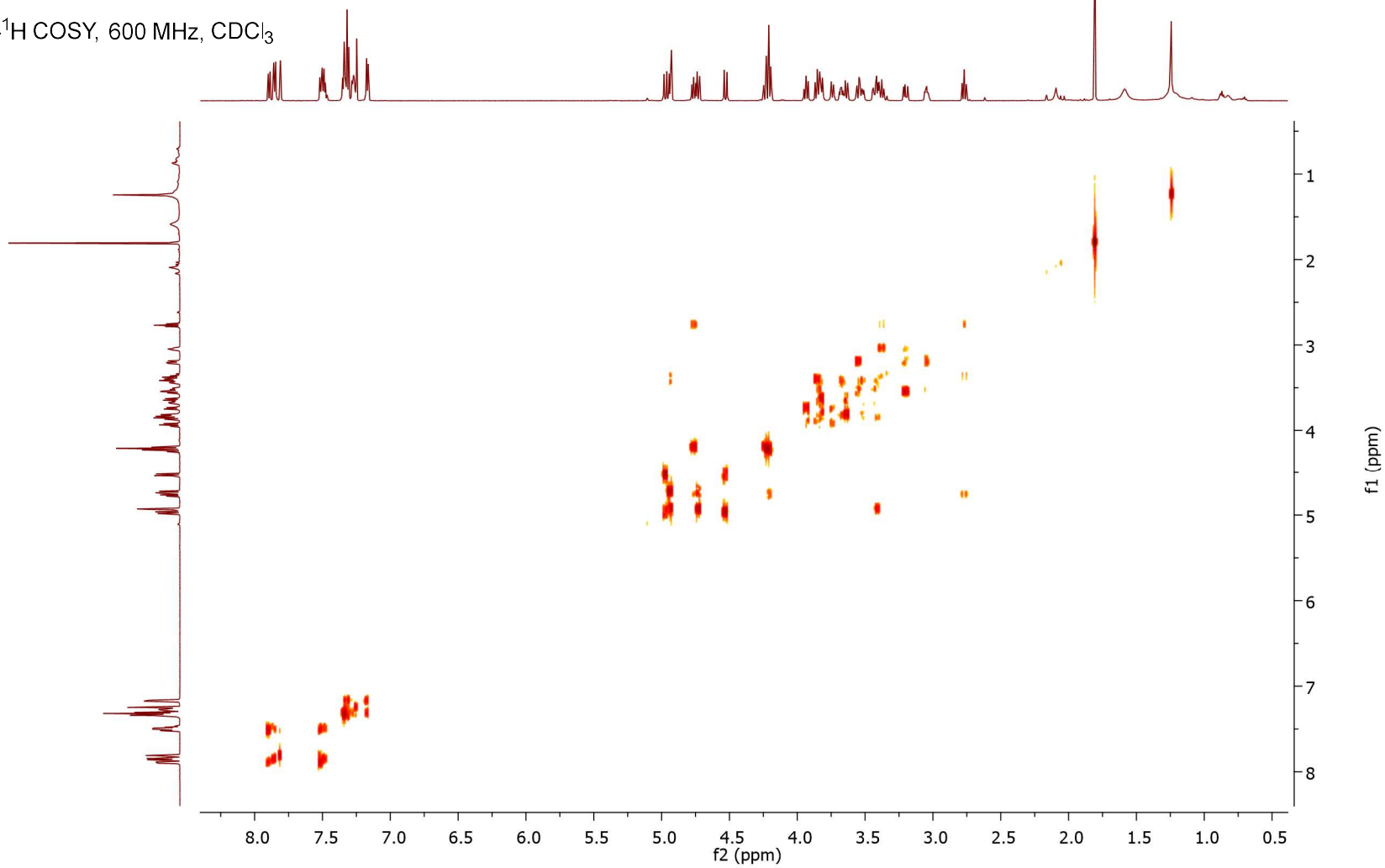
¹H NMR, 600 MHz, CDCl₃

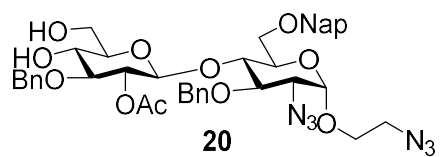




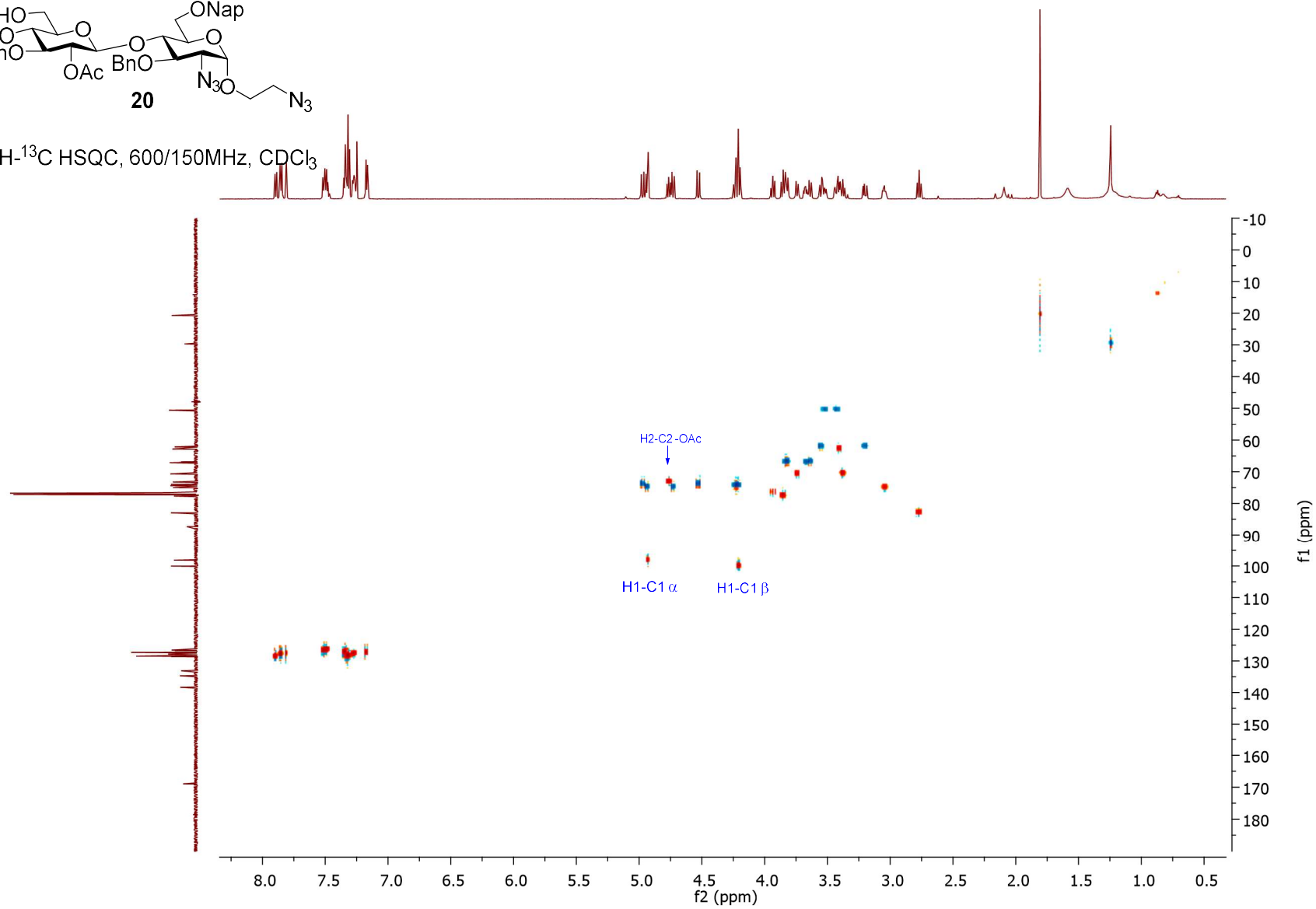


^1H - ^1H COSY, 600 MHz, CDCl_3

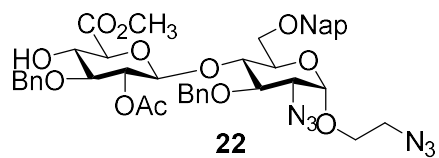




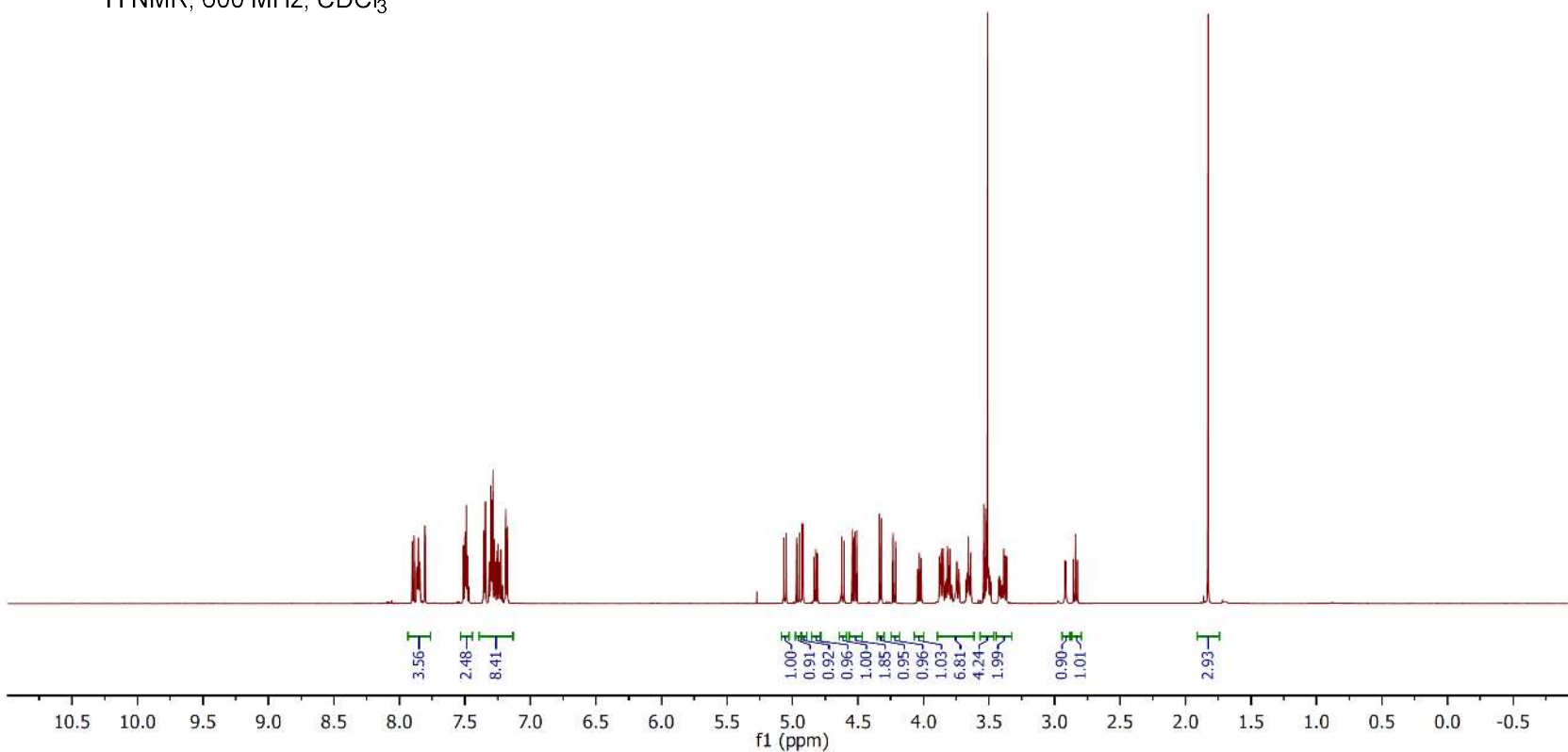
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

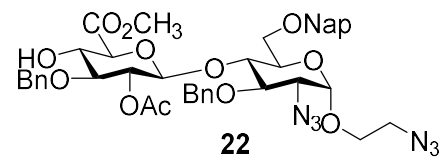


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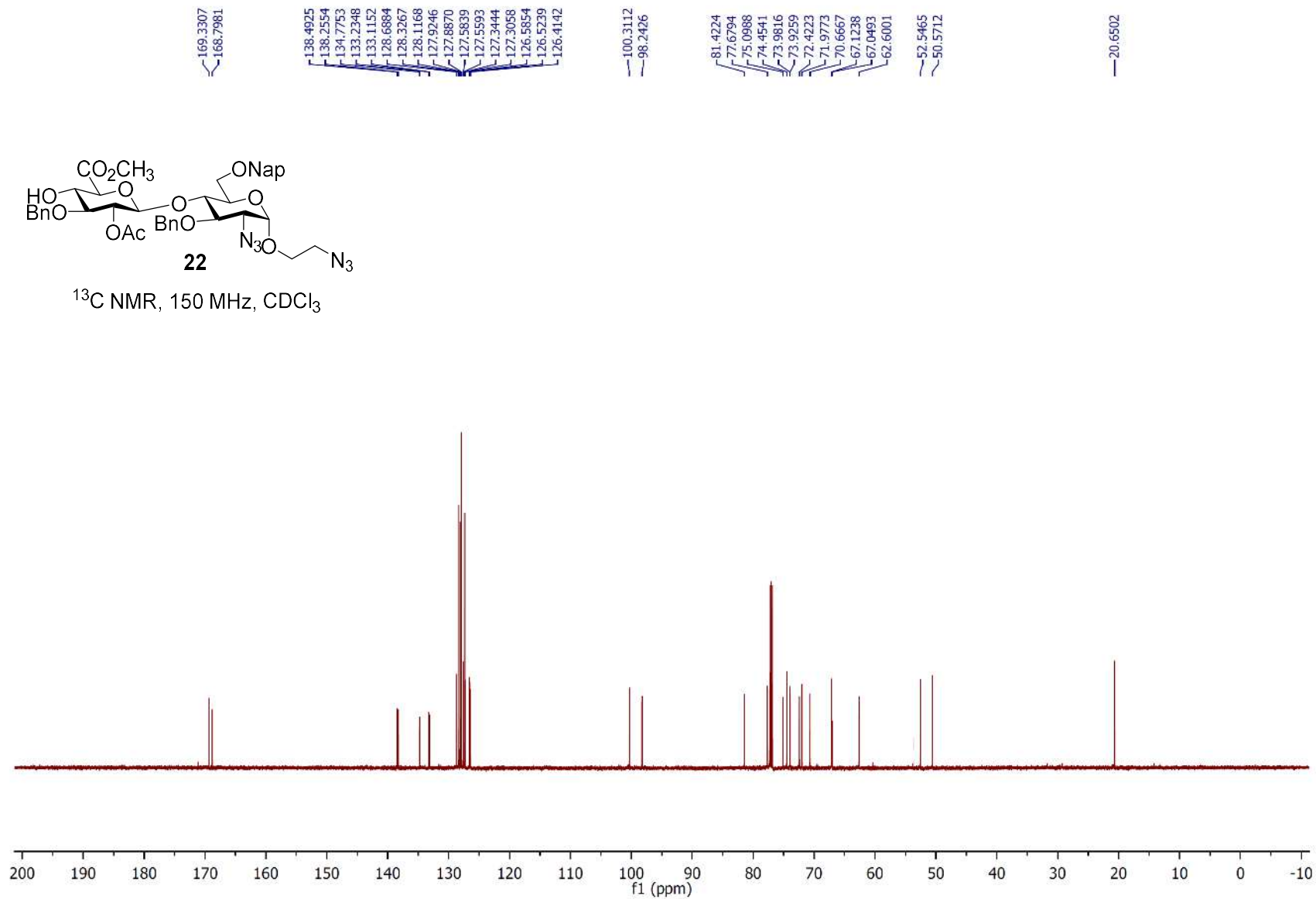


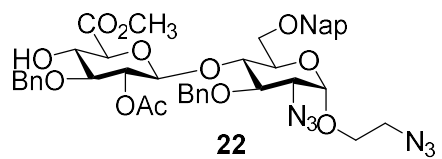
$^1\text{H NMR}$, 600 MHz, CDCl_3



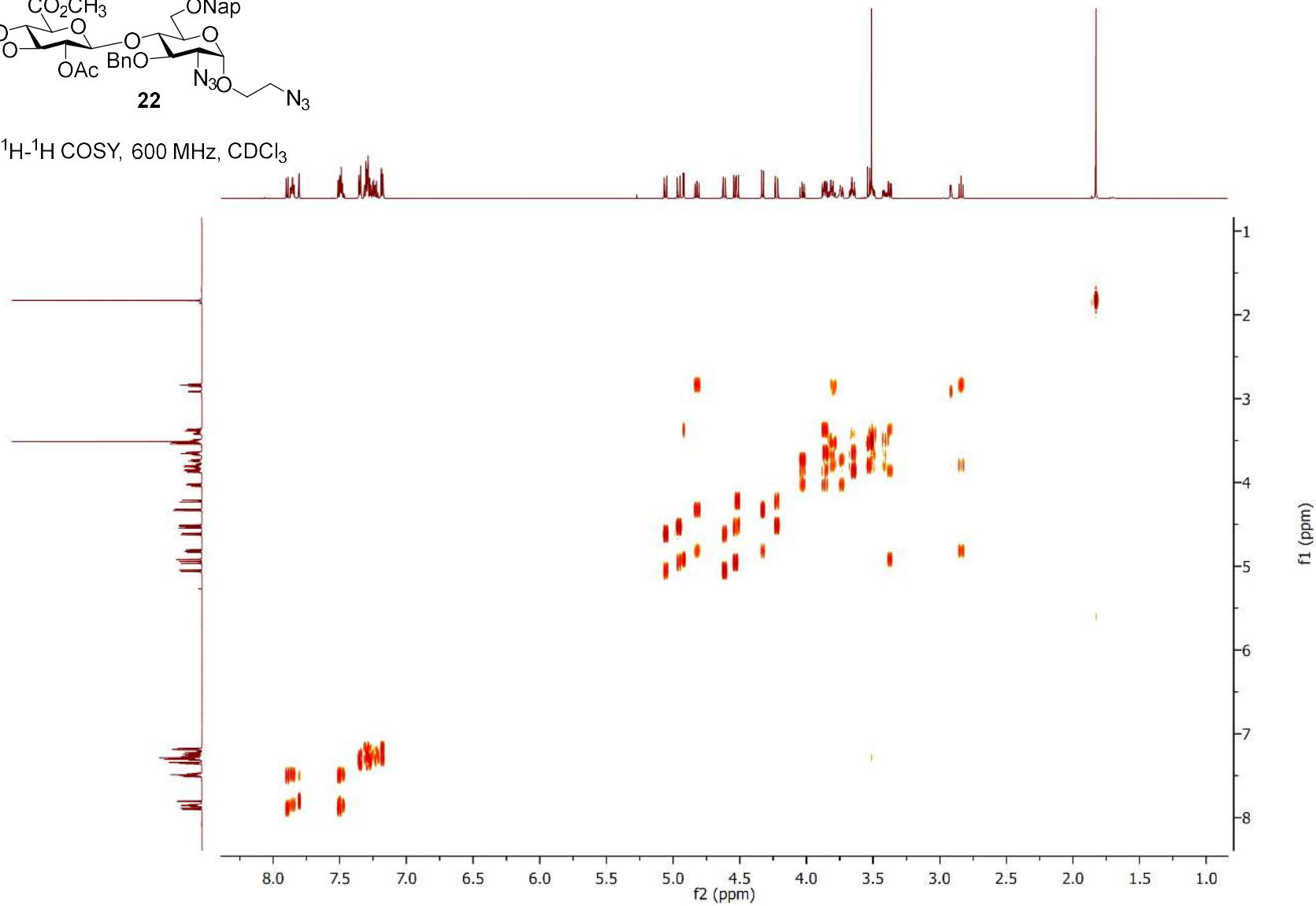


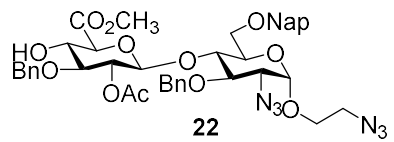
^{13}C NMR, 150 MHz, CDCl_3



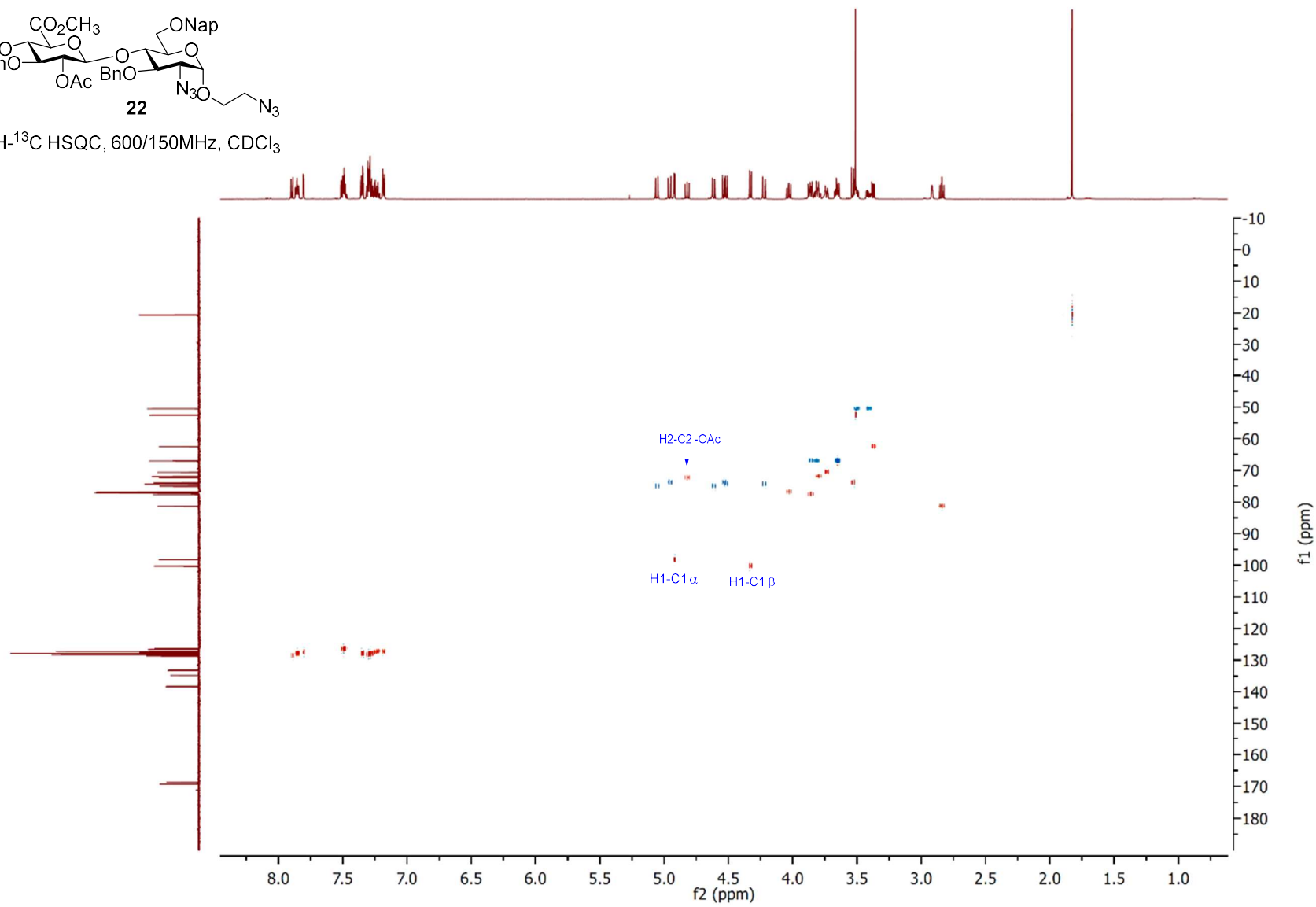


^1H - ^1H COSY, 600 MHz, CDCl_3

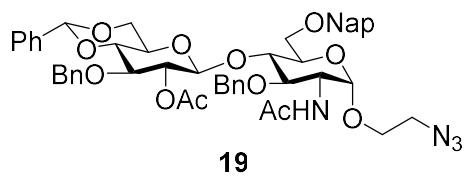




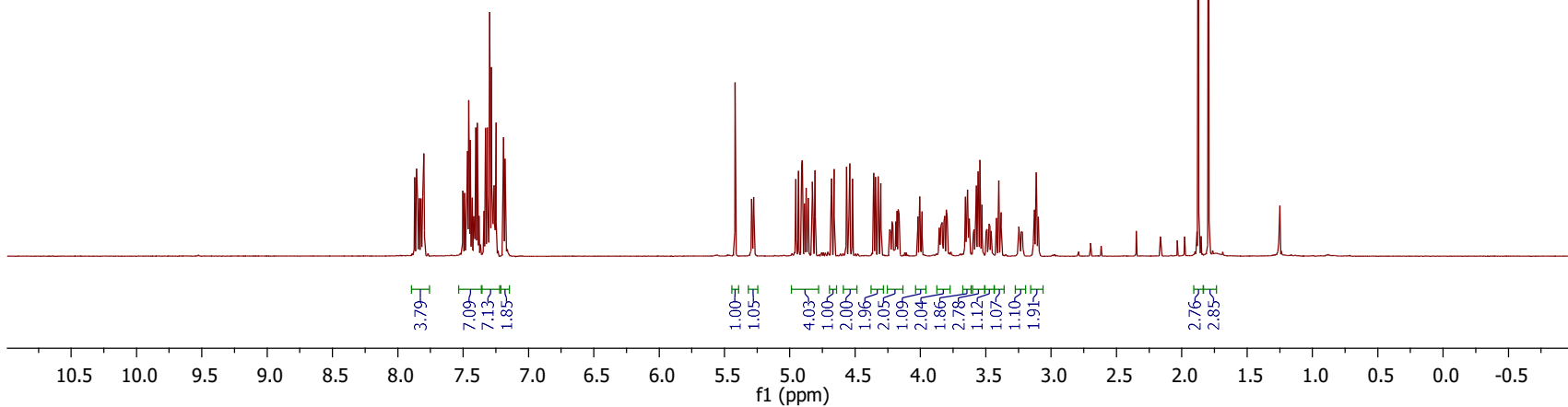
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

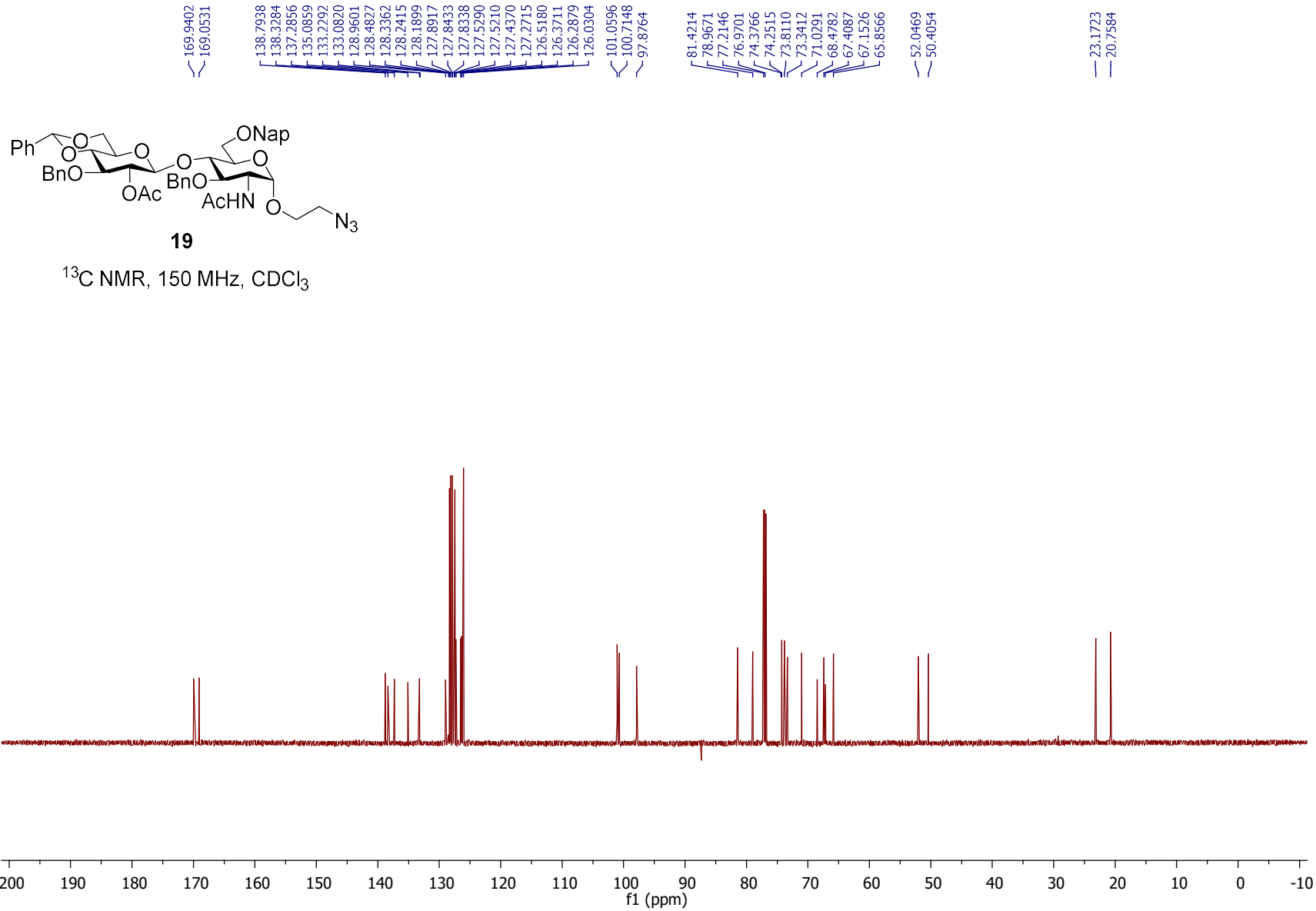


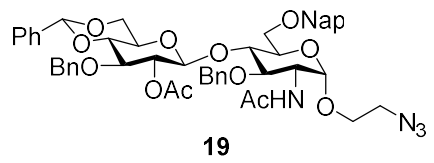
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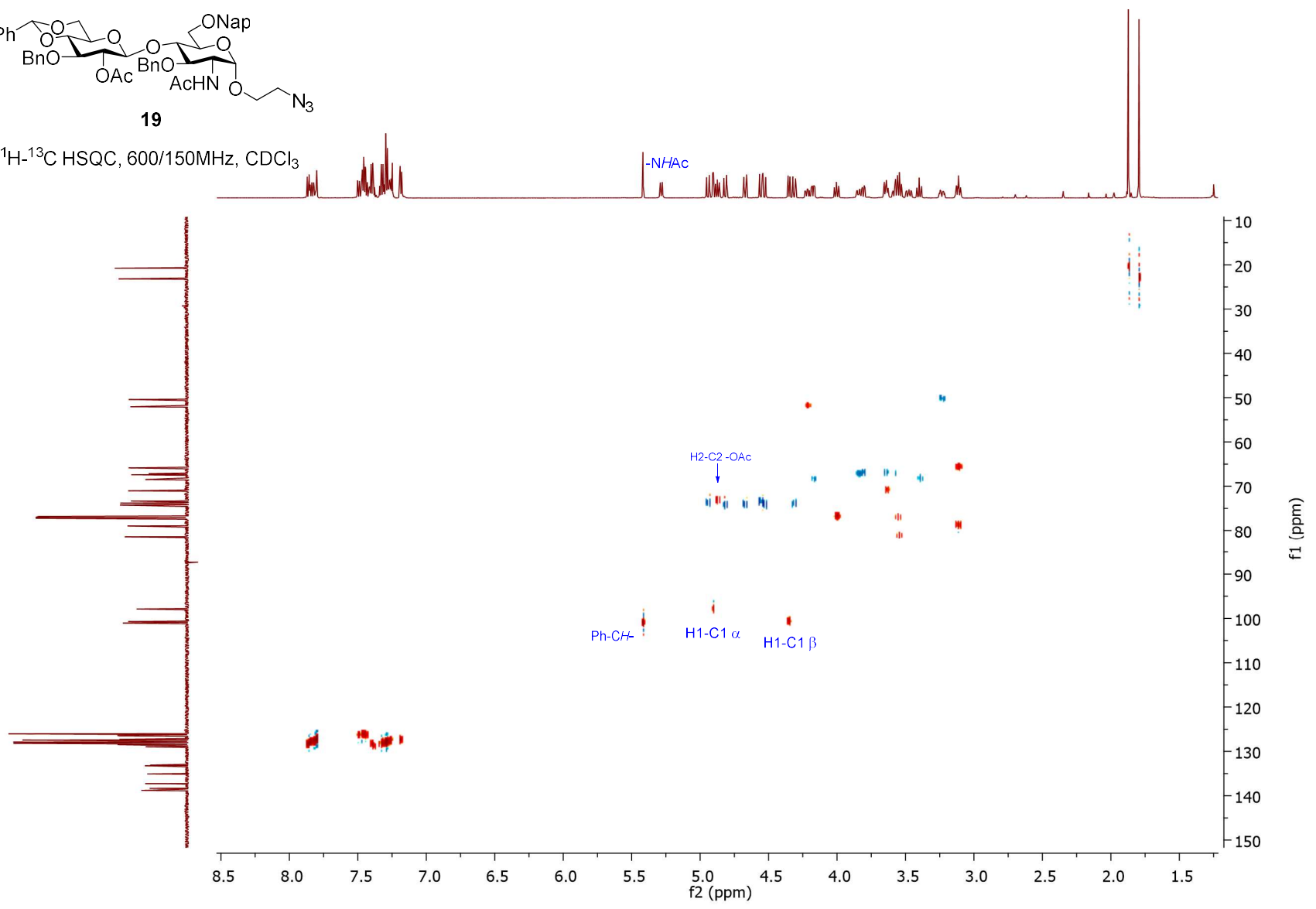
$^1\text{H NMR}$, 600 MHz, CDCl_3



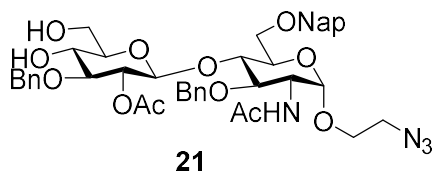




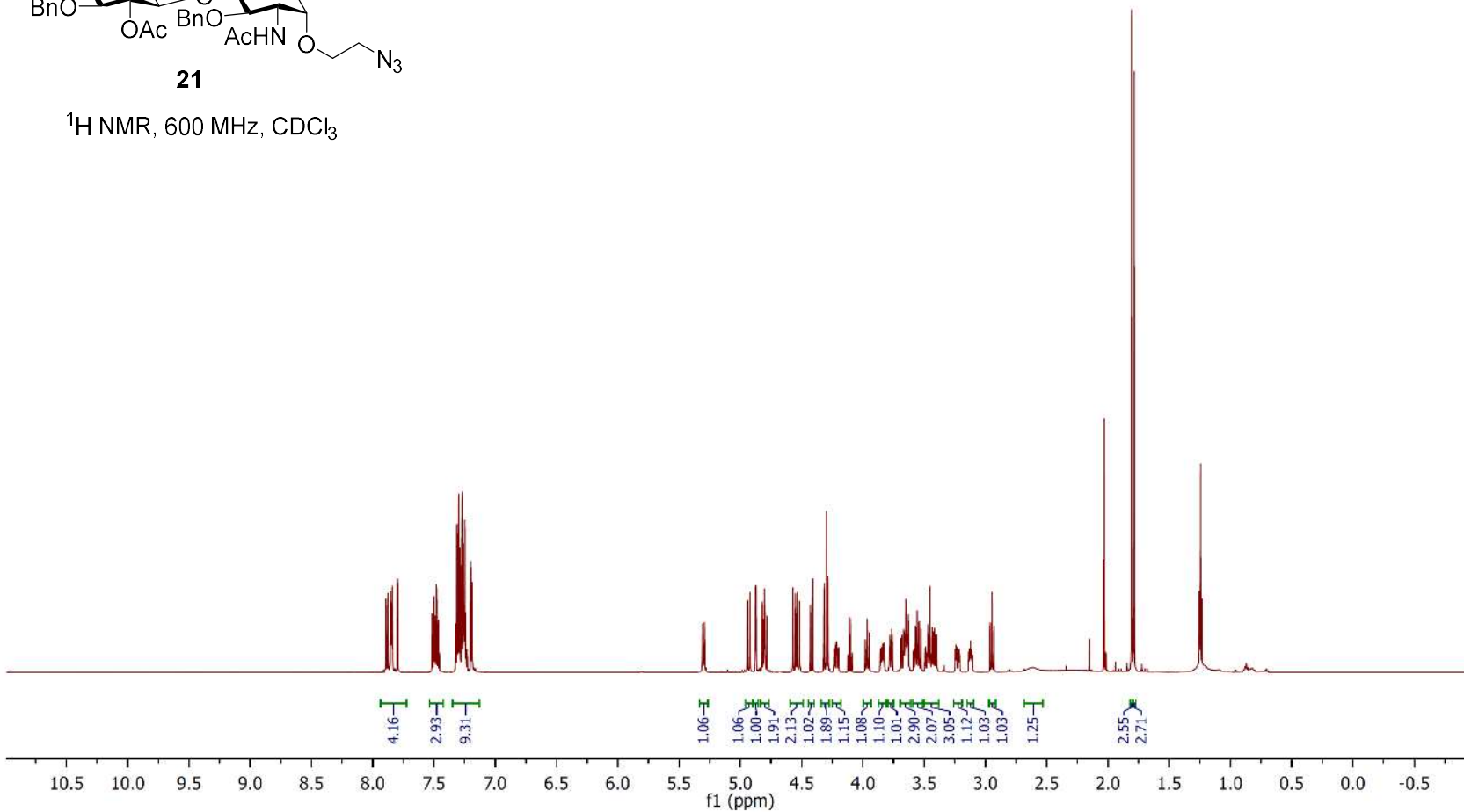
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

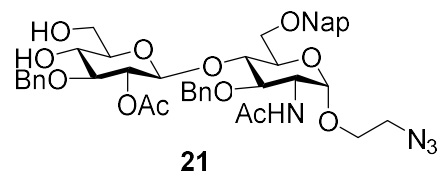


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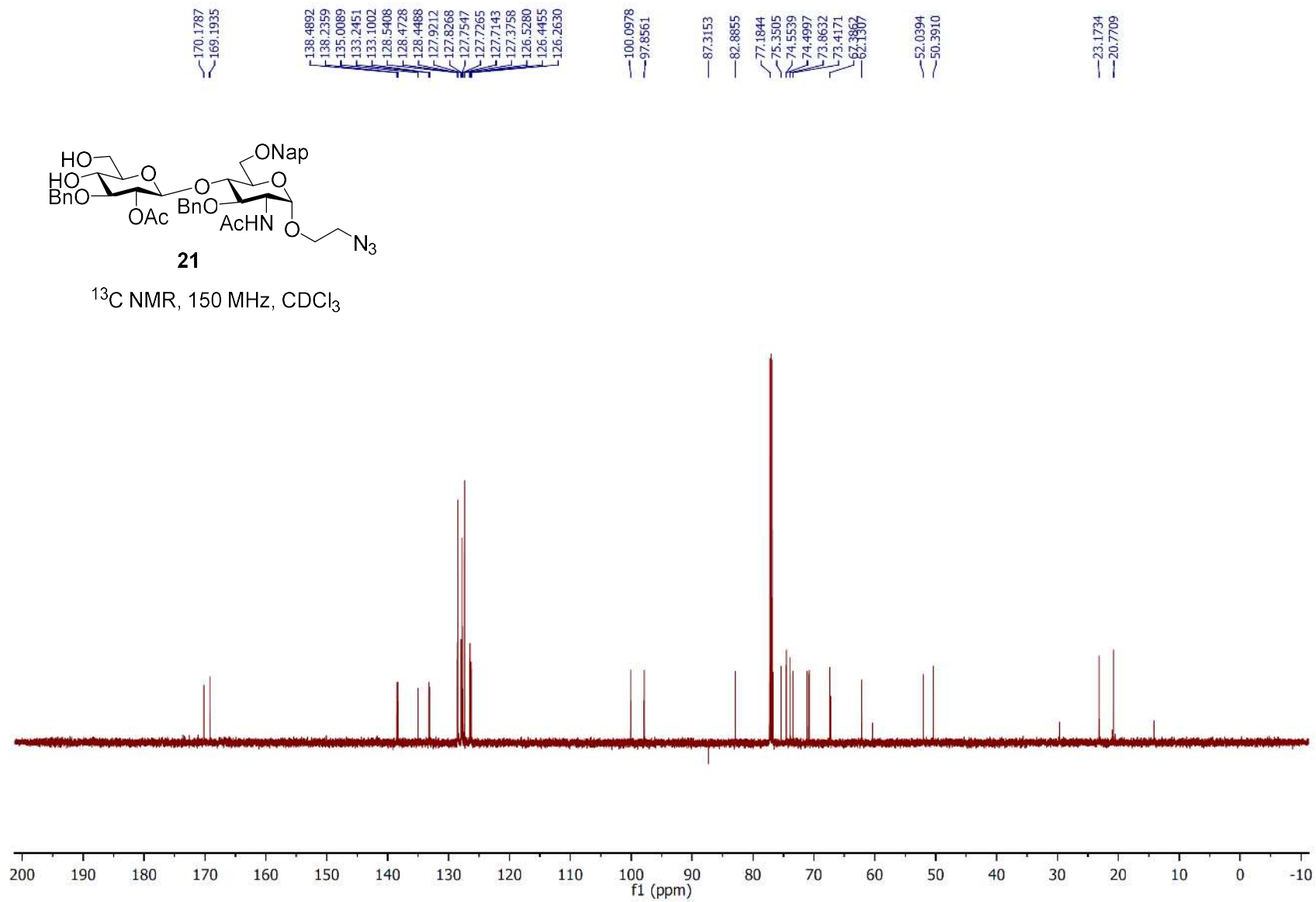


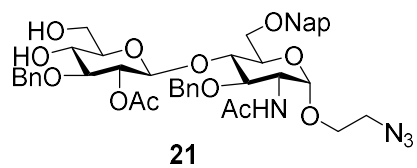
$^1\text{H NMR}$, 600 MHz, CDCl_3



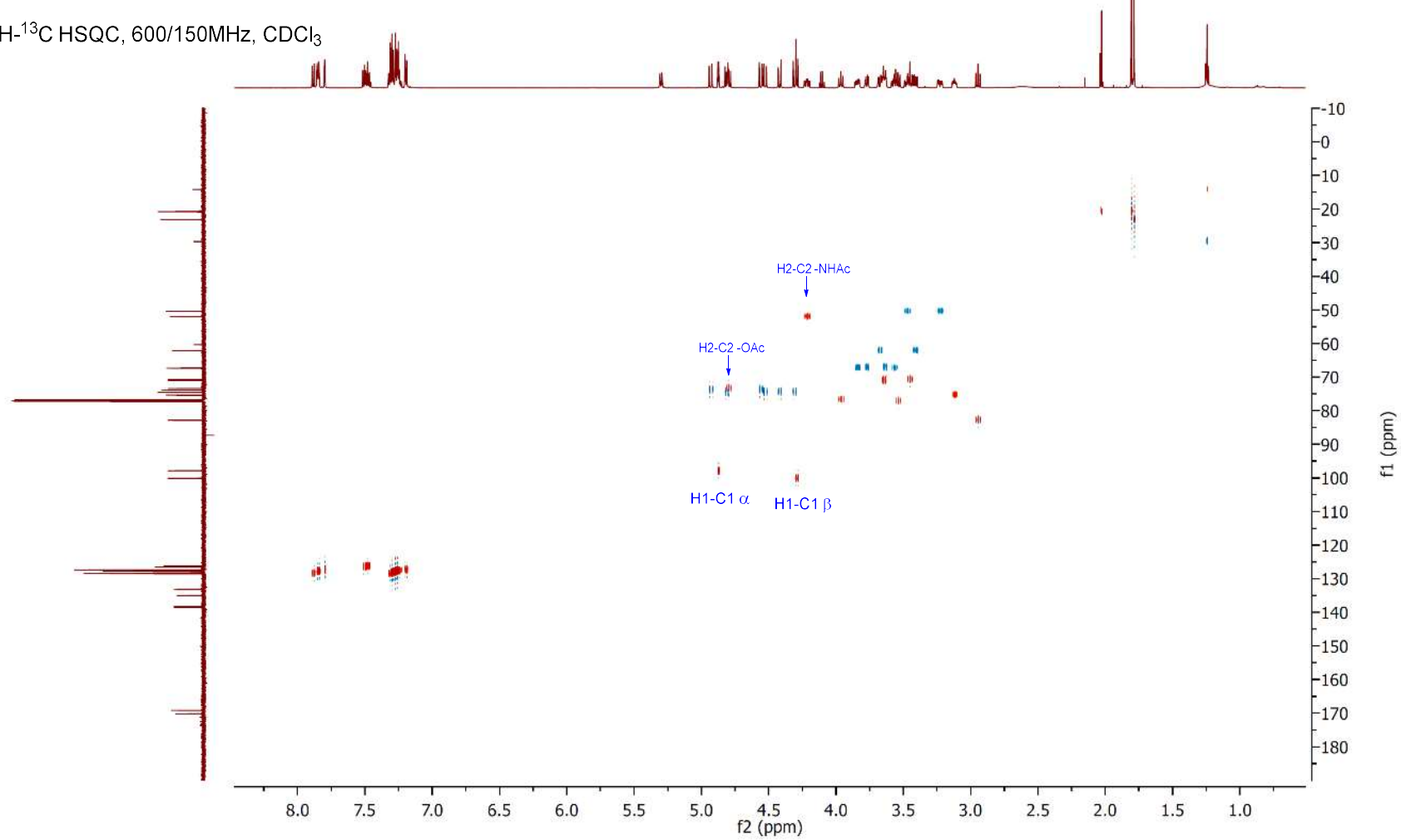


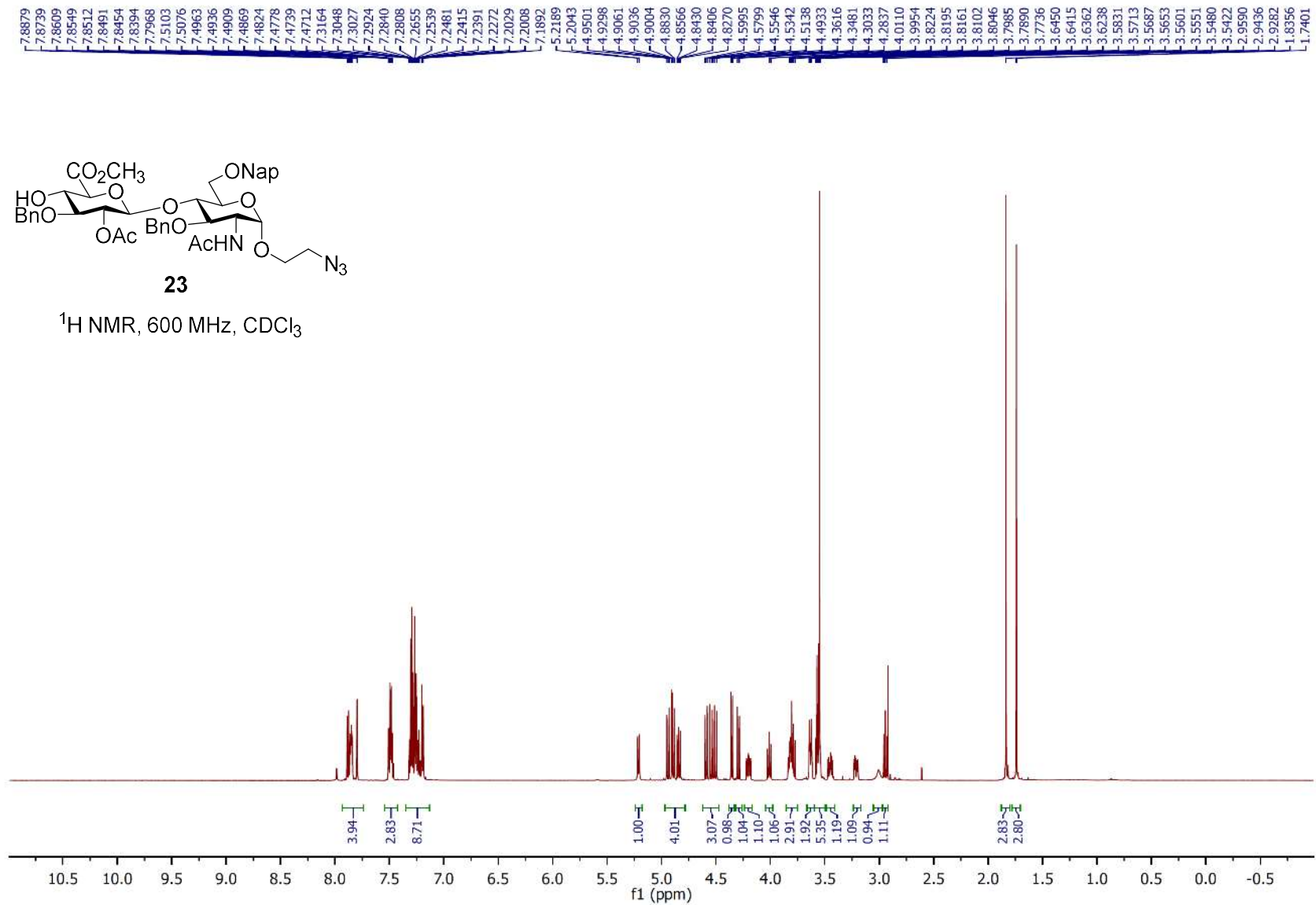
^{13}C NMR, 150 MHz, CDCl_3

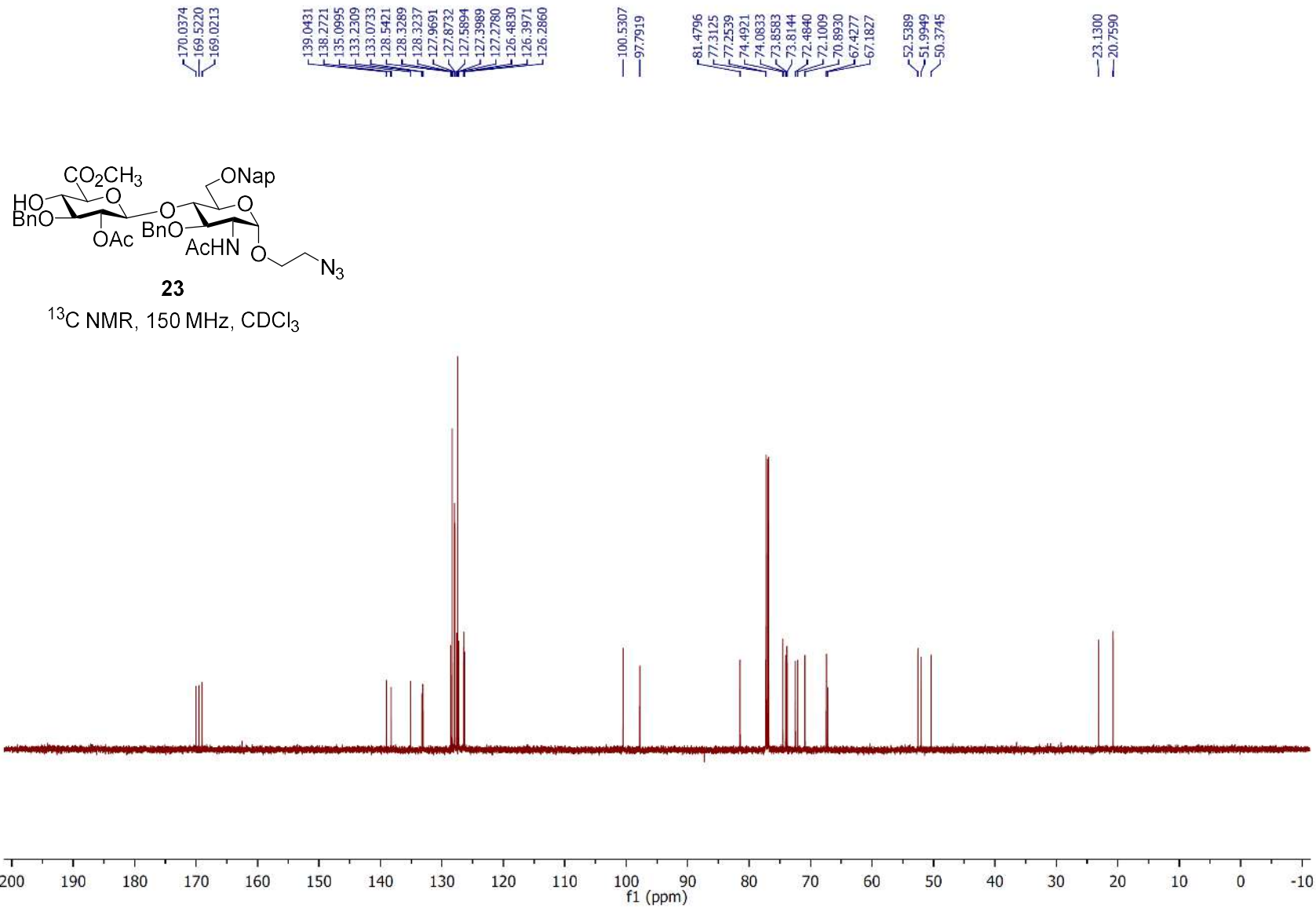


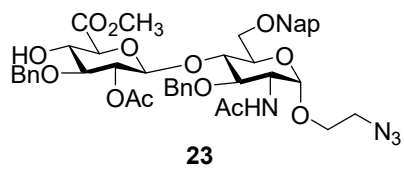


¹H-¹³C HSQC, 600/150MHz, CDCl₃

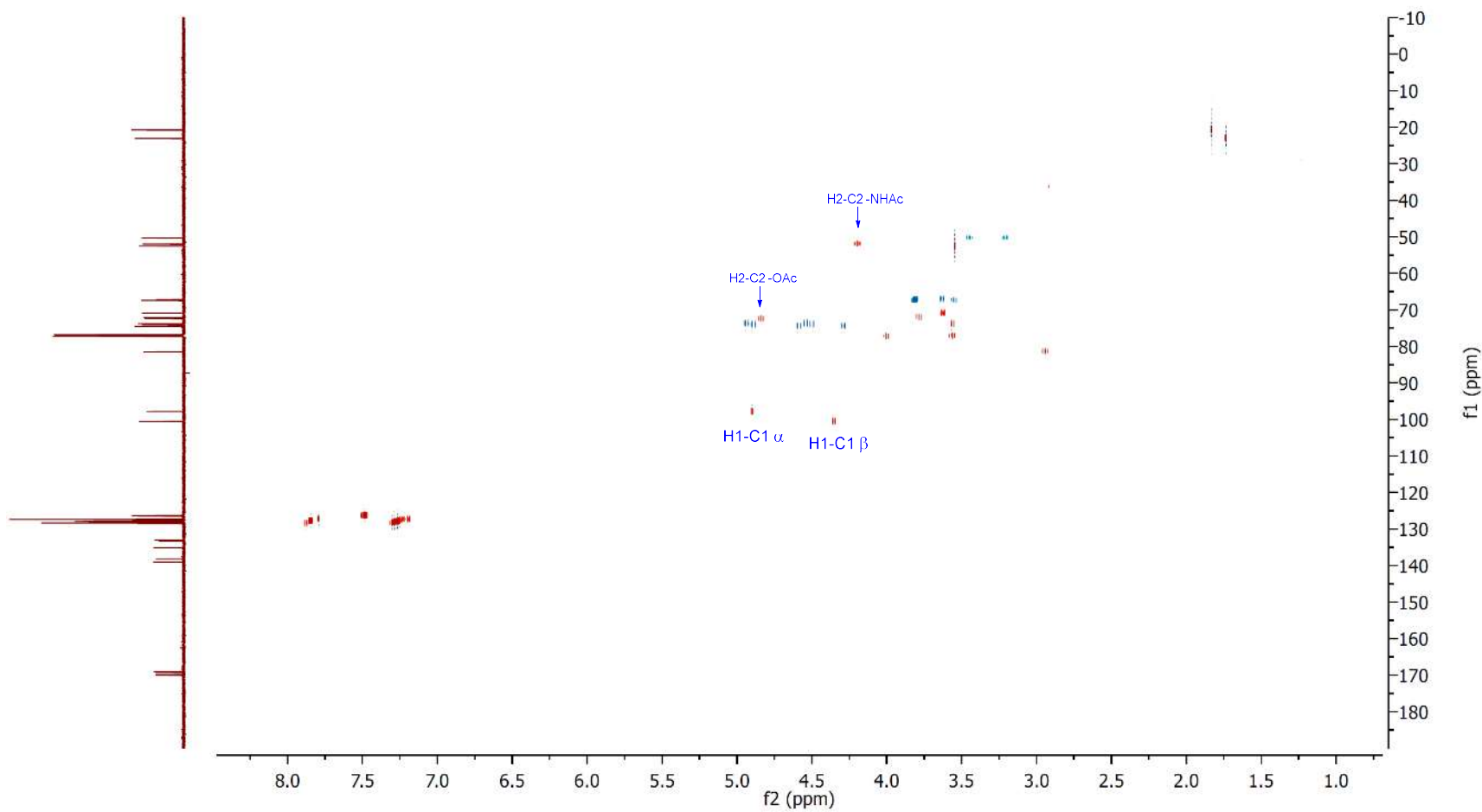




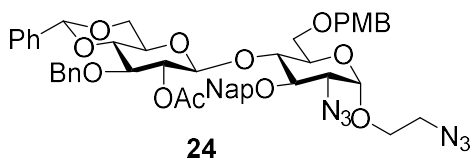




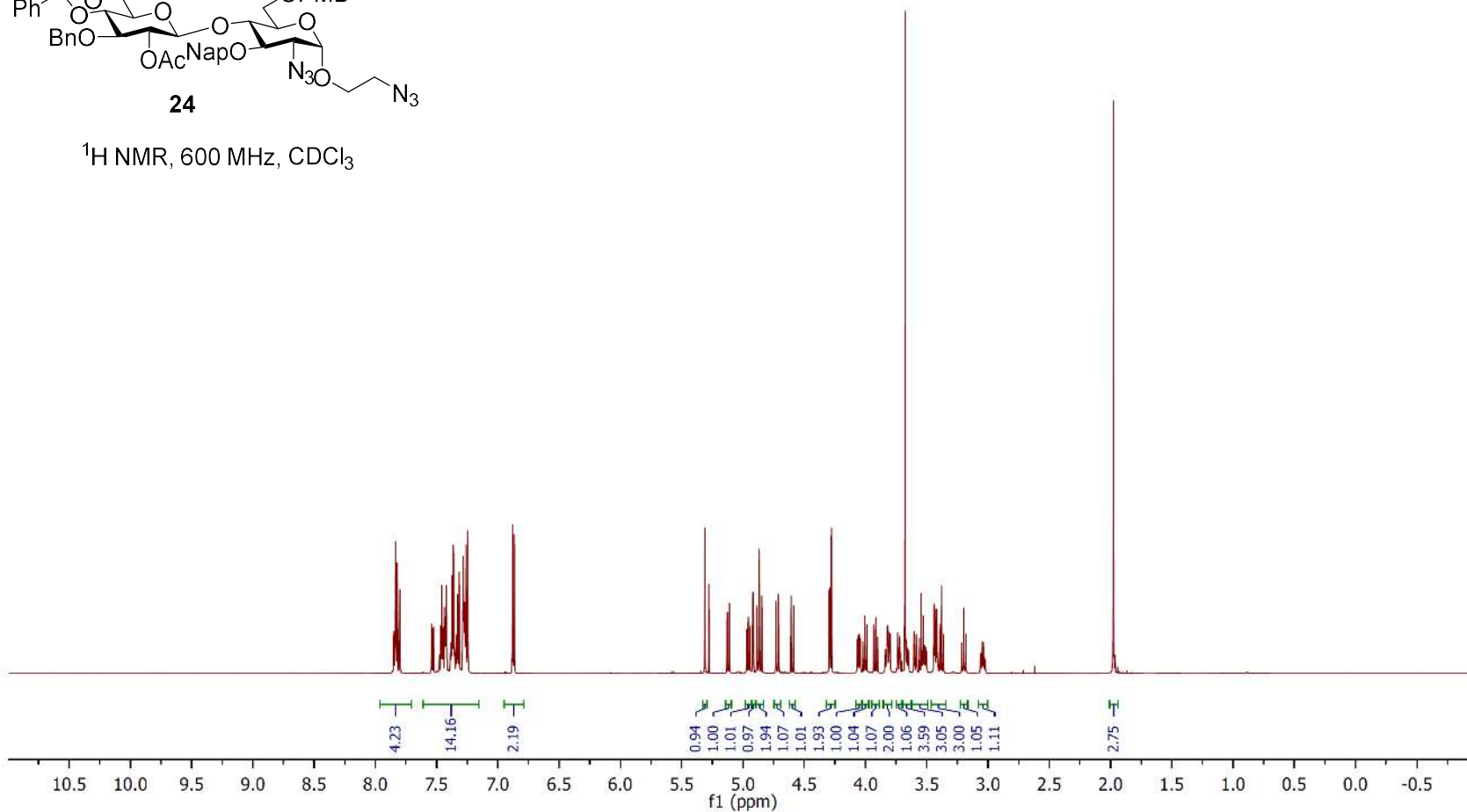
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

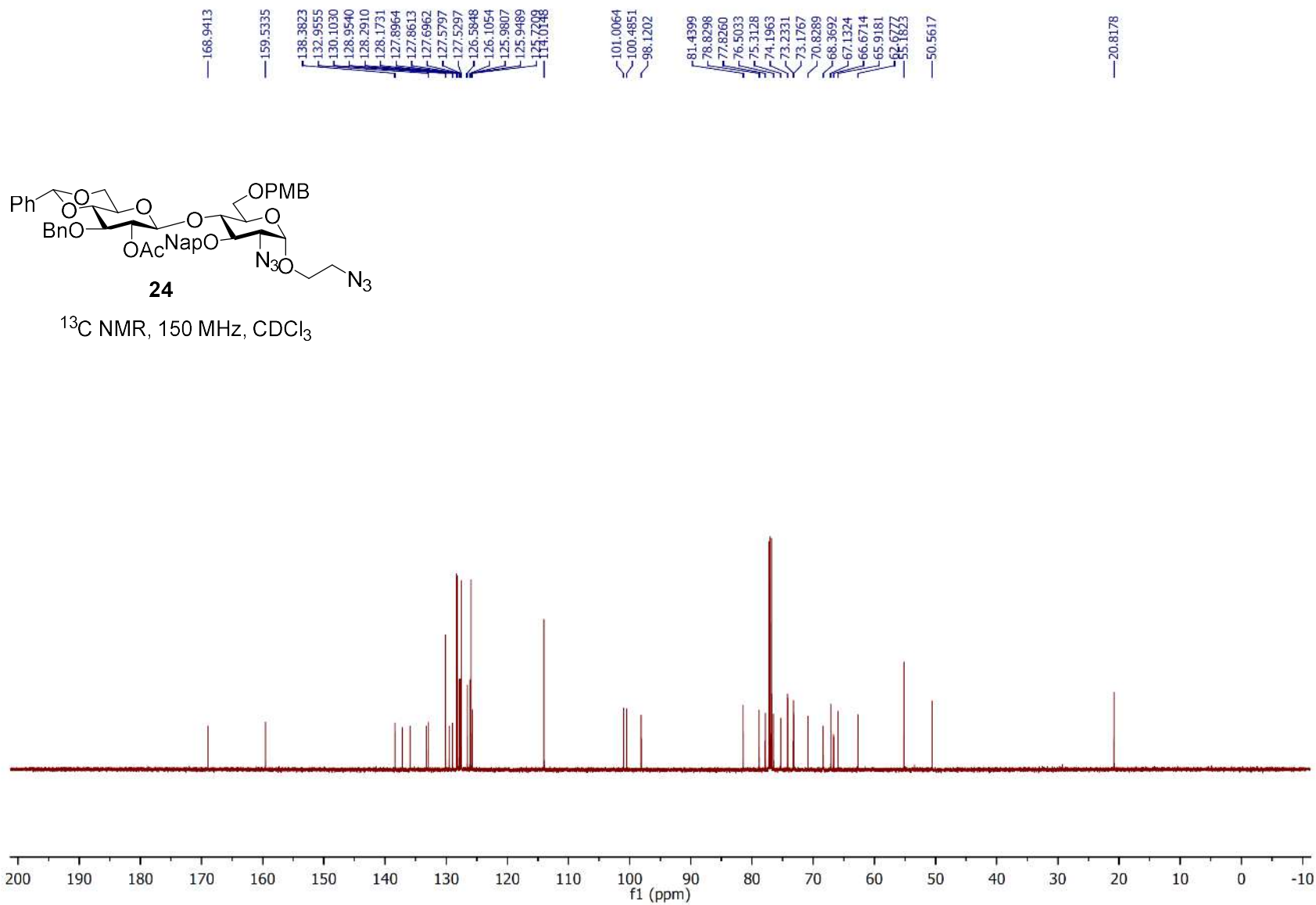


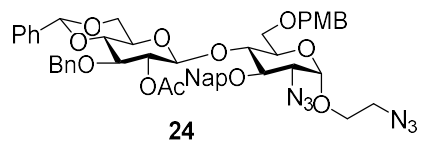
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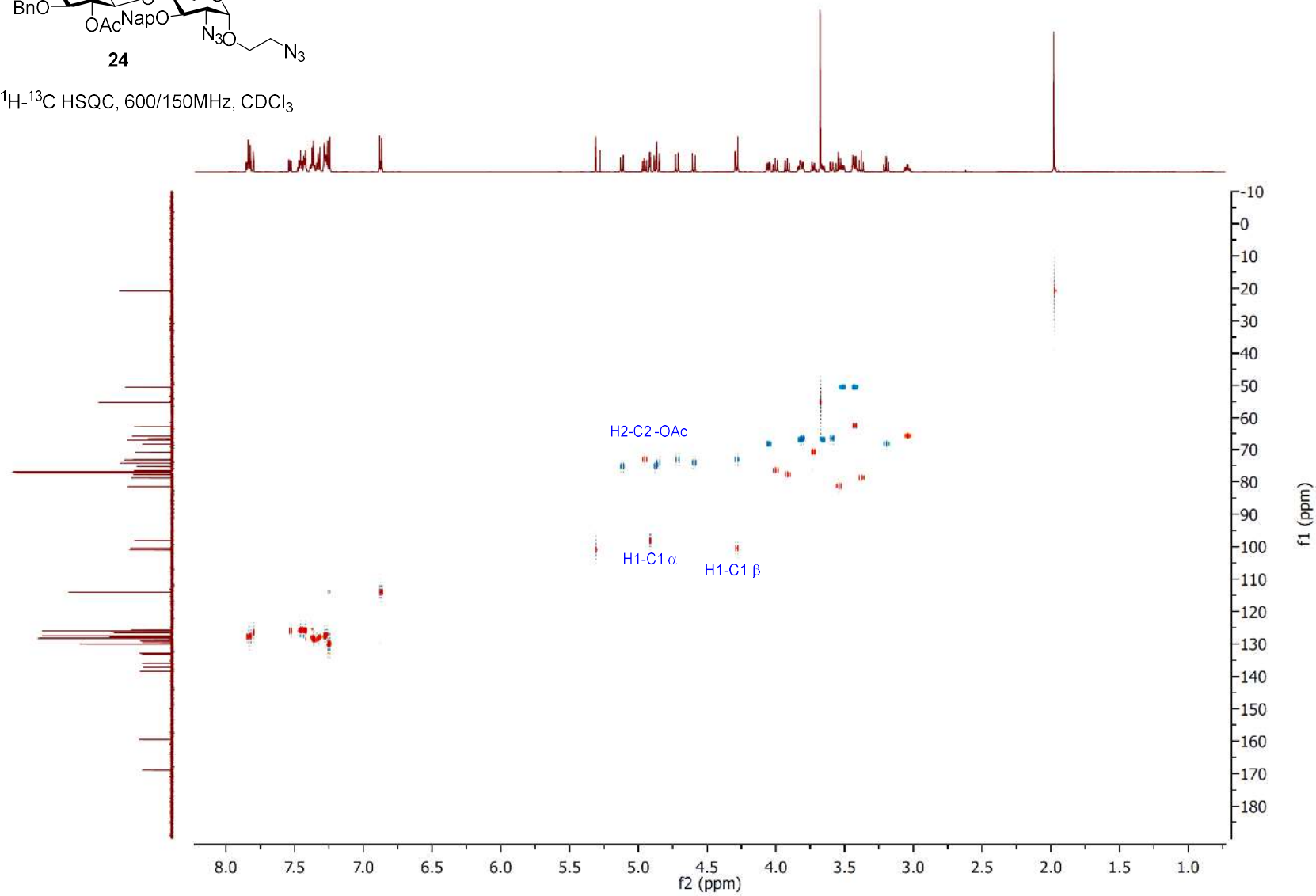
$^1\text{H NMR}$, 600 MHz, CDCl_3



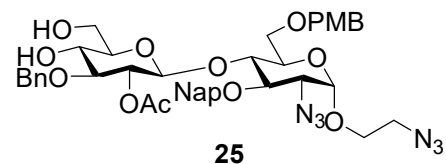




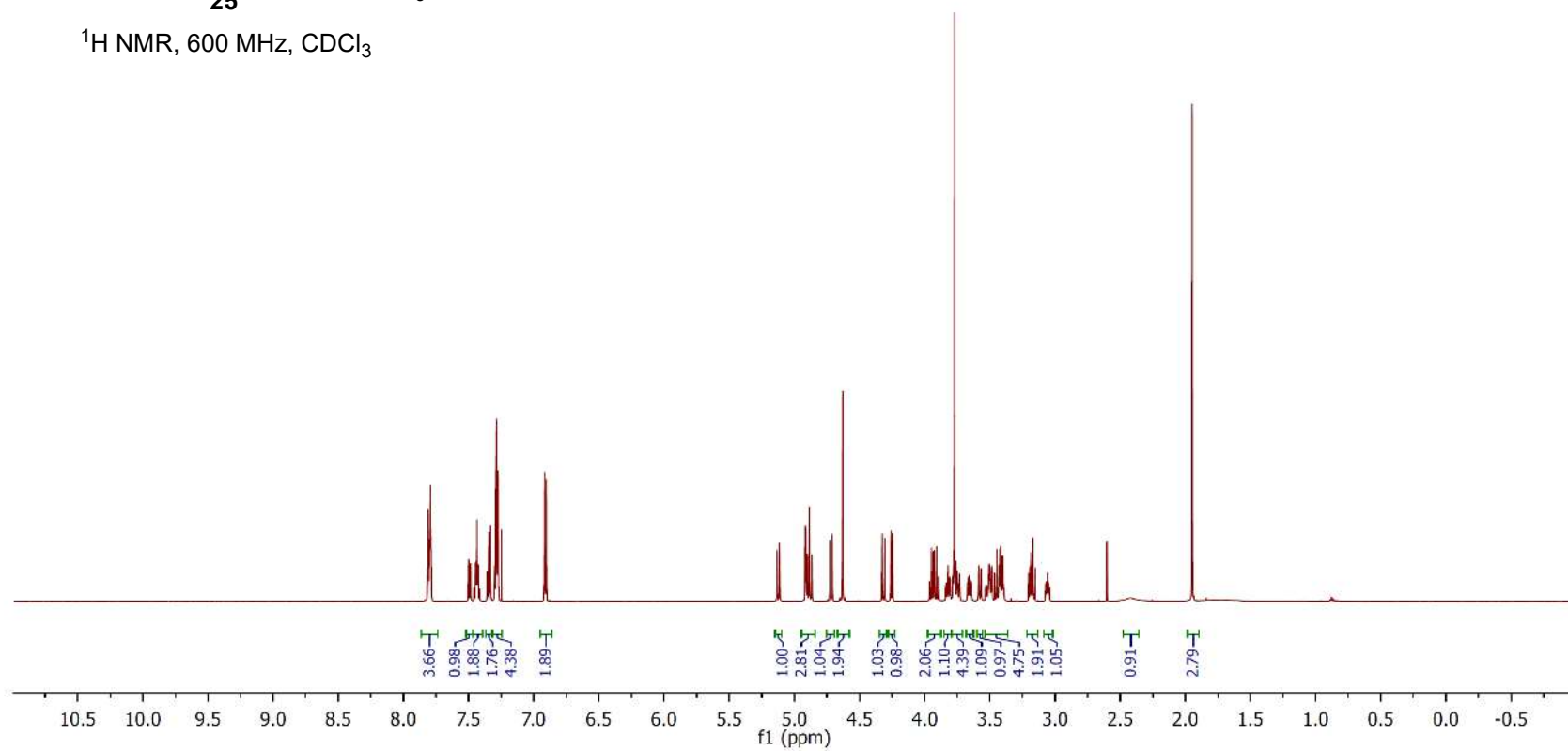
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3



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$^1\text{H NMR}$, 600 MHz, CDCl_3

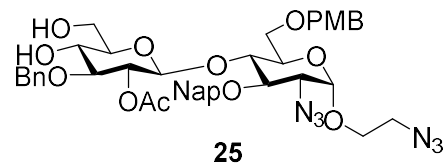


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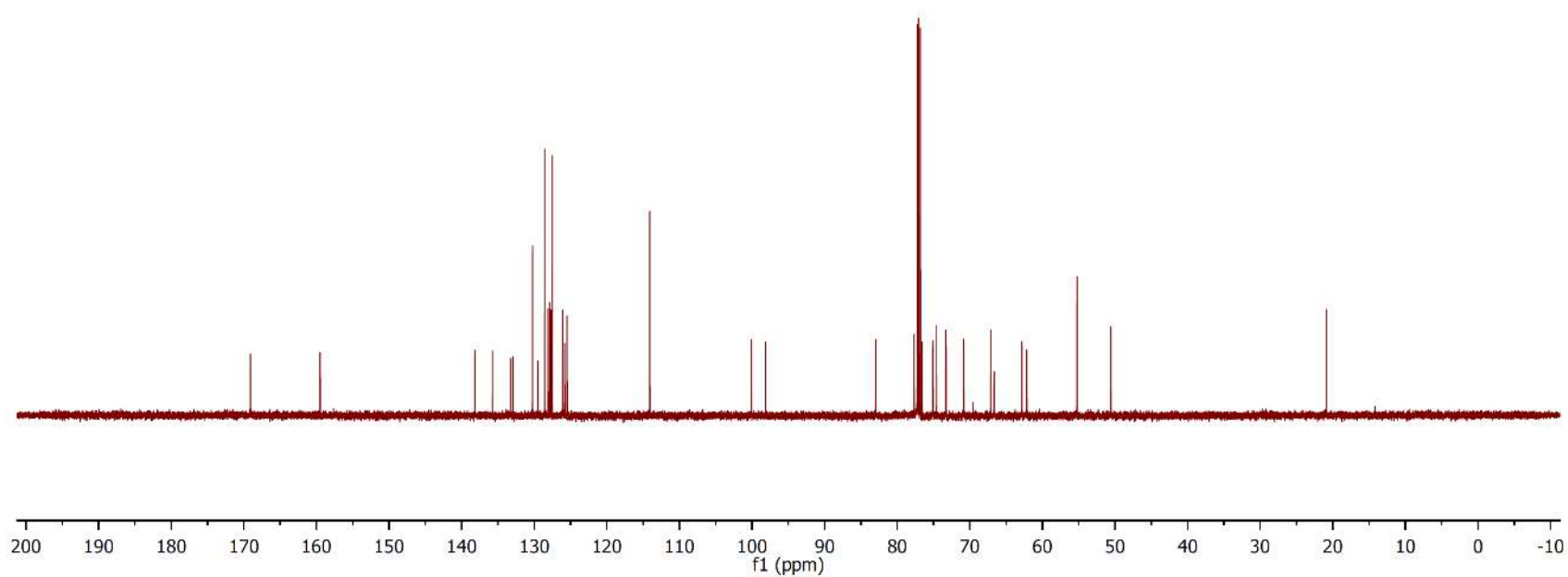
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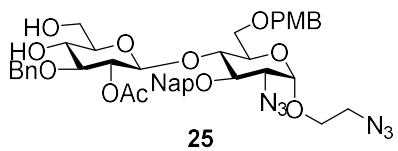
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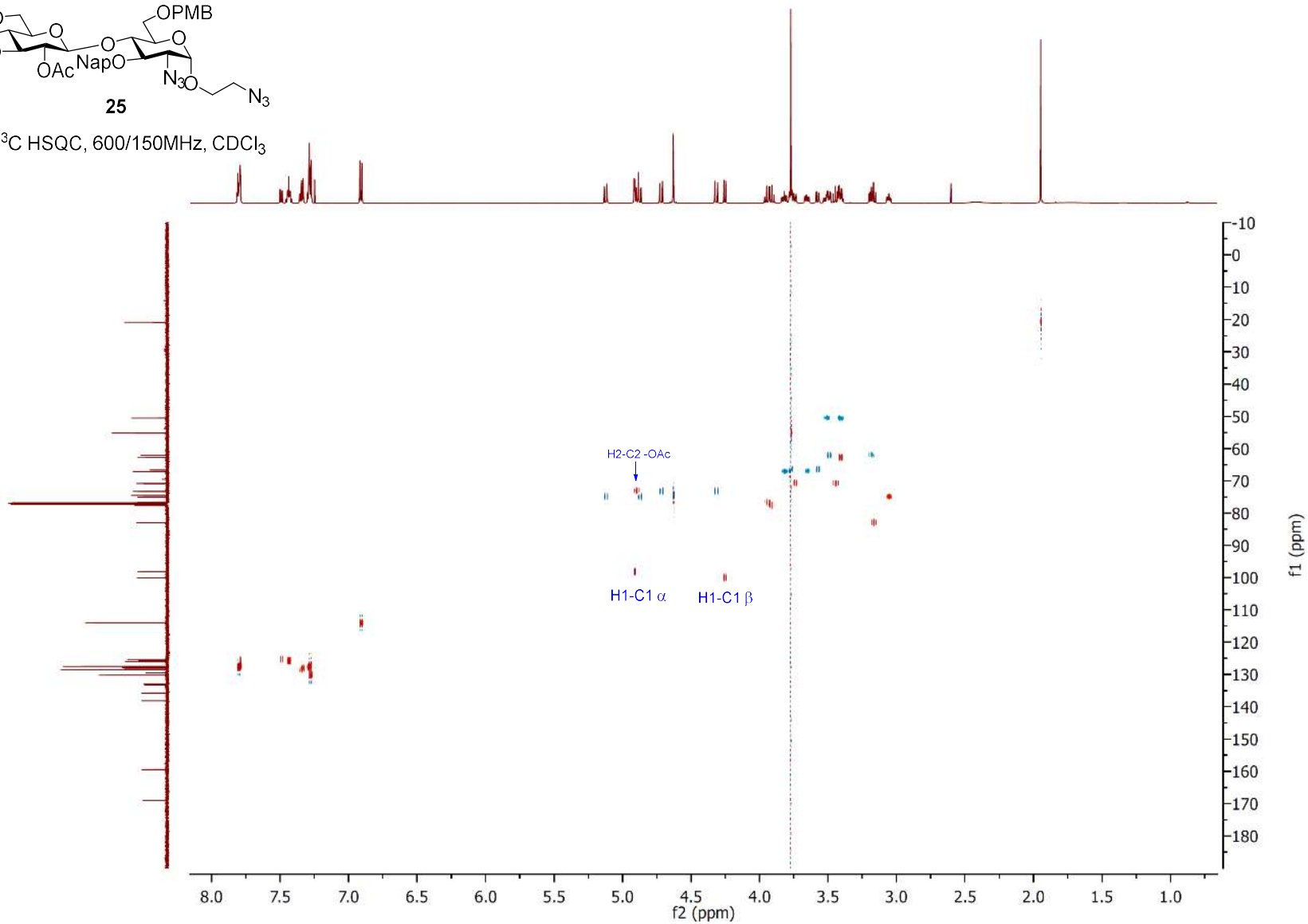


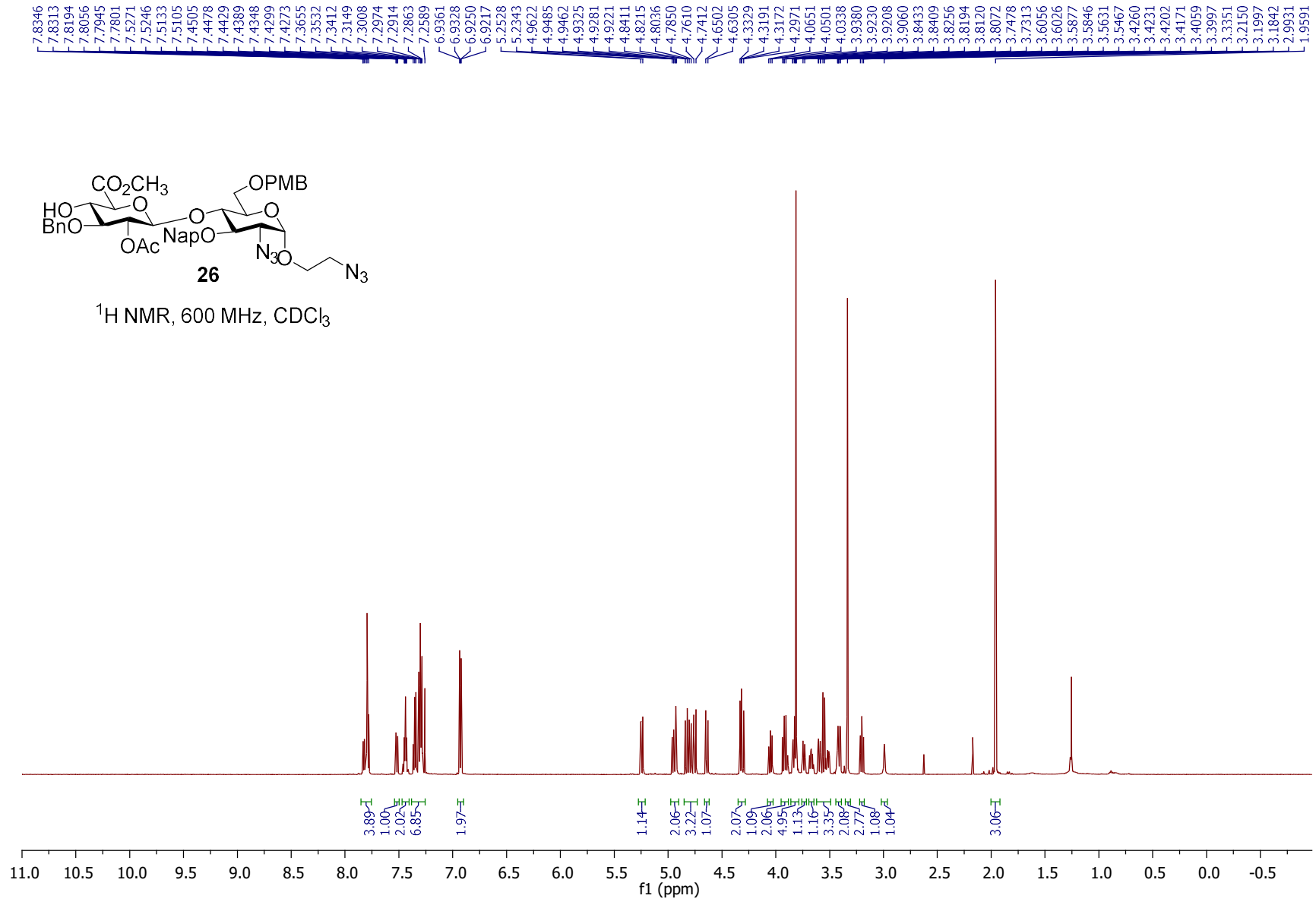
^{13}C NMR, 150 MHz, CDCl_3

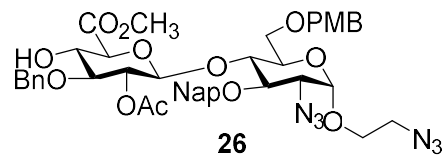




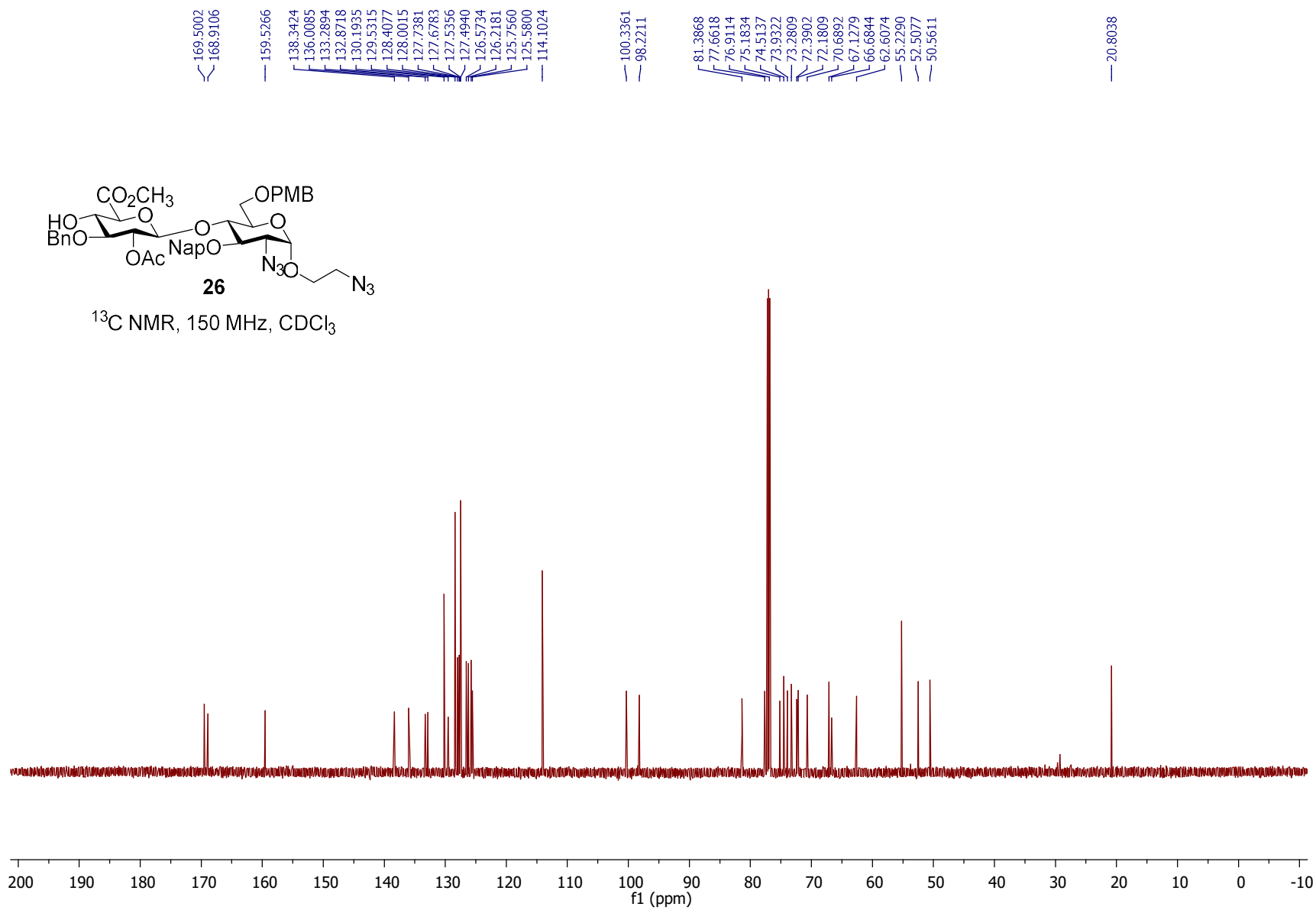
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

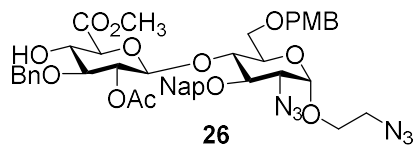




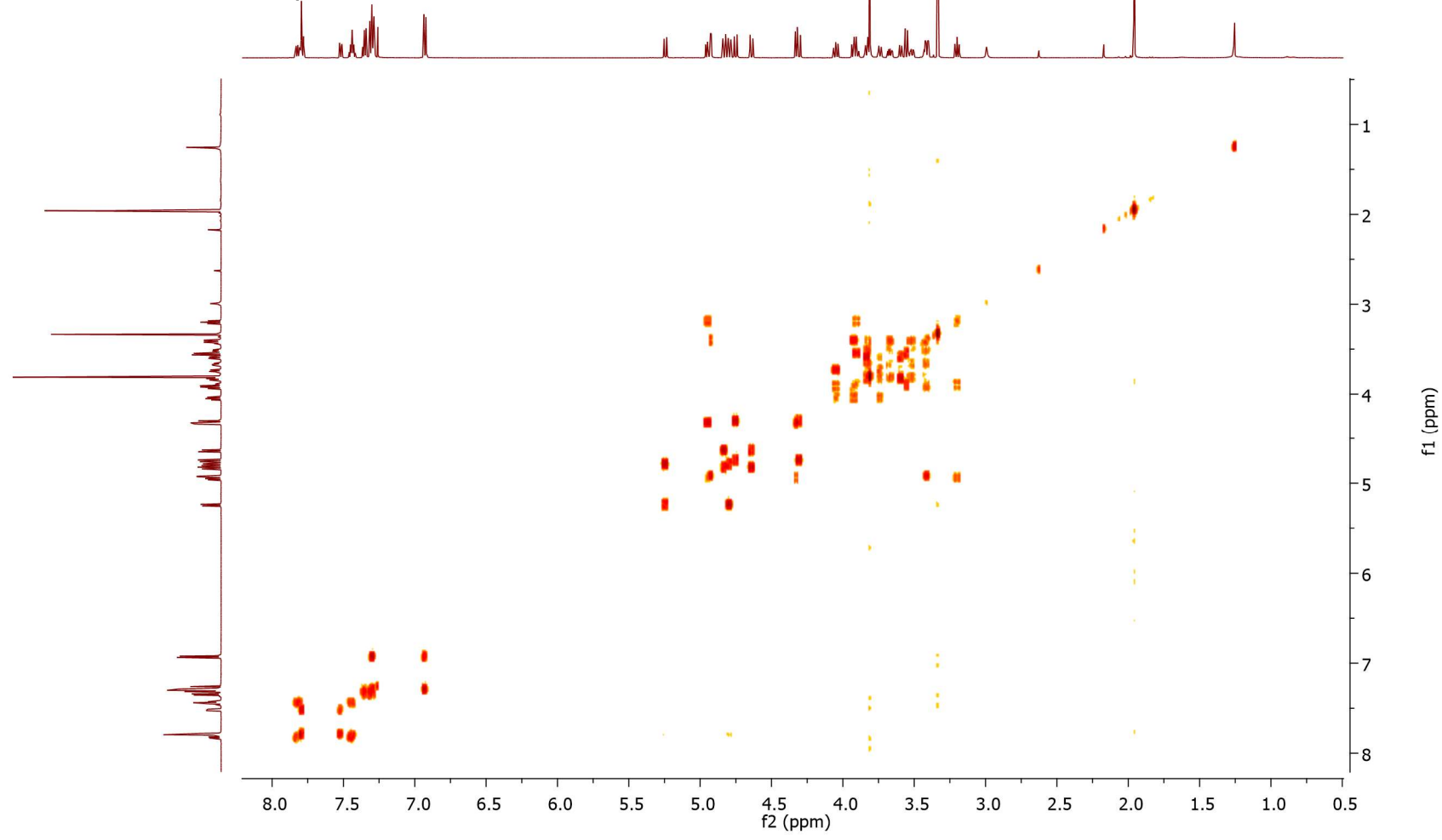


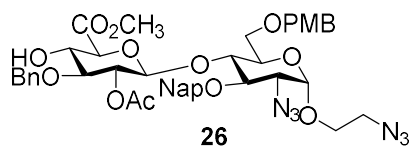
^{13}C NMR, 150 MHz, CDCl_3



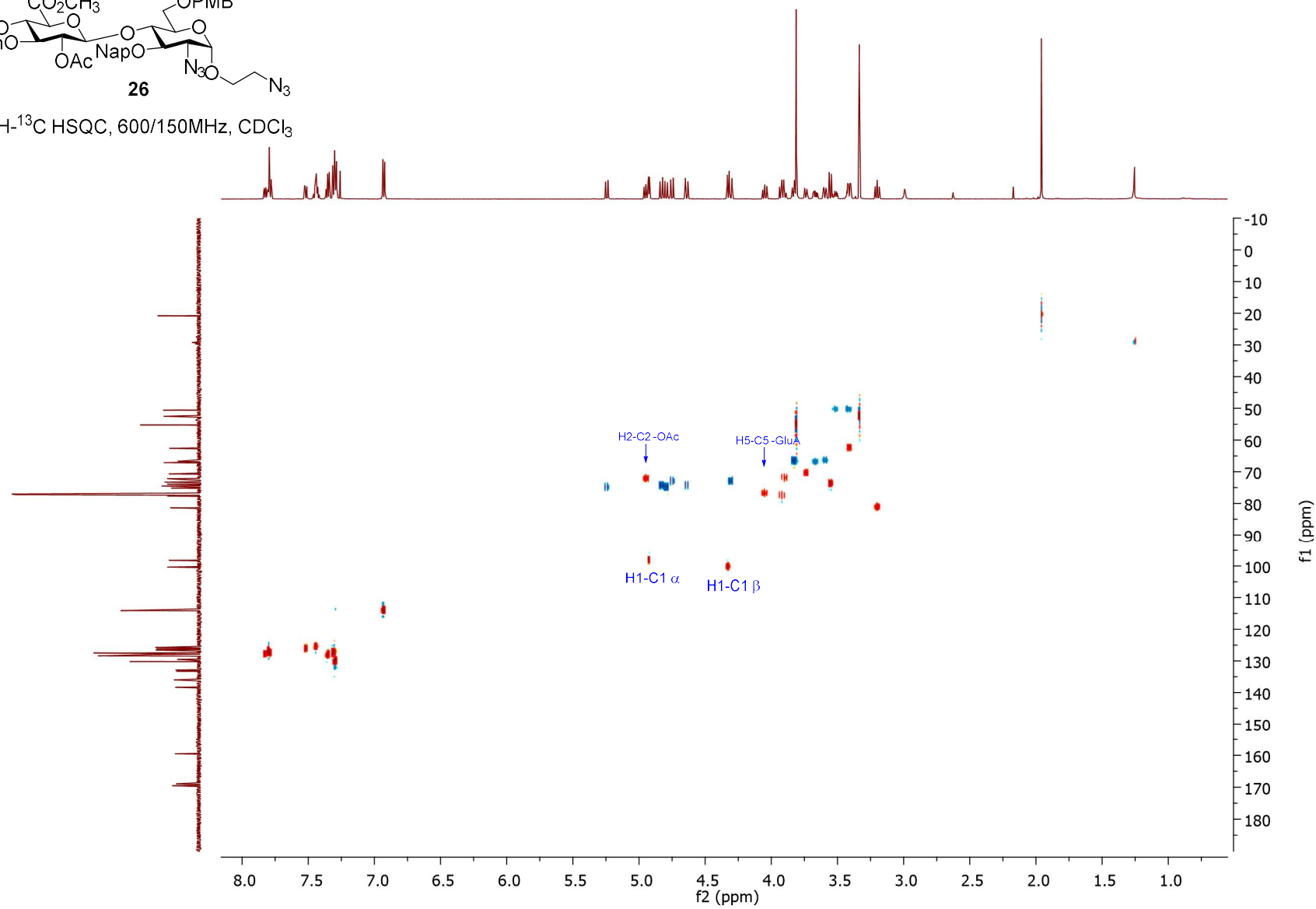


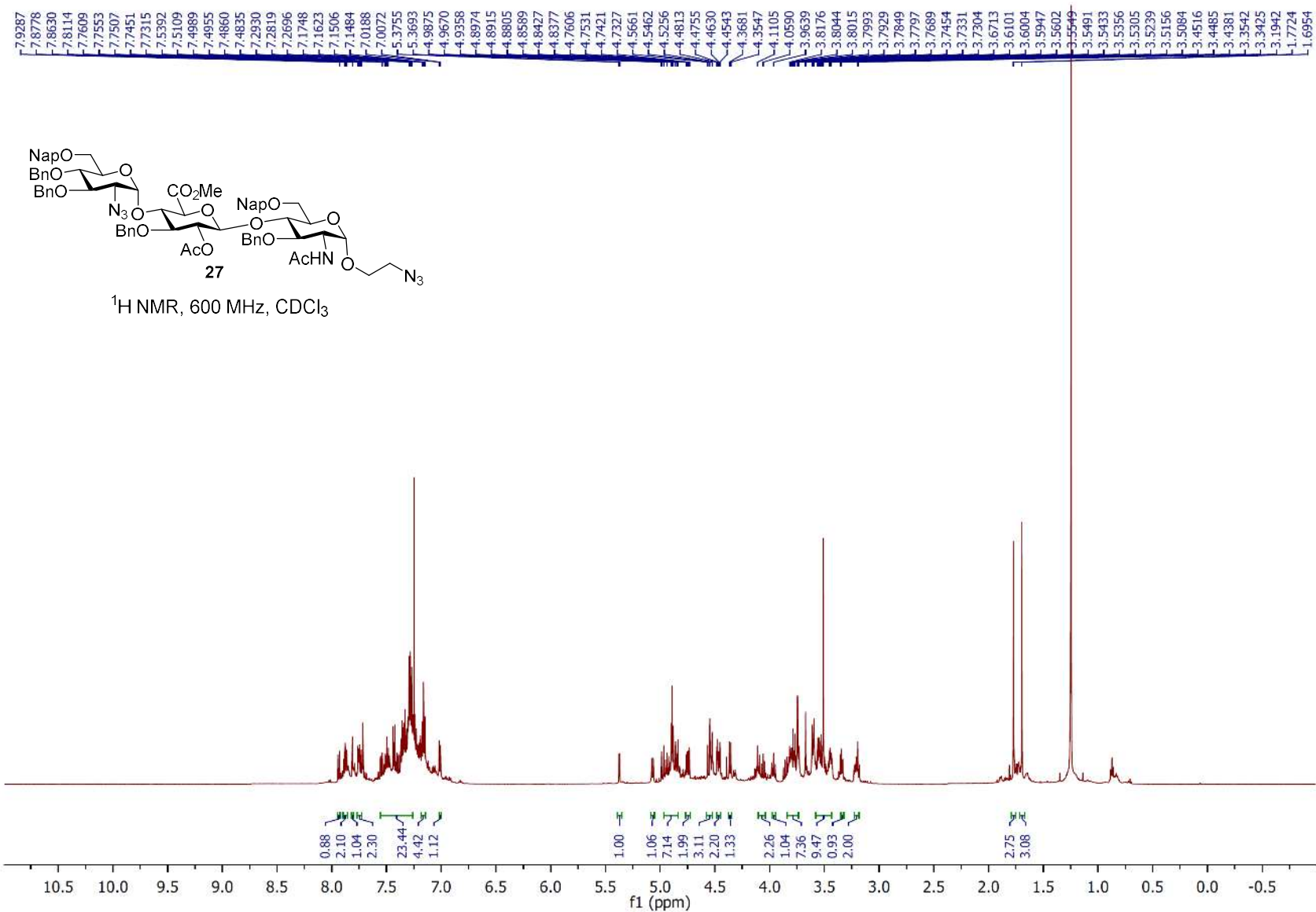
¹H-¹H COSY, 600 MHz, CDCl₃

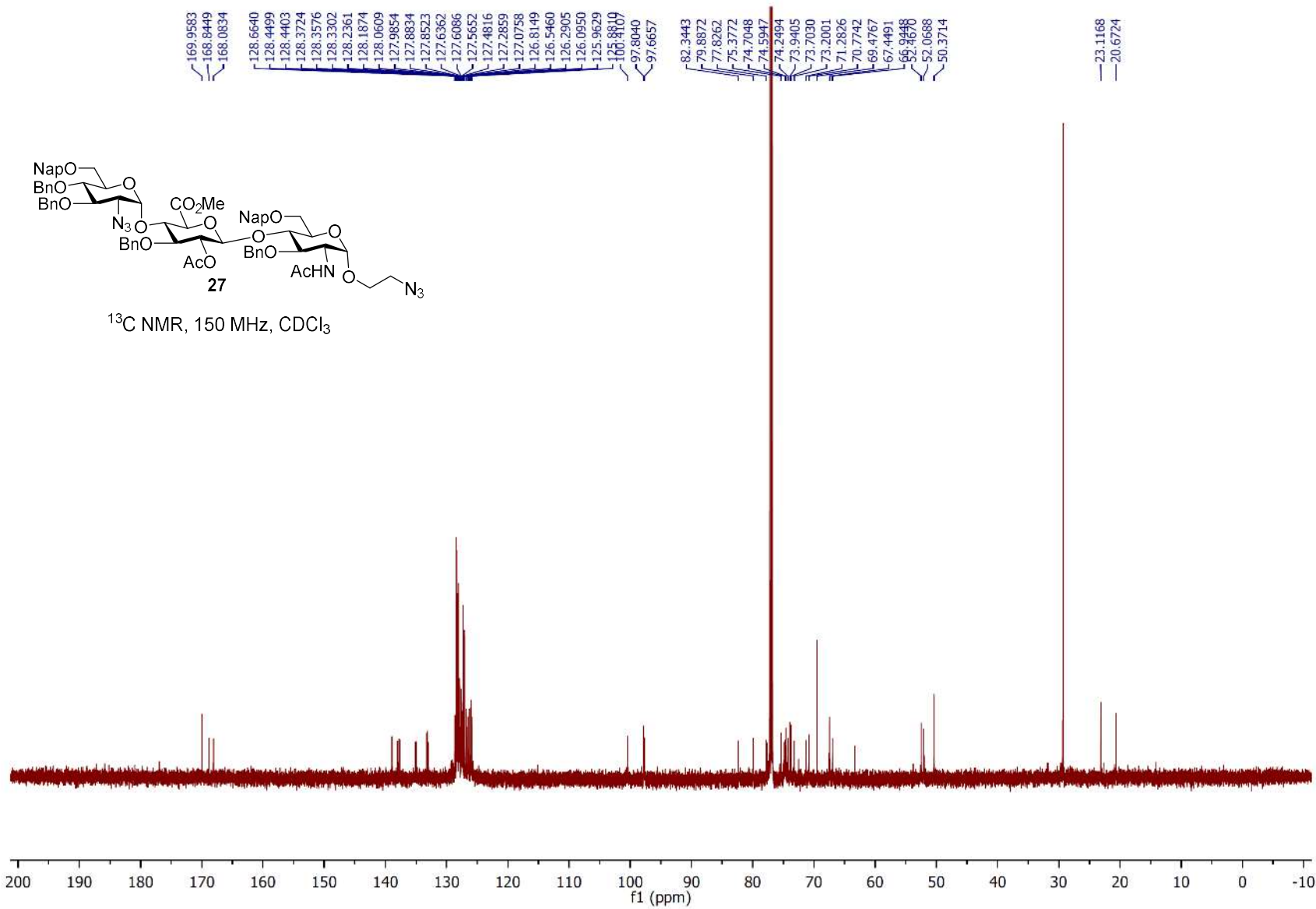


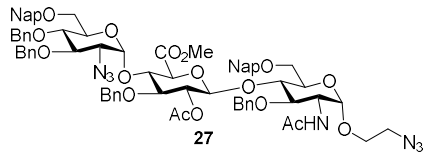


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

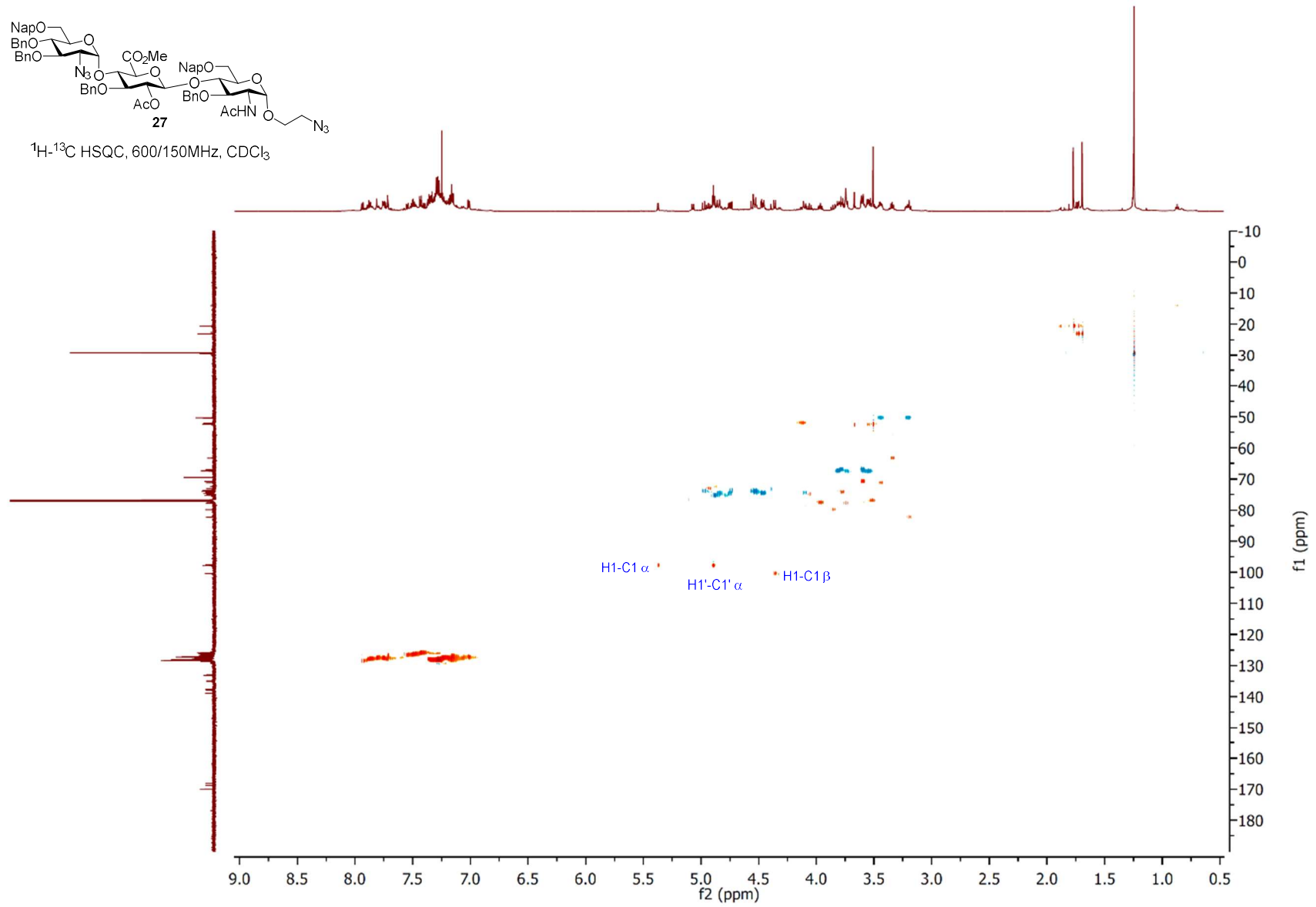




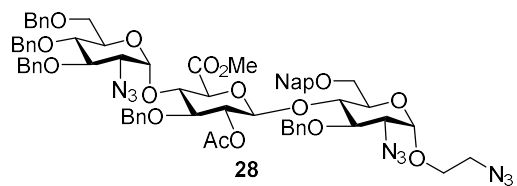




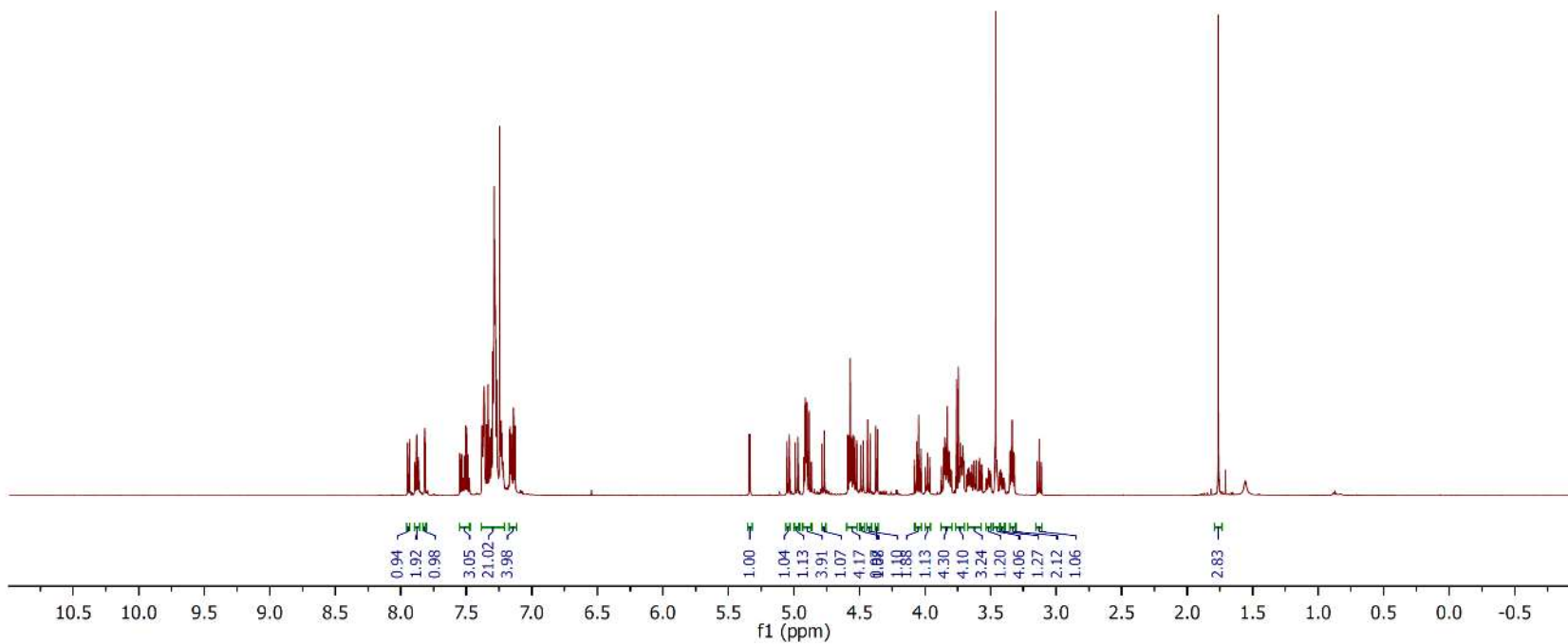
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

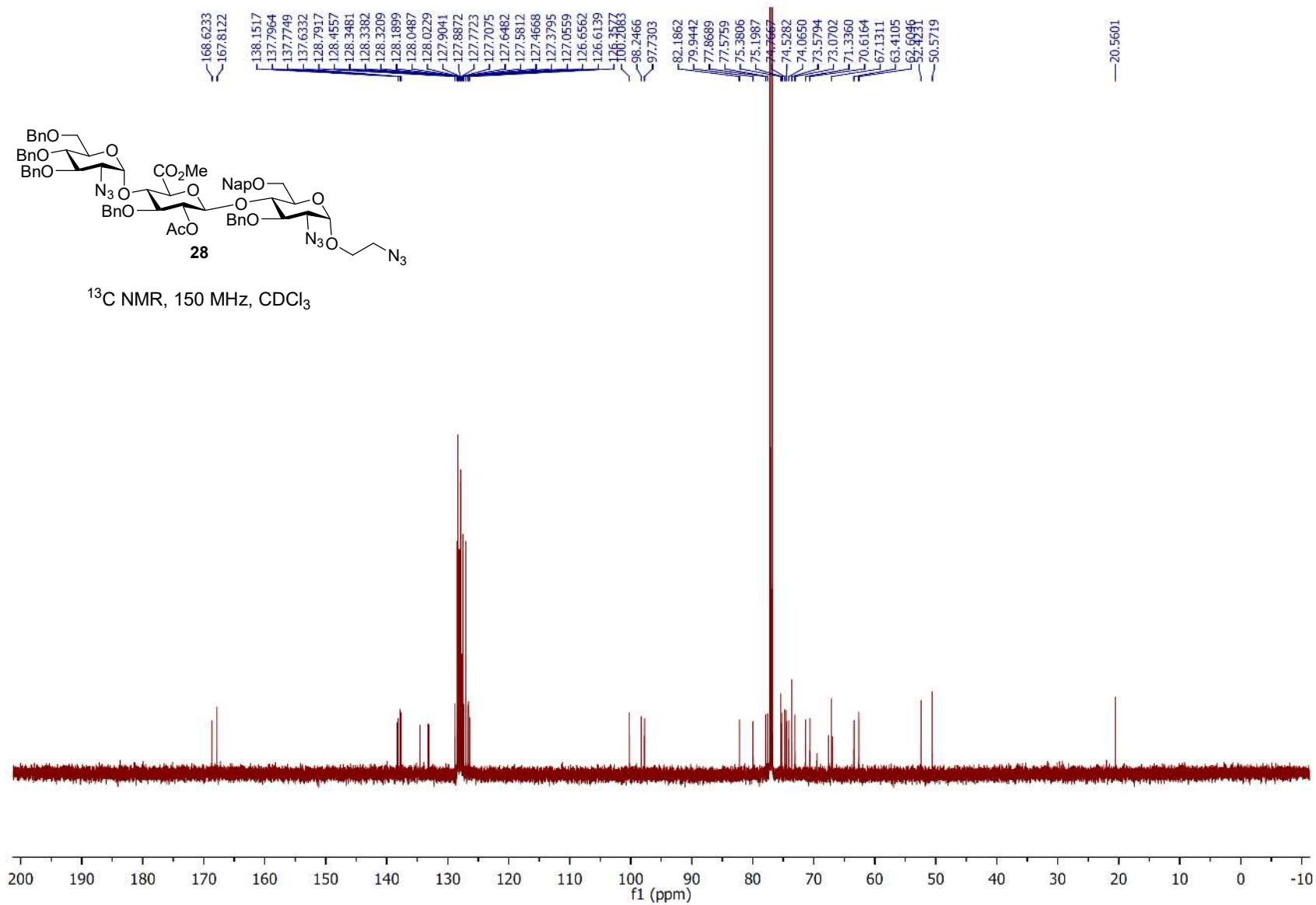


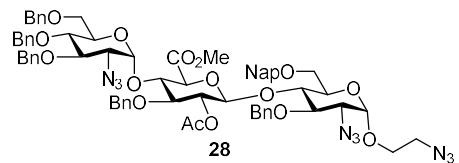
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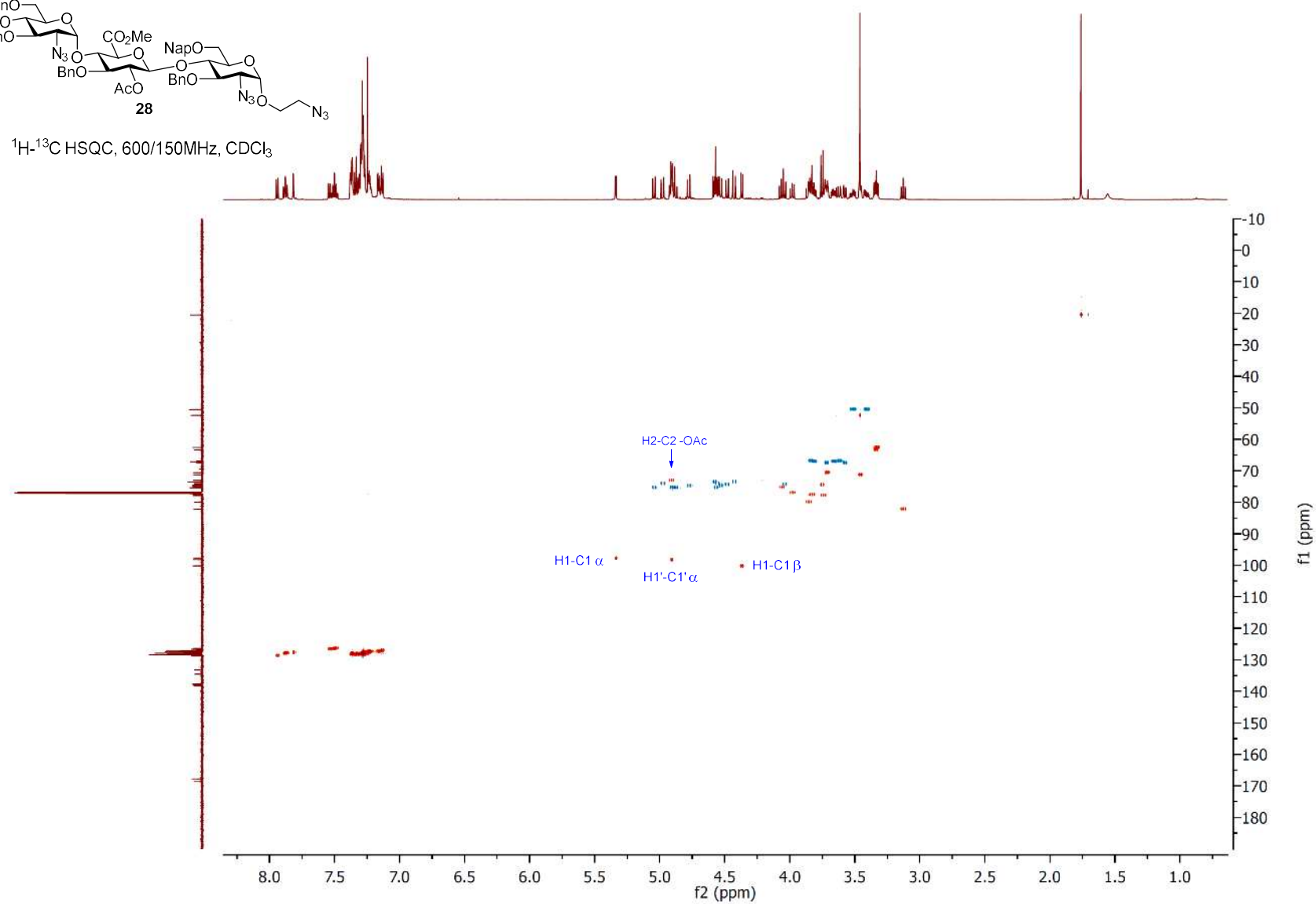
¹H NMR, 600 MHz, CDCl₃

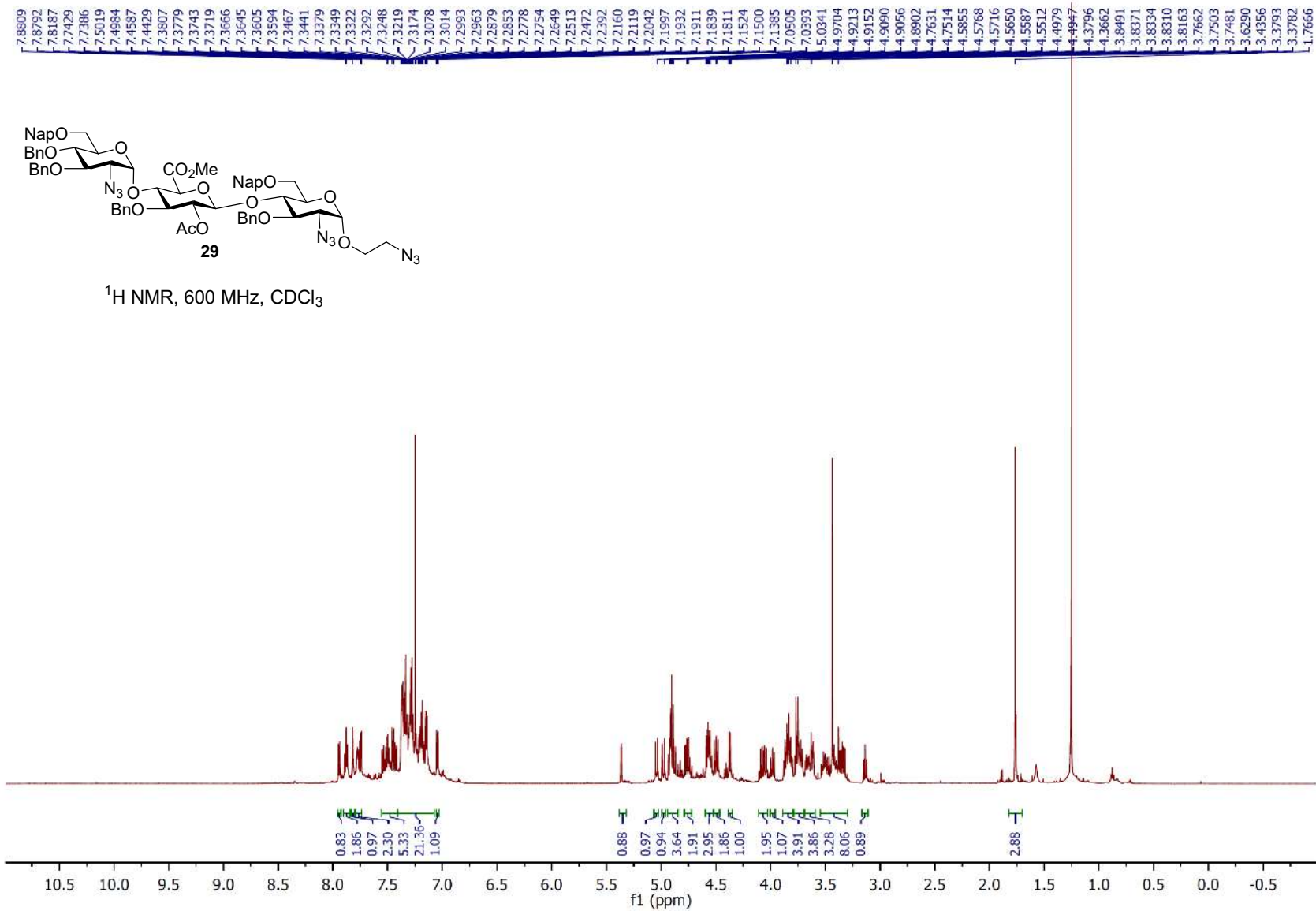


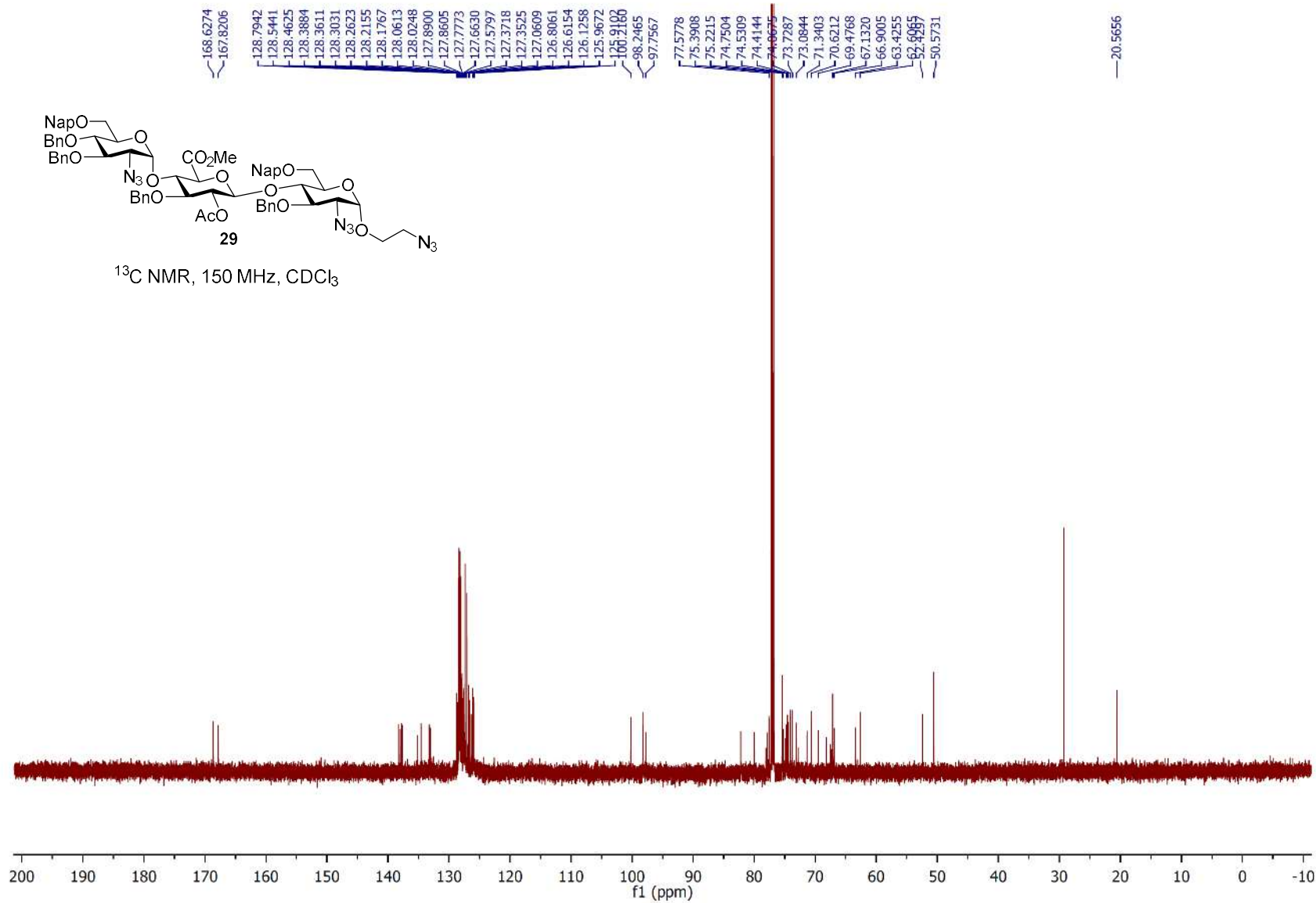


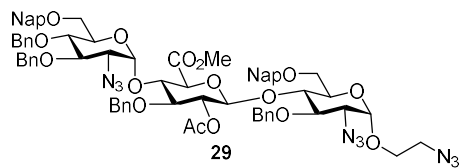


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

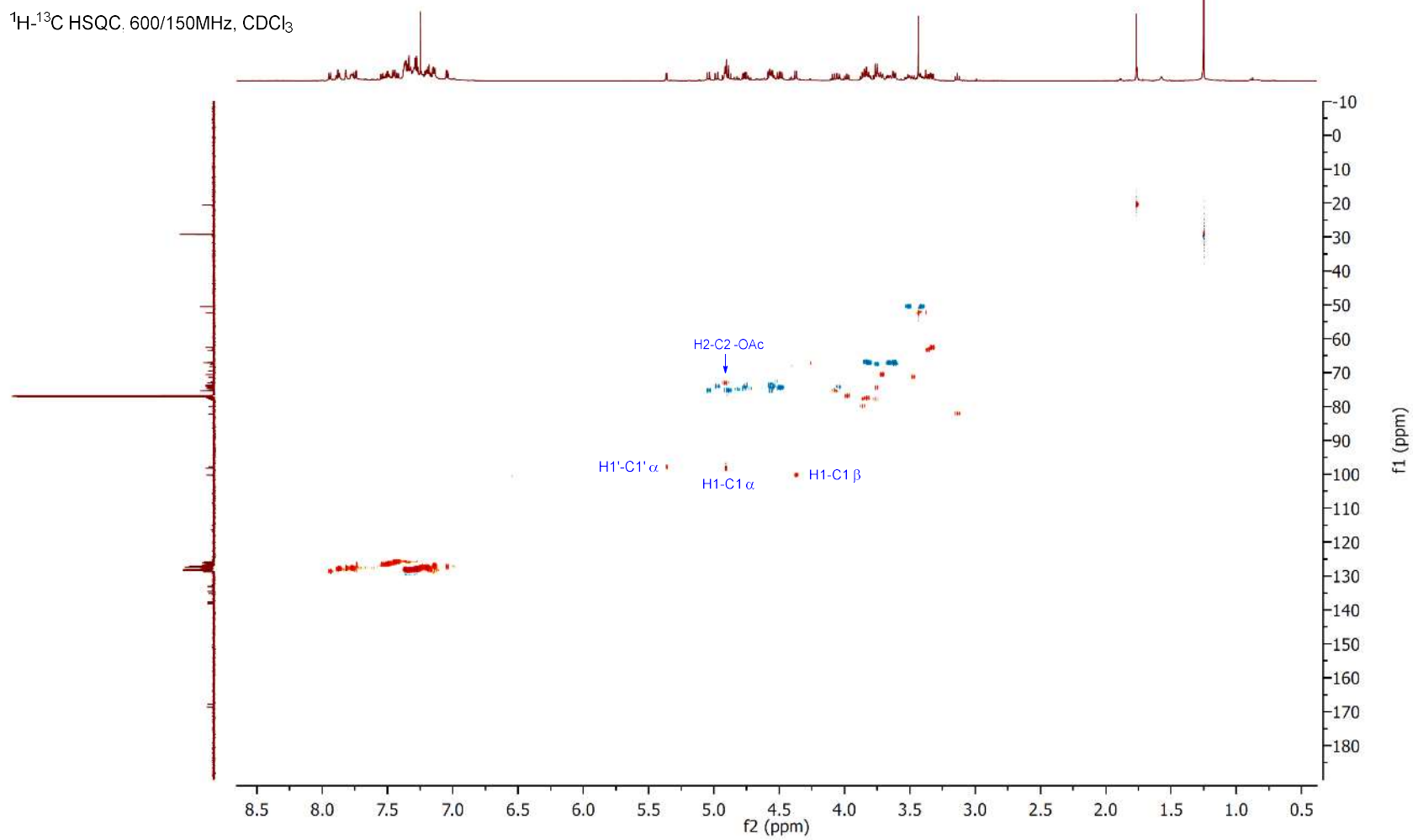


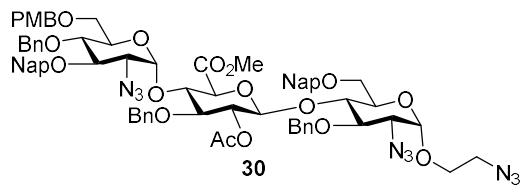




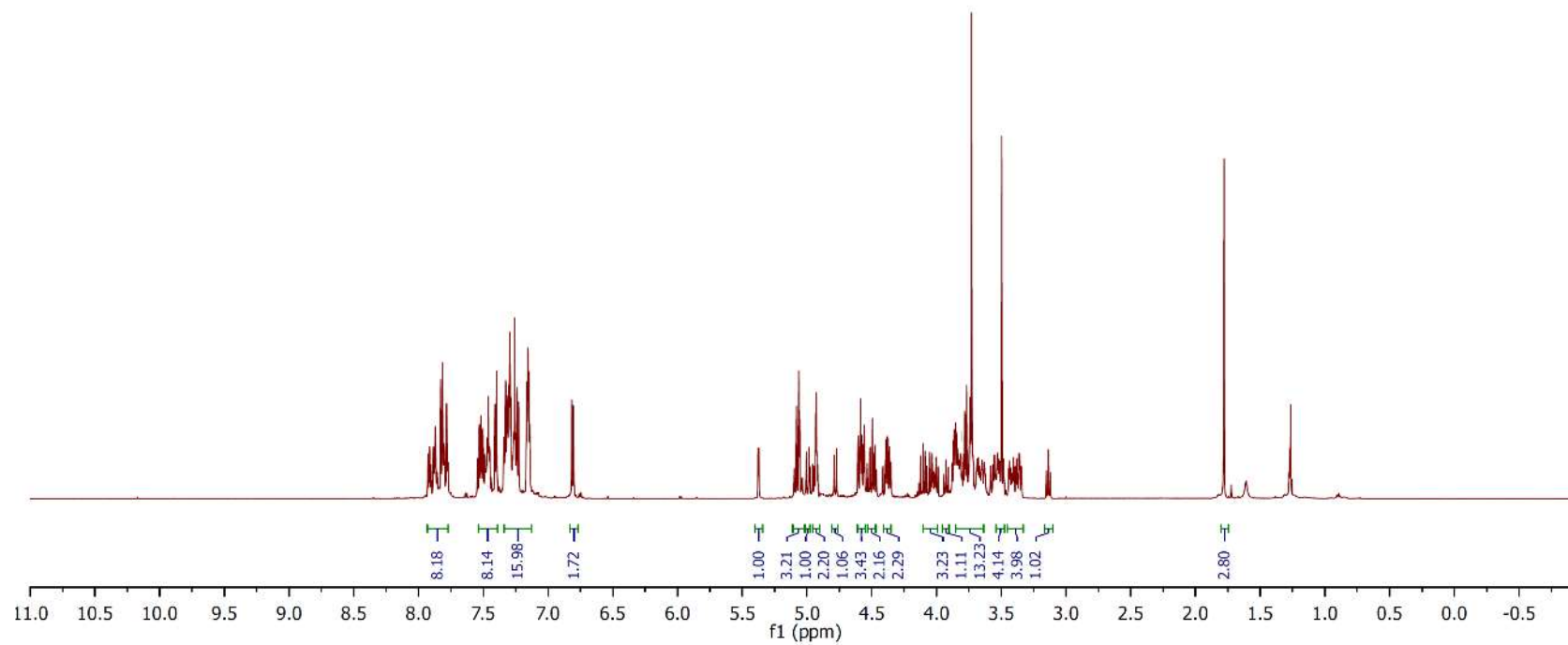


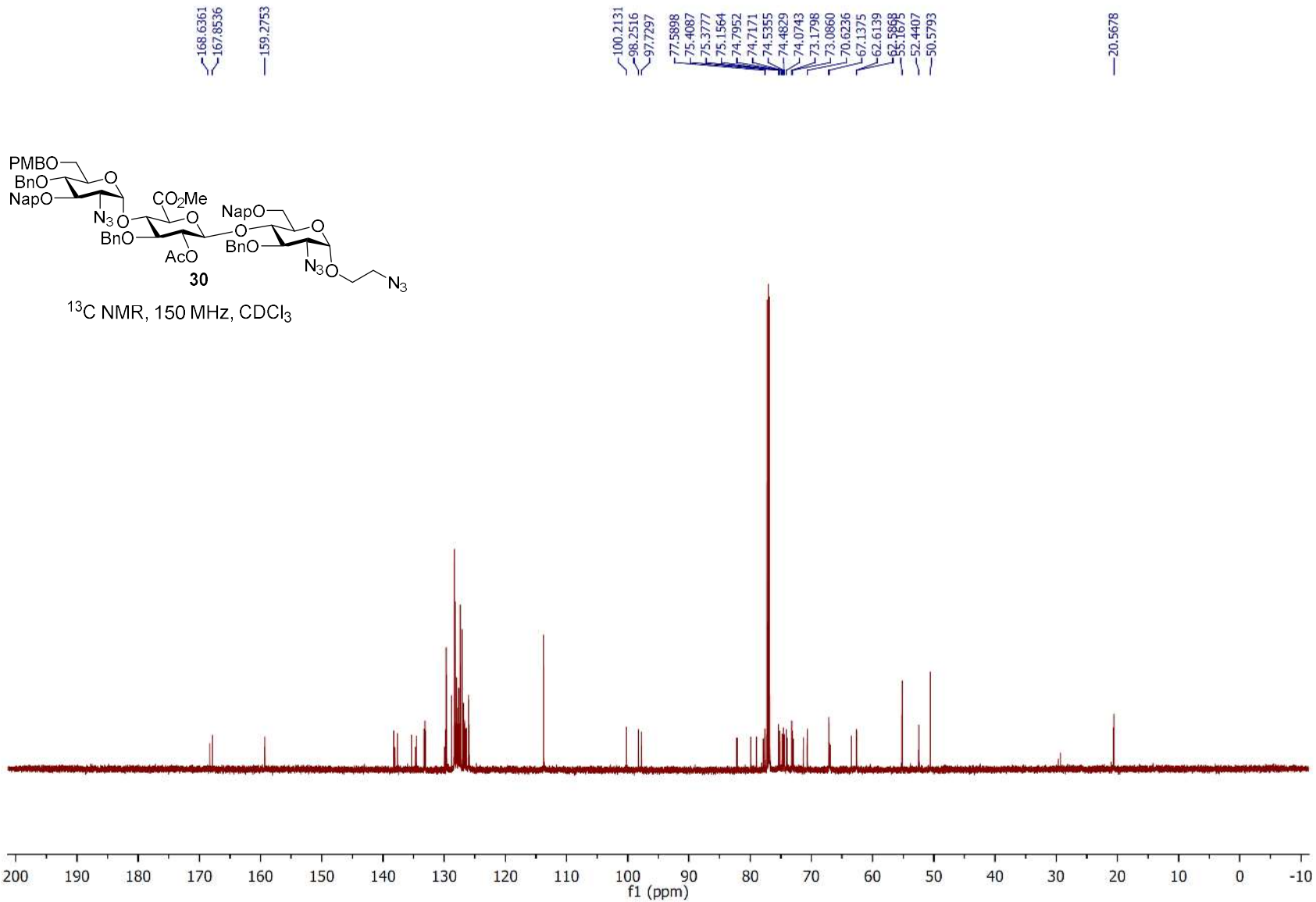
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

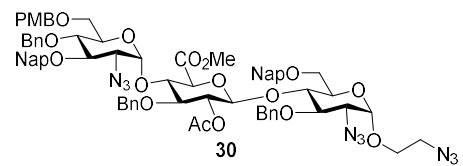




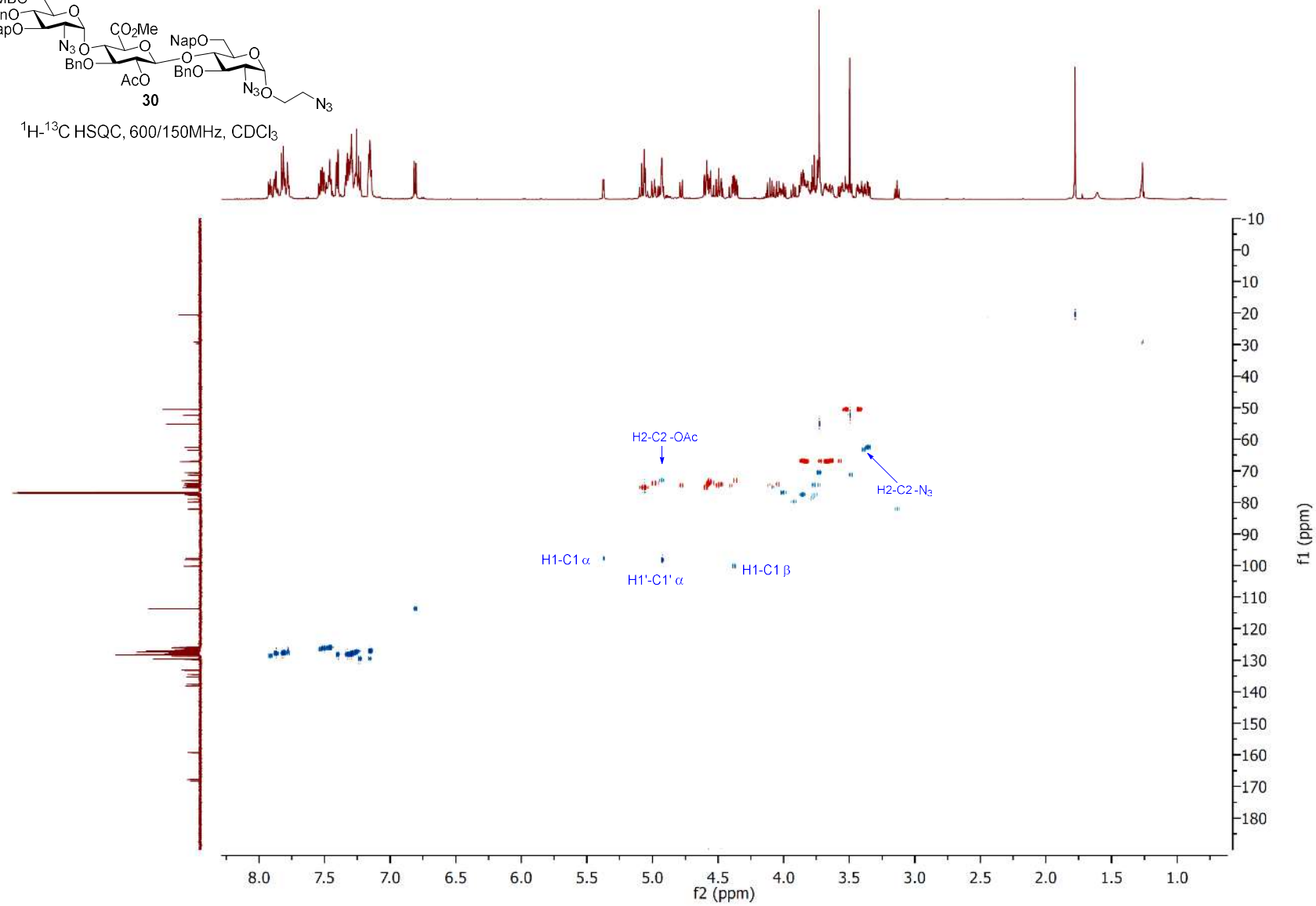
$^1\text{H NMR}$, 600 MHz, CDCl_3

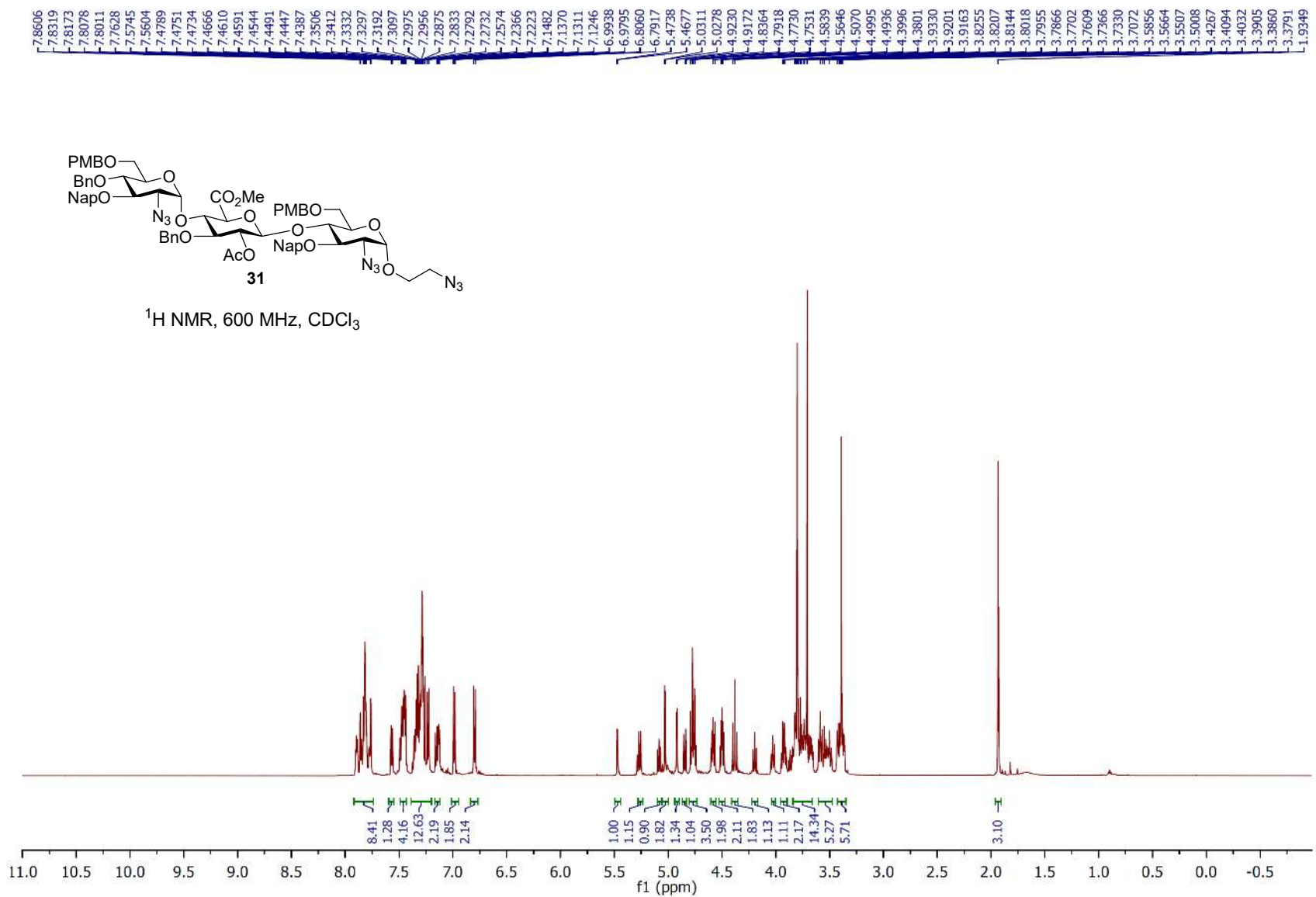


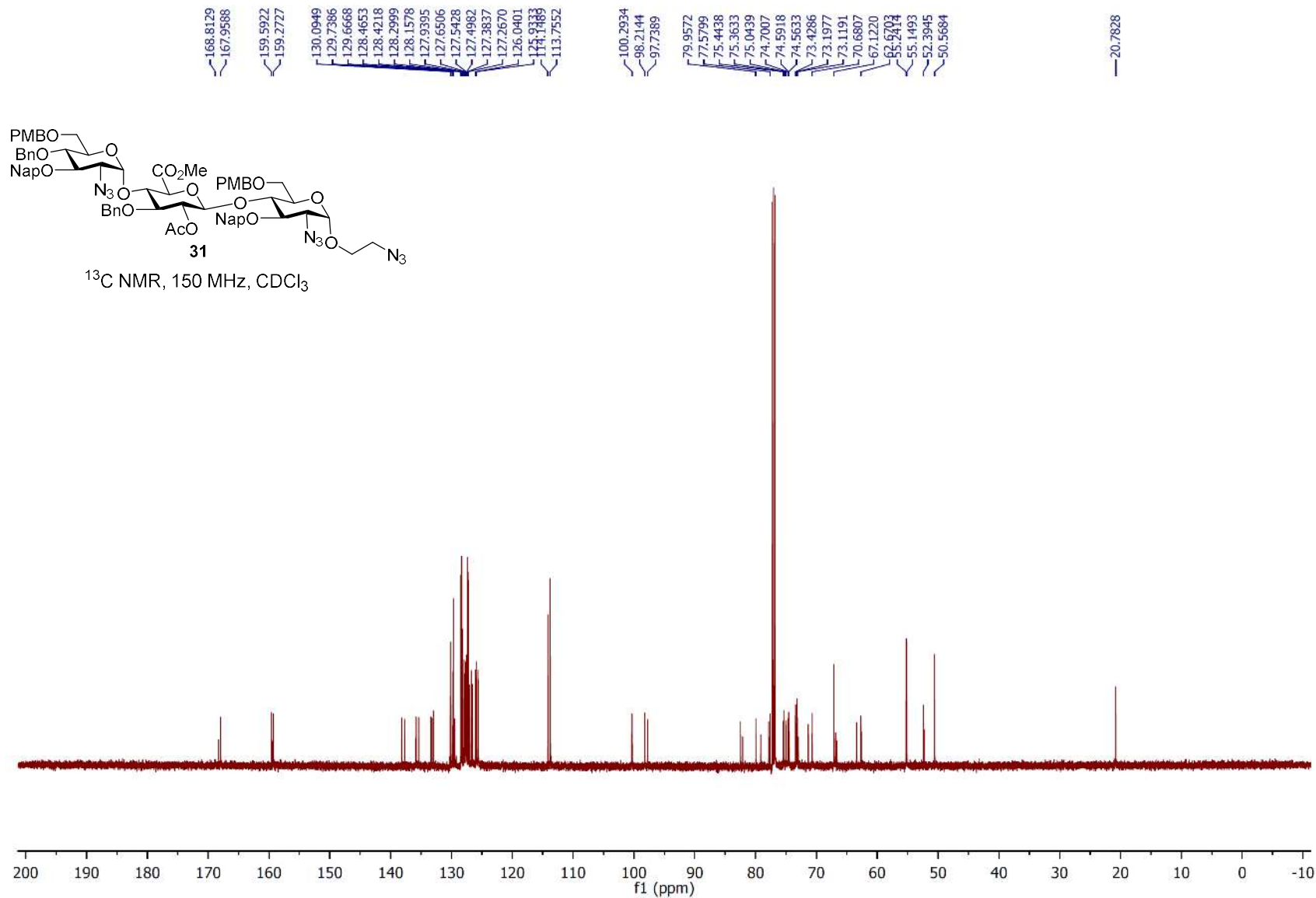


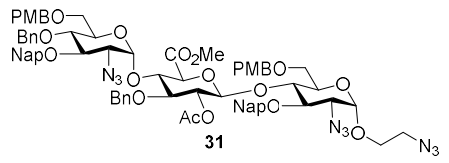


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

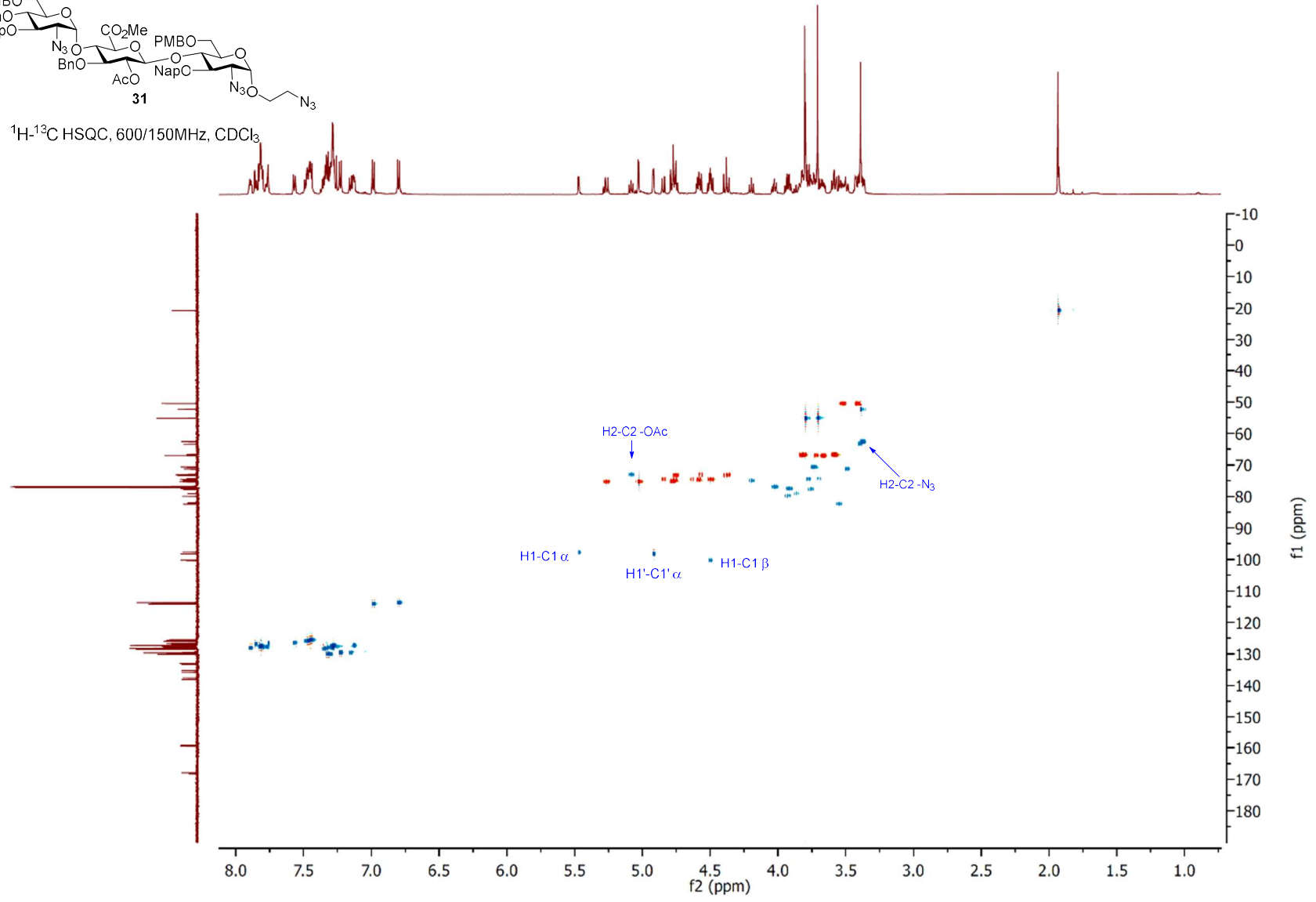




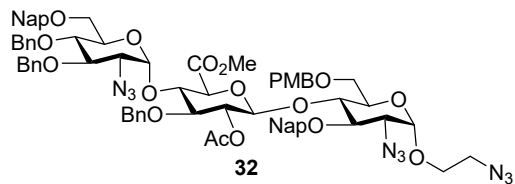




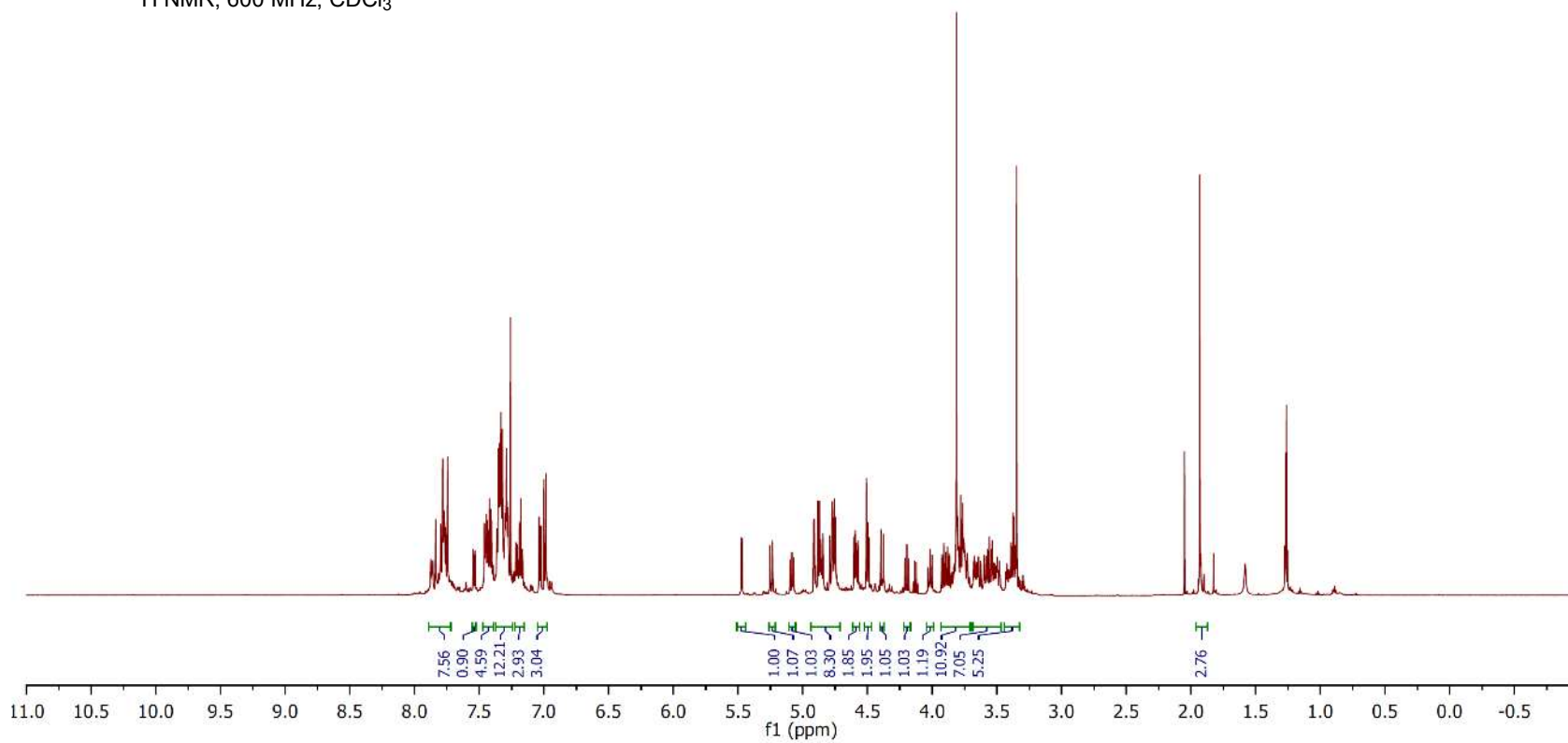
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

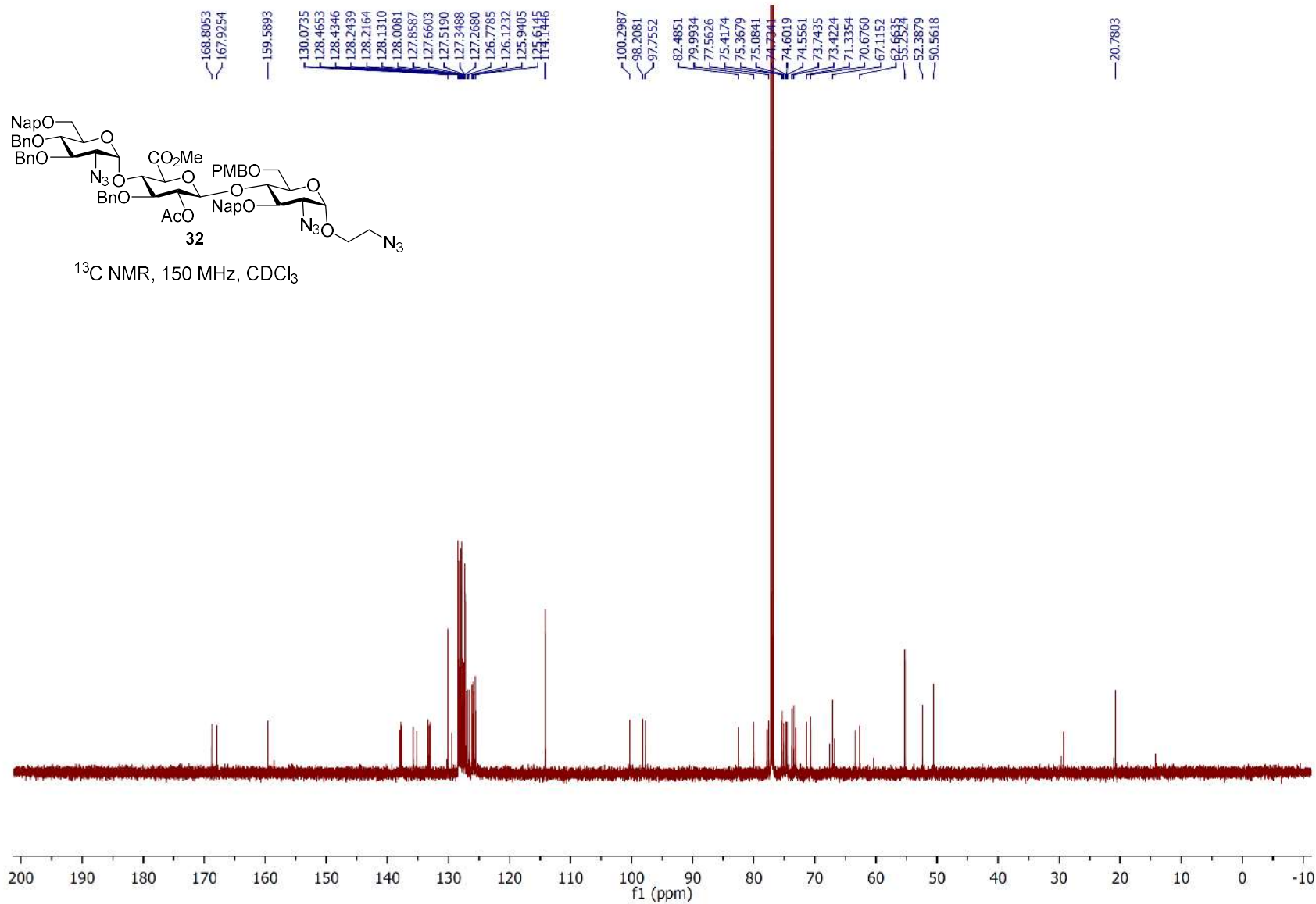


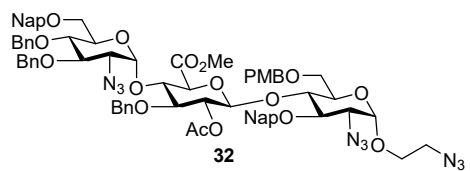
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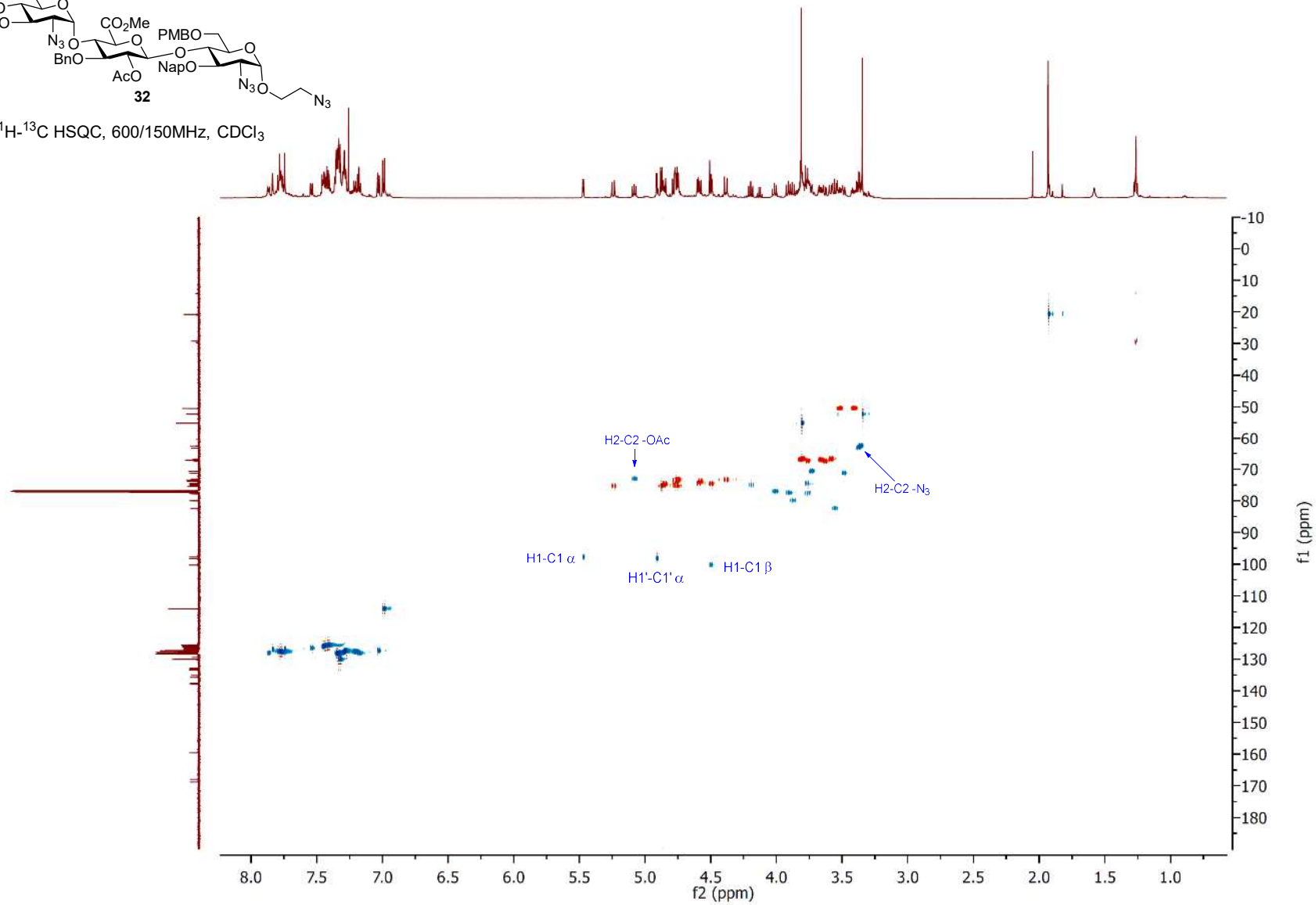
¹H NMR, 600 MHz, CDCl₃

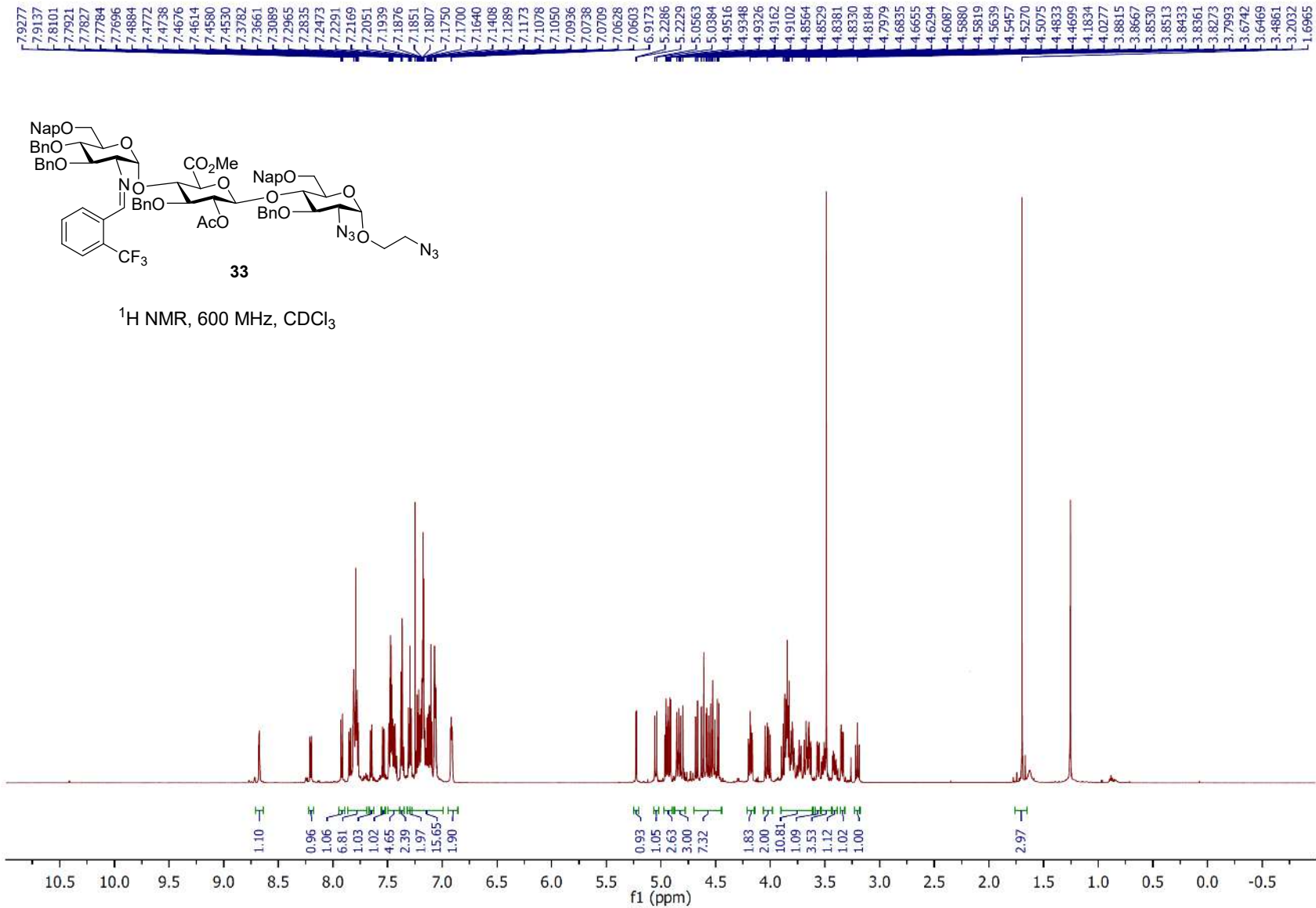


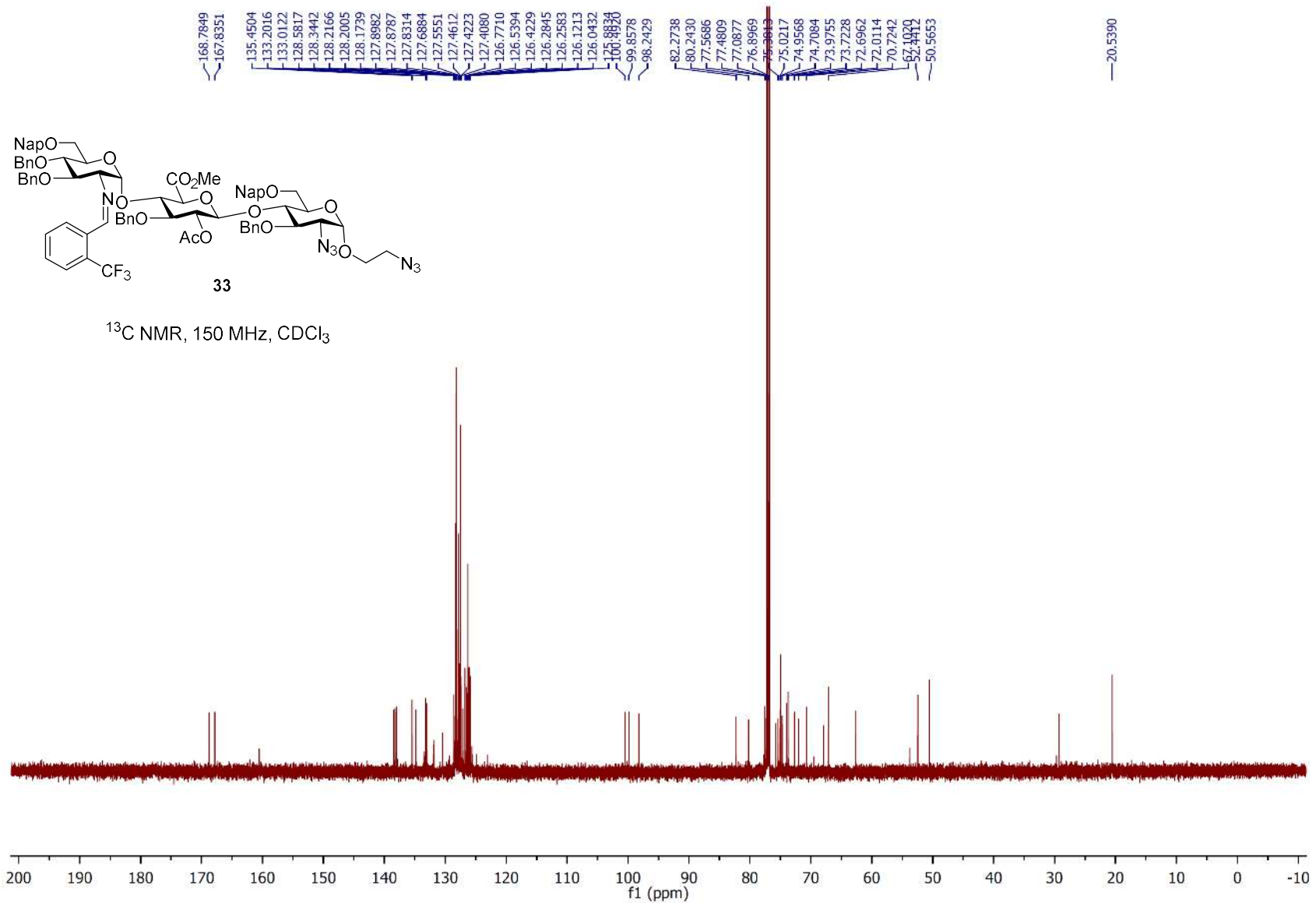


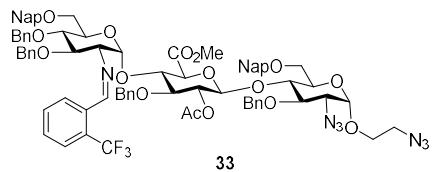


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

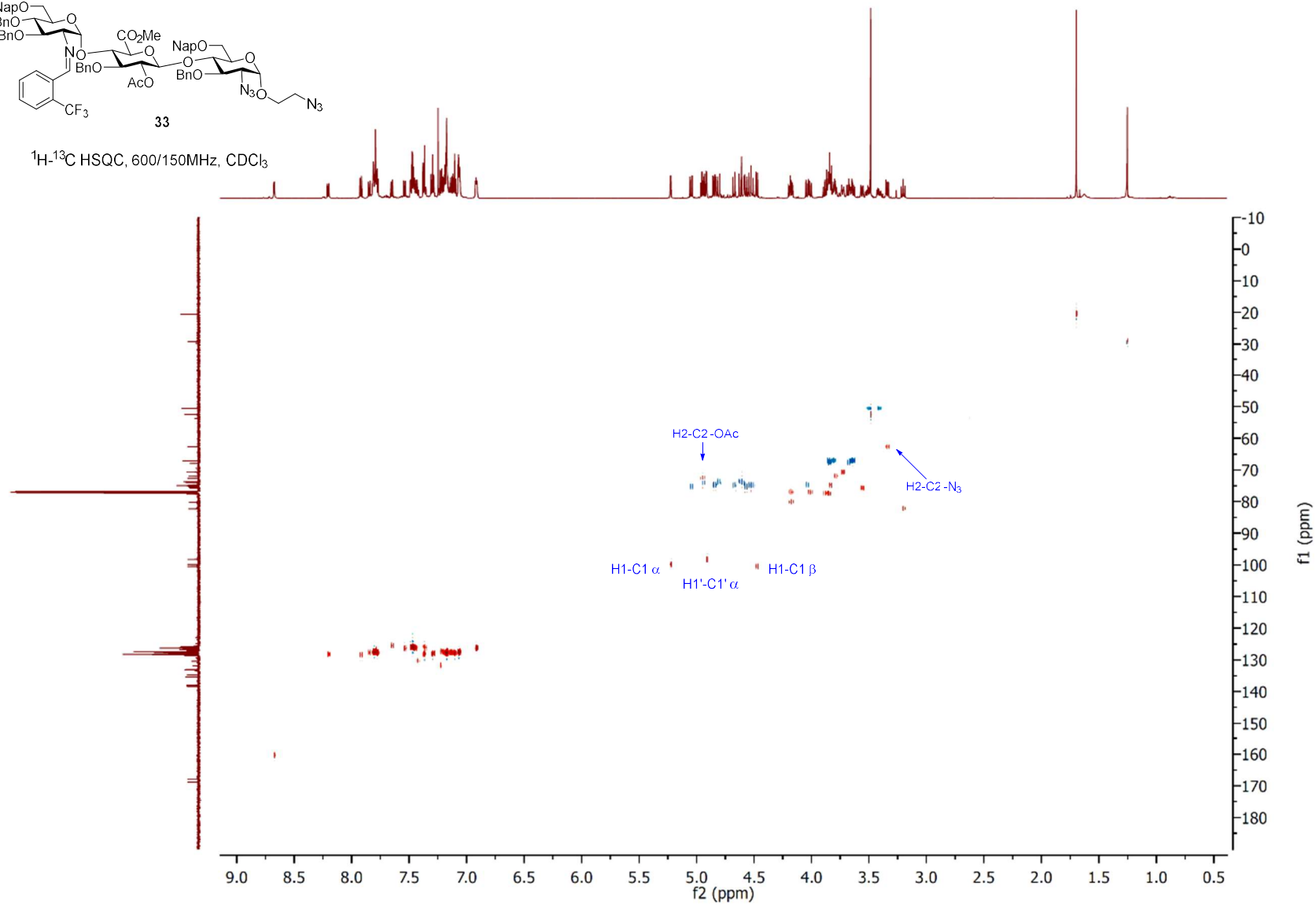


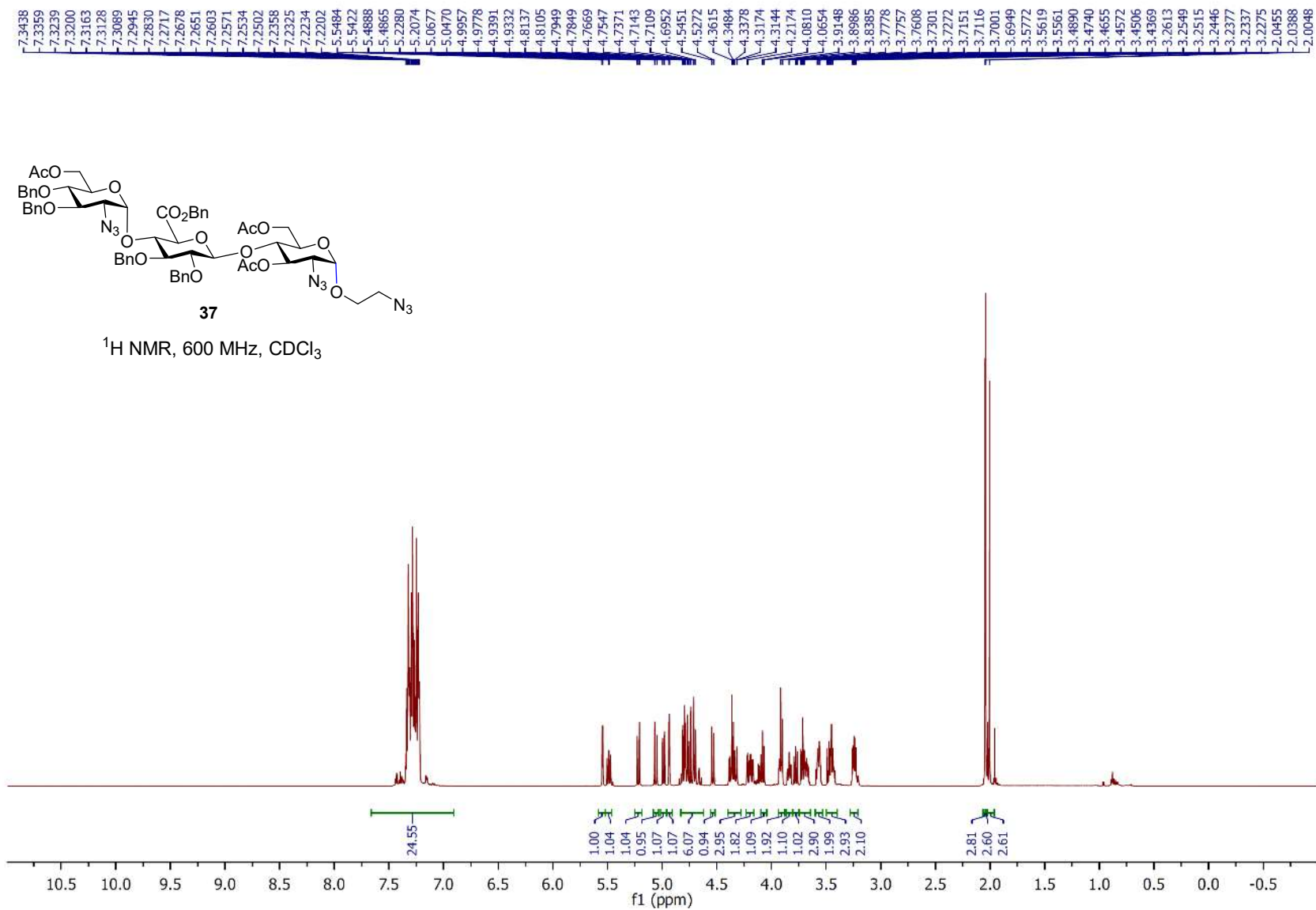


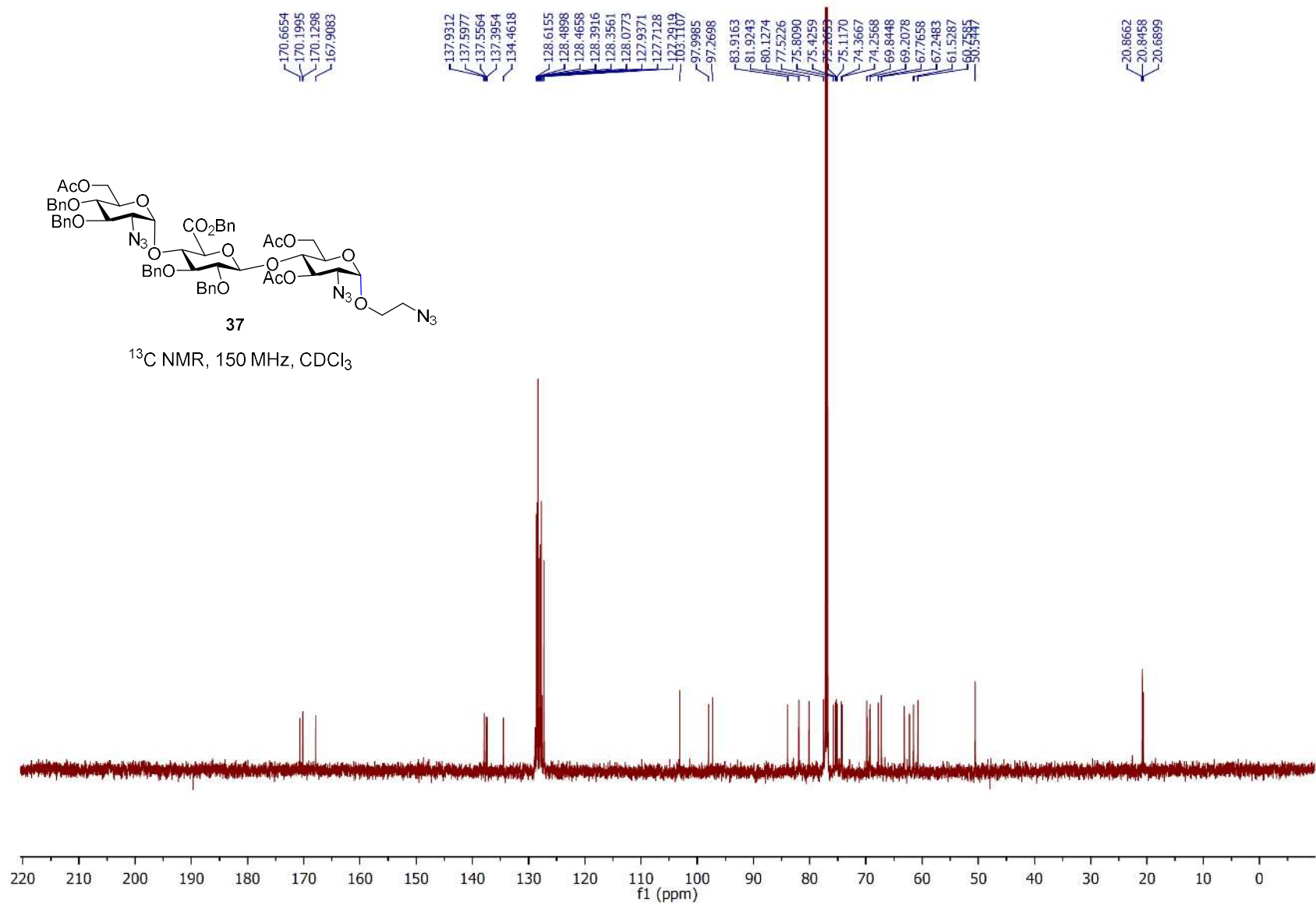


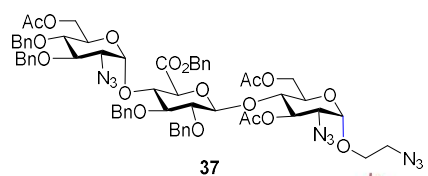


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

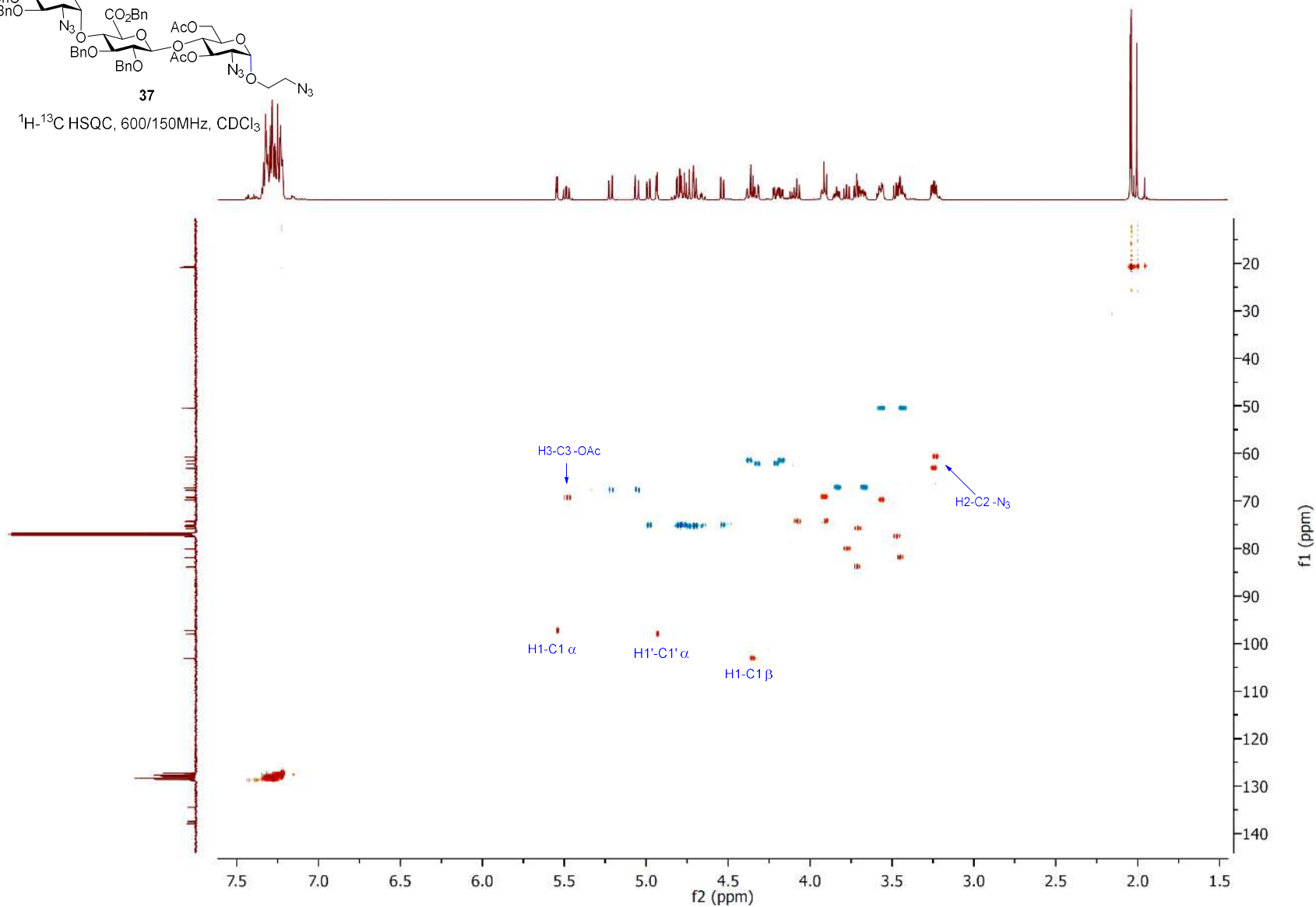




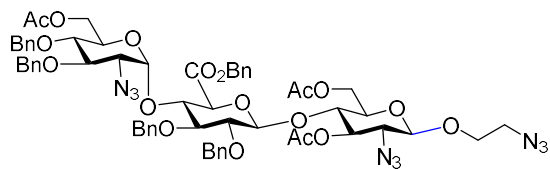




^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

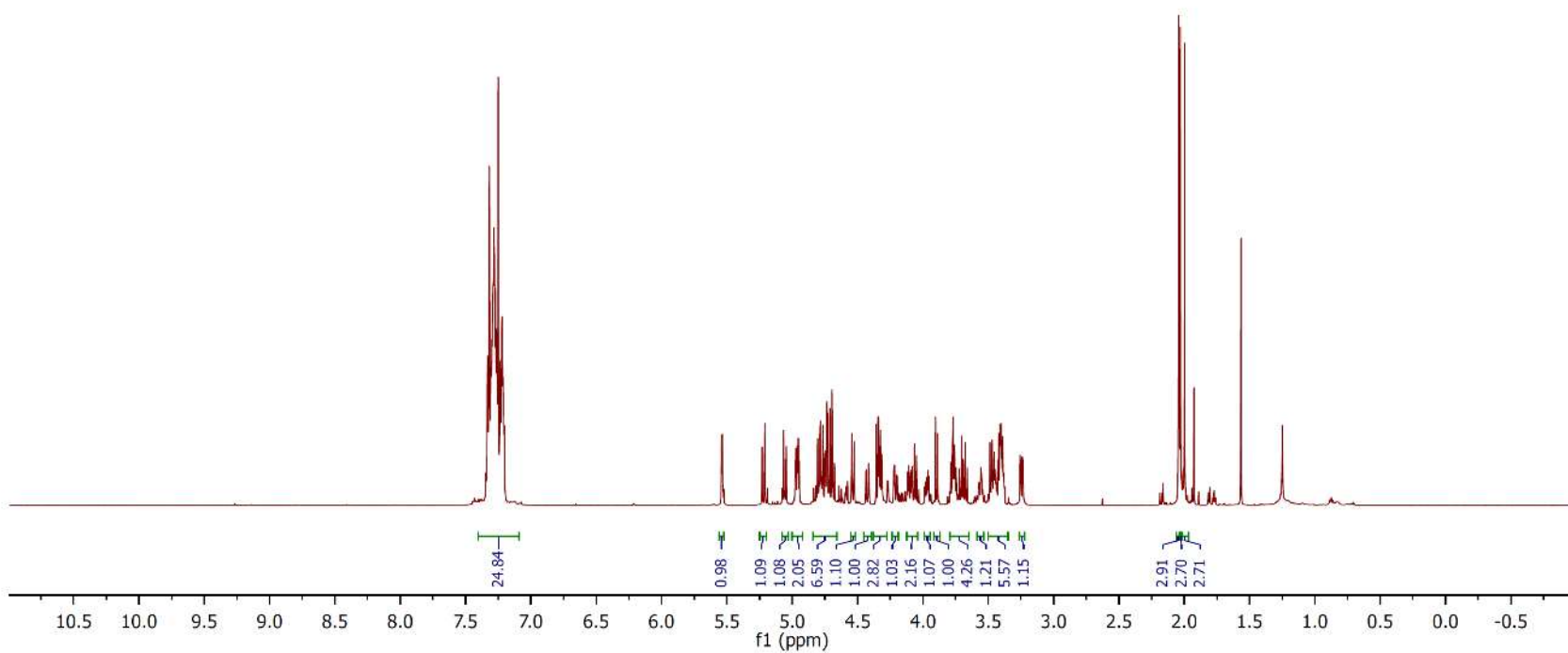


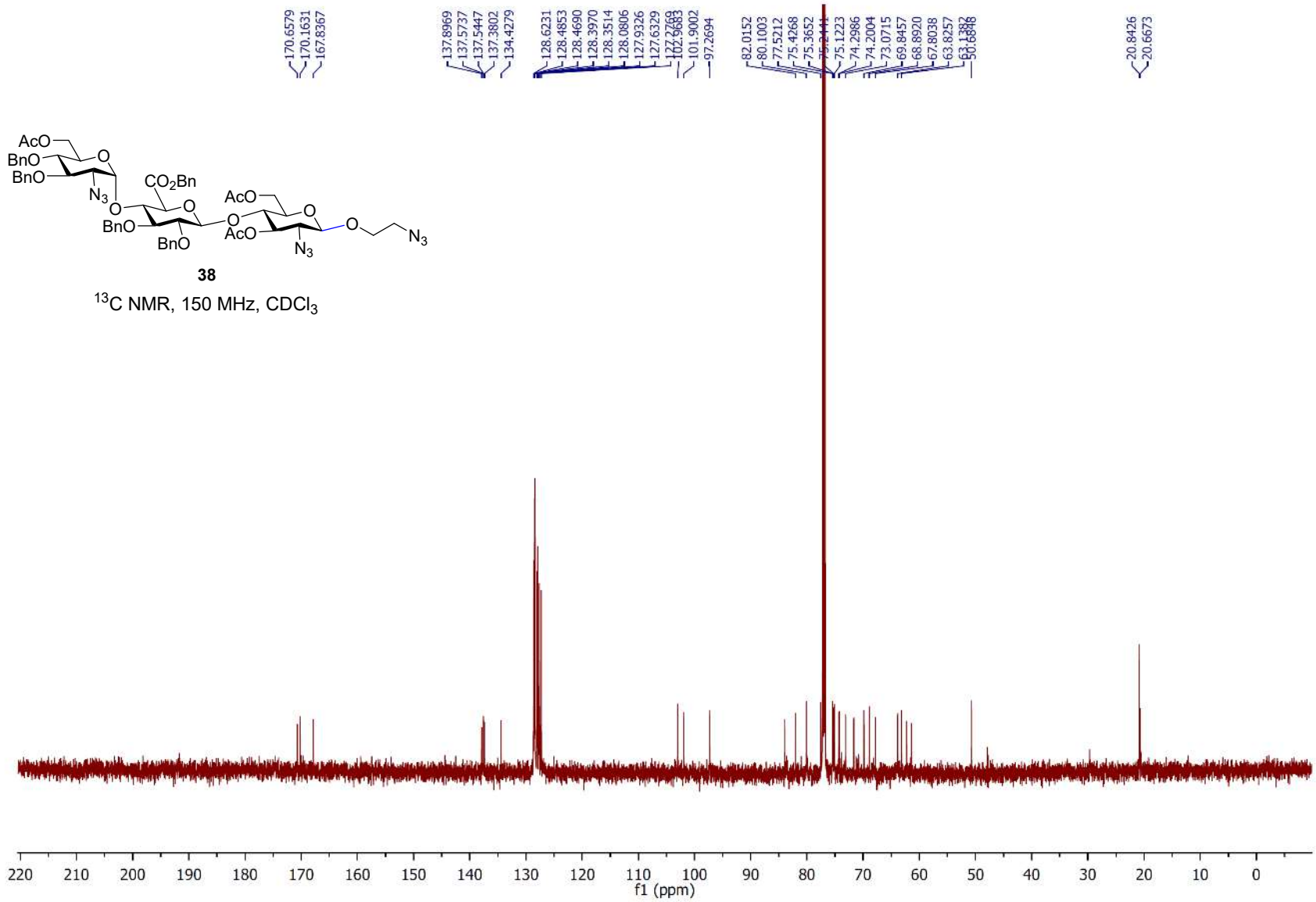
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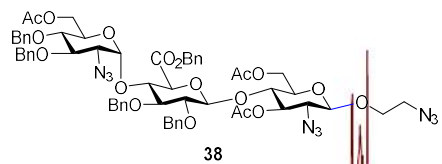


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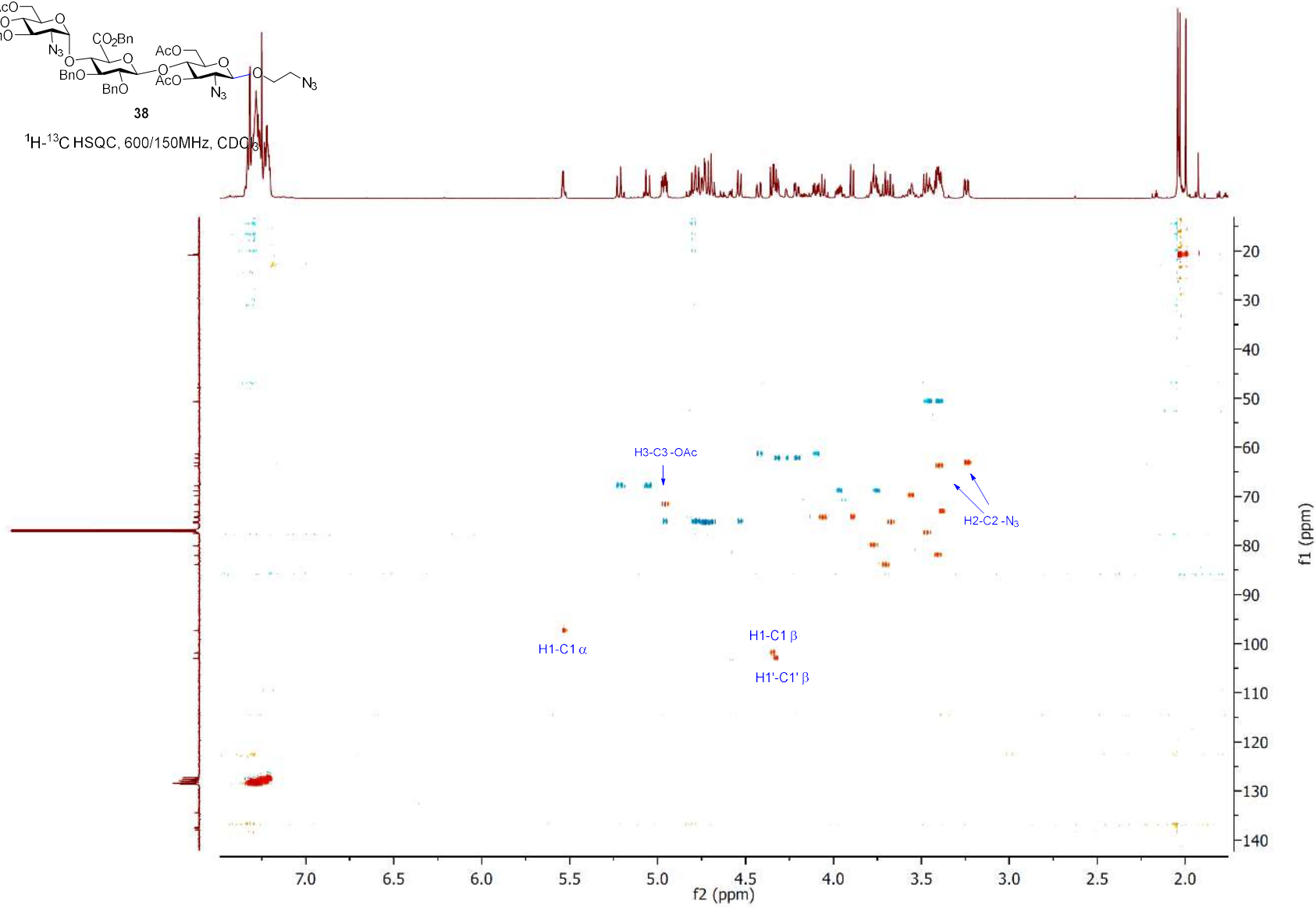
^1H NMR, 600 MHz, CDCl_3

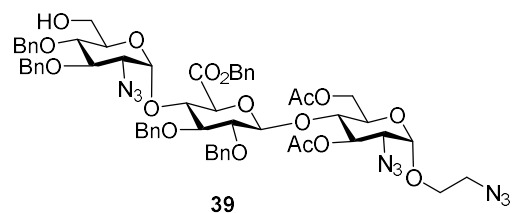






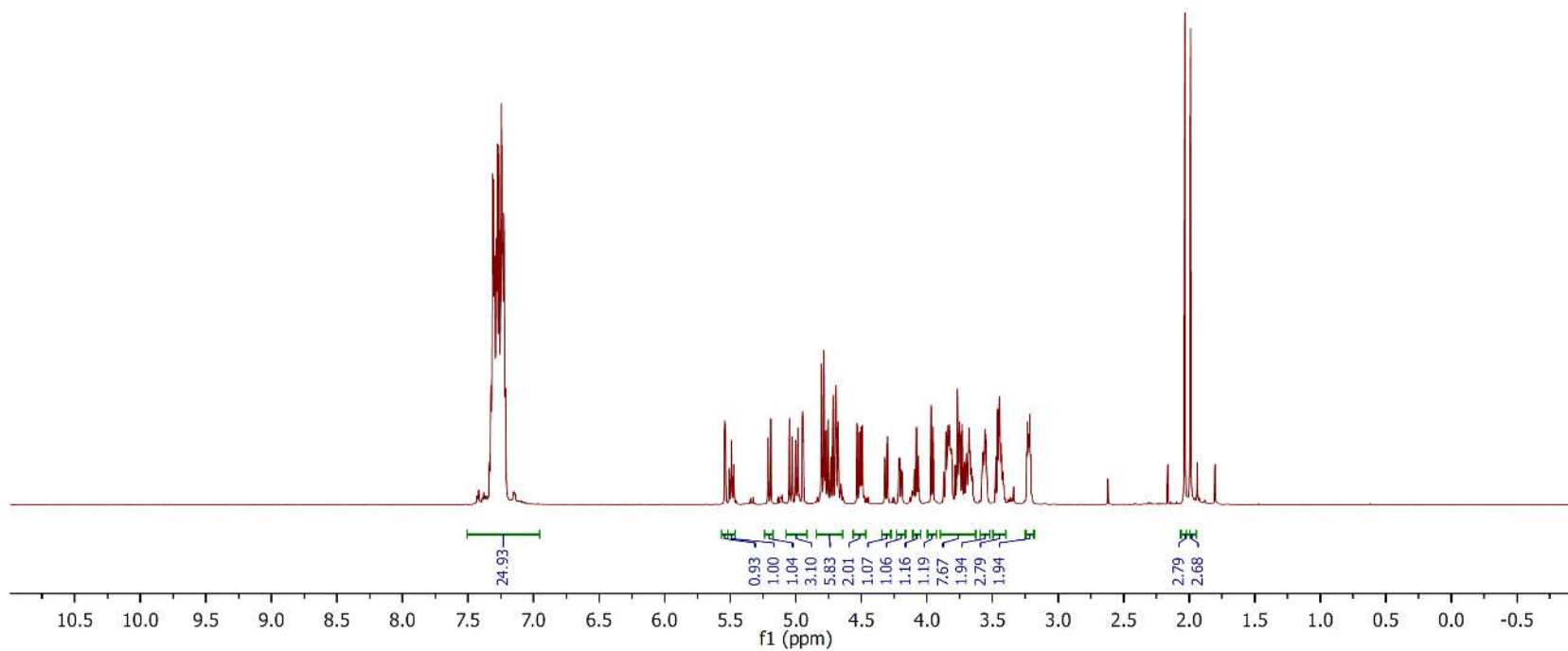
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

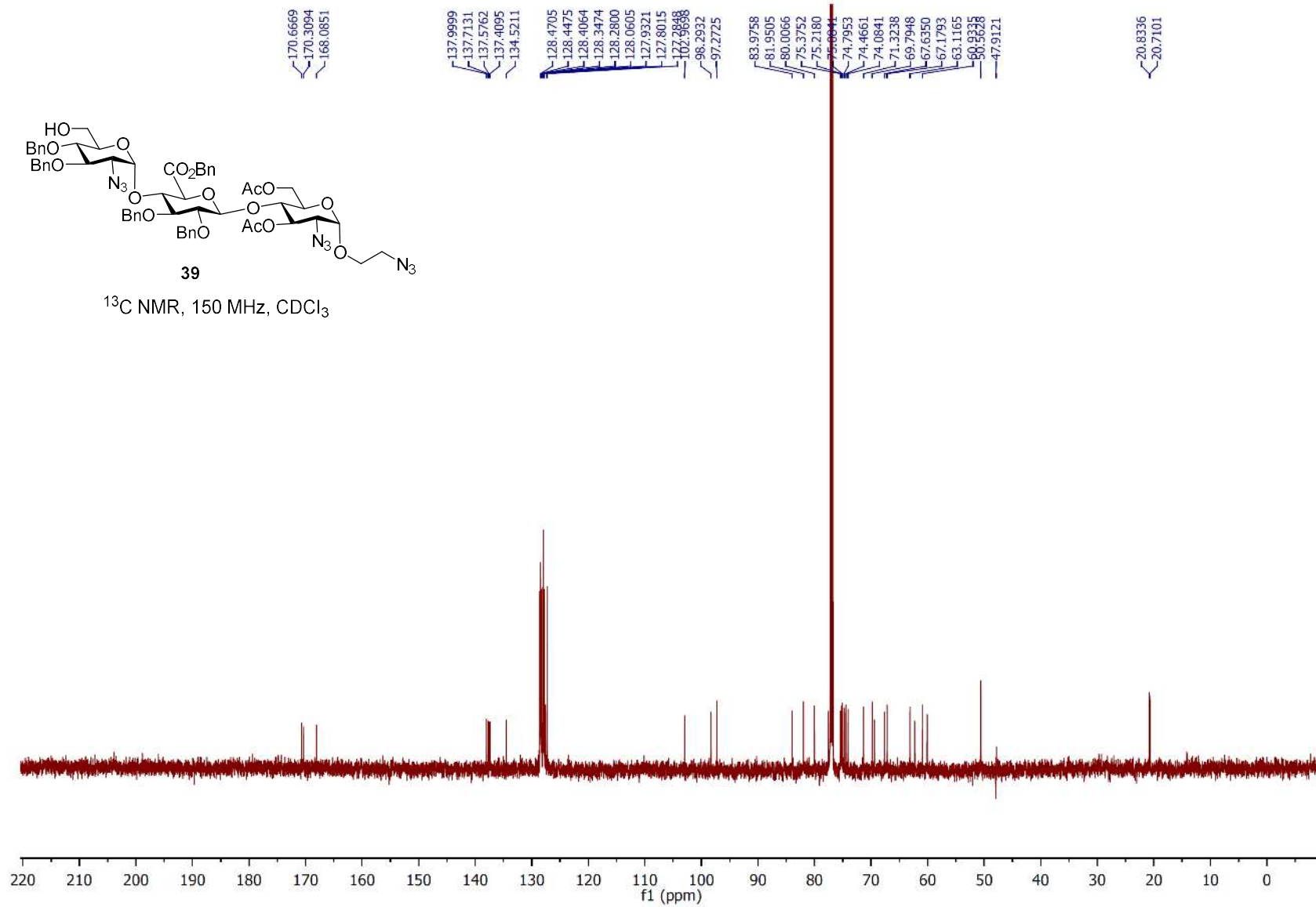


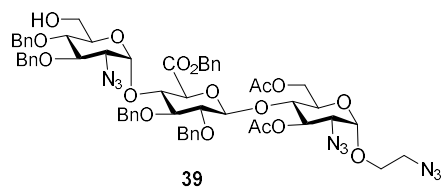


¹H NMR, 600 MHz, CDCl₃

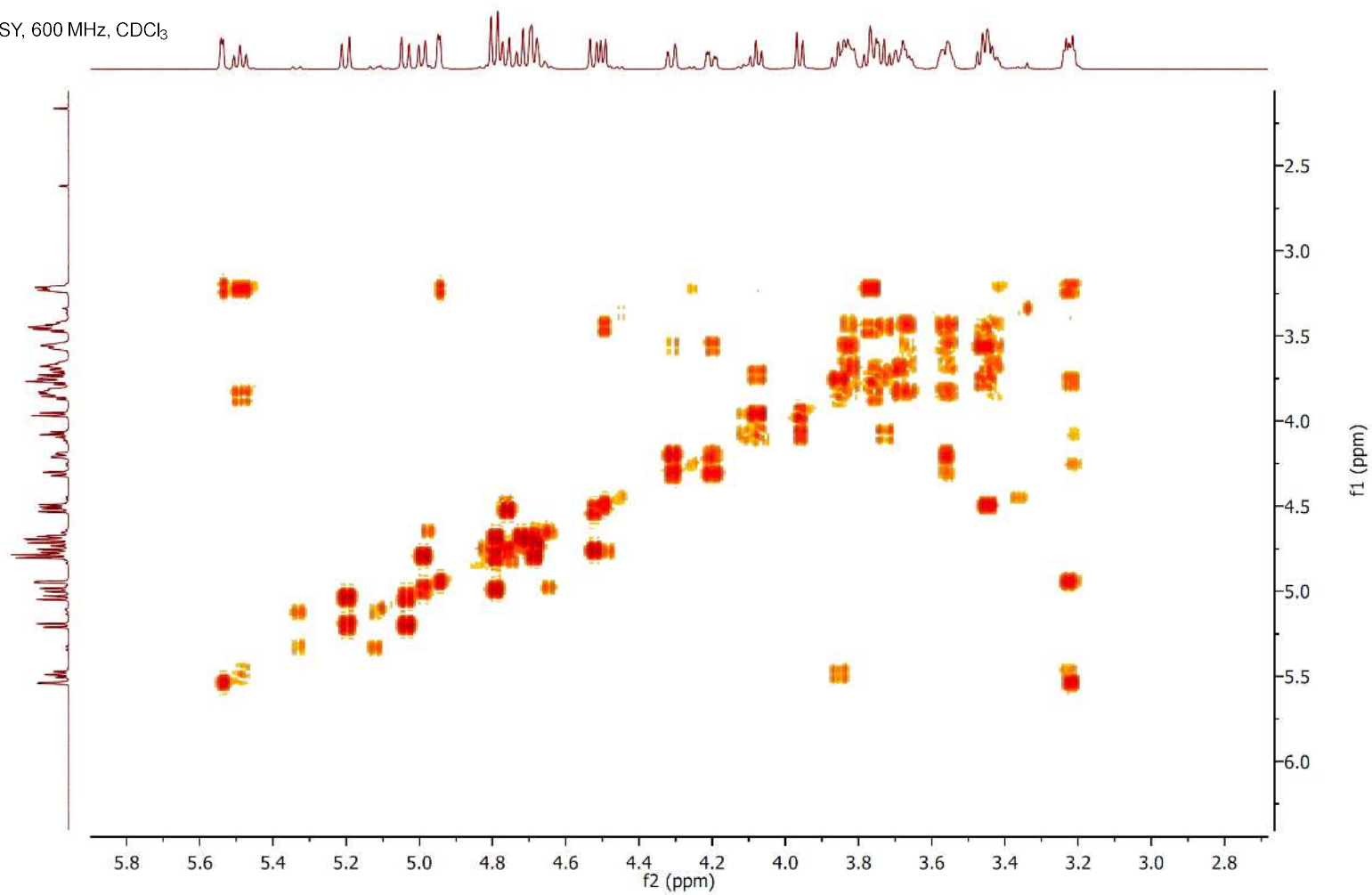
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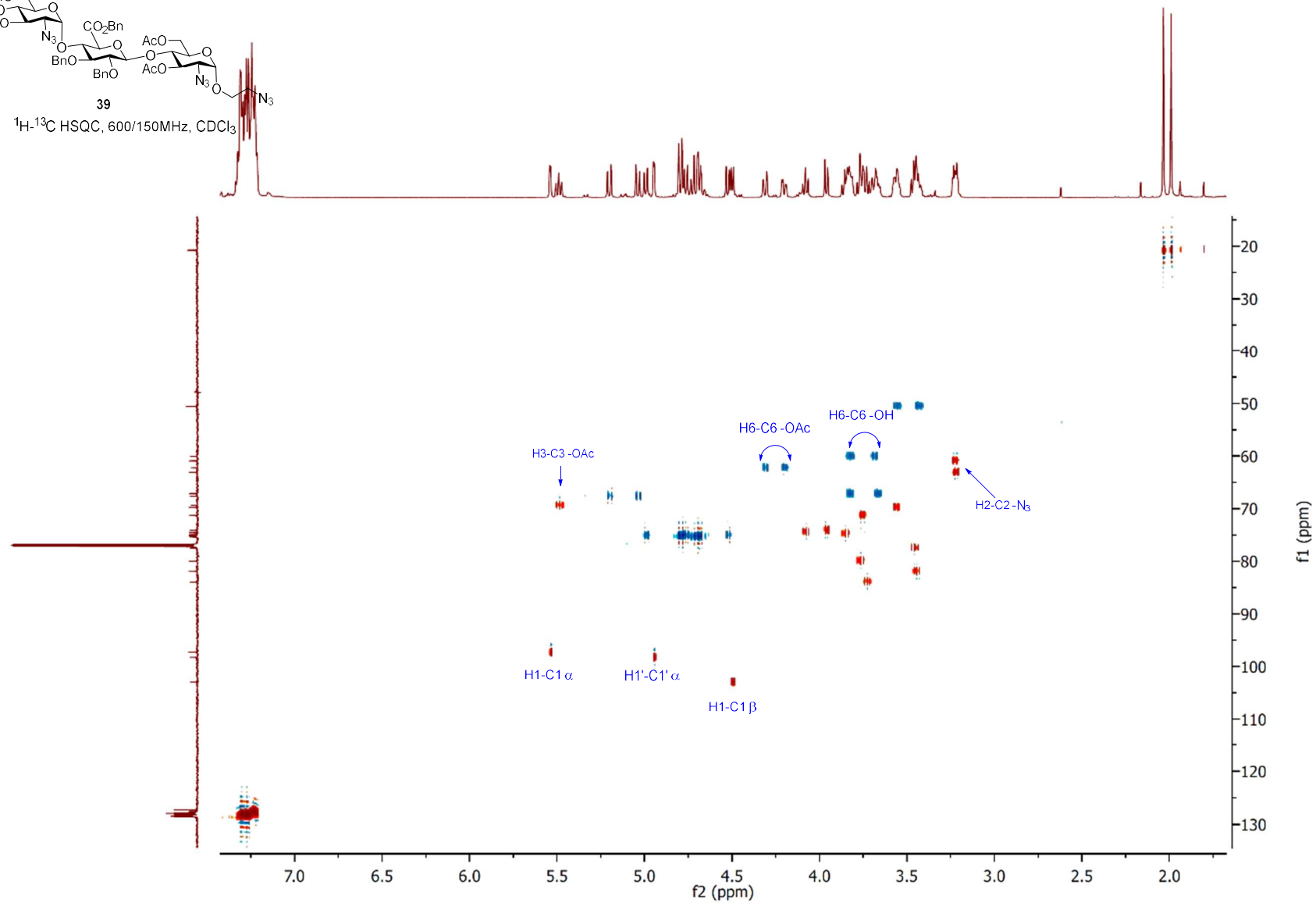
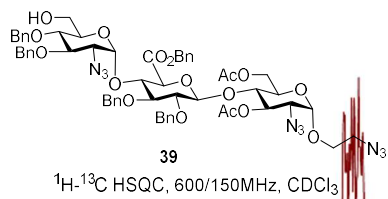


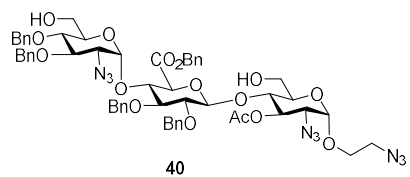




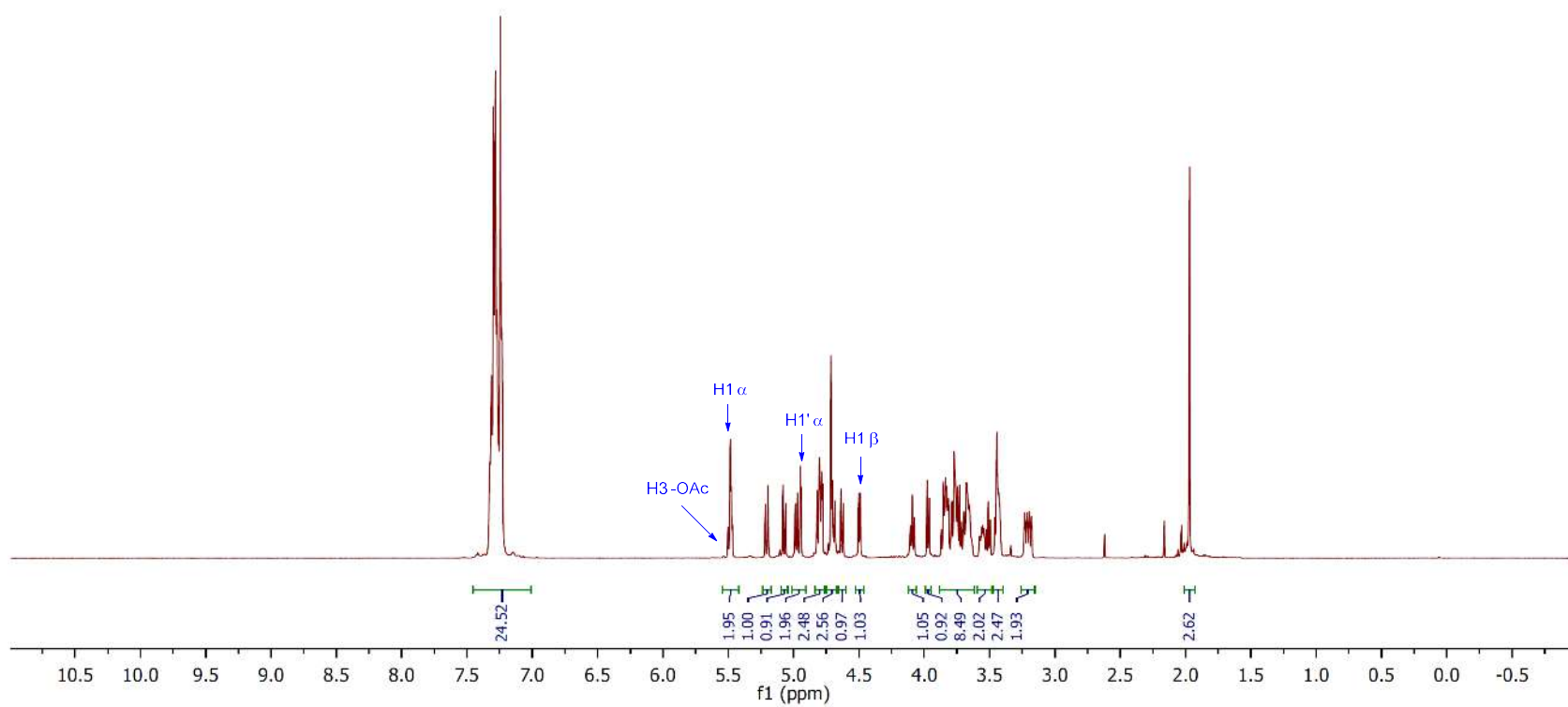
^1H - ^1H COSY, 600 MHz, CDCl_3

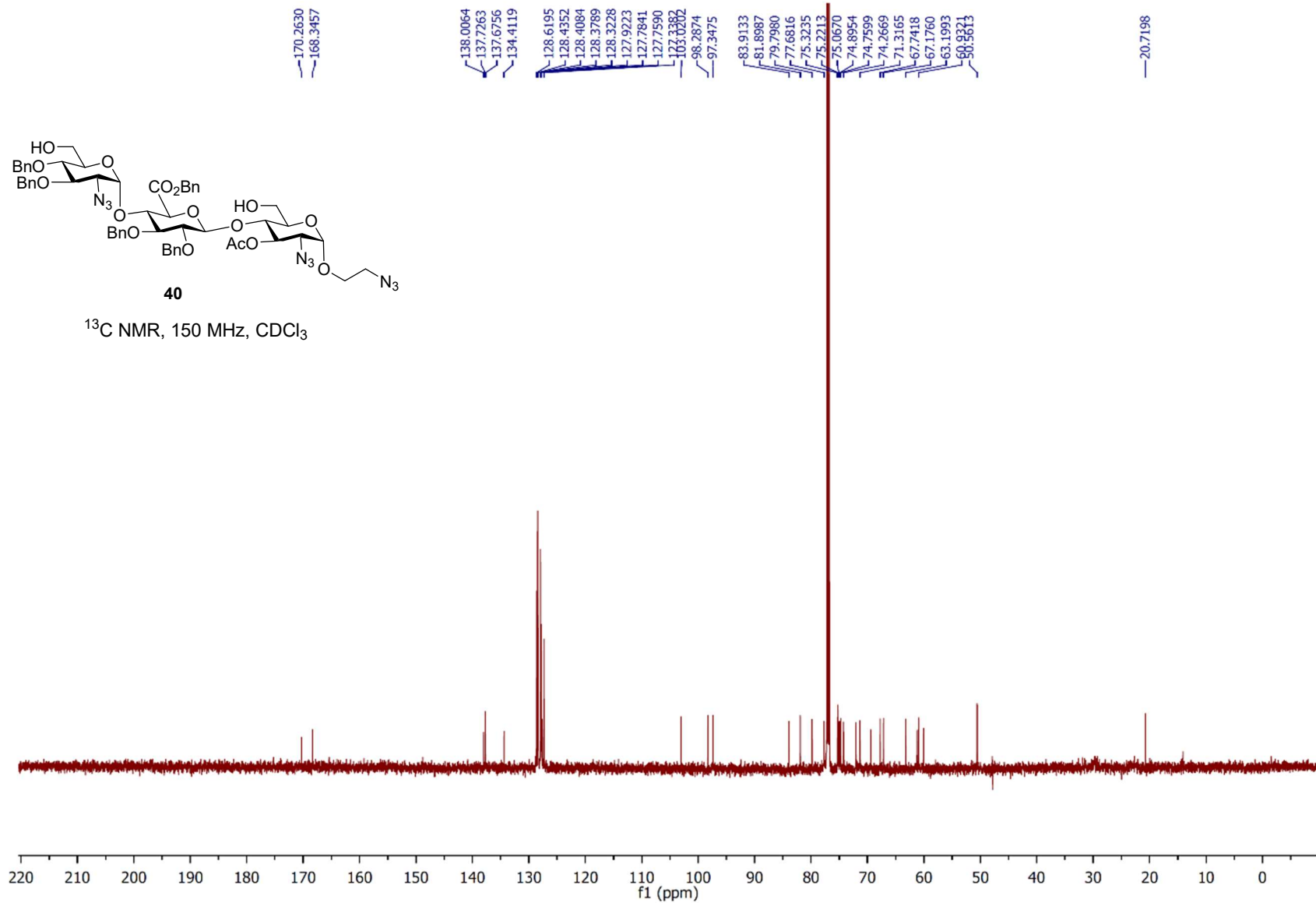




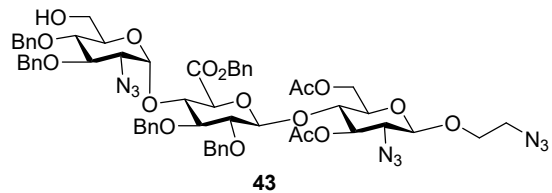


¹H NMR, 600 MHz, CDCl₃

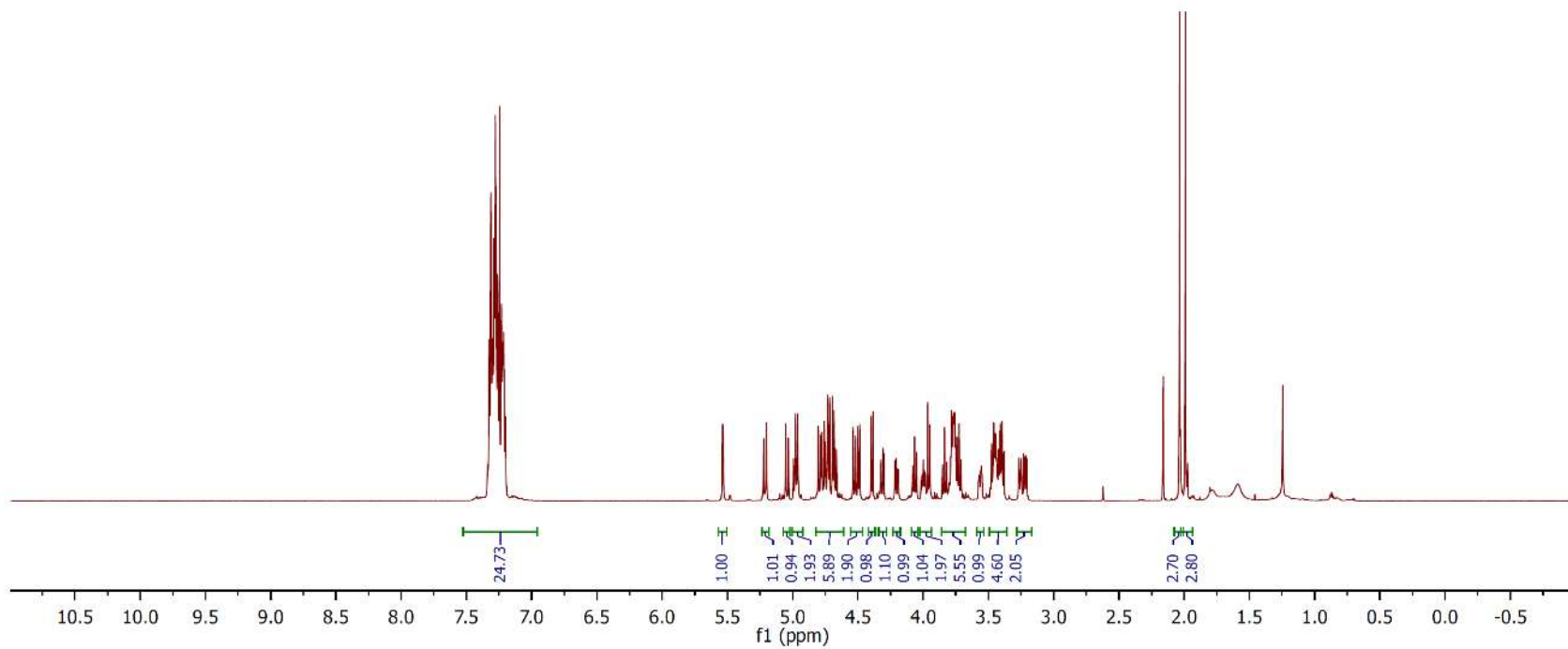


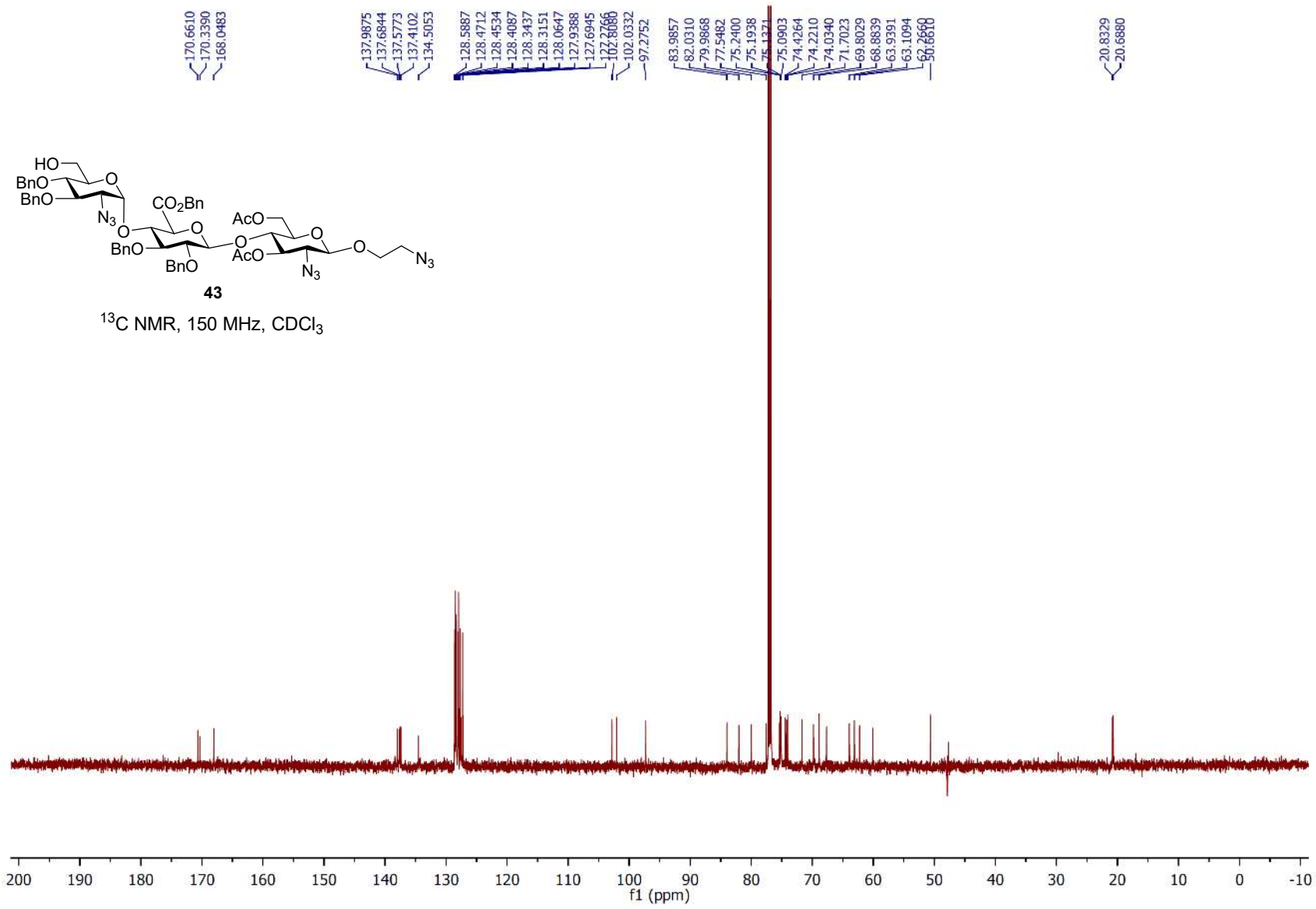


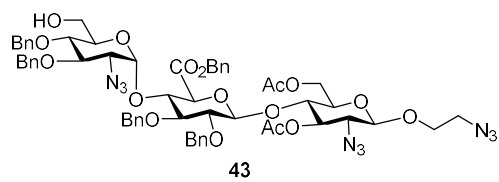
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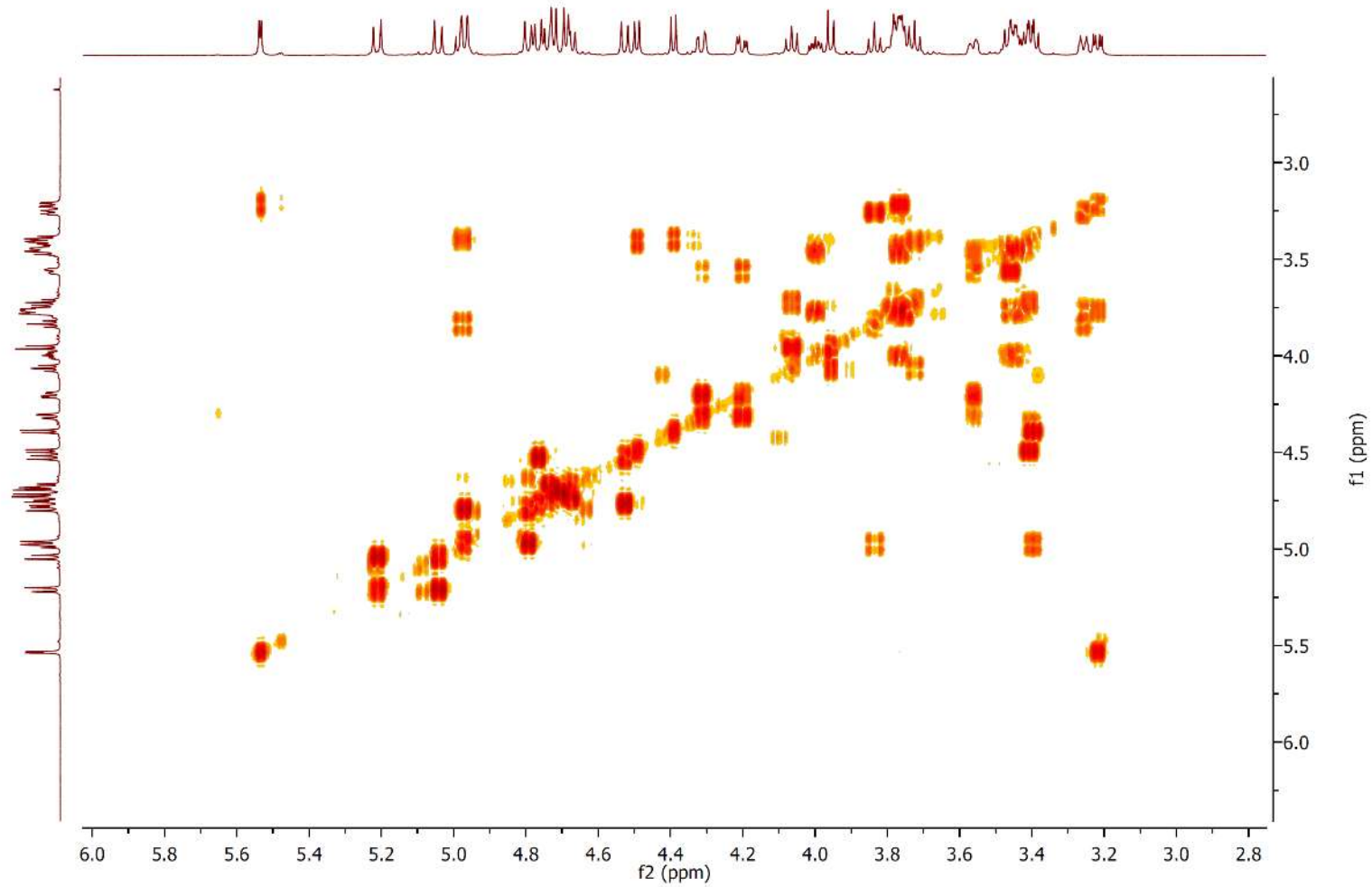
$^1\text{H NMR}$, 600 MHz, CDCl_3

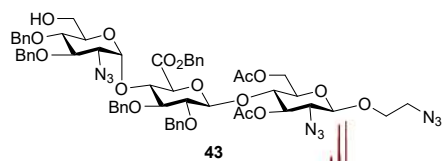




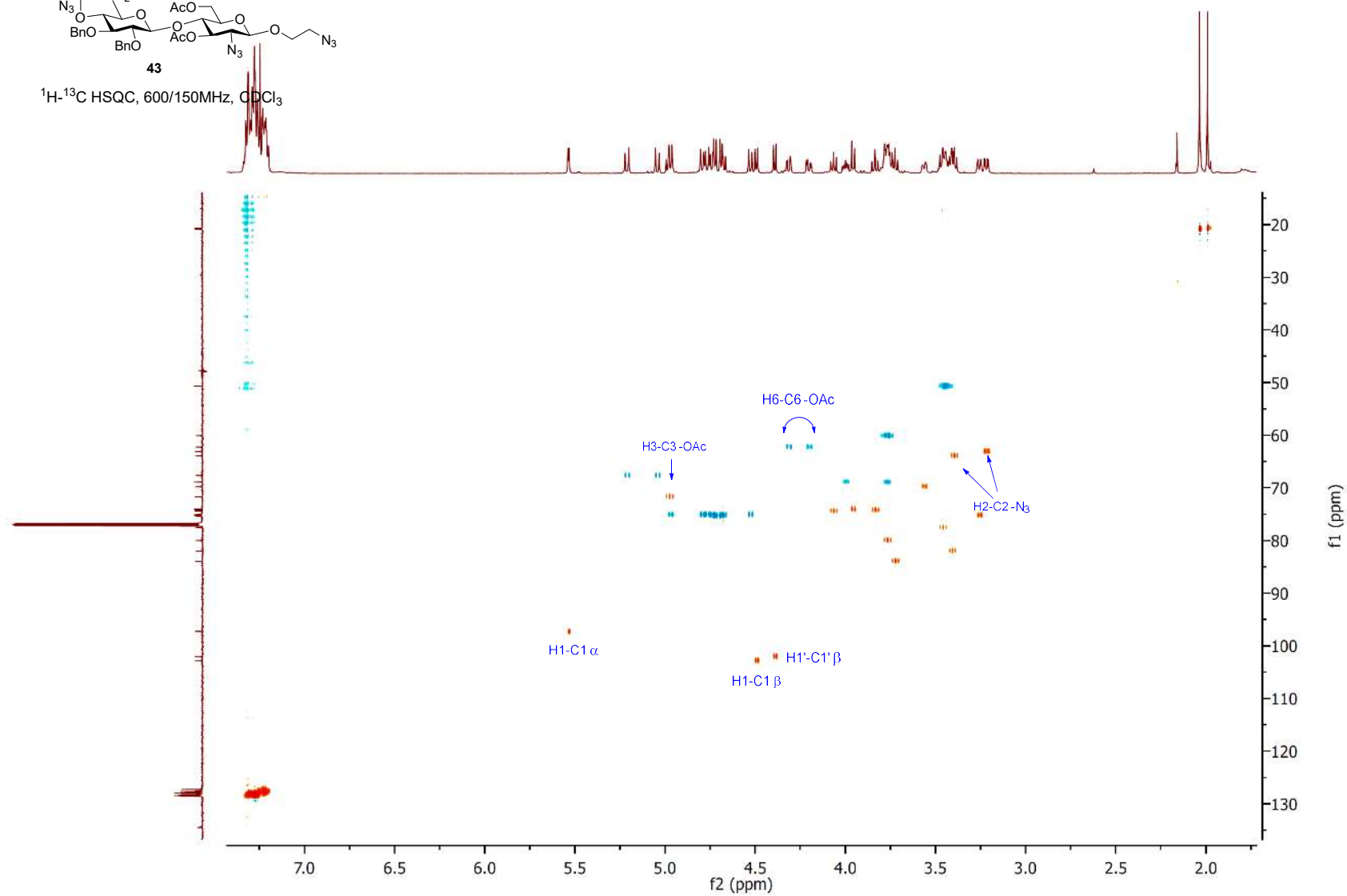


^1H - ^1H COSY, 600 MHz, CDCl_3

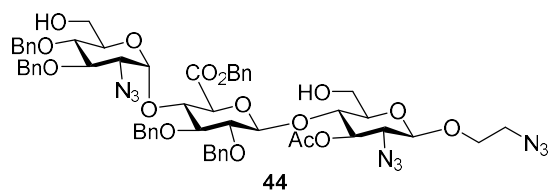




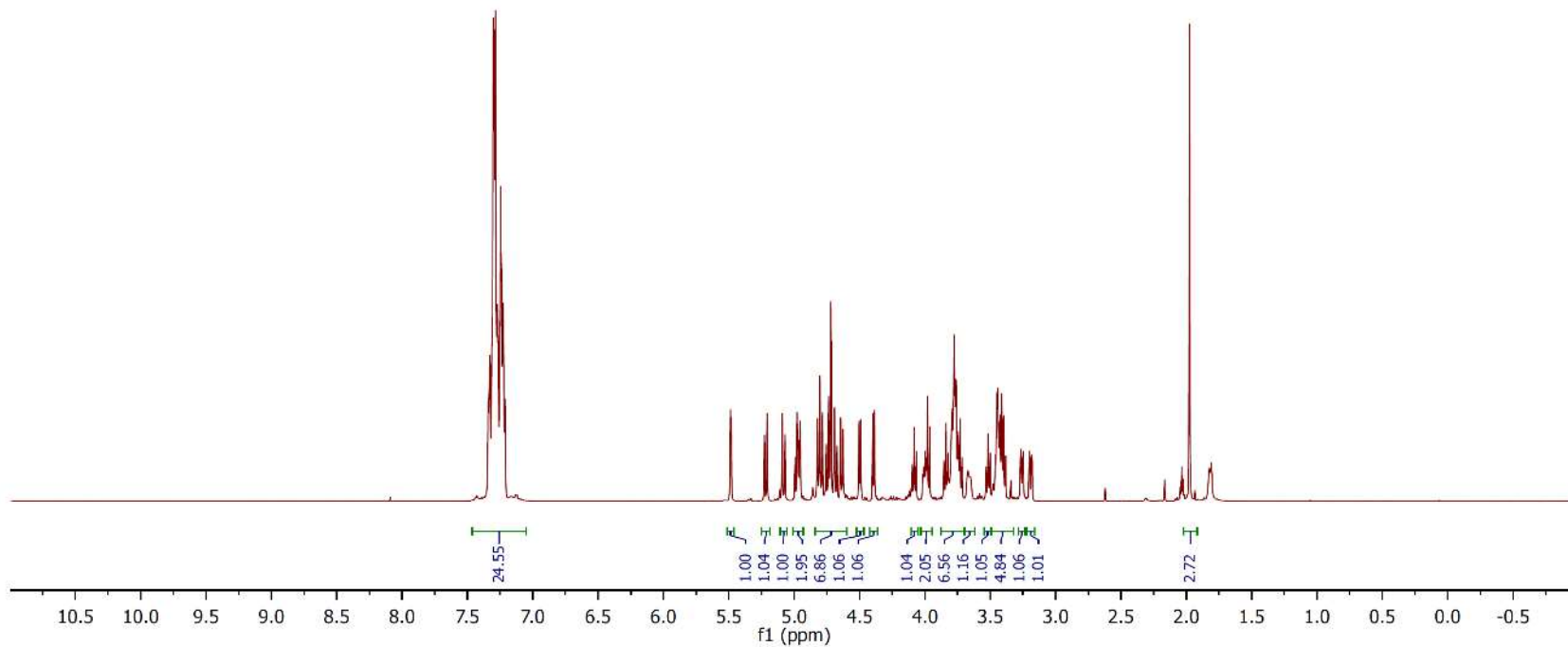
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

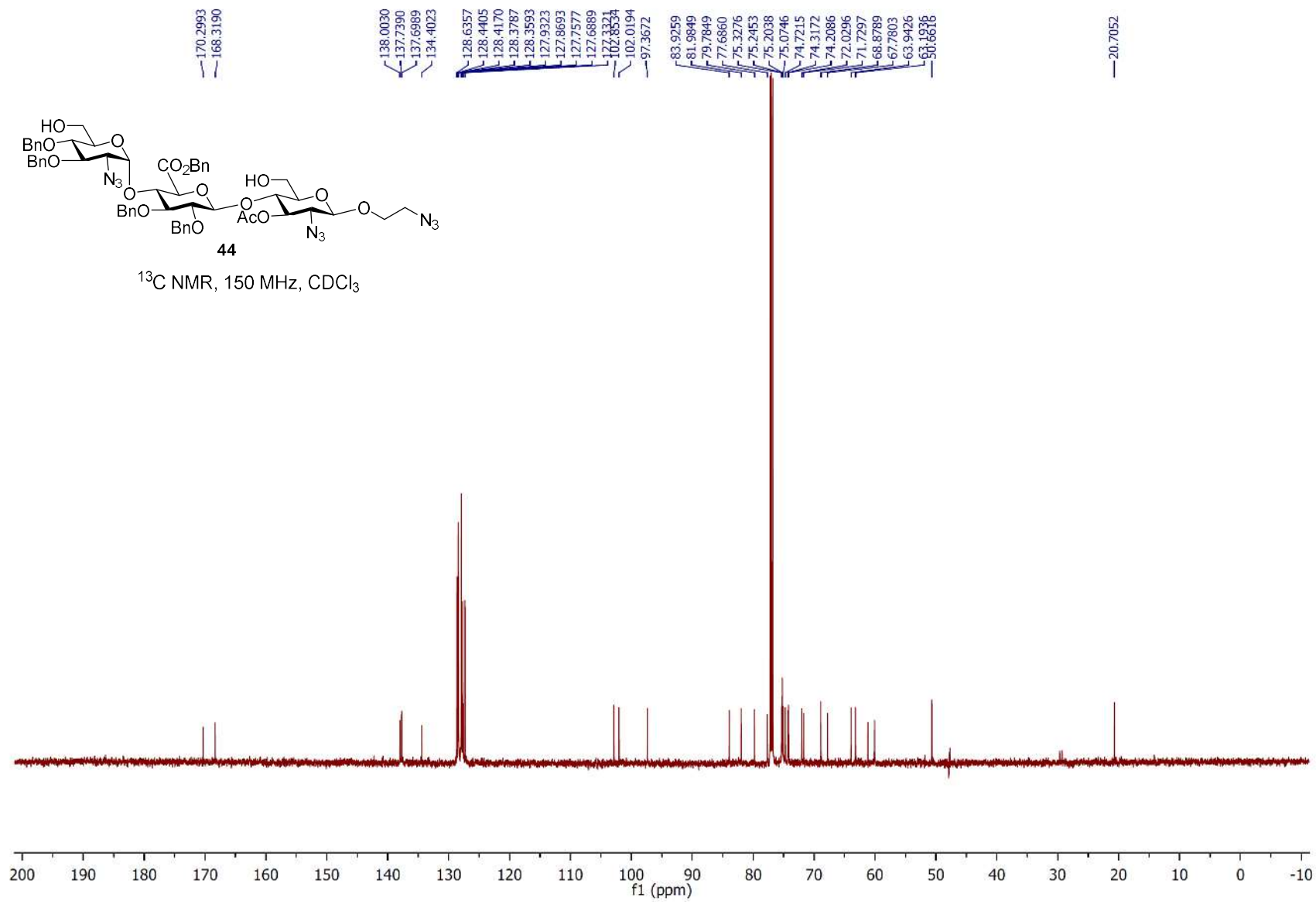


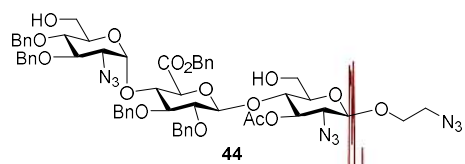
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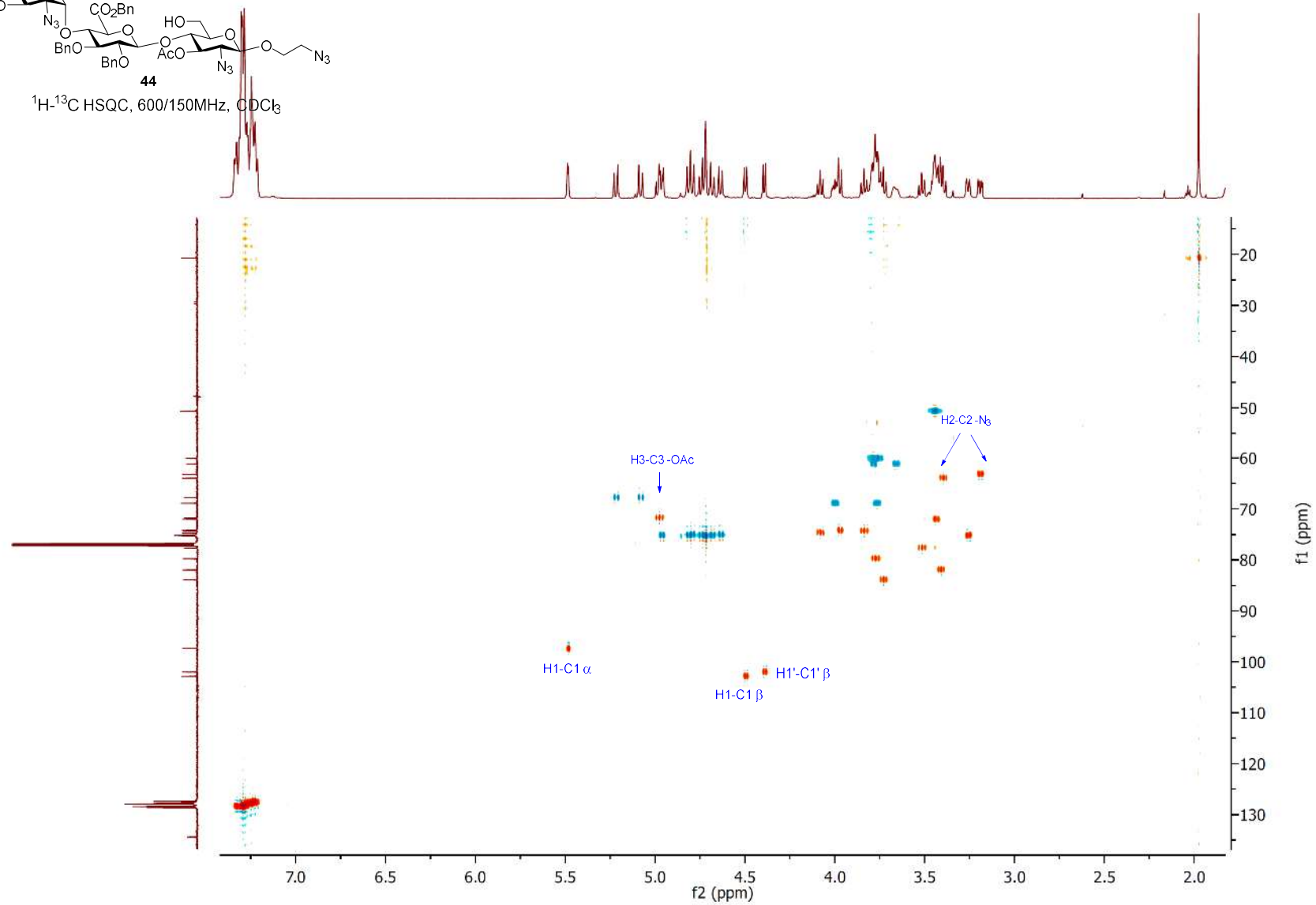
¹H NMR, 600 MHz, CDCl₃



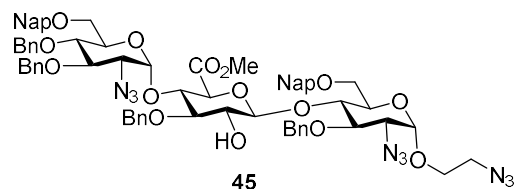




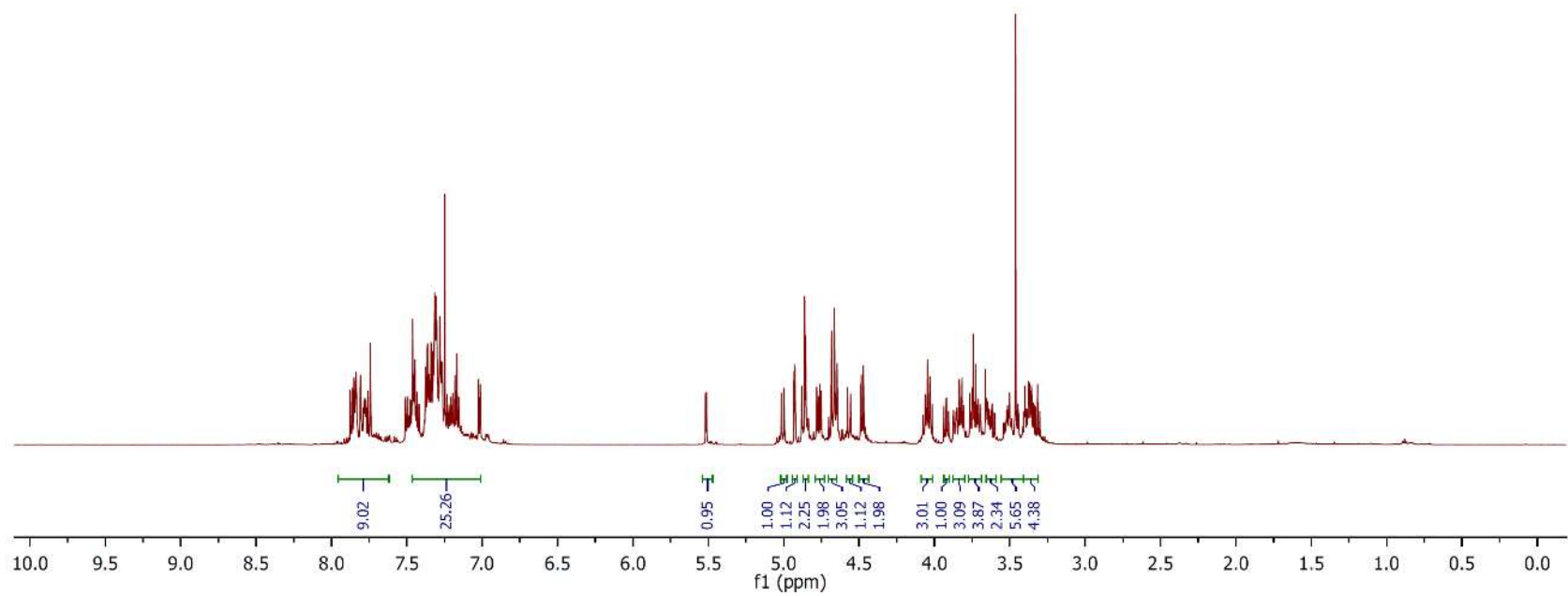
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

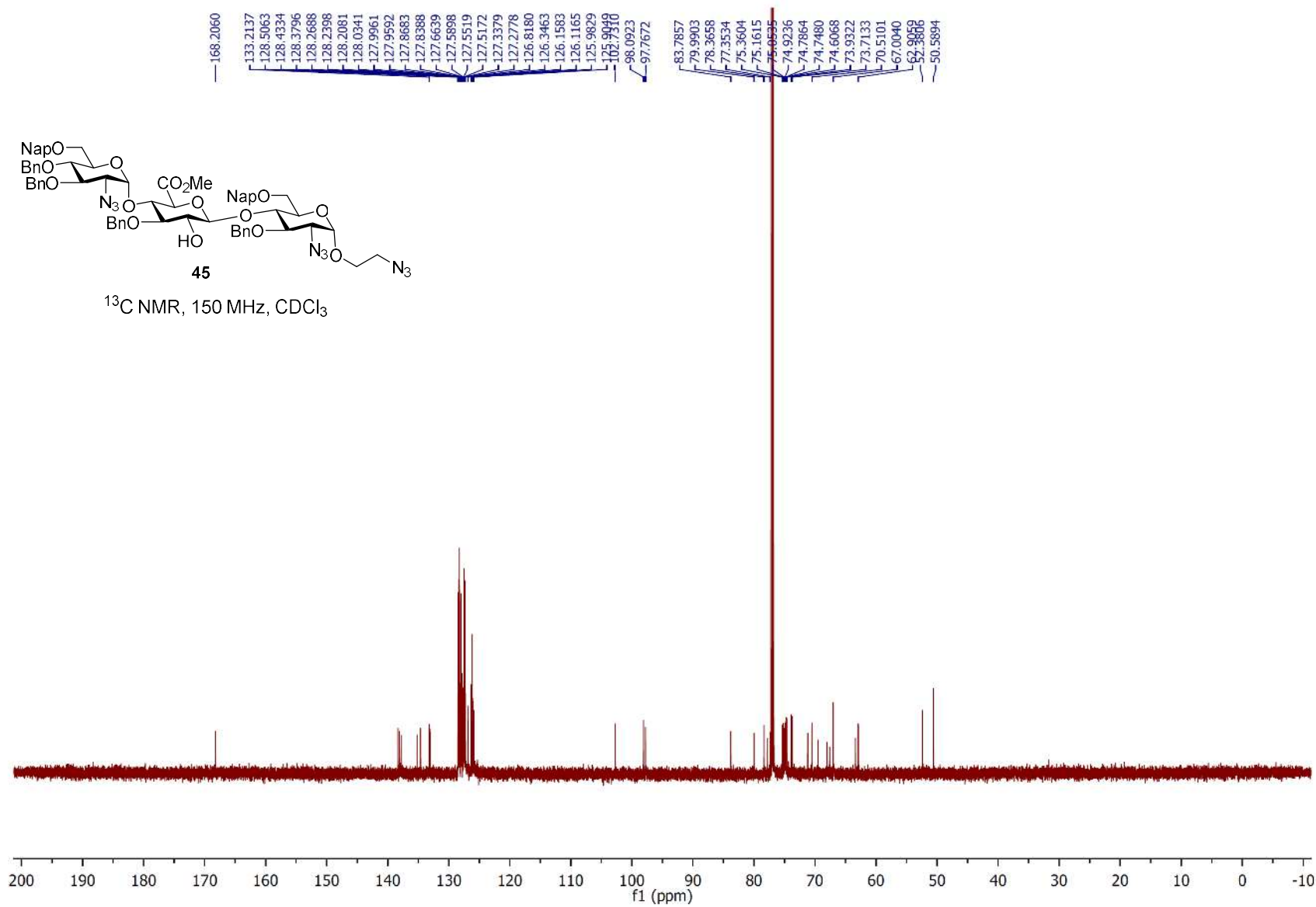


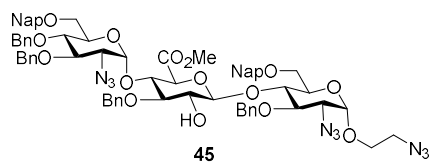
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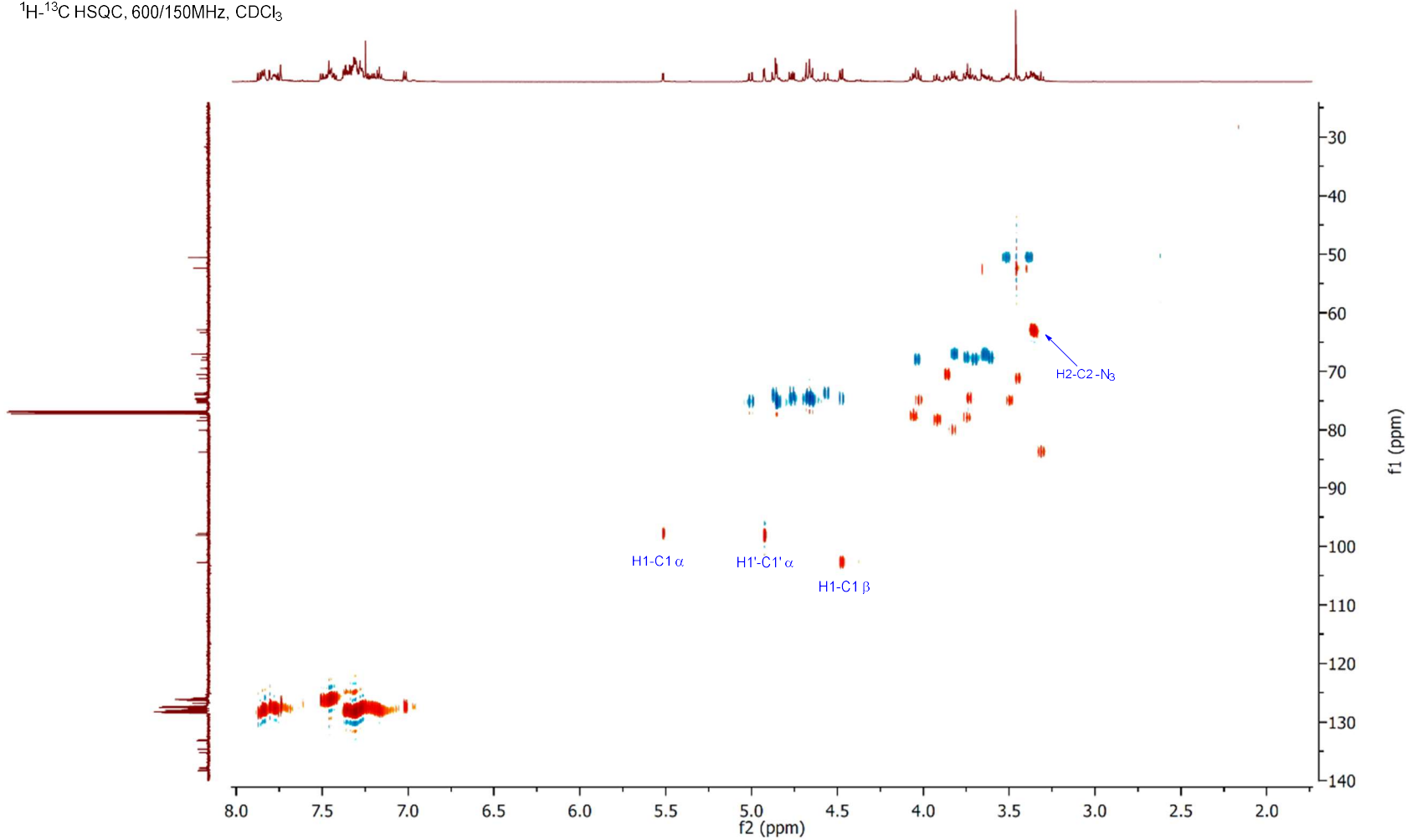
^1H NMR, 600 MHz, CDCl_3

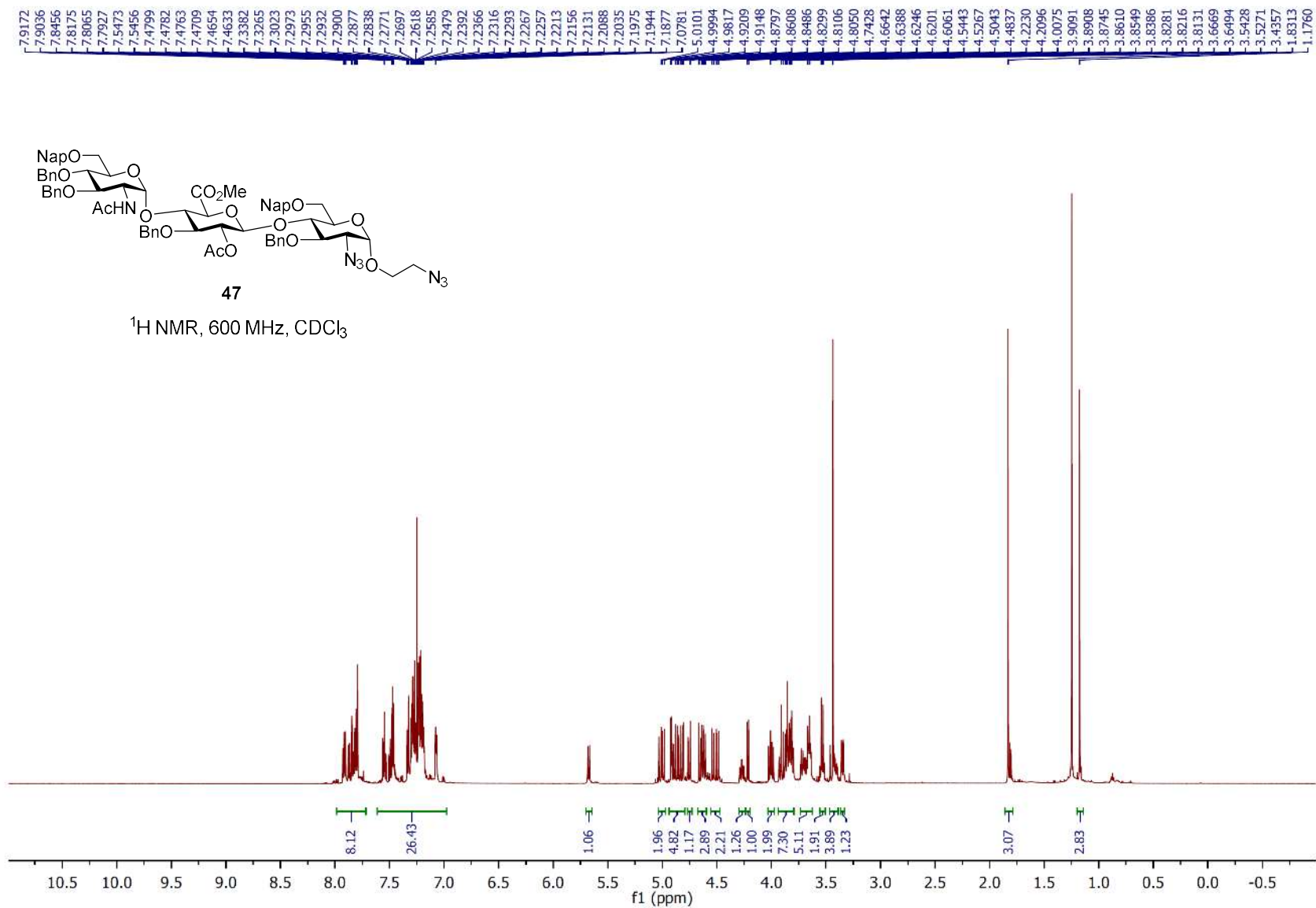


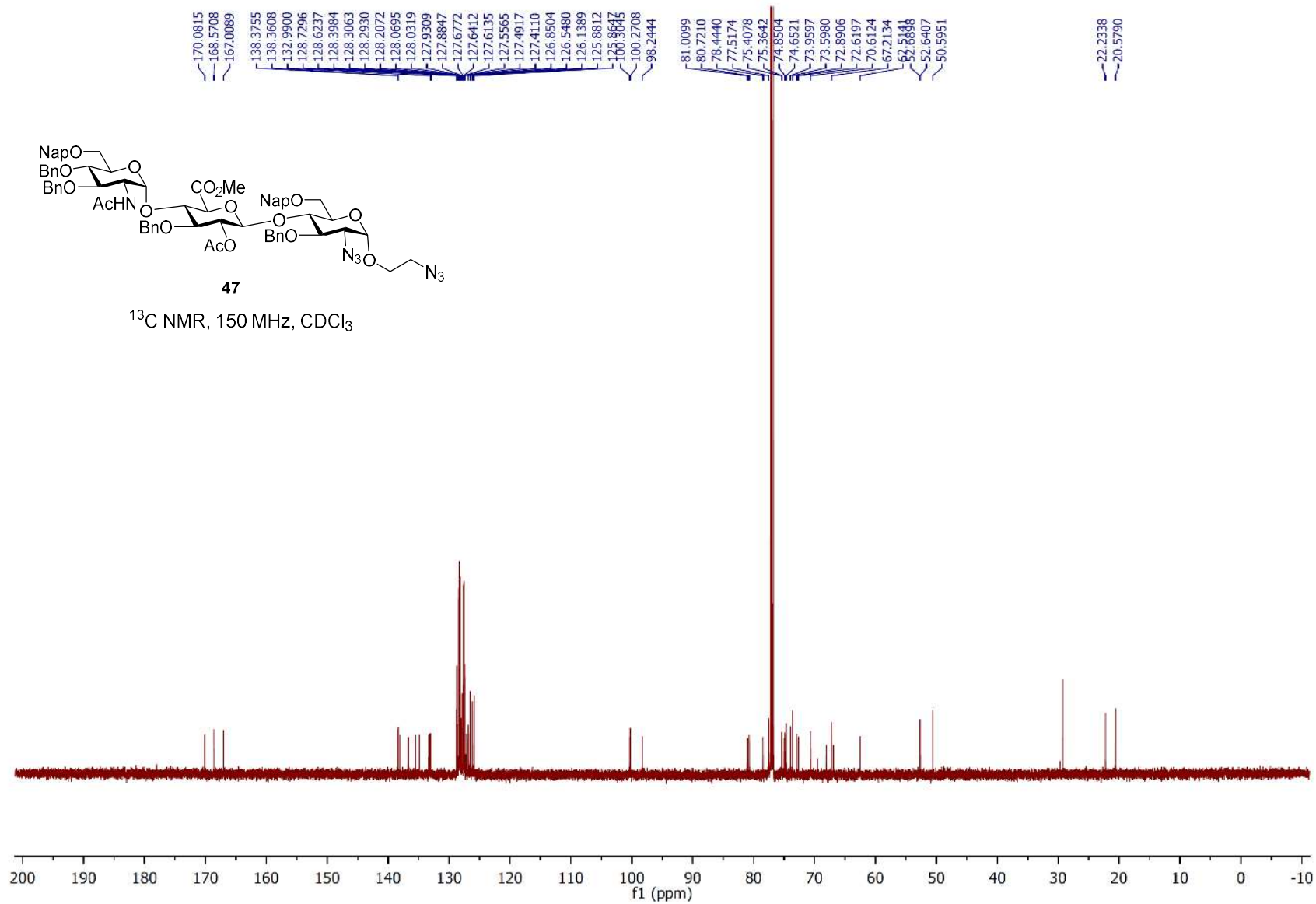


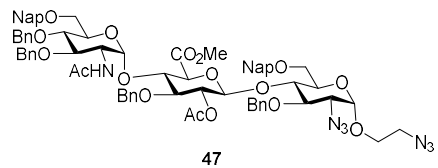


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

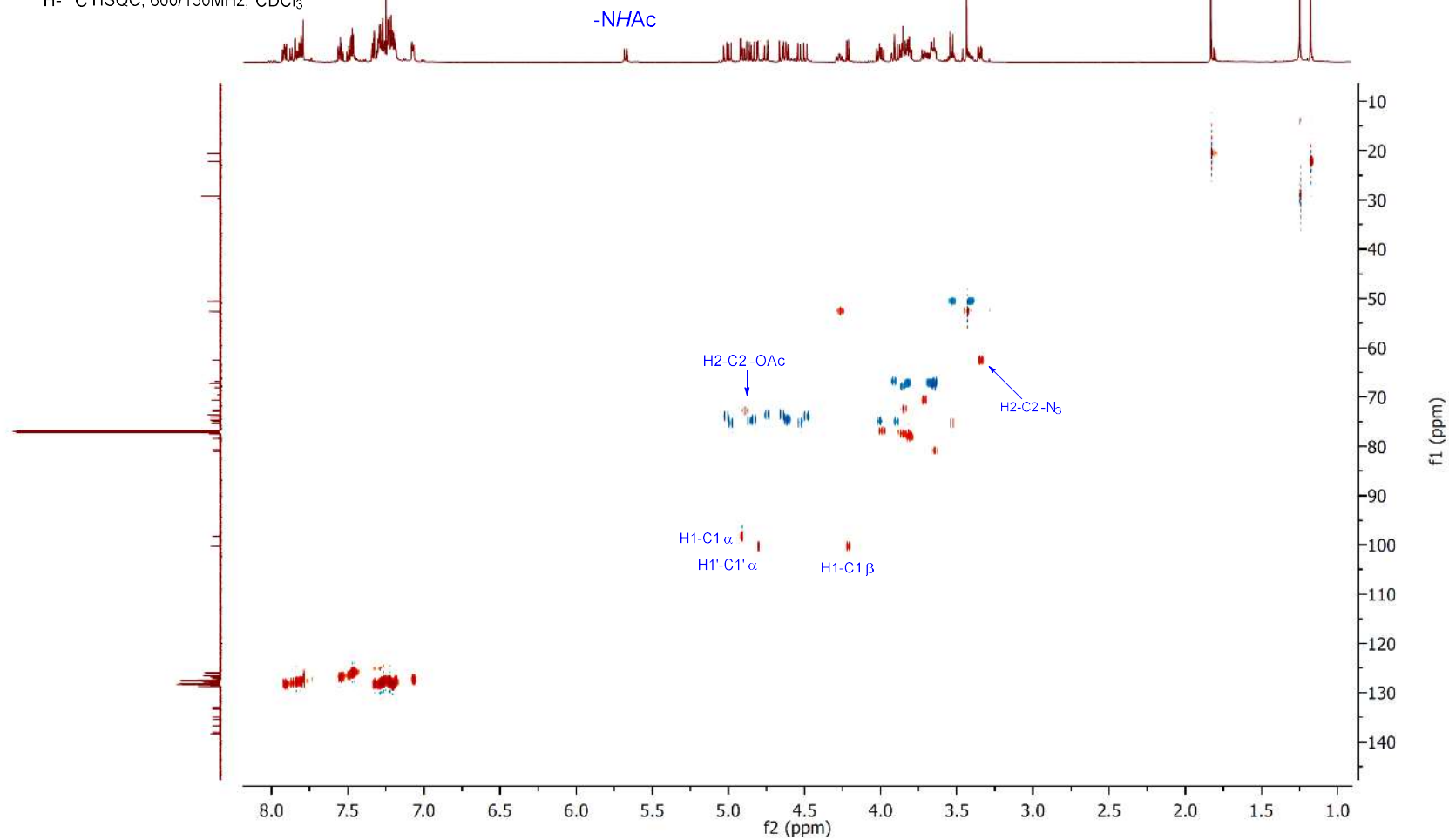


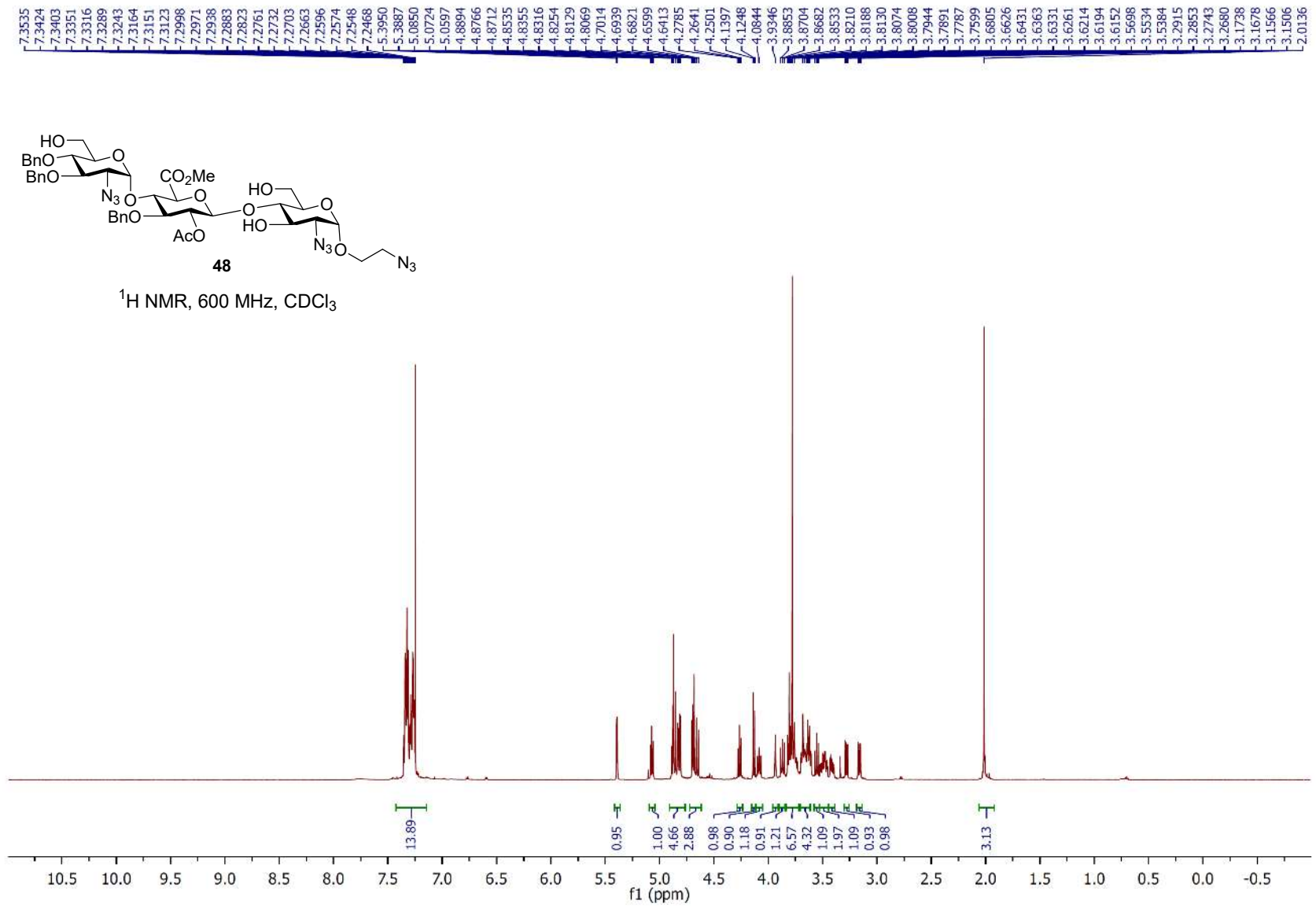


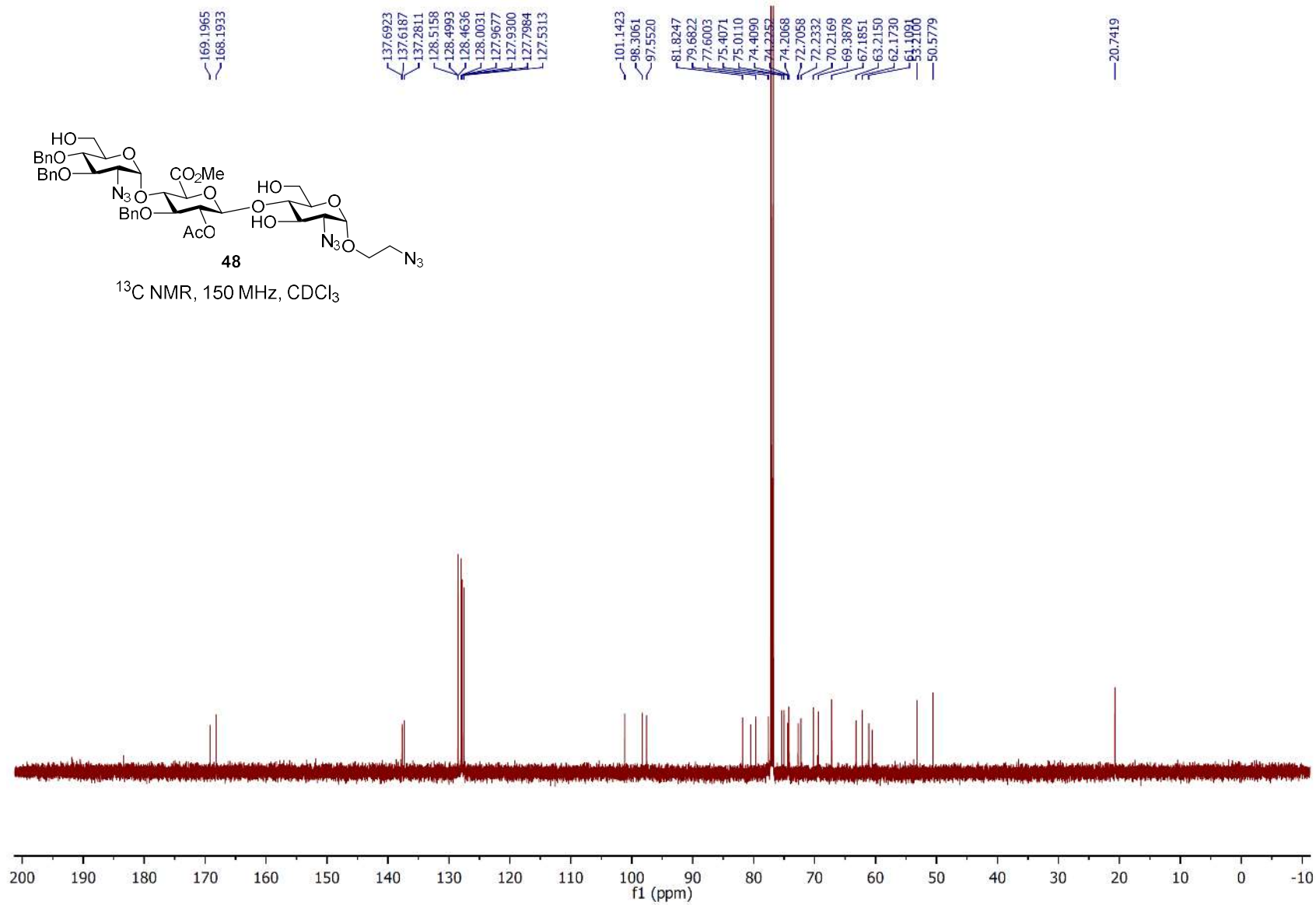


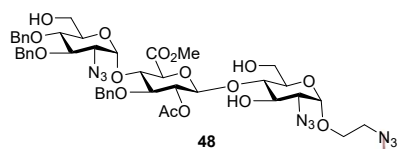


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

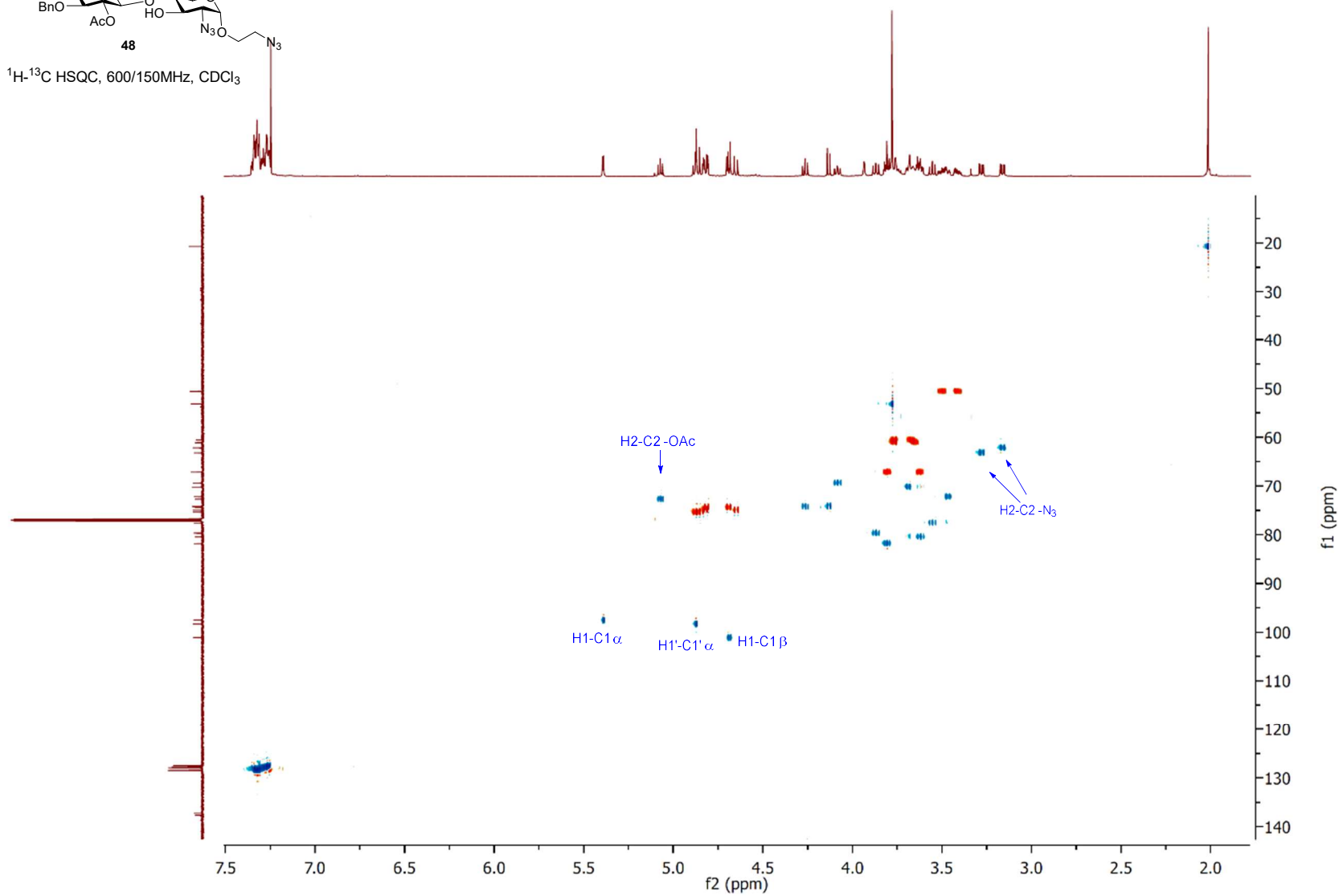




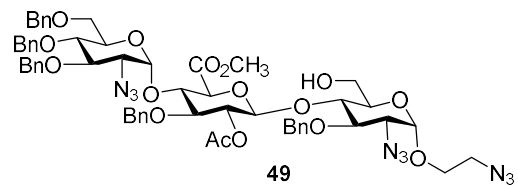




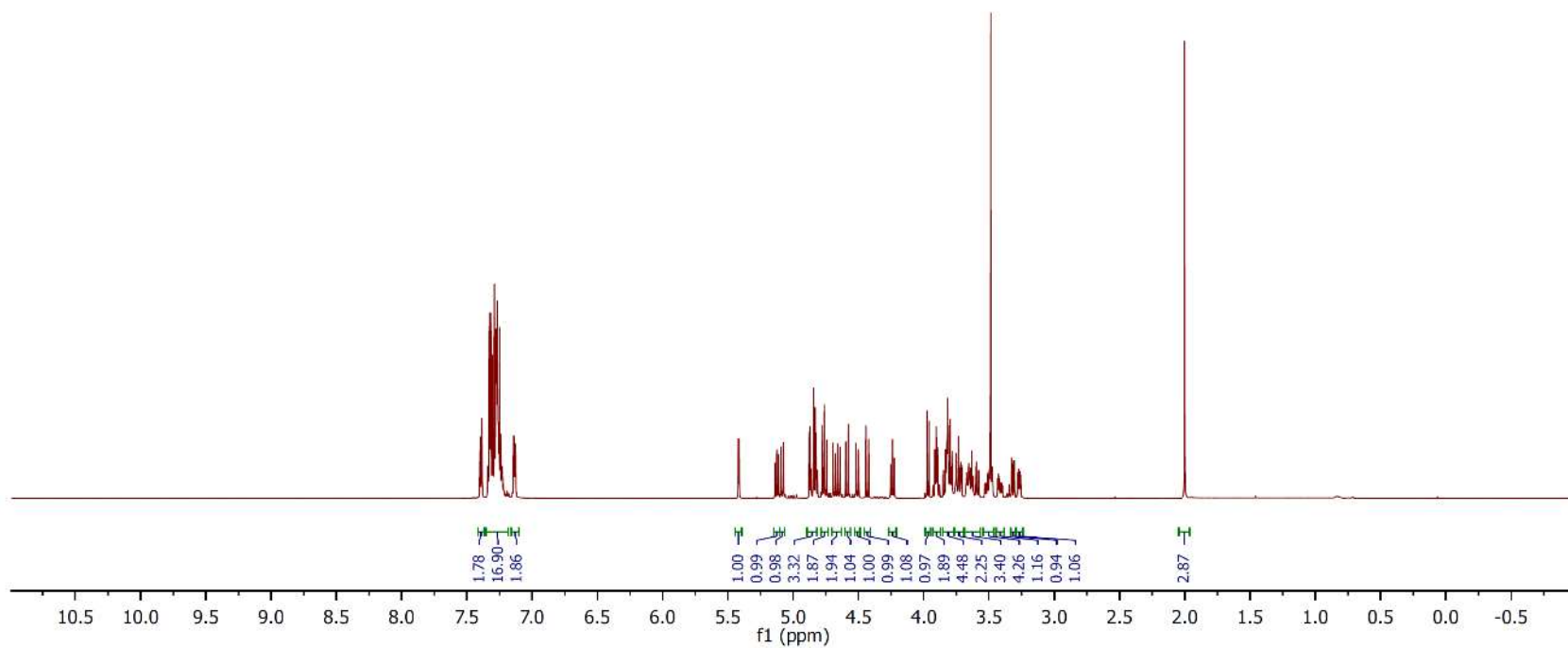
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

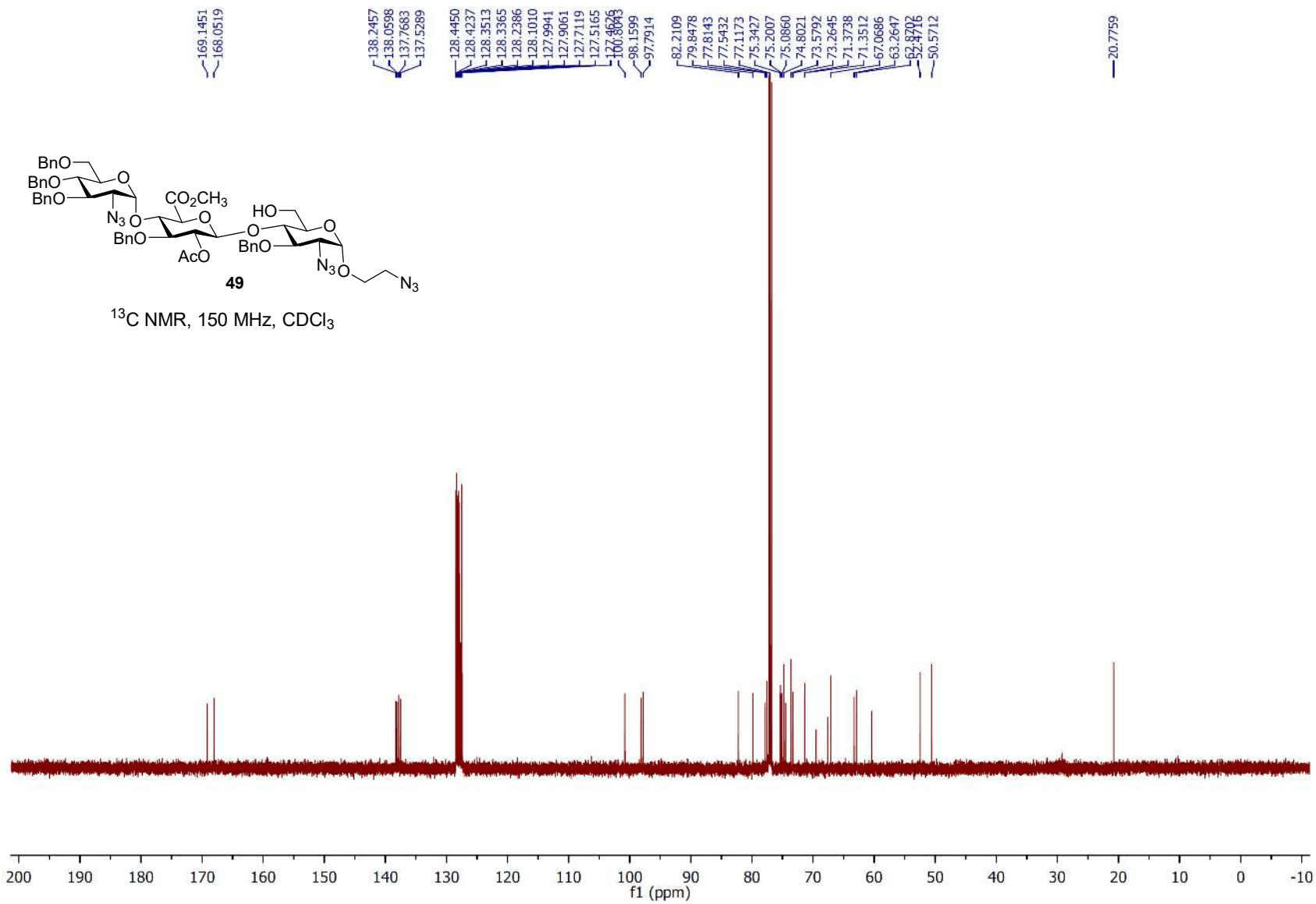


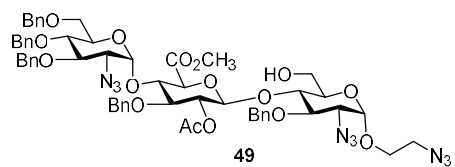
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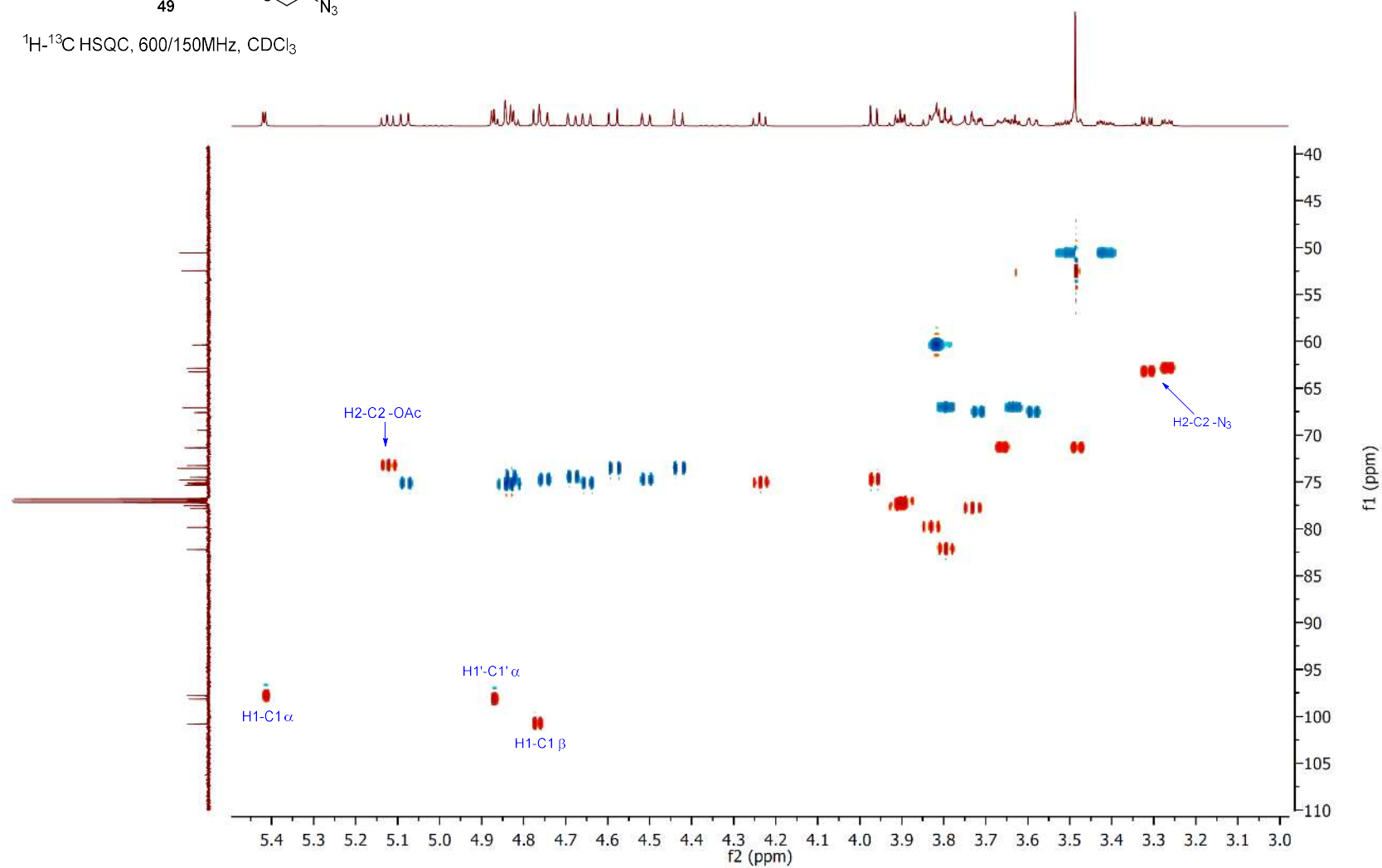
^1H NMR, 600 MHz, CDCl_3



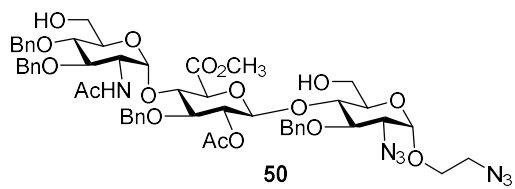




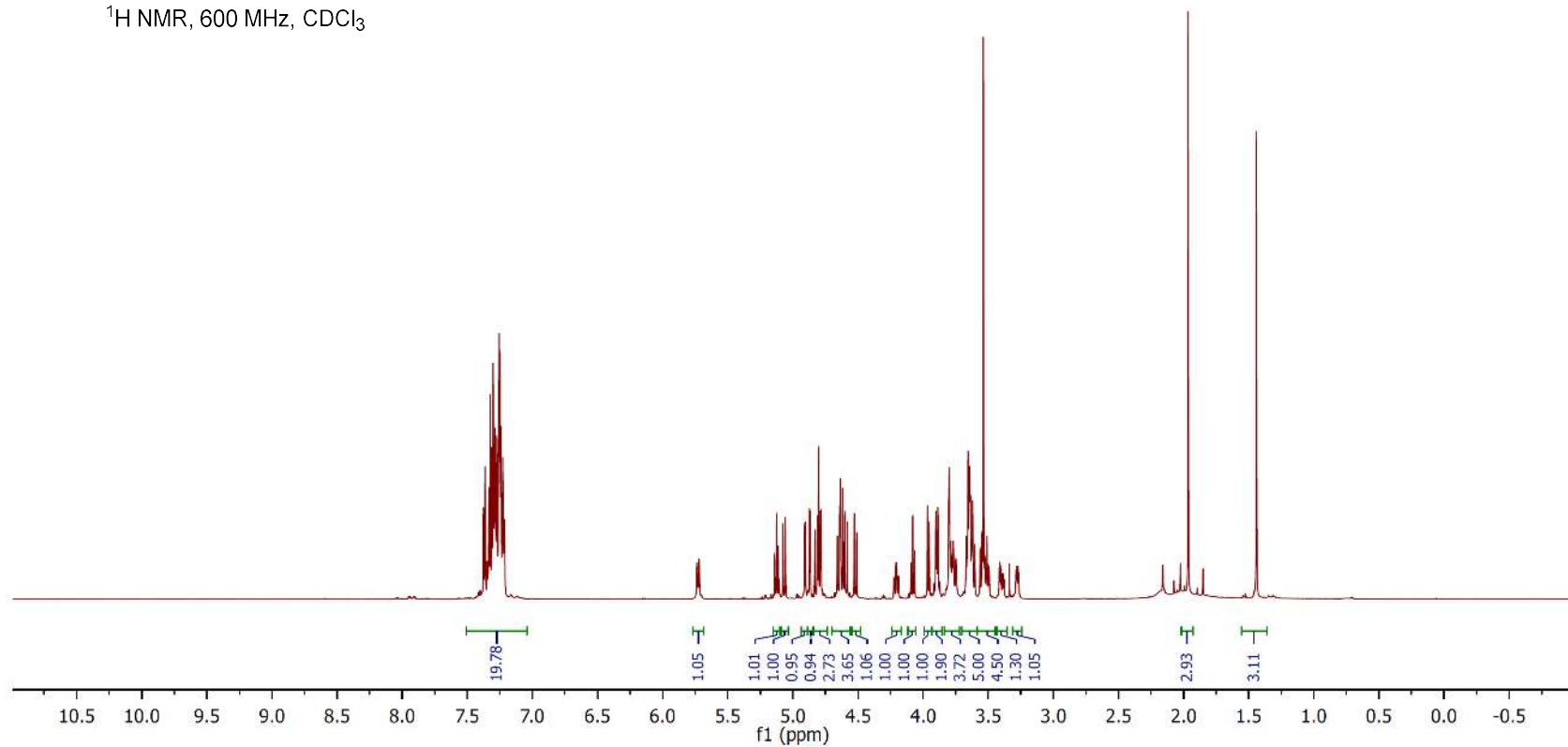
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

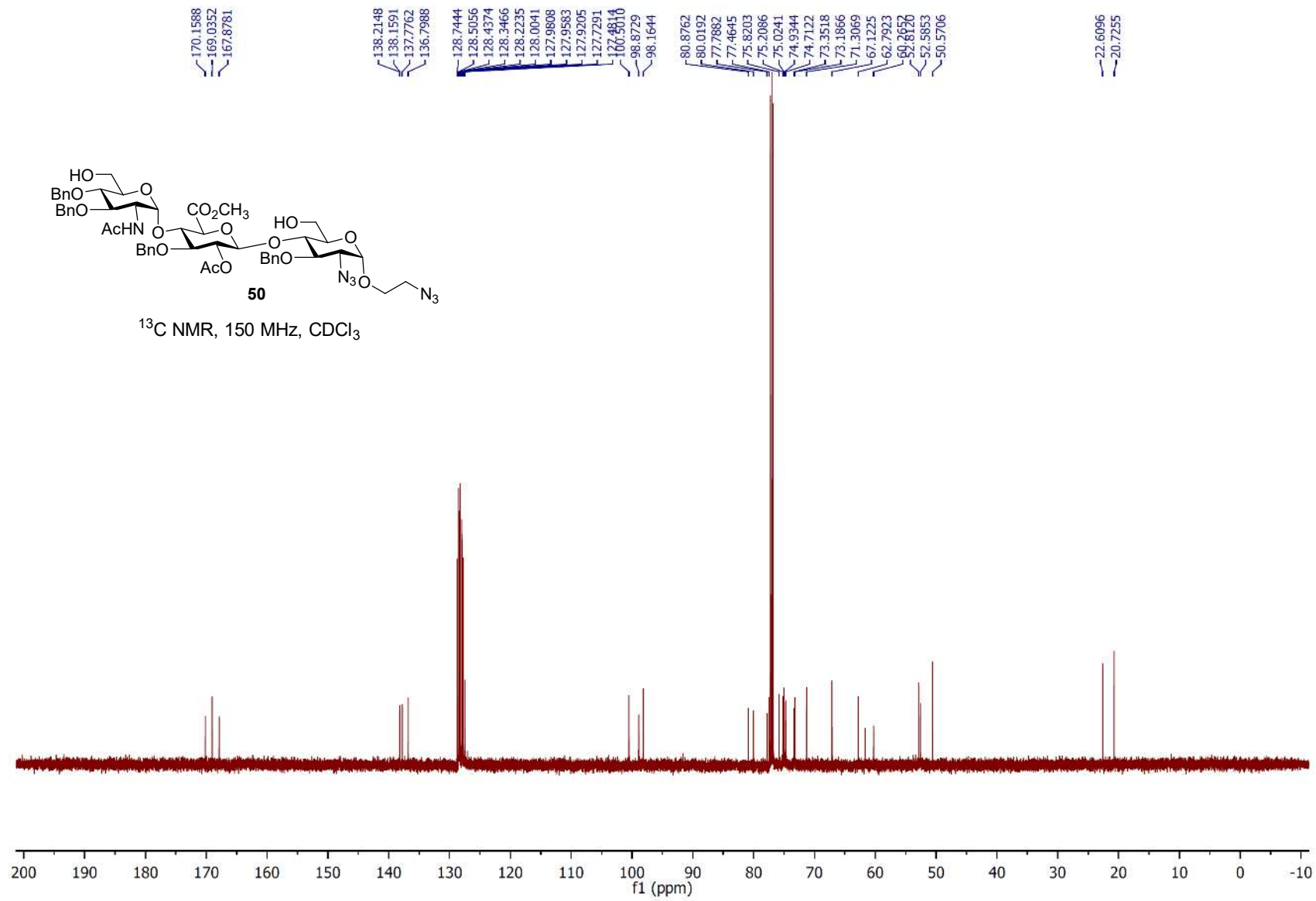


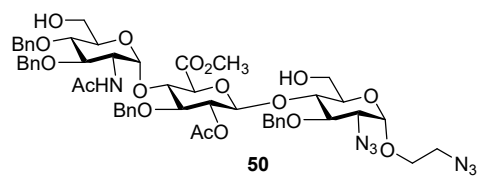
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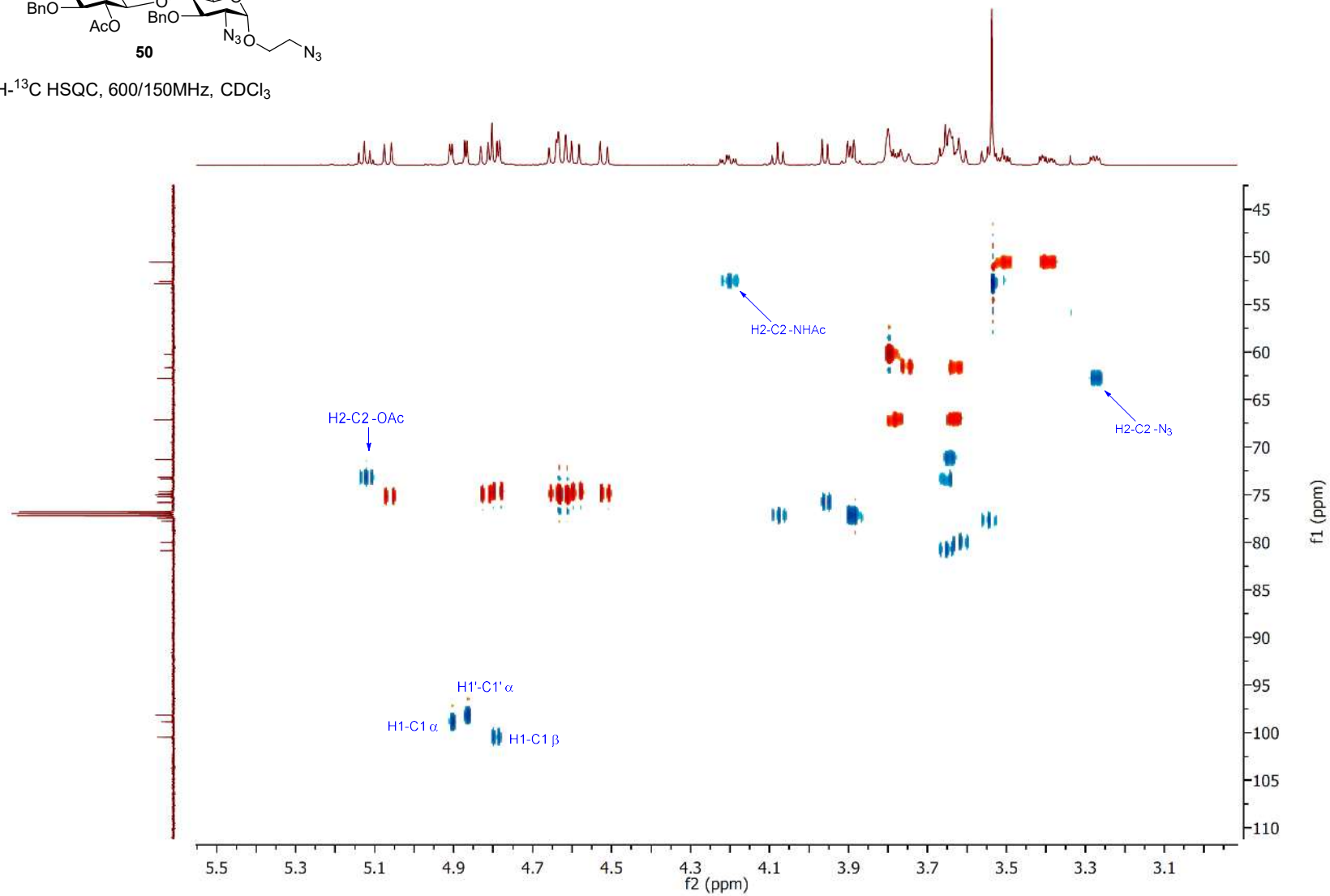
¹H NMR, 600 MHz, CDCl₃



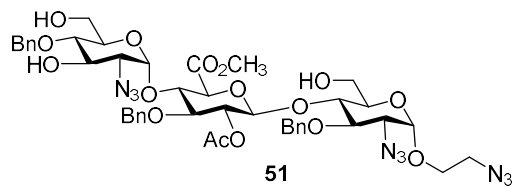




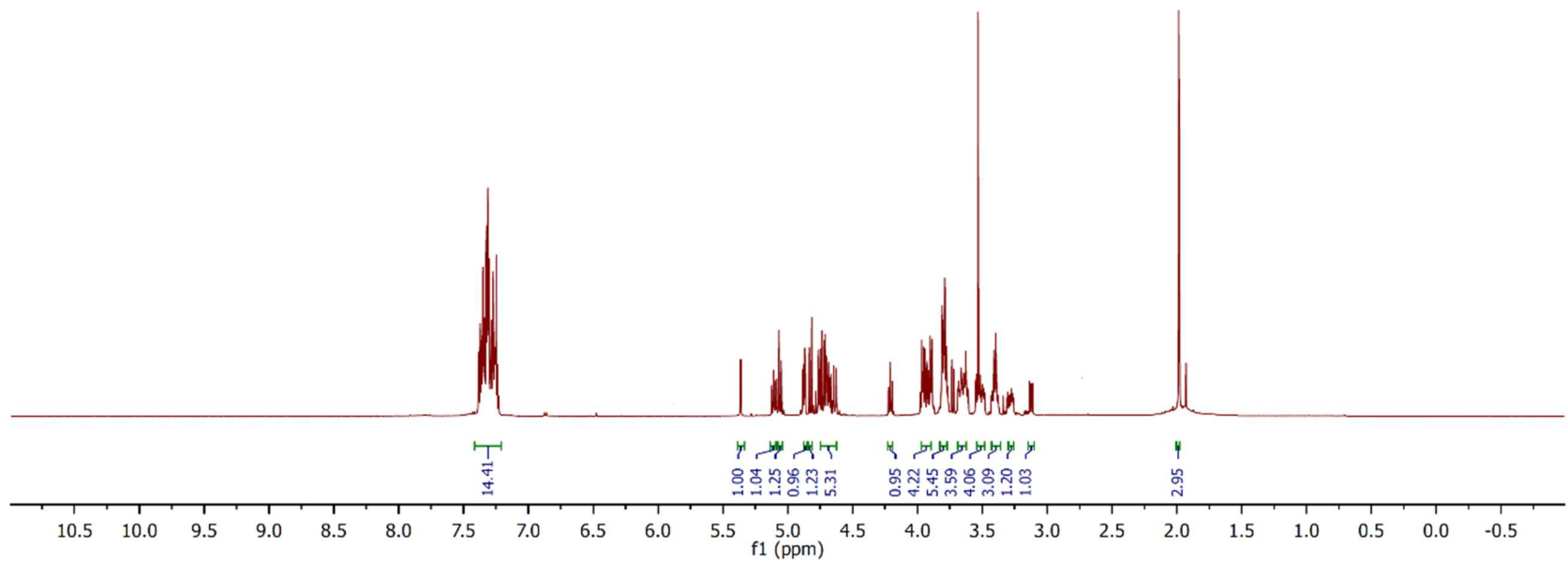
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

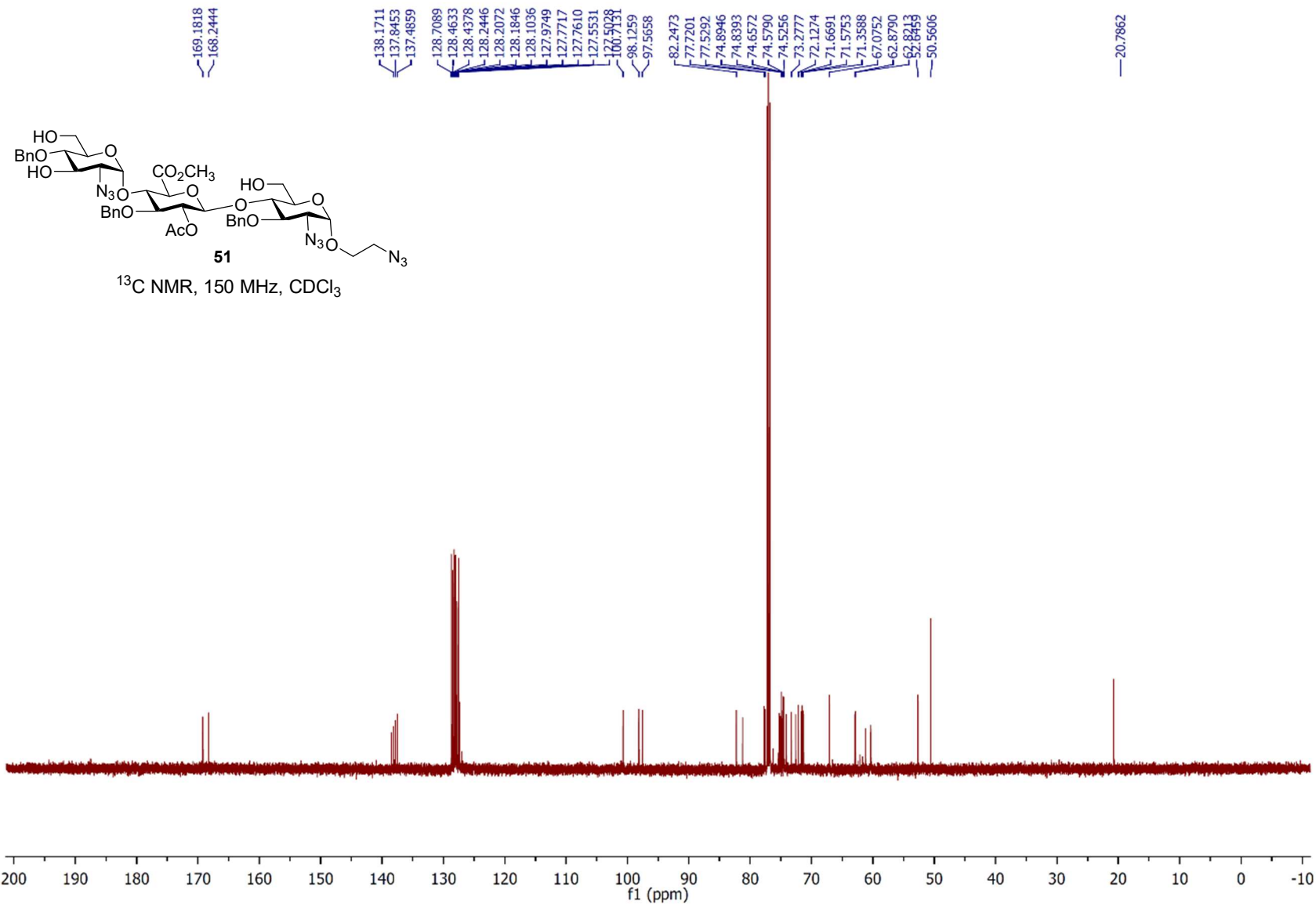


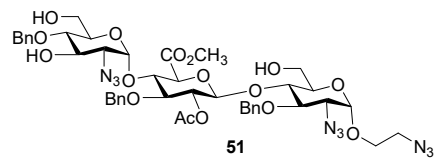
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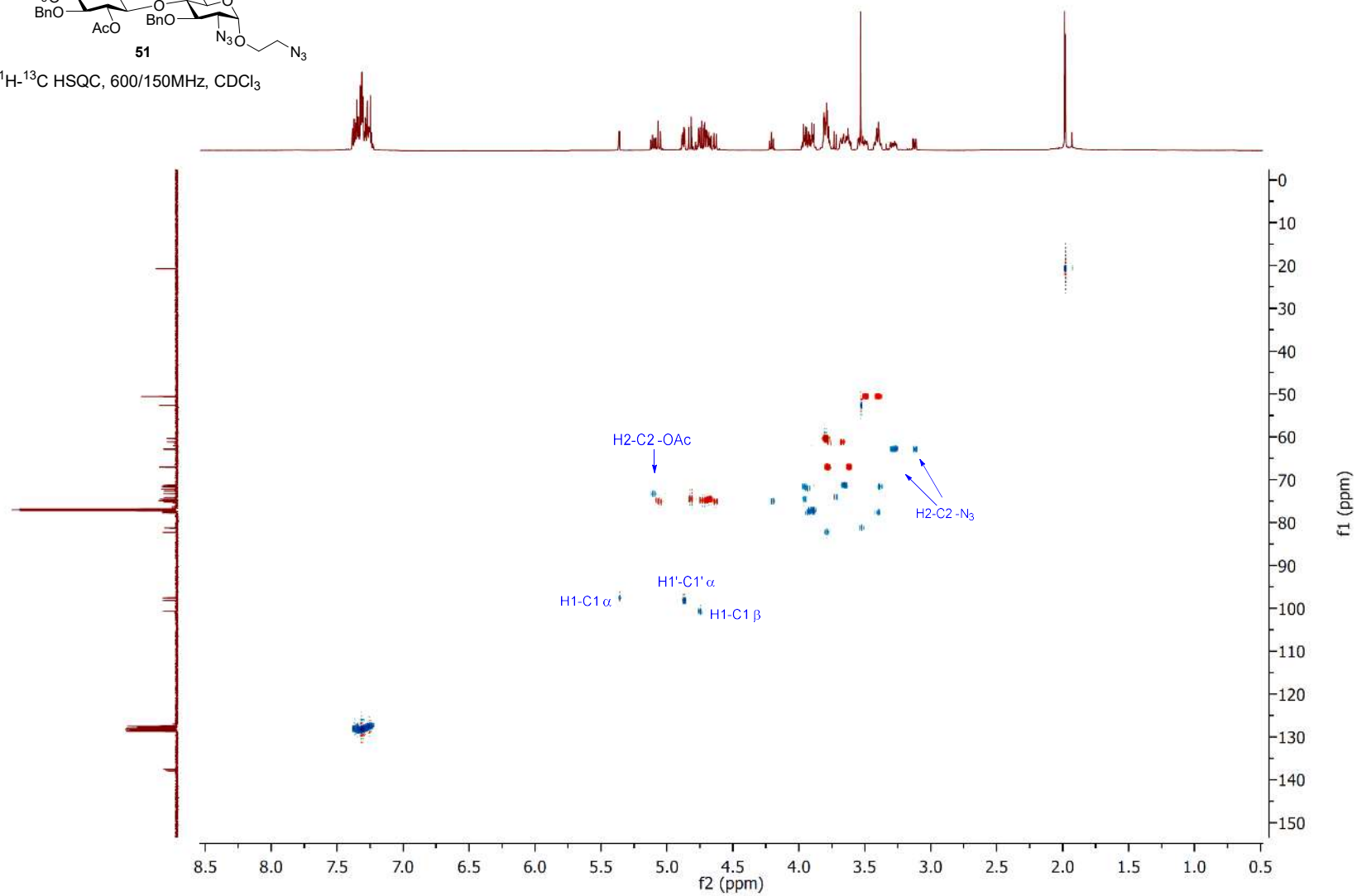
$^1\text{H NMR}$, 600 MHz, CDCl_3

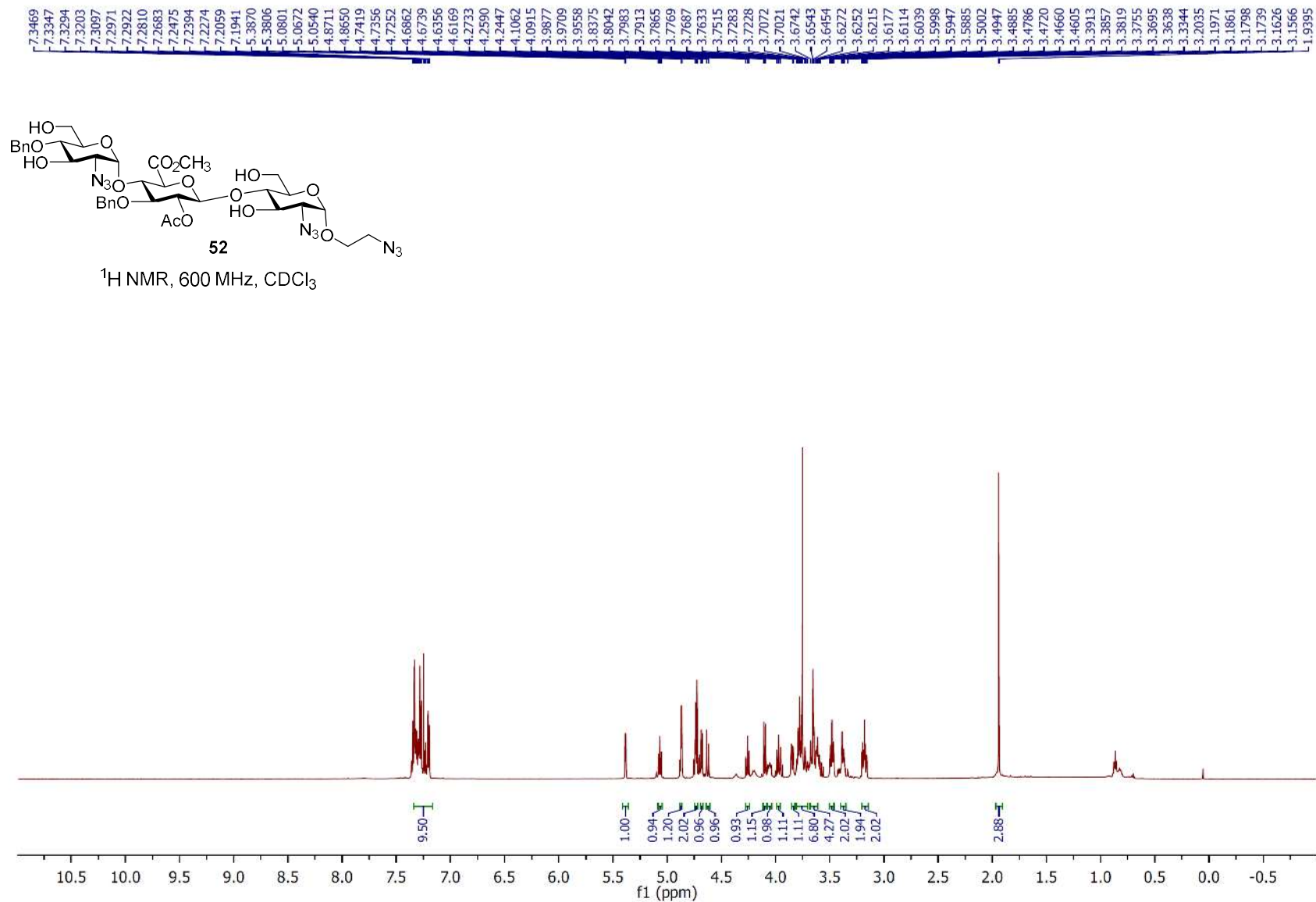


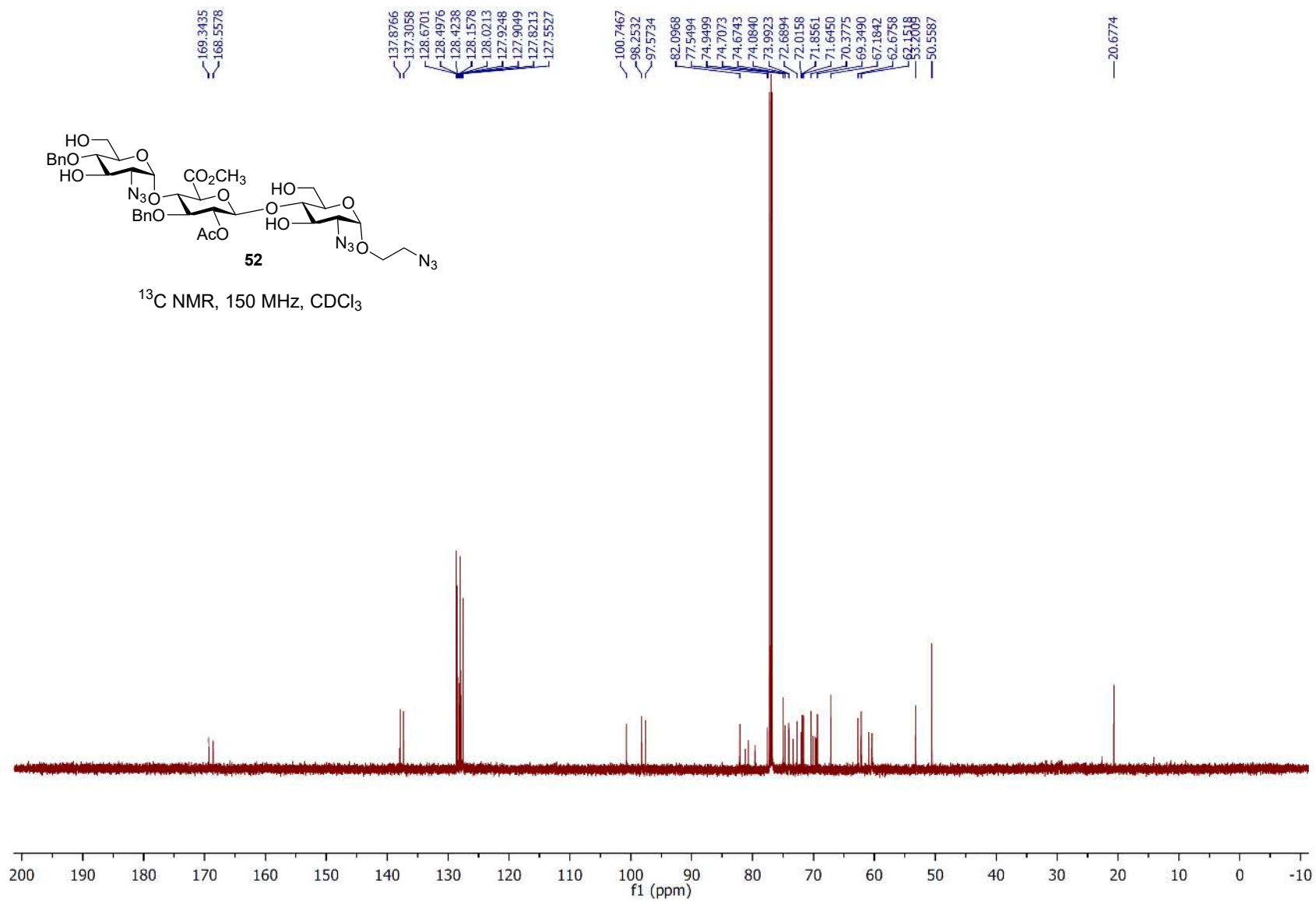




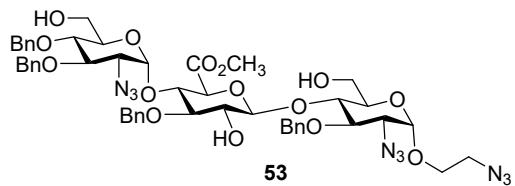
^1H - ^{13}C HSQC, 600/150MHz, CDCl_3



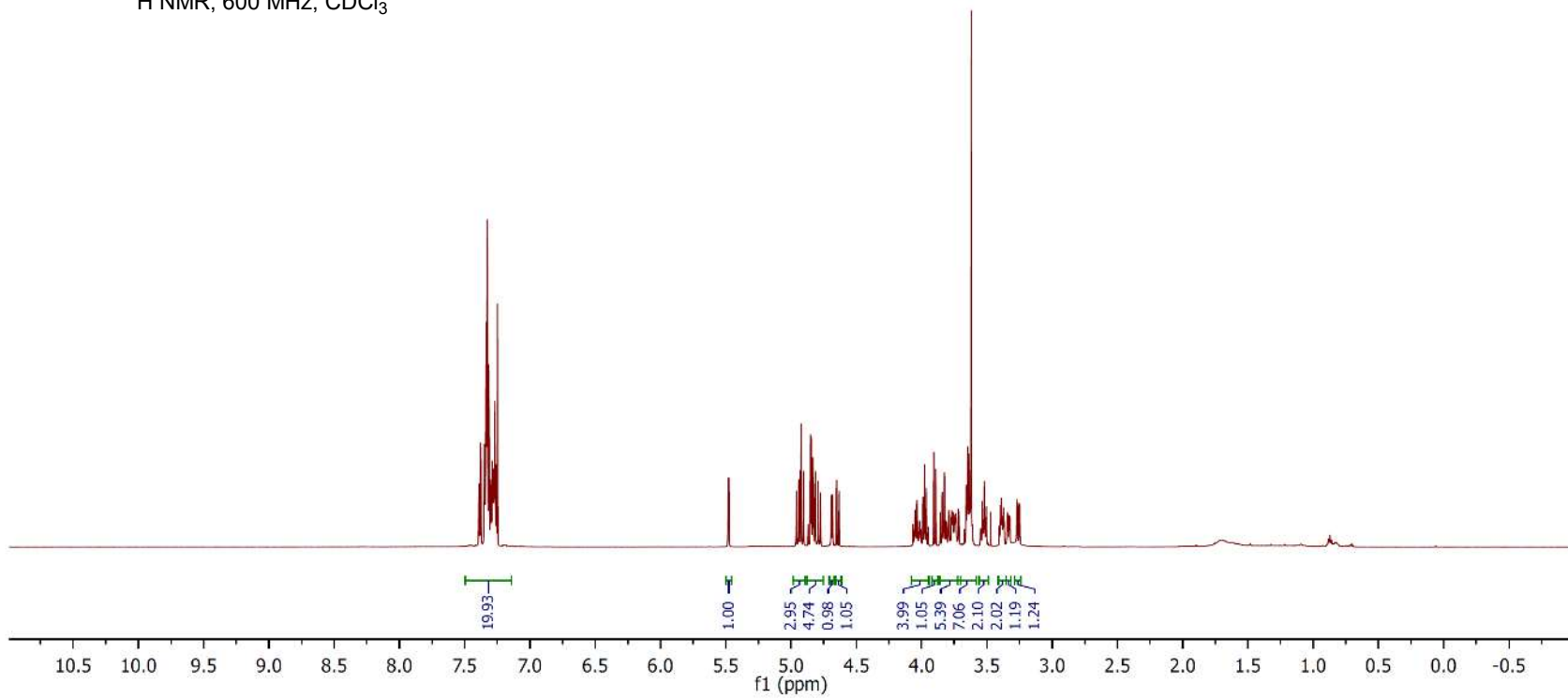


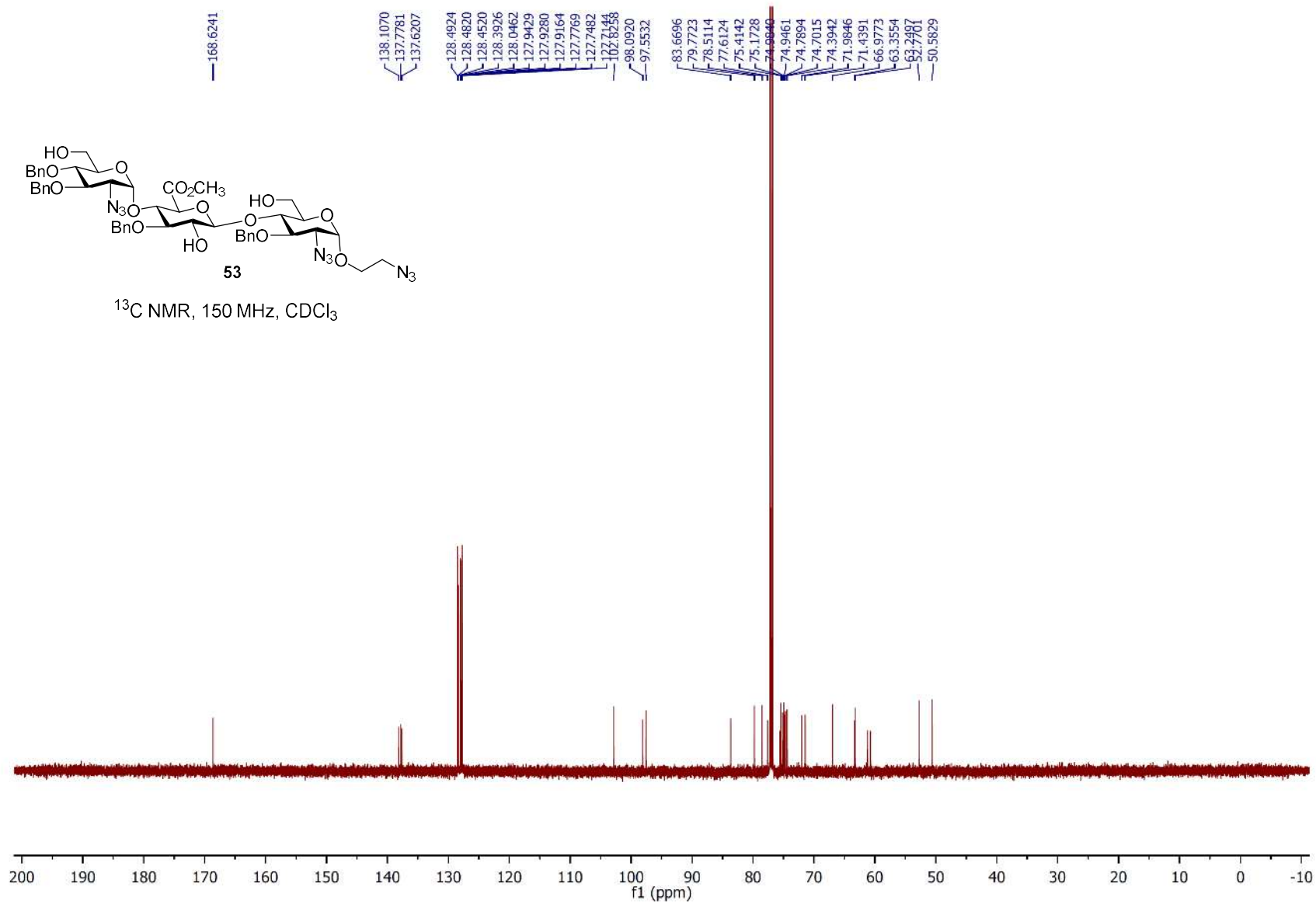


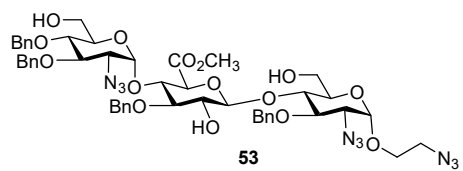
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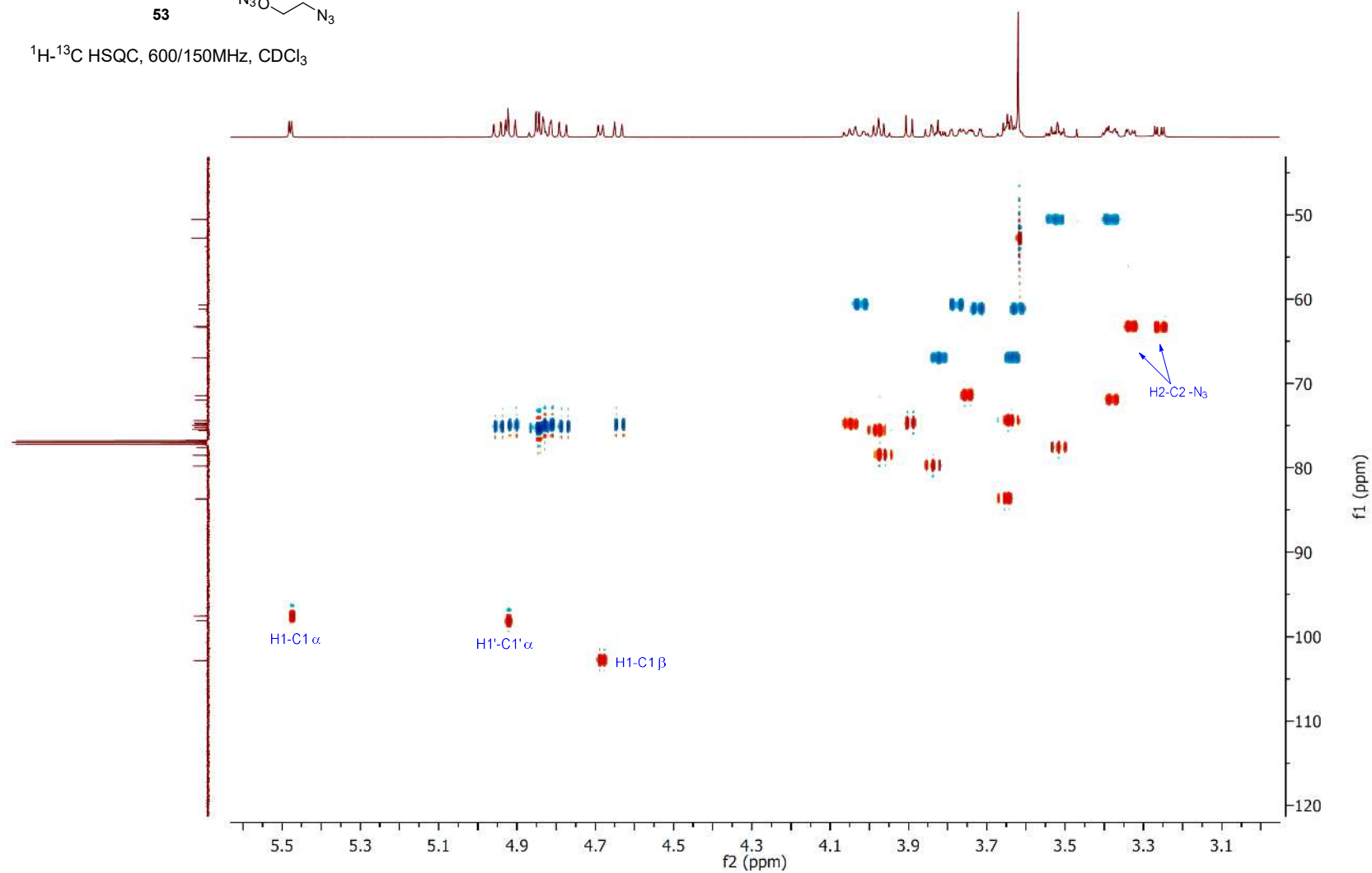
$^1\text{H NMR}$, 600 MHz, CDCl_3

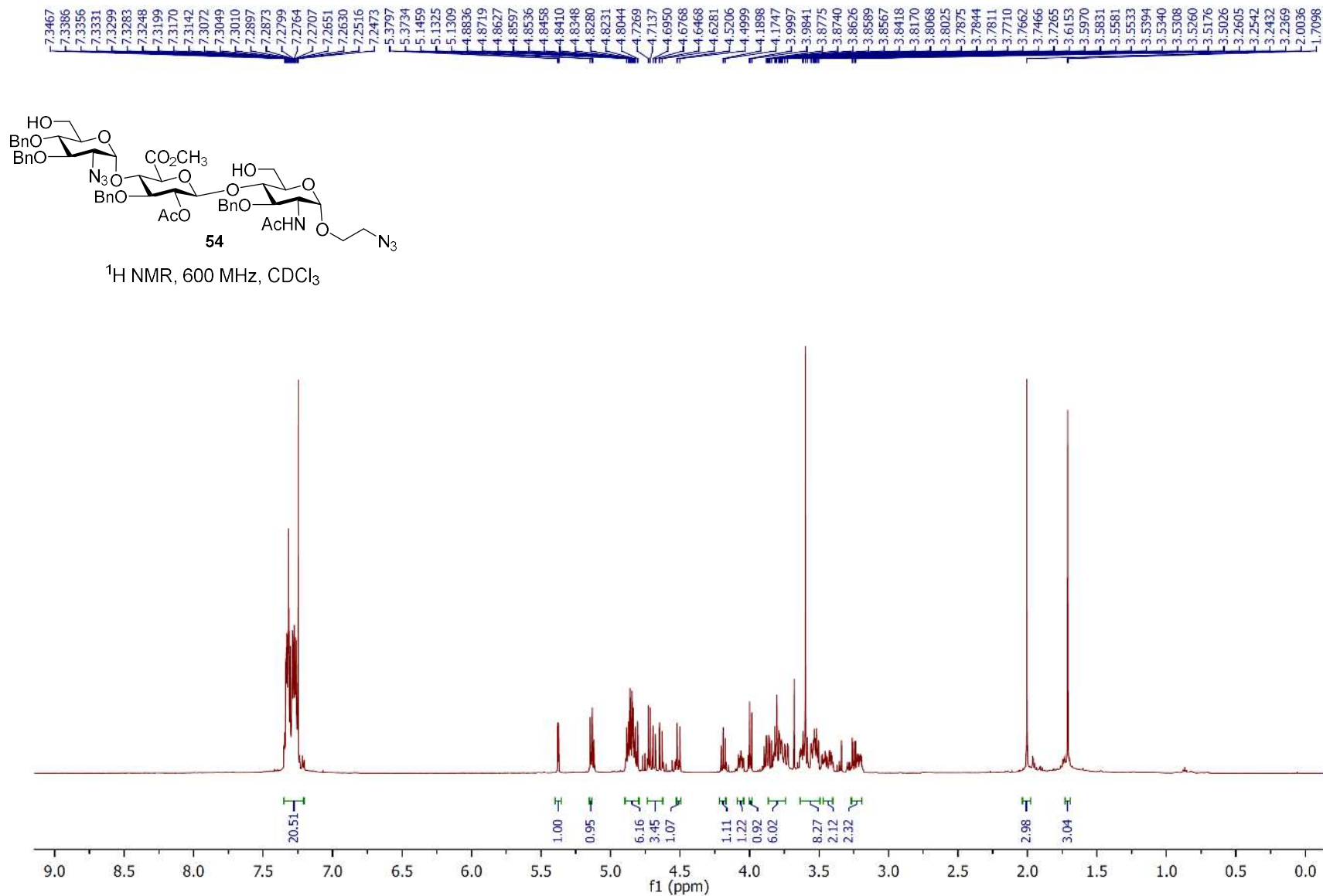


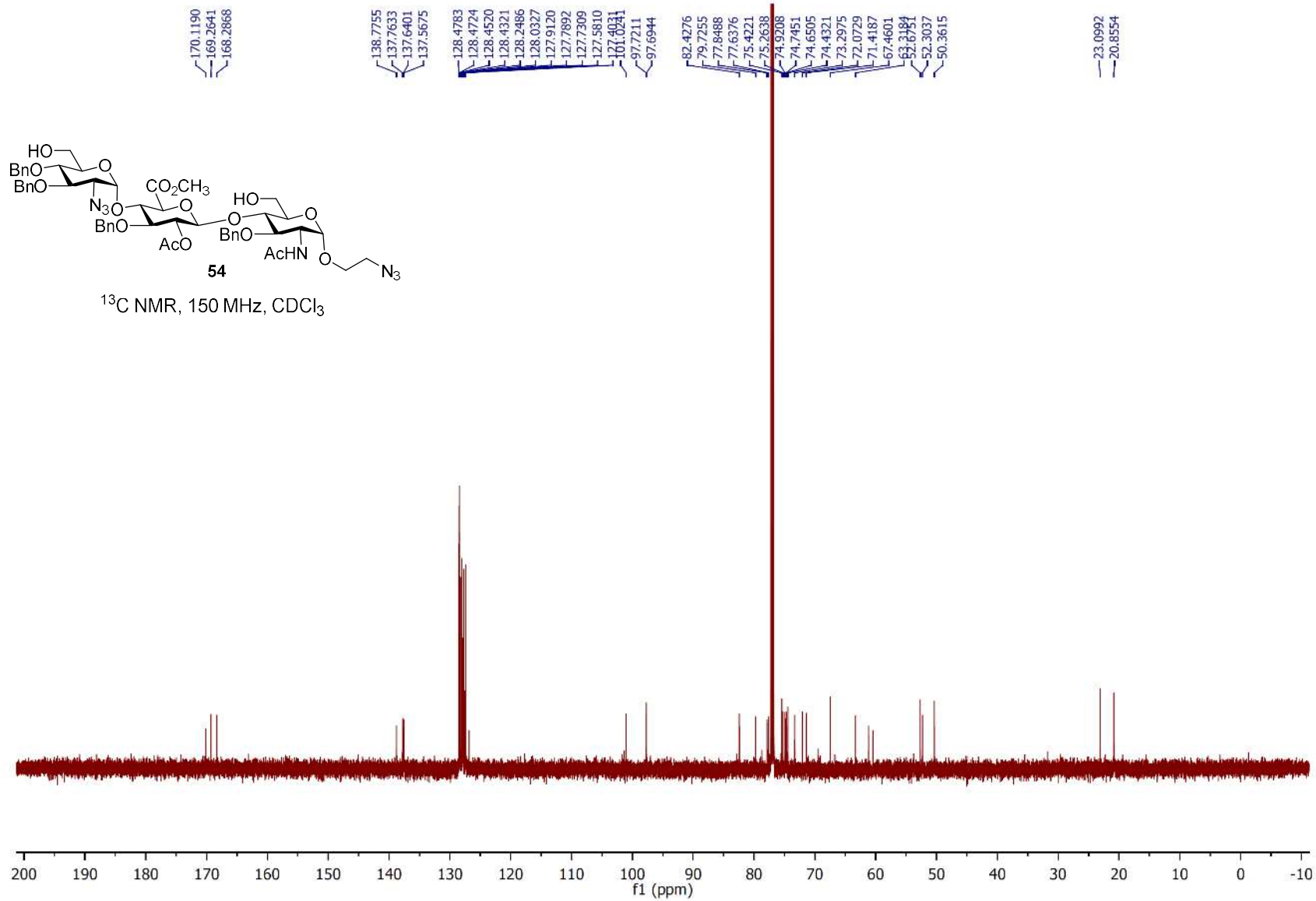


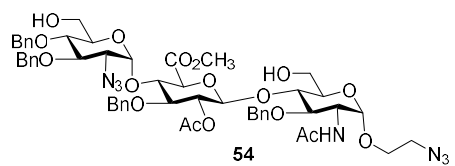


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

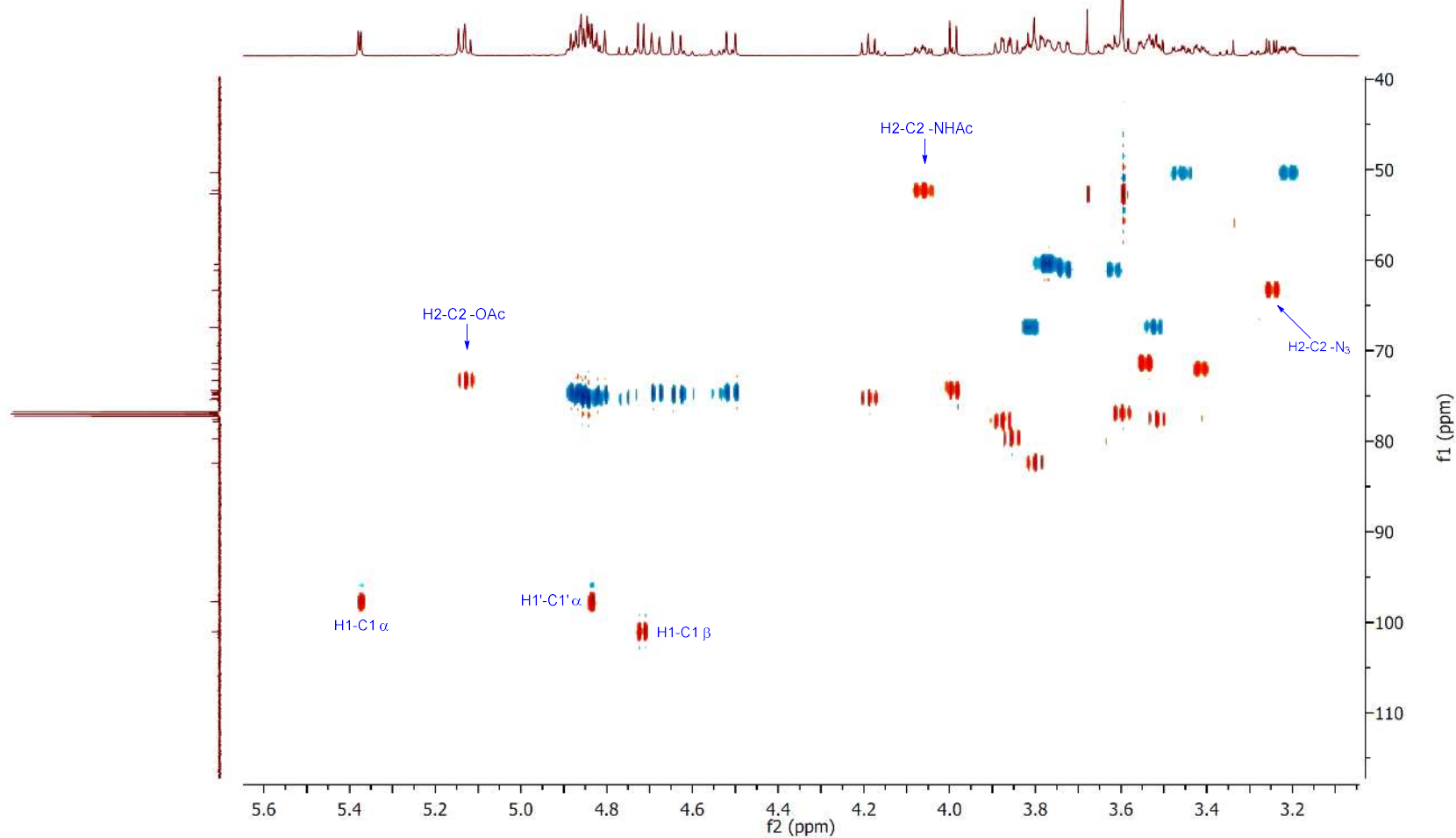


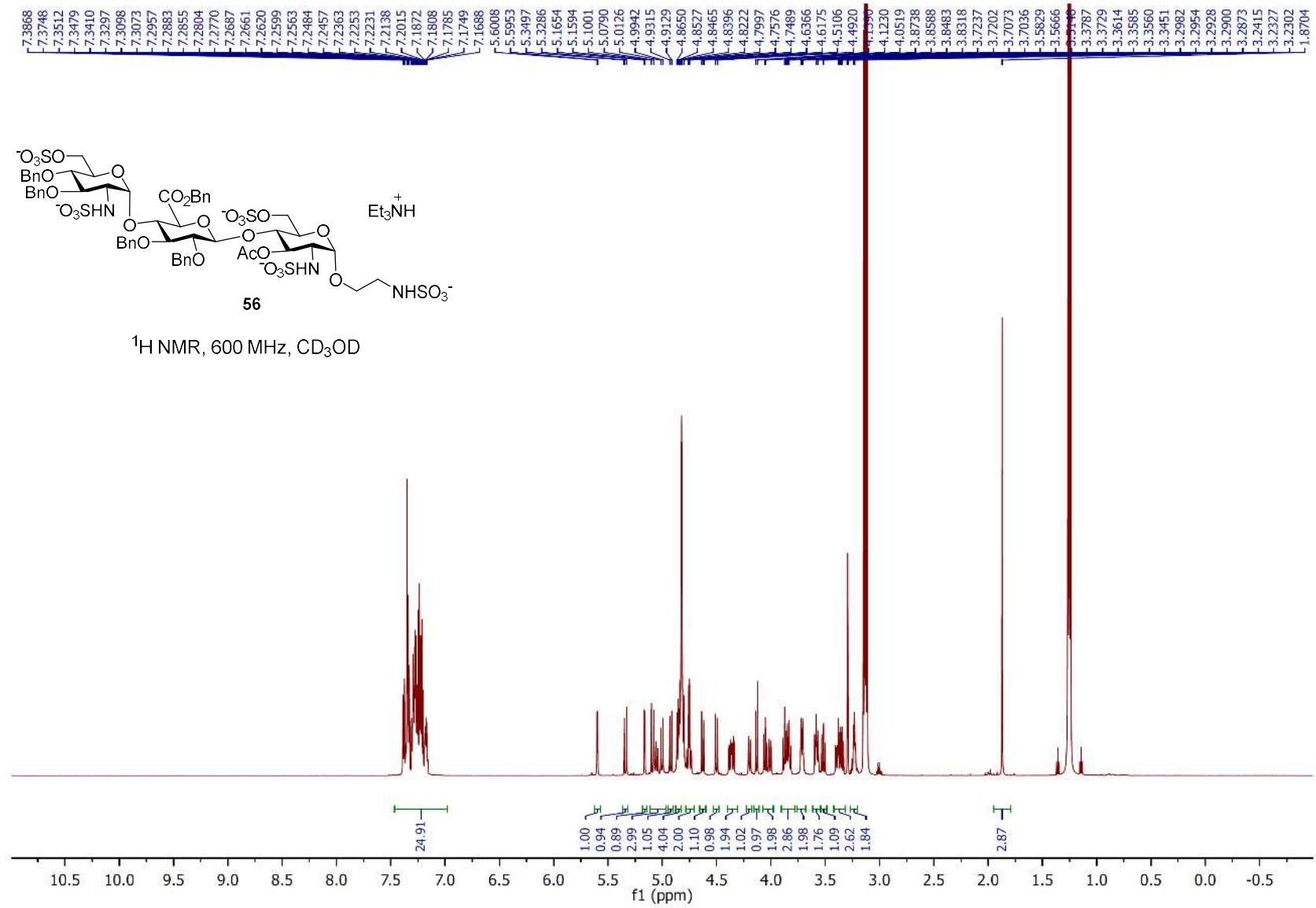


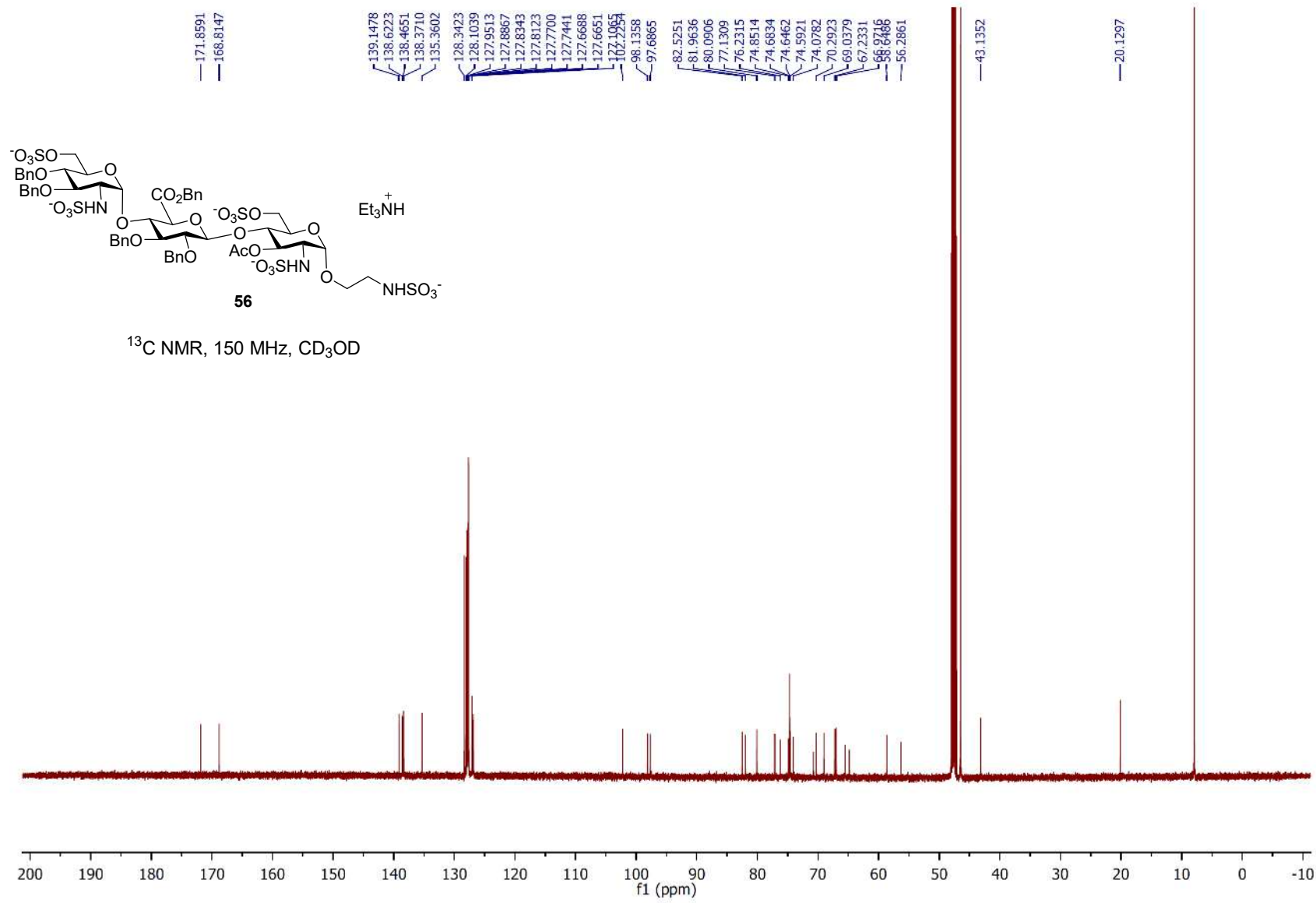


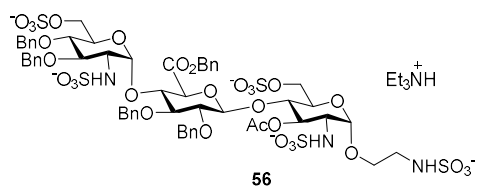


^1H - ^{13}C HSQC, 600/150MHz, CDCl_3

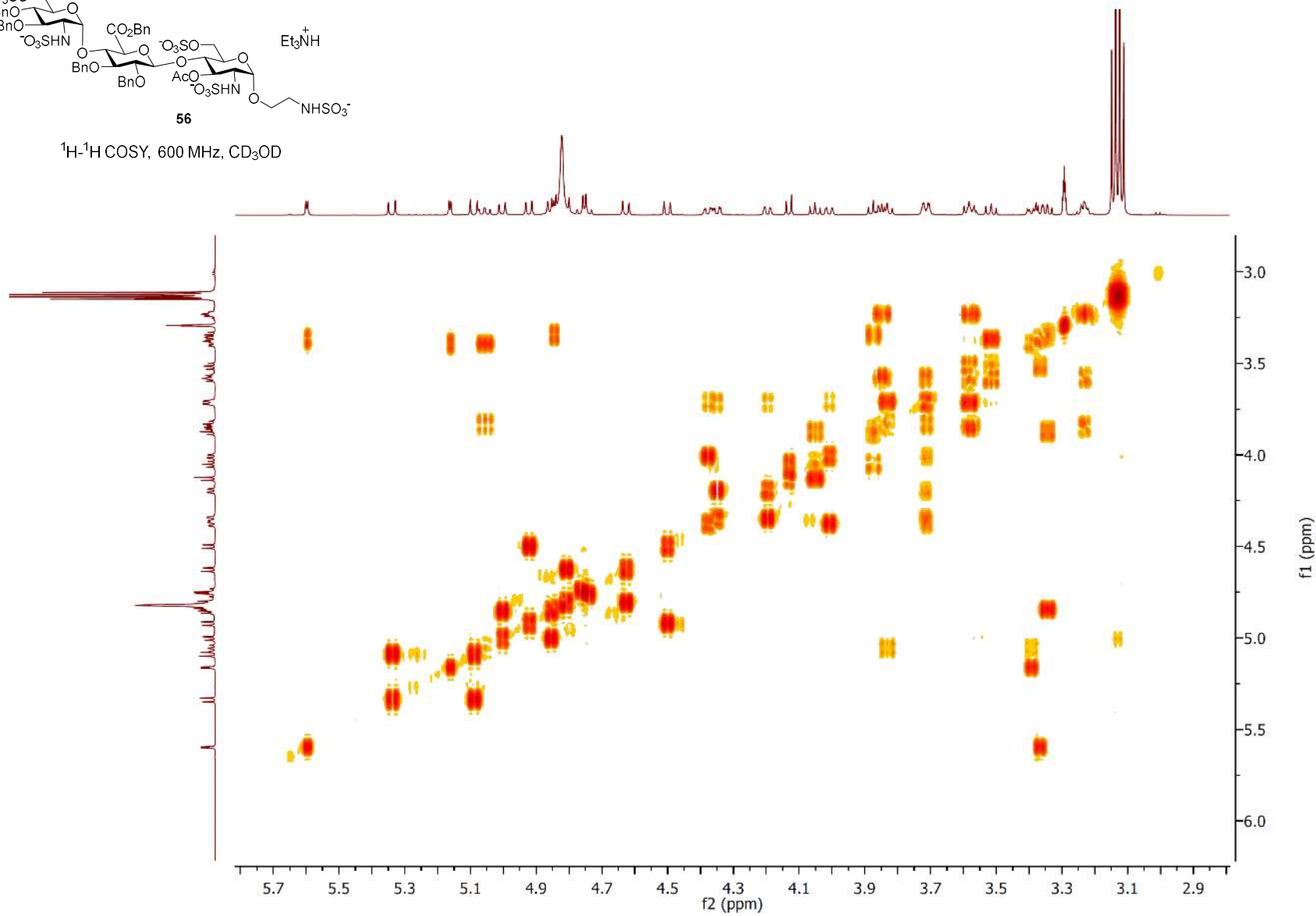


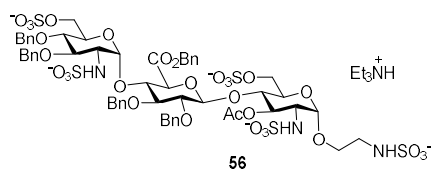




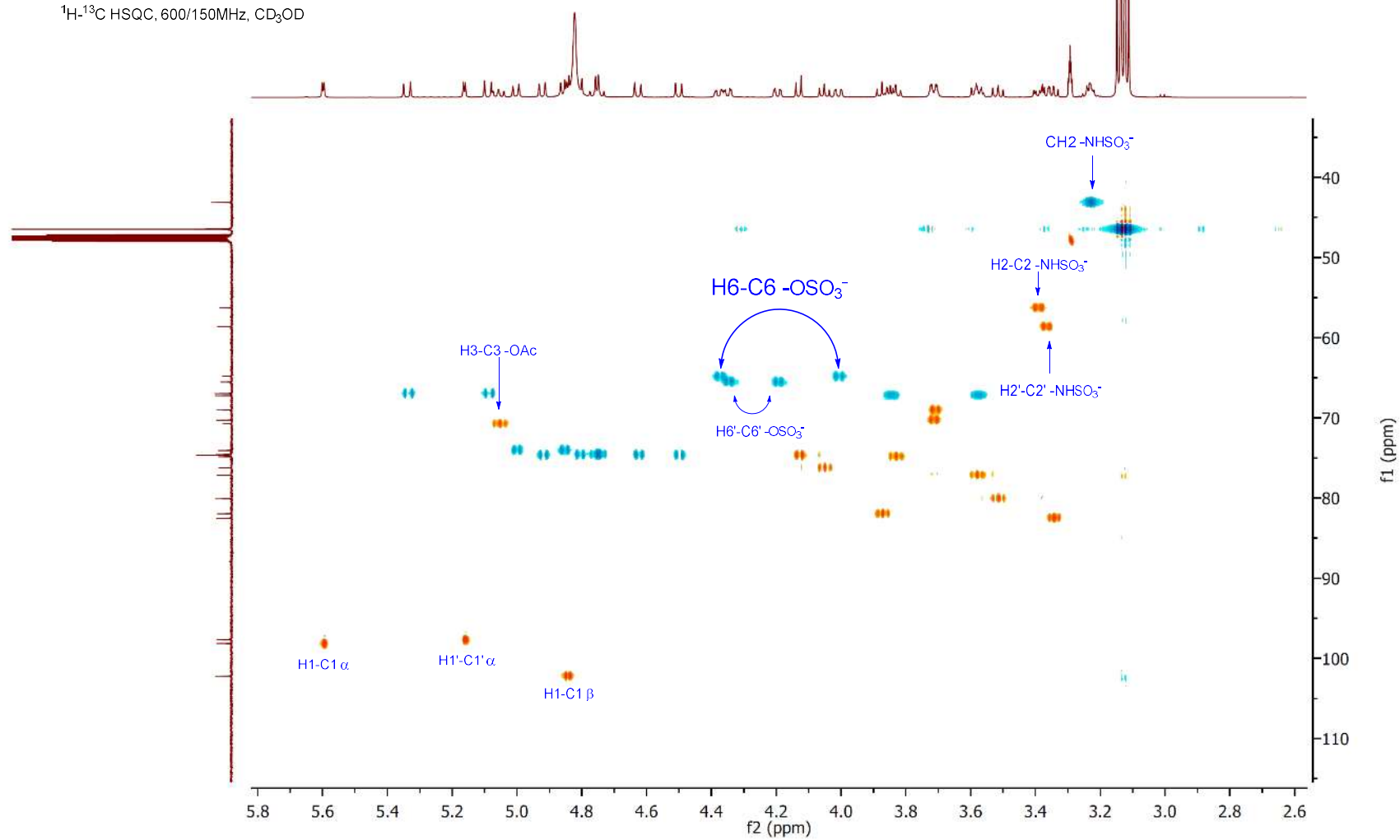


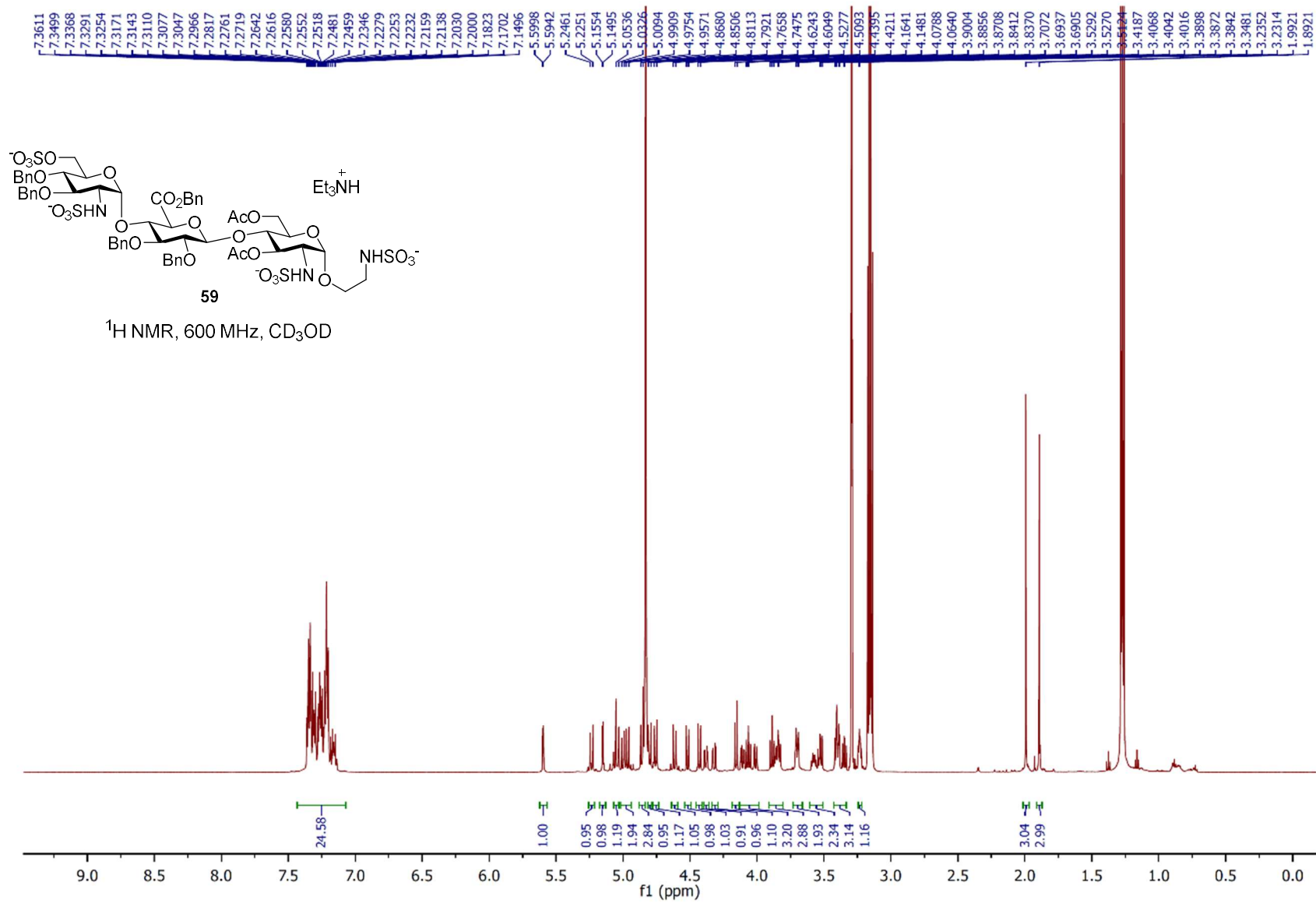
^1H - ^1H COSY, 600 MHz, CD_3OD

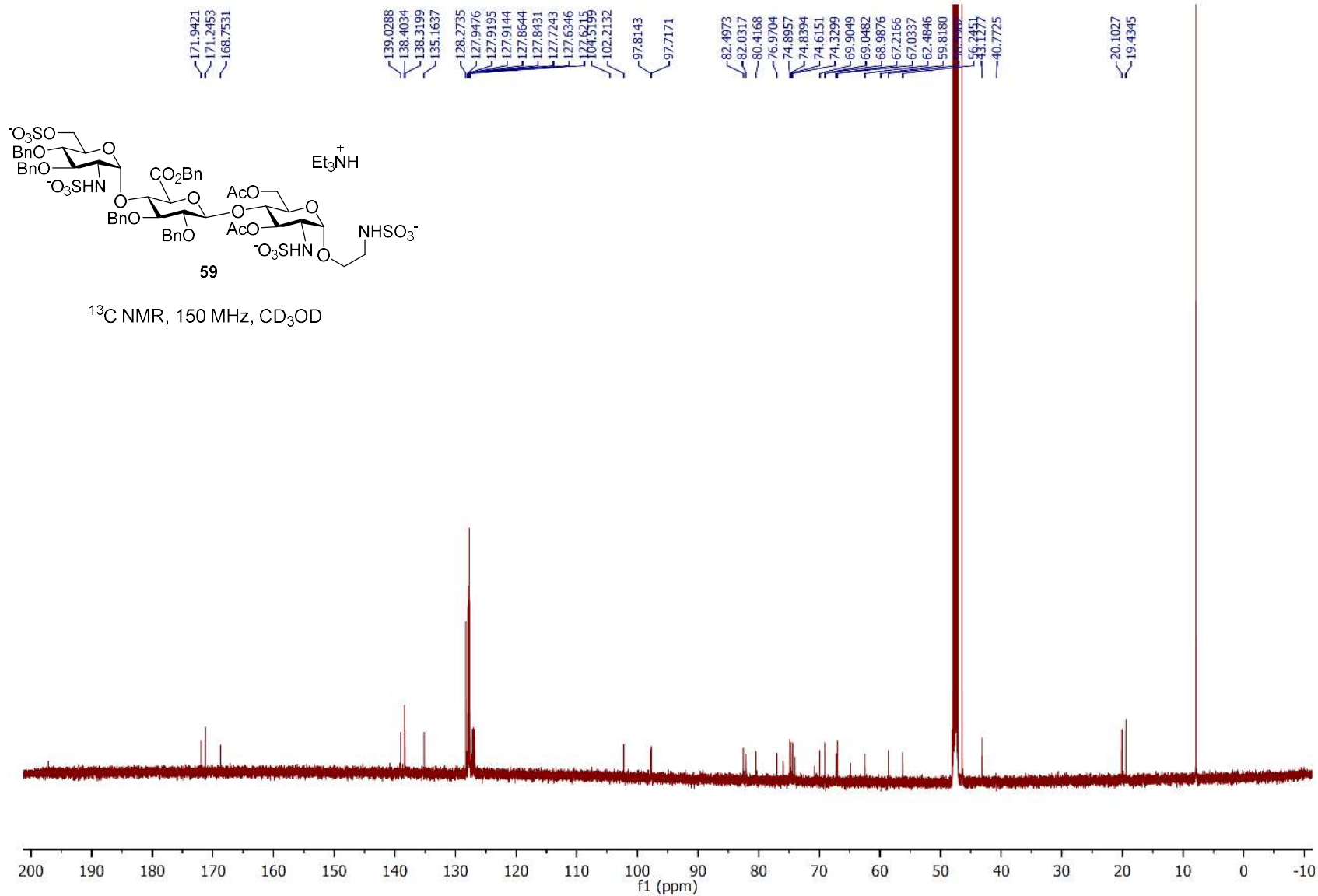


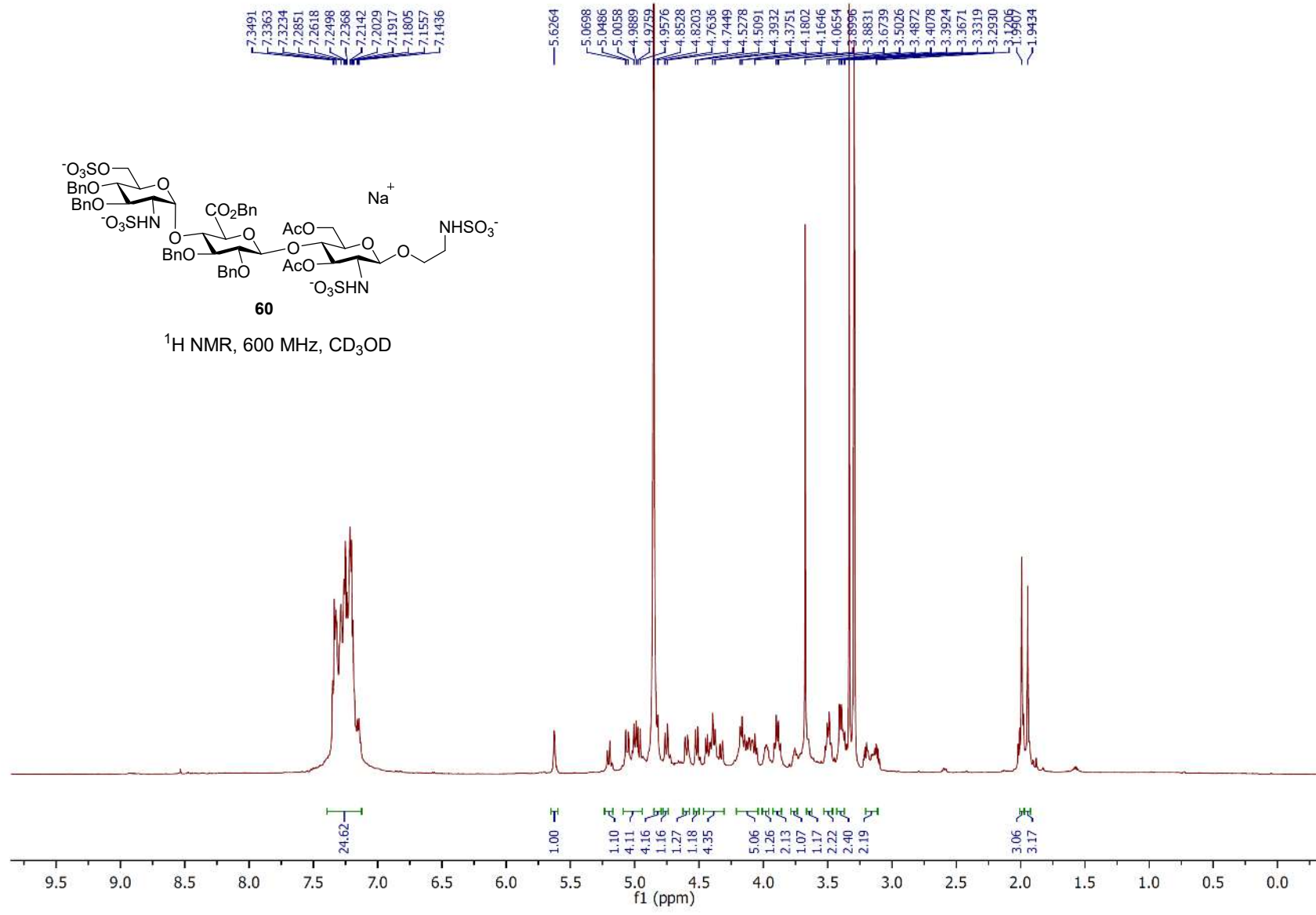


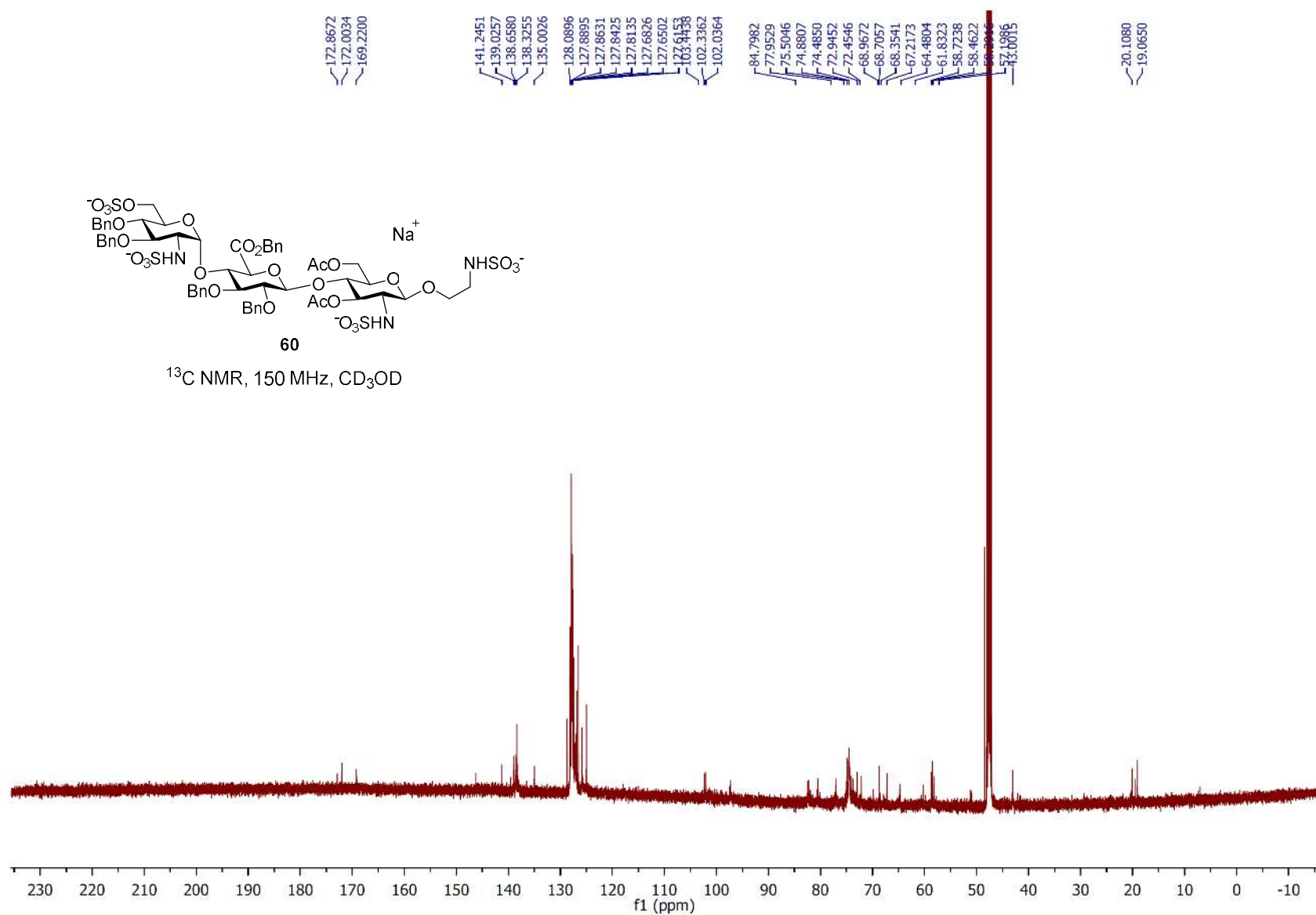
^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

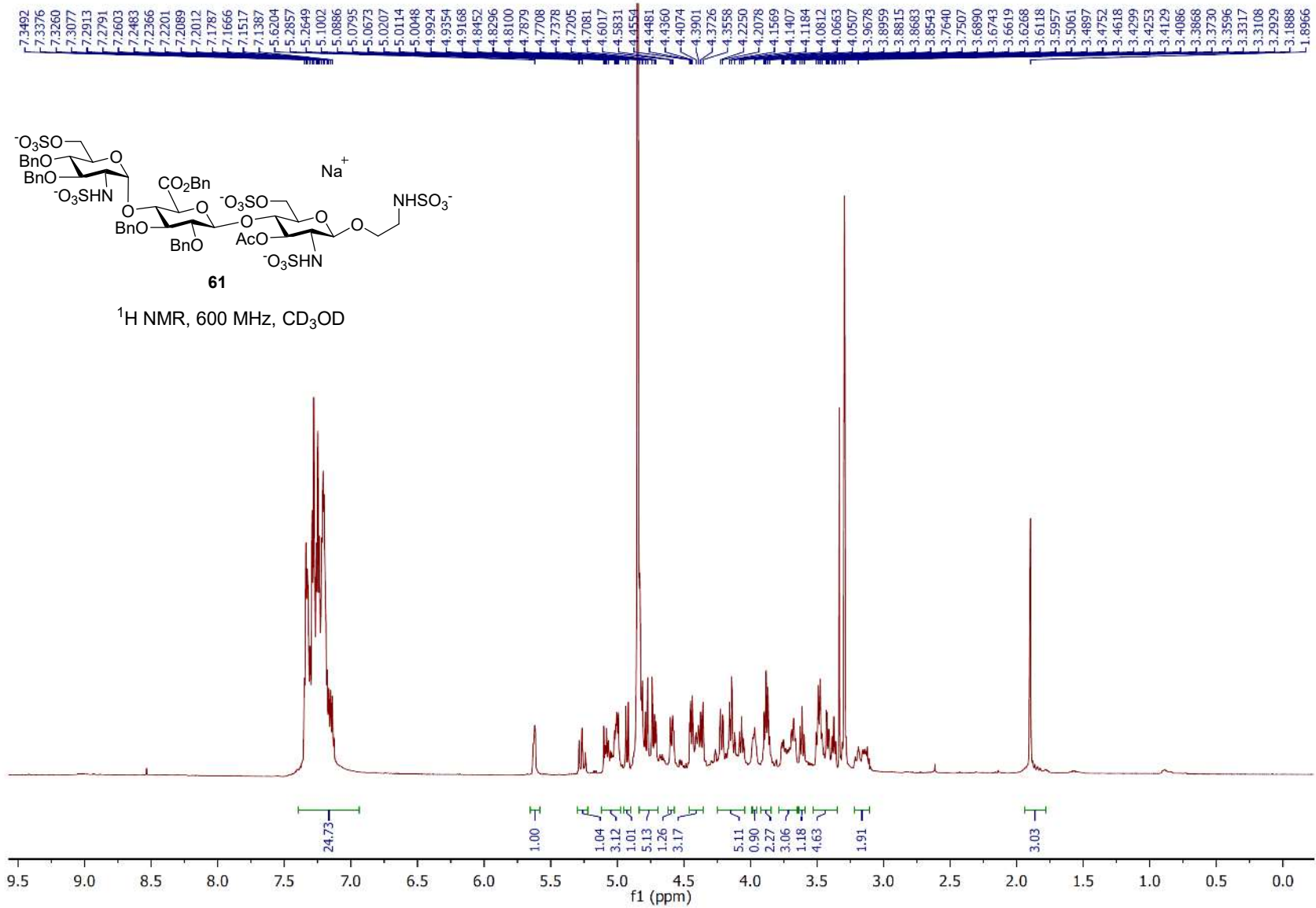


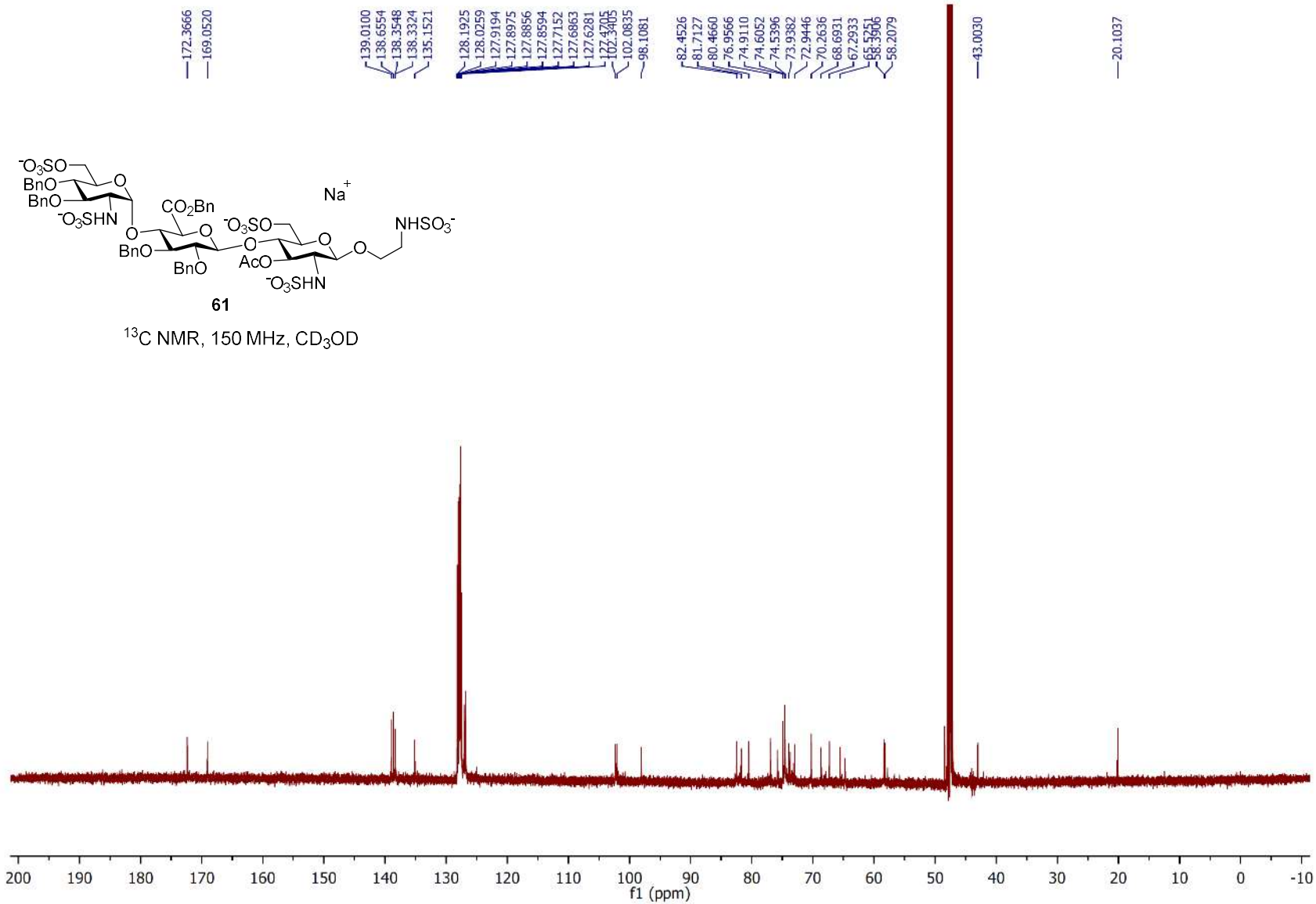


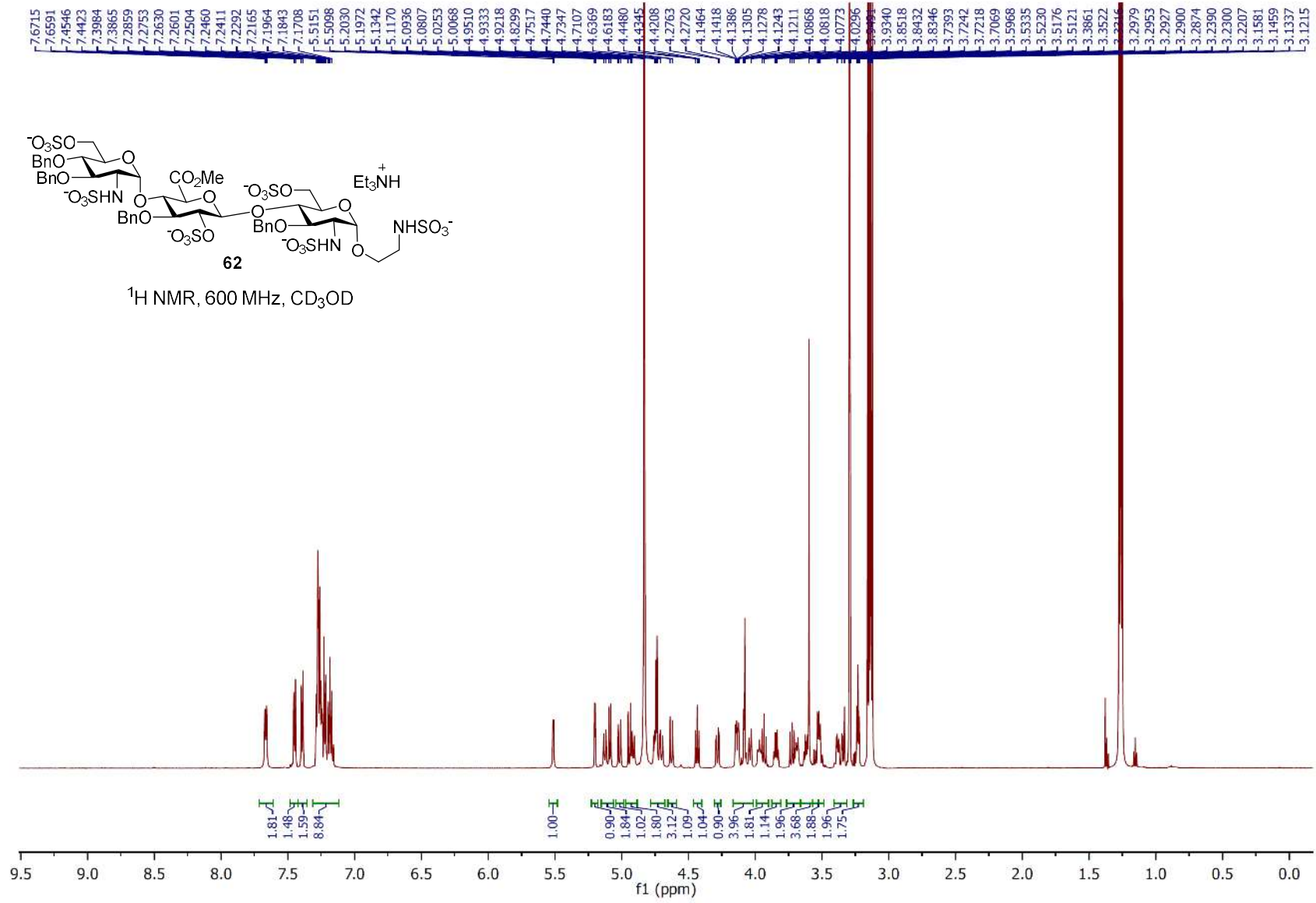


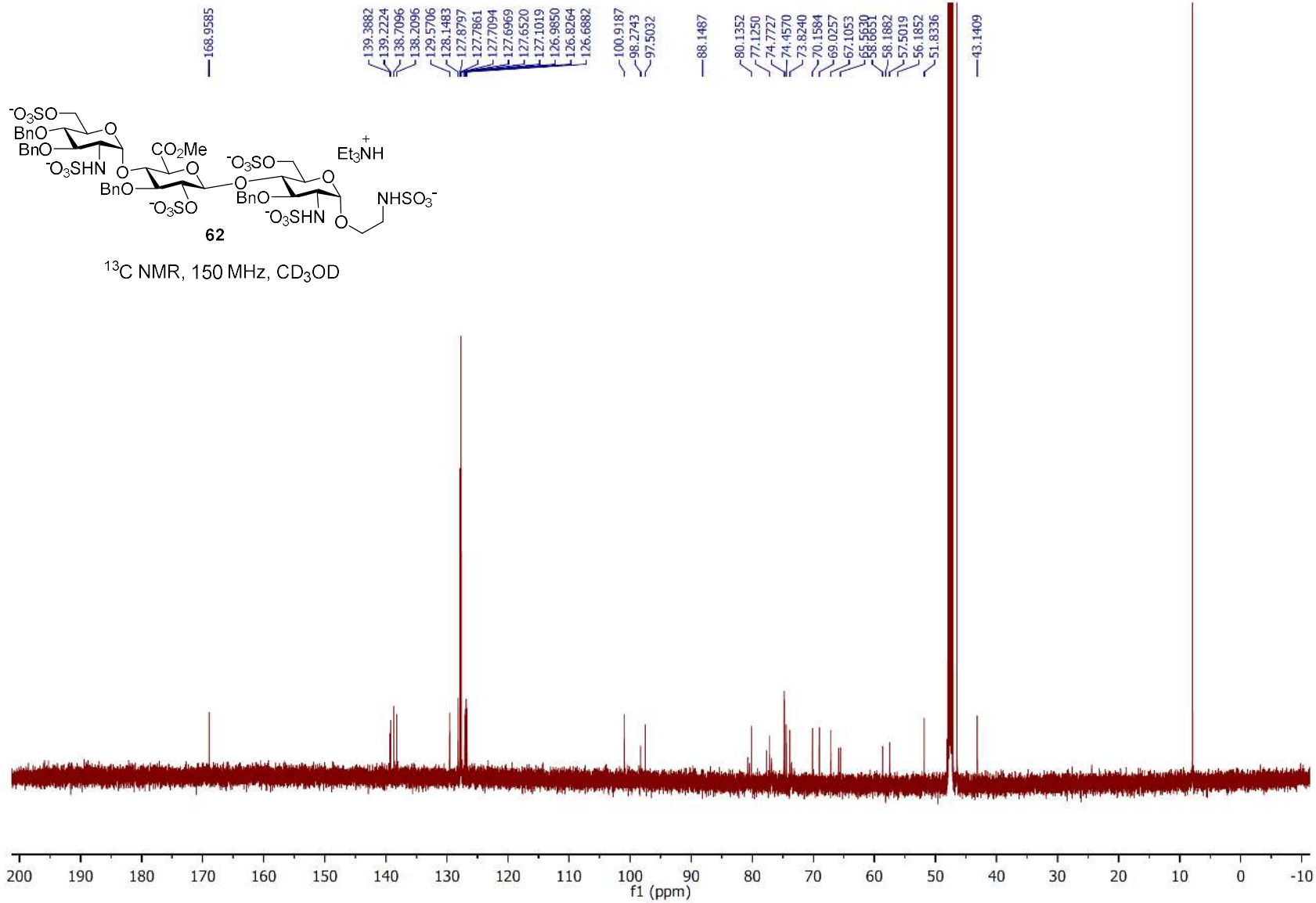


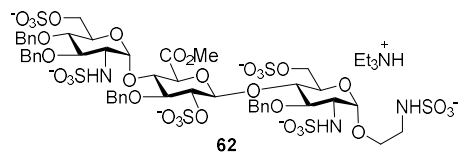




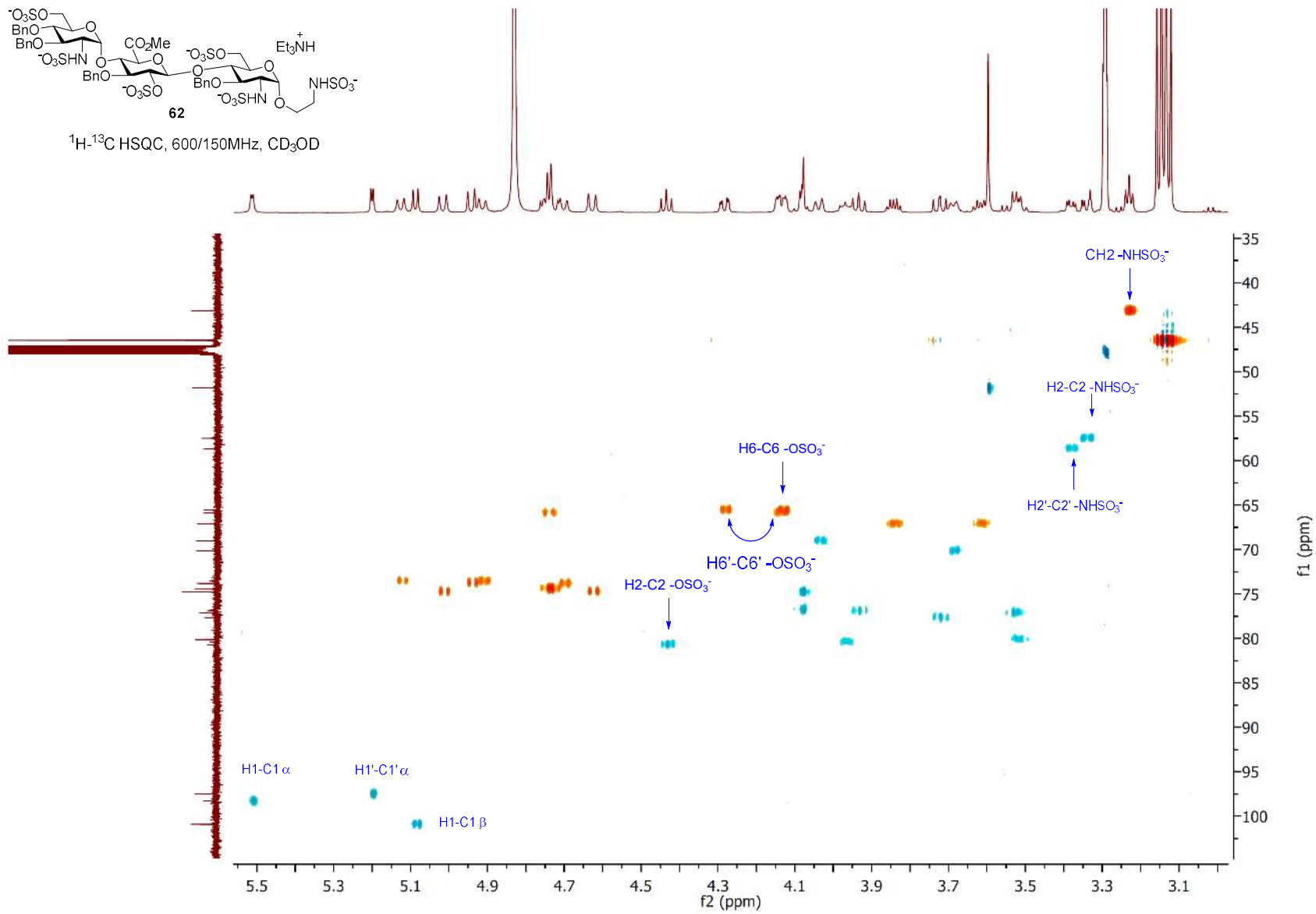


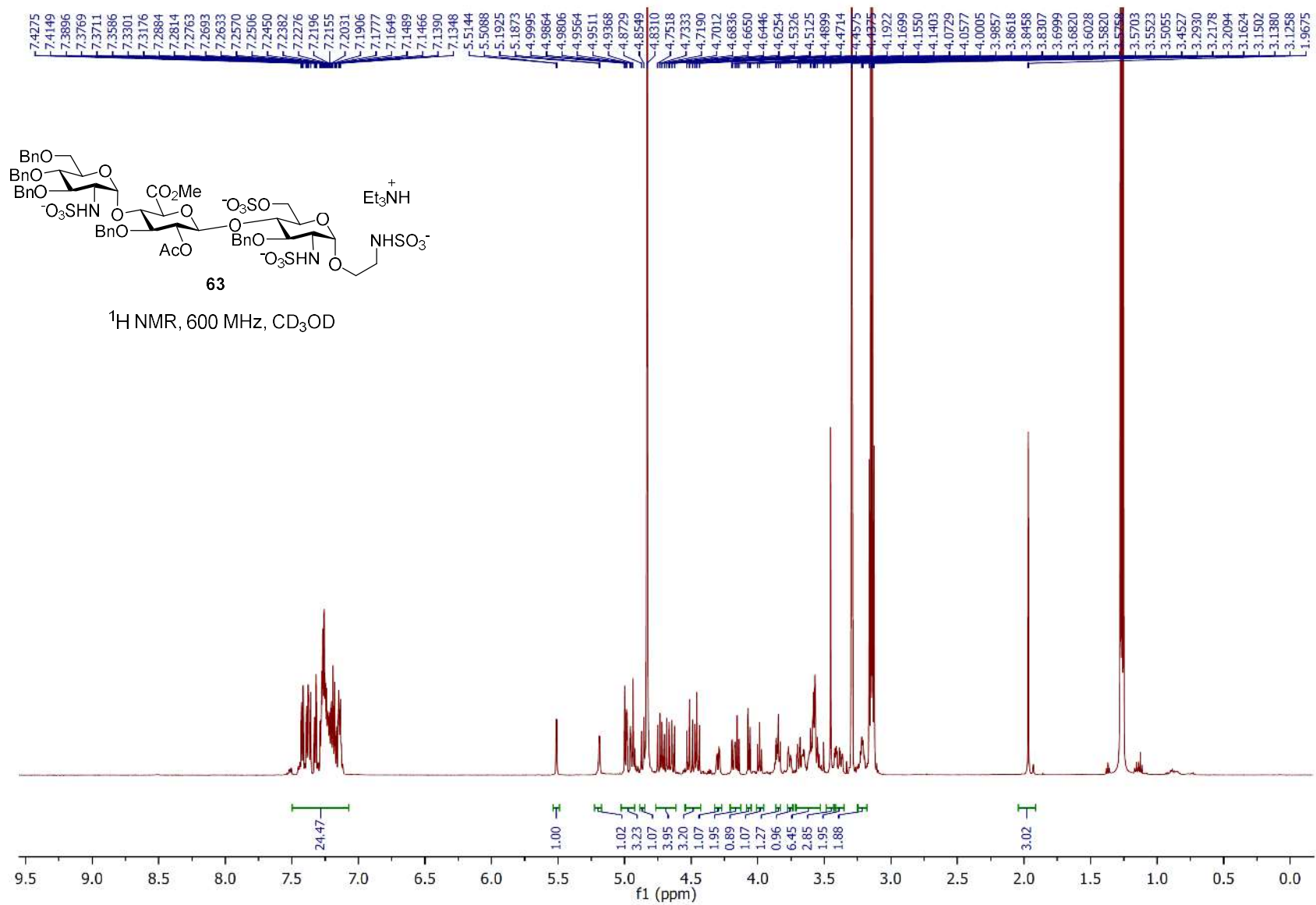


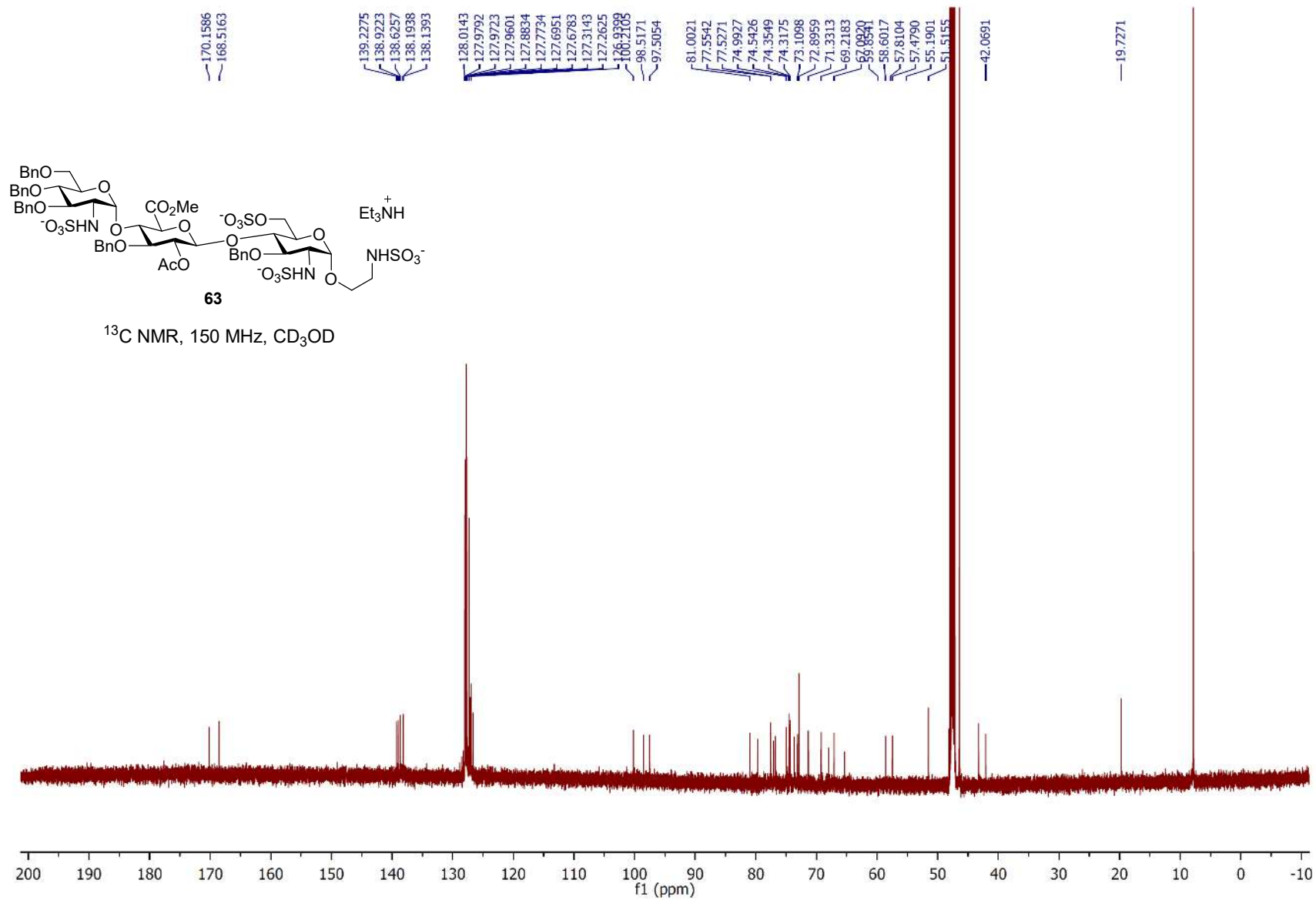


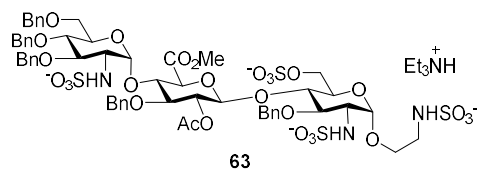


^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

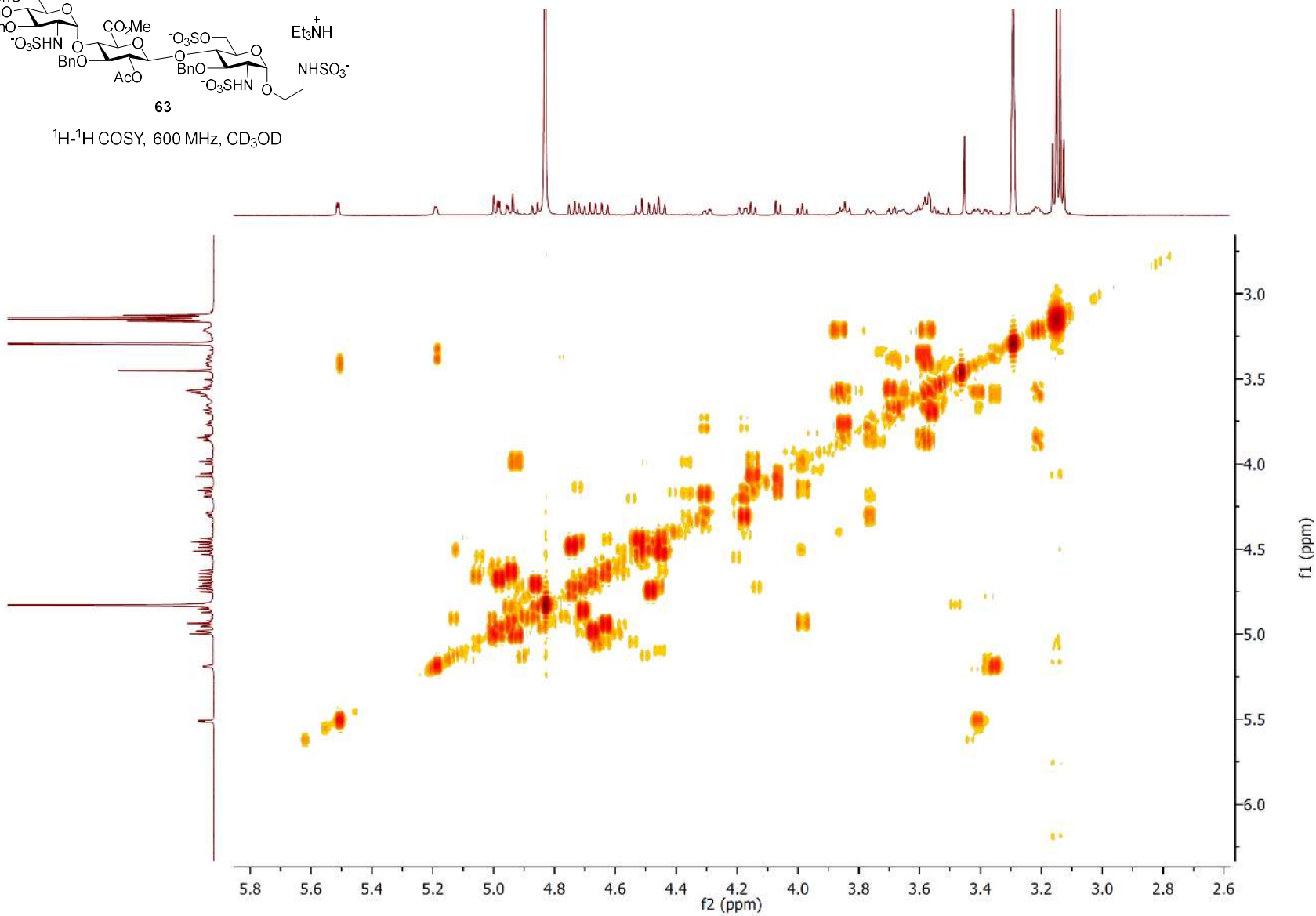


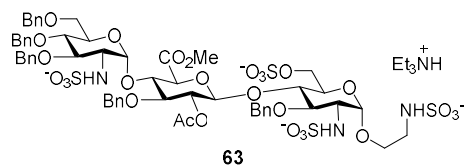




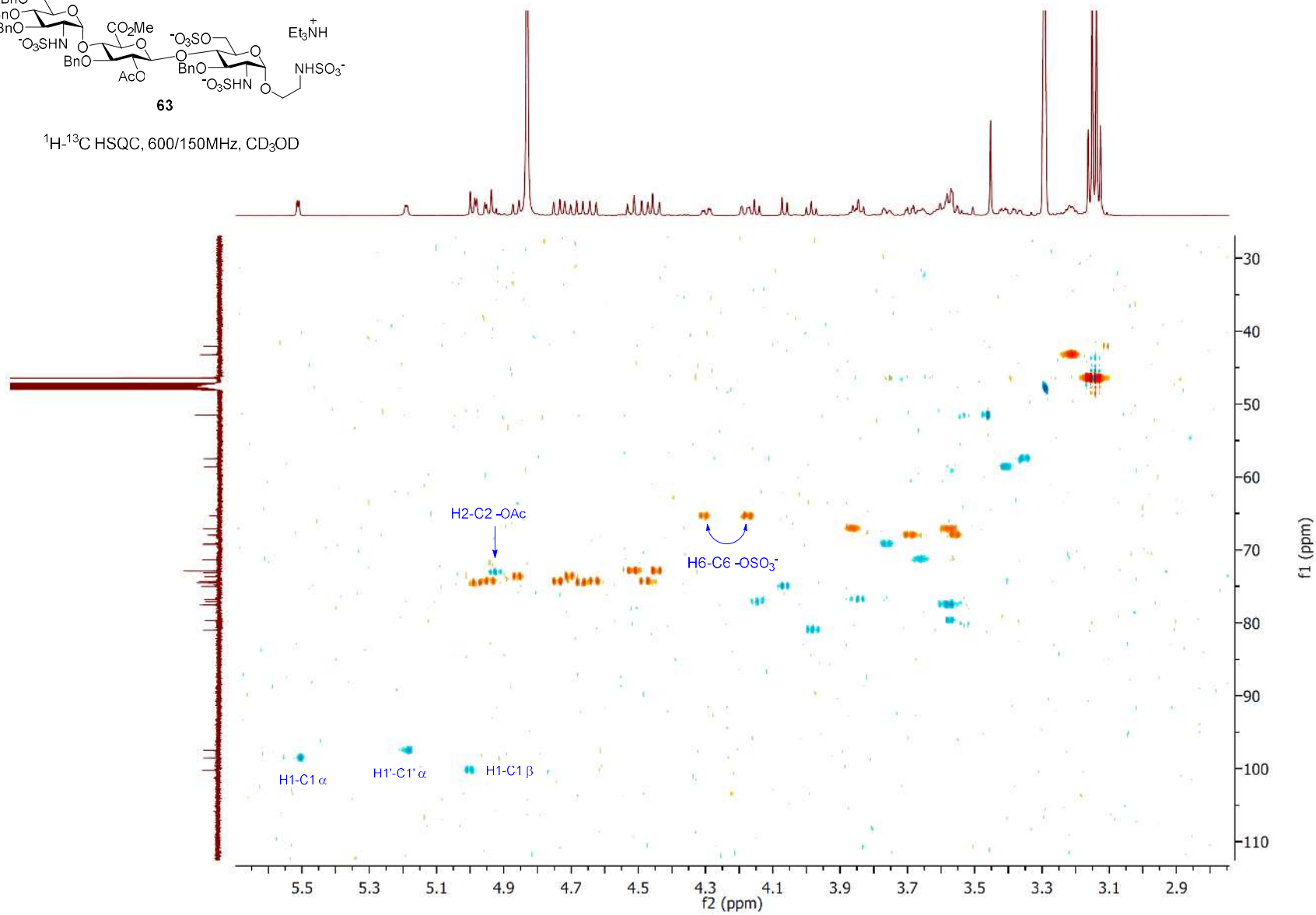


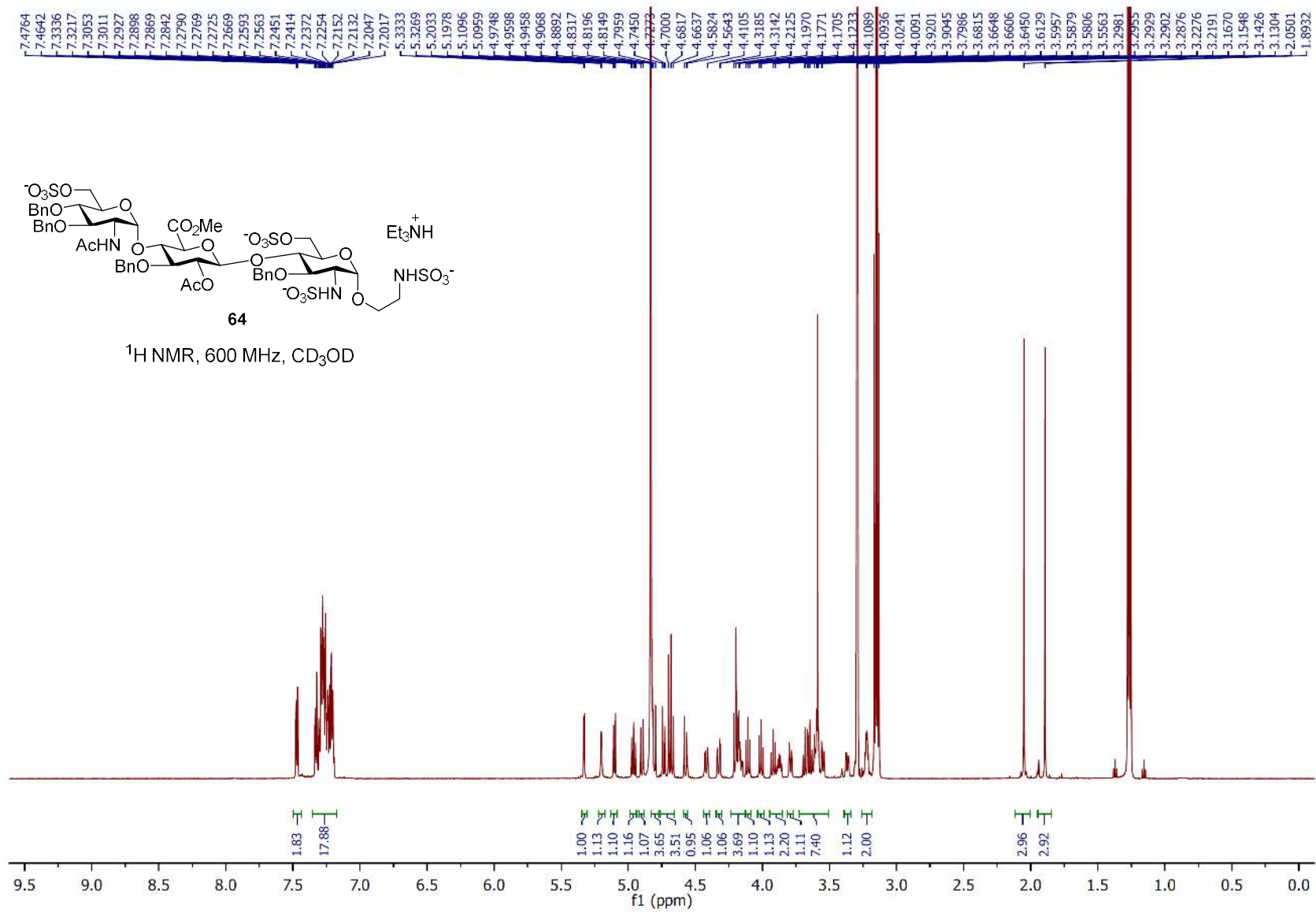
^1H - ^1H COSY, 600 MHz, CD_3OD

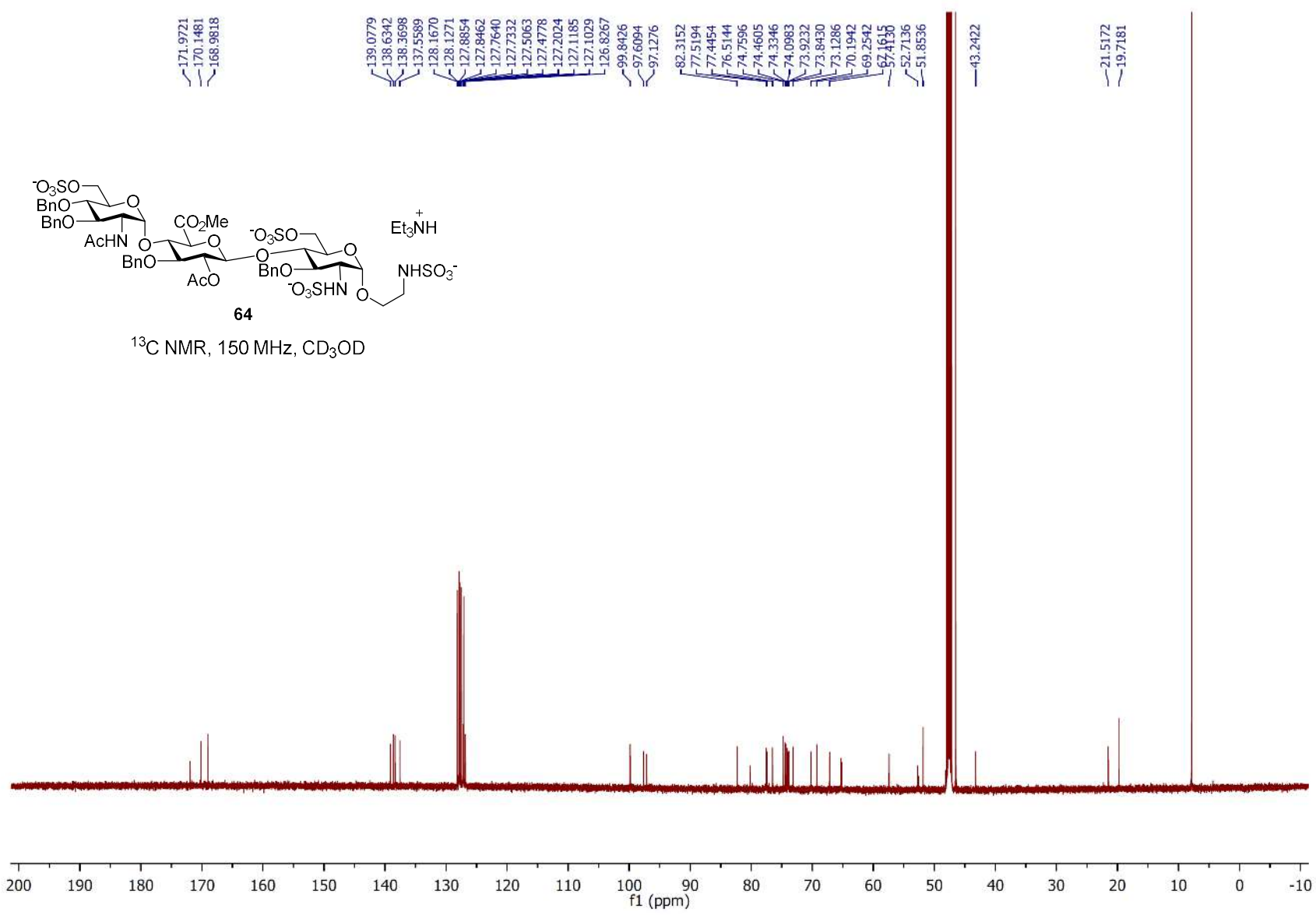


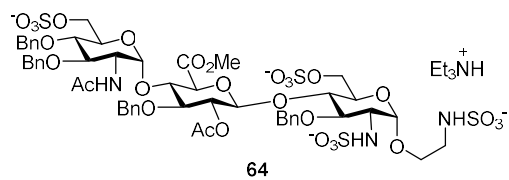


^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

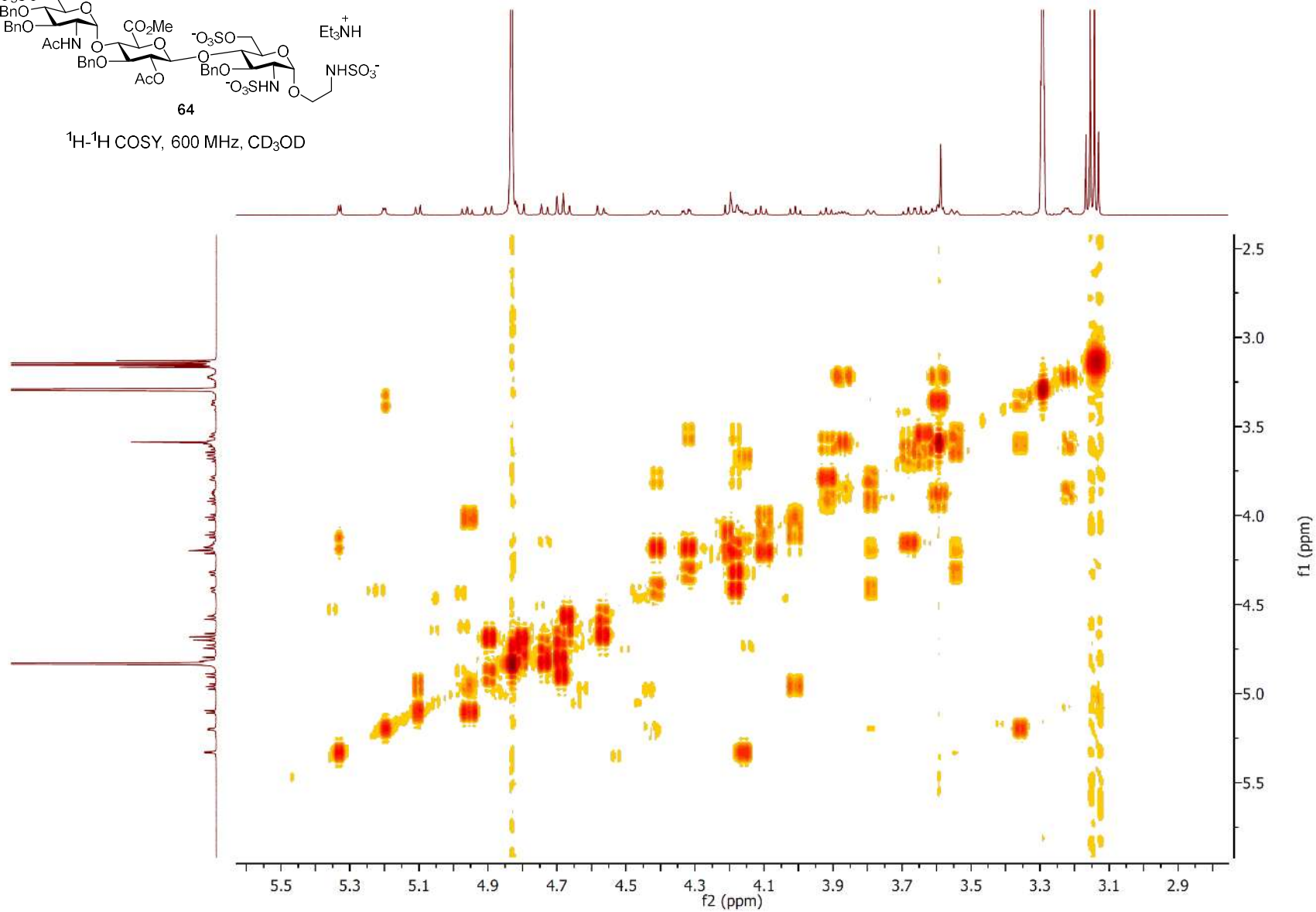


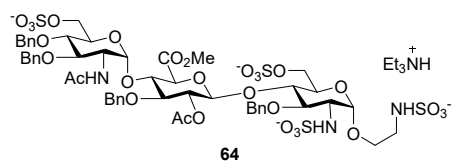




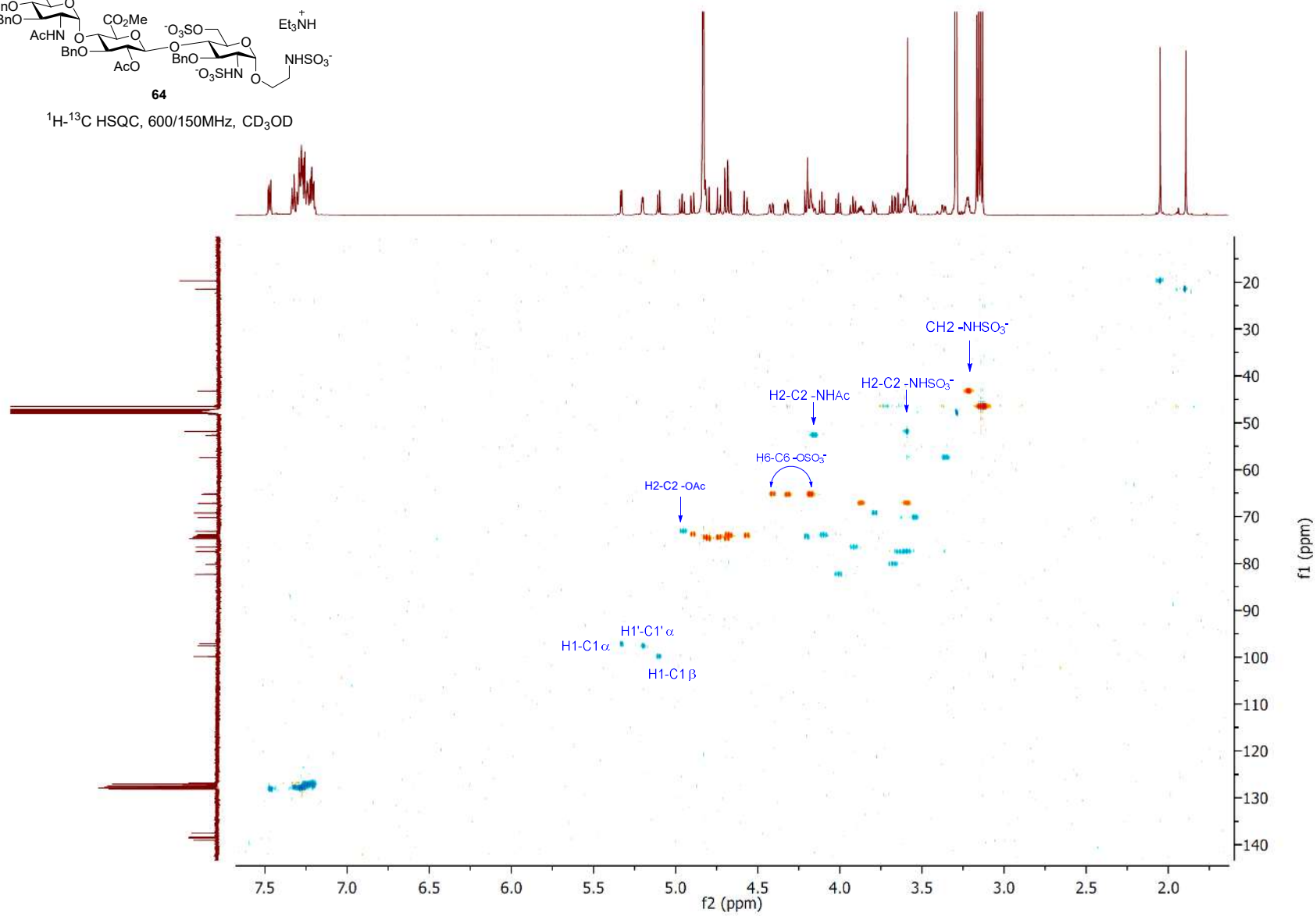


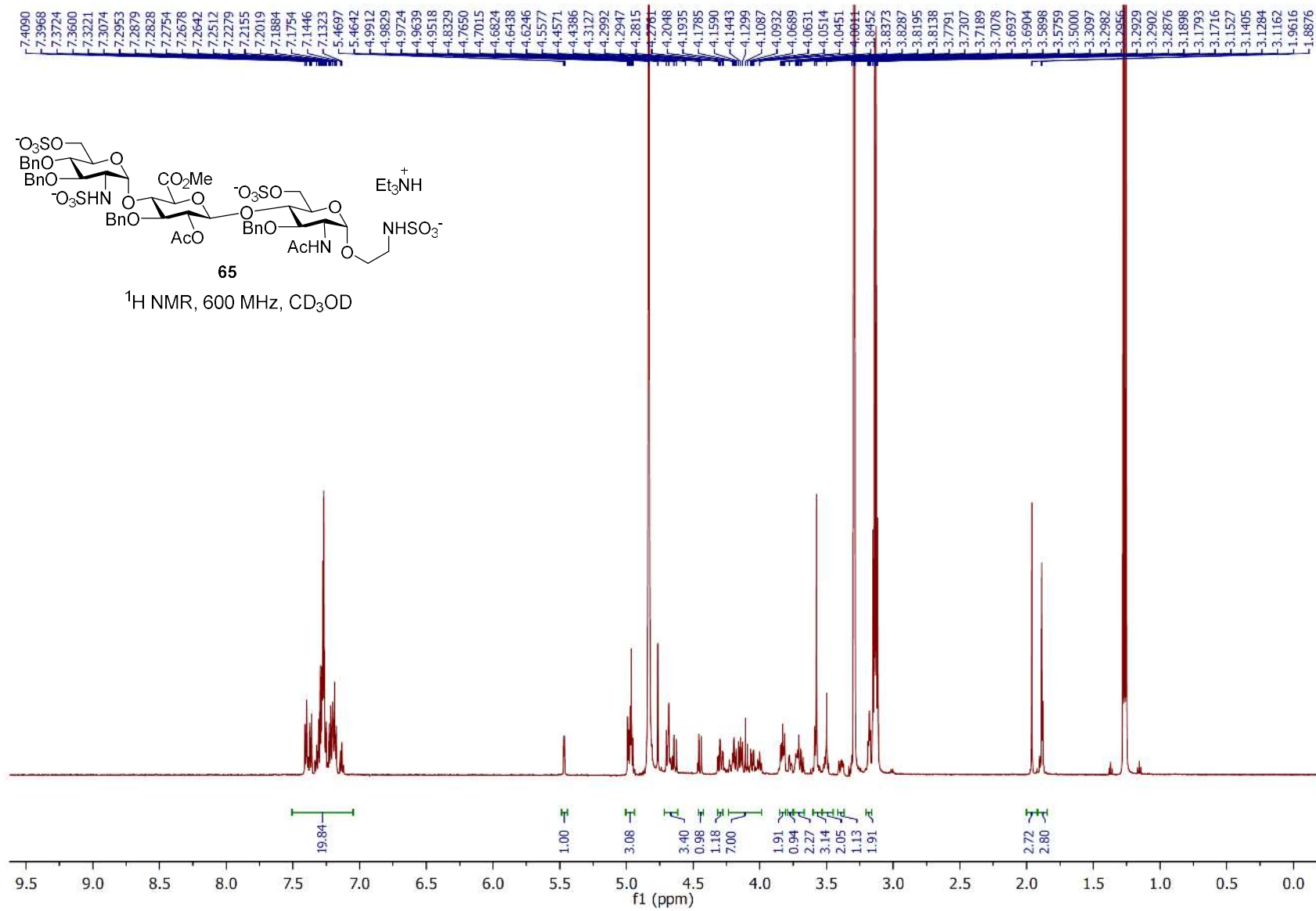
^1H - ^1H COSY, 600 MHz, CD_3OD

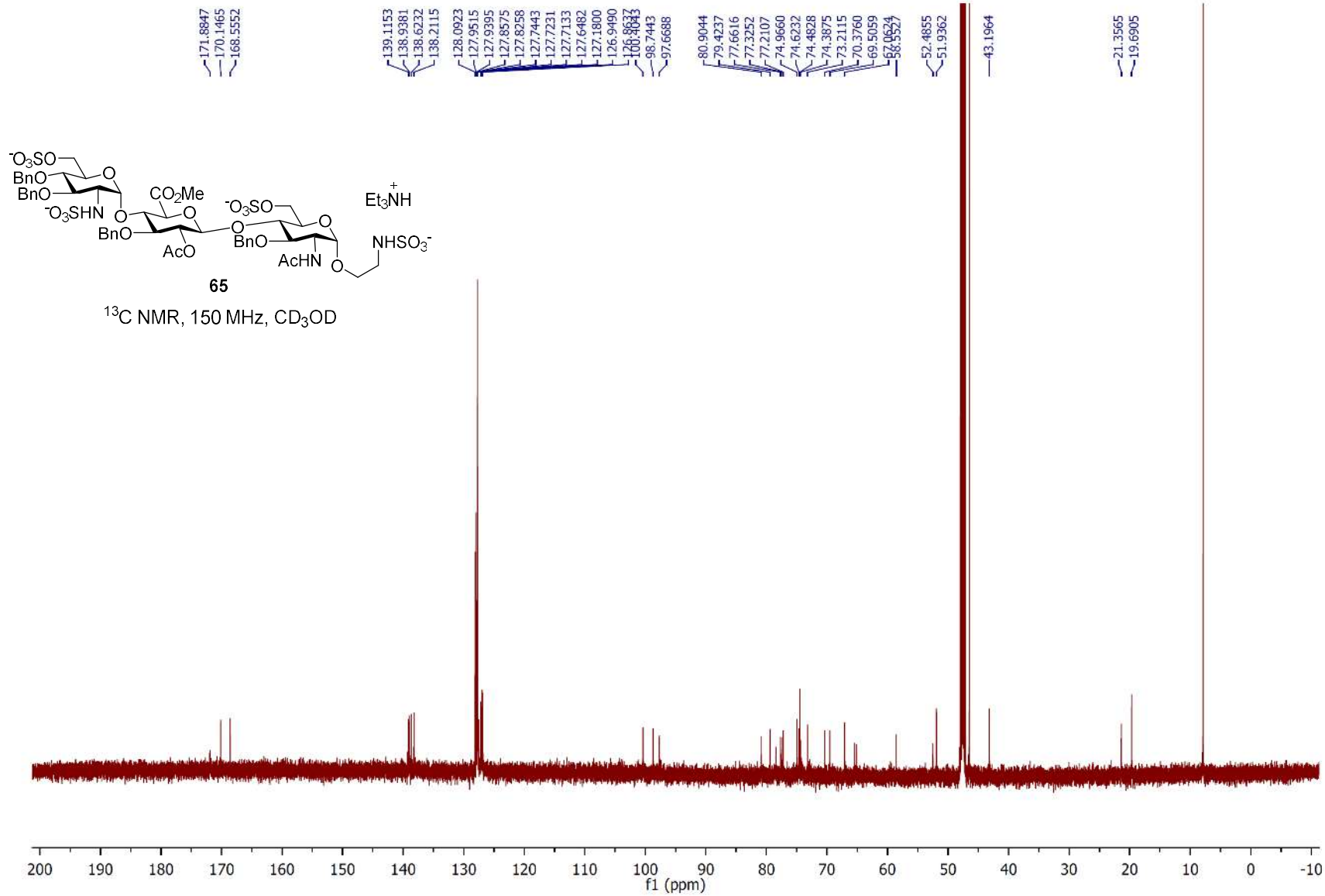


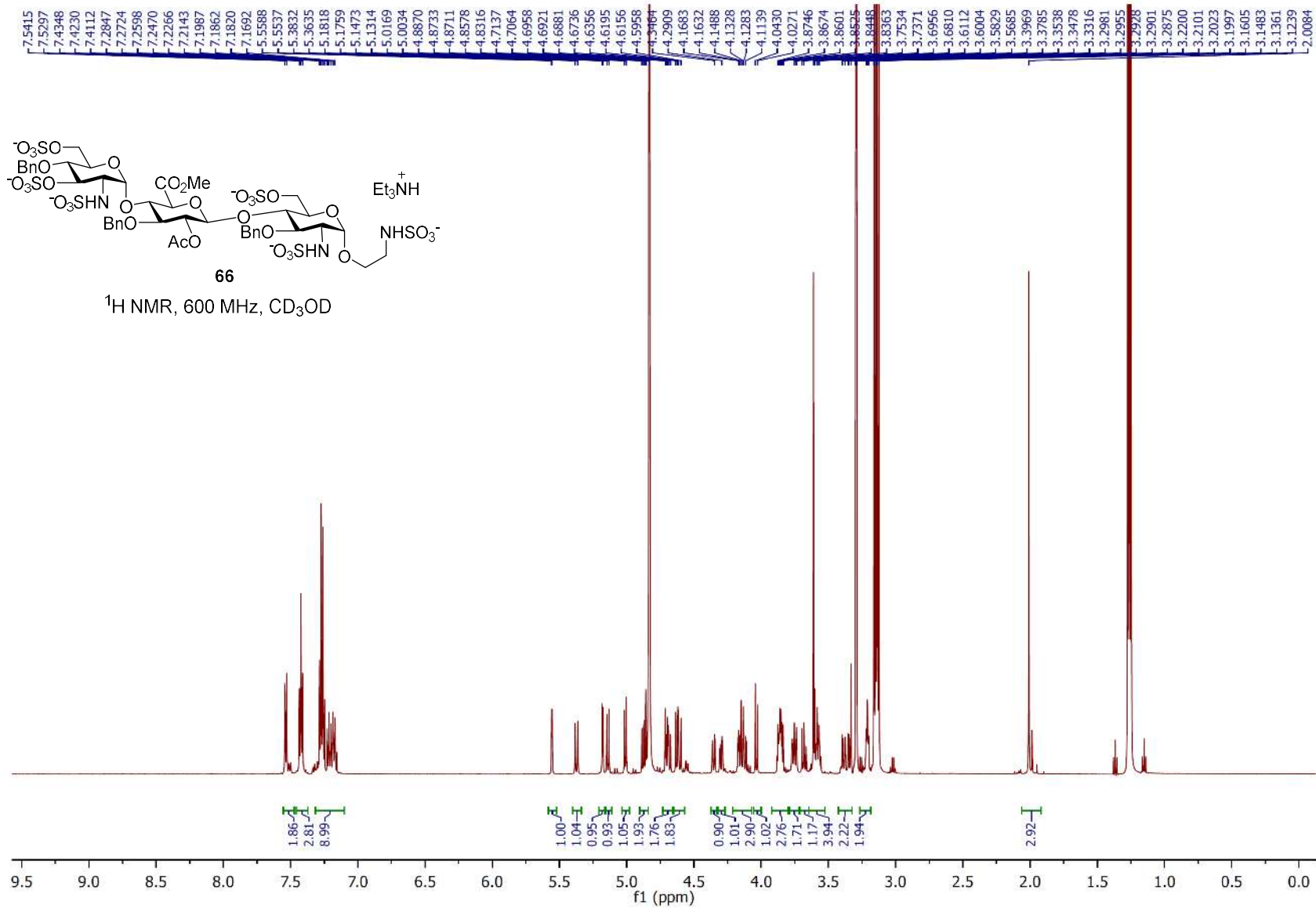


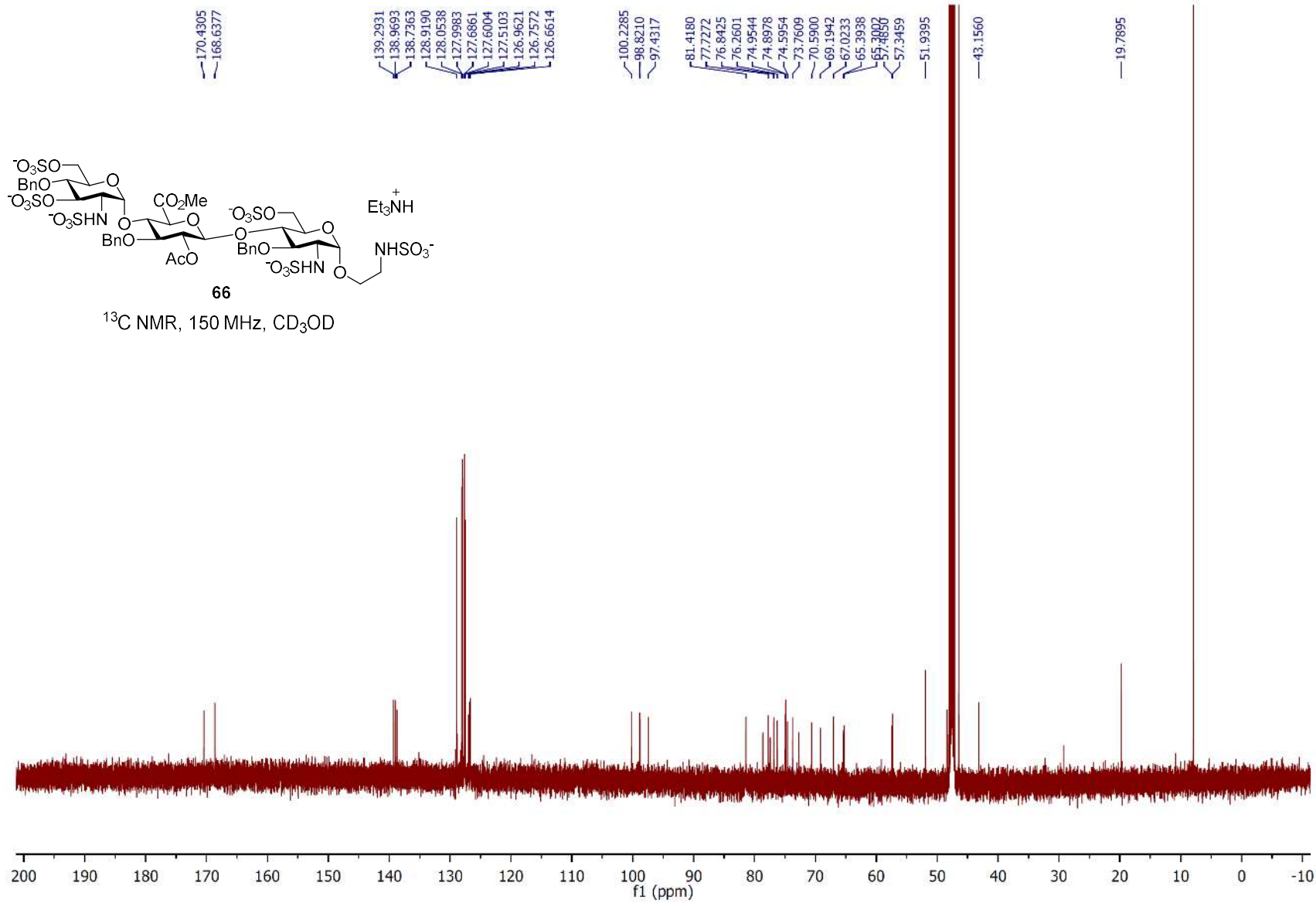
^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

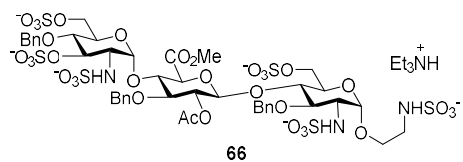




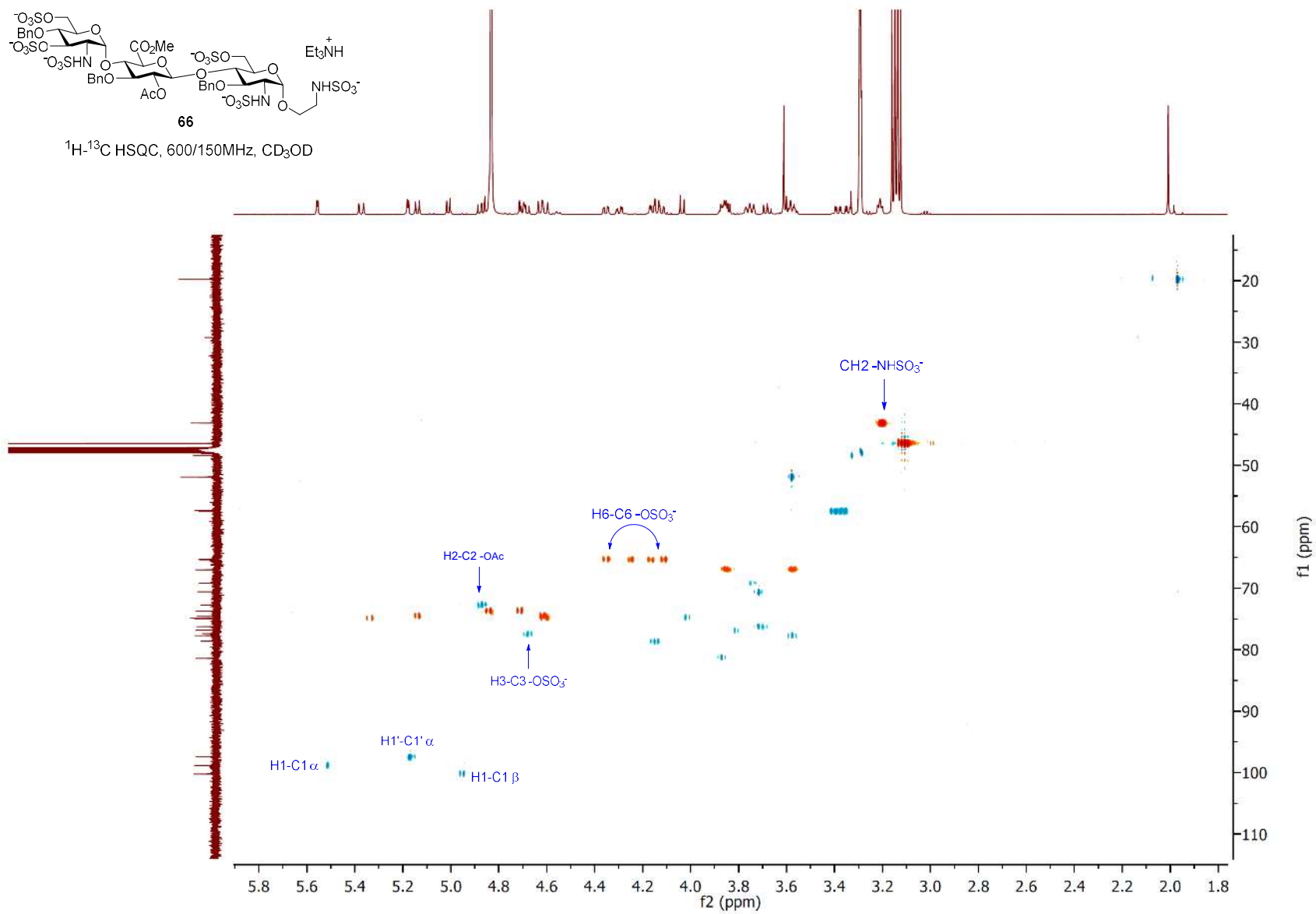


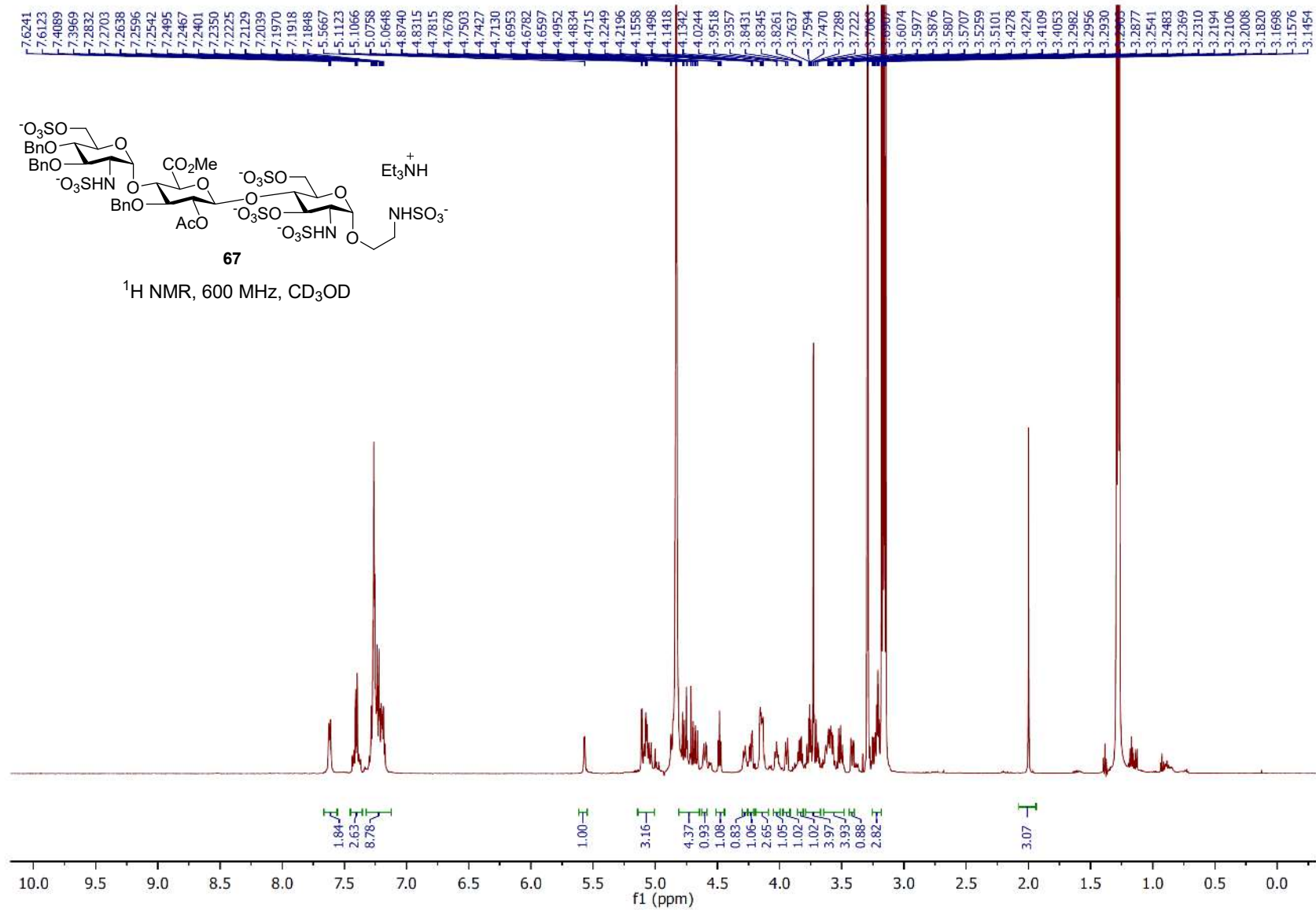


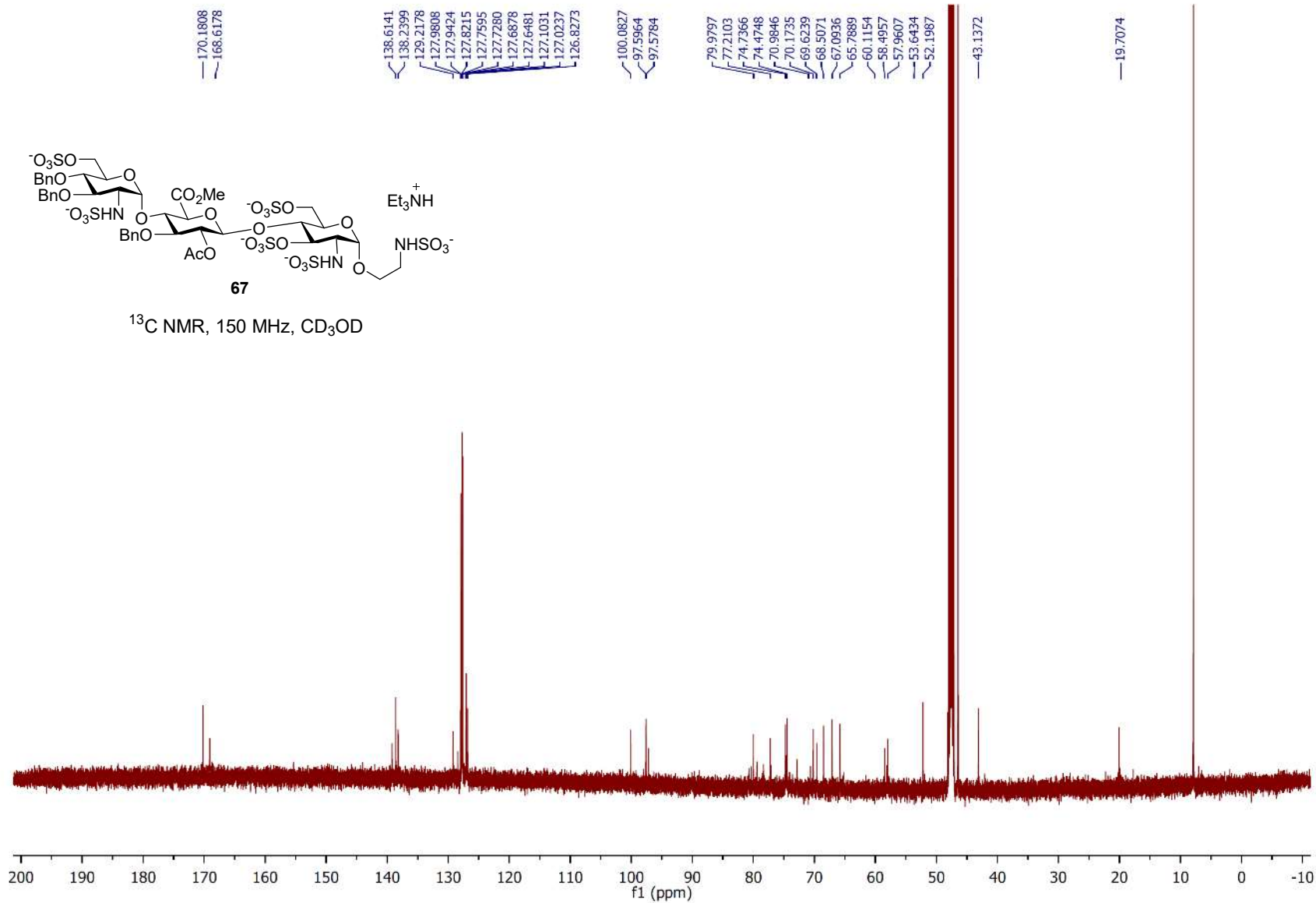


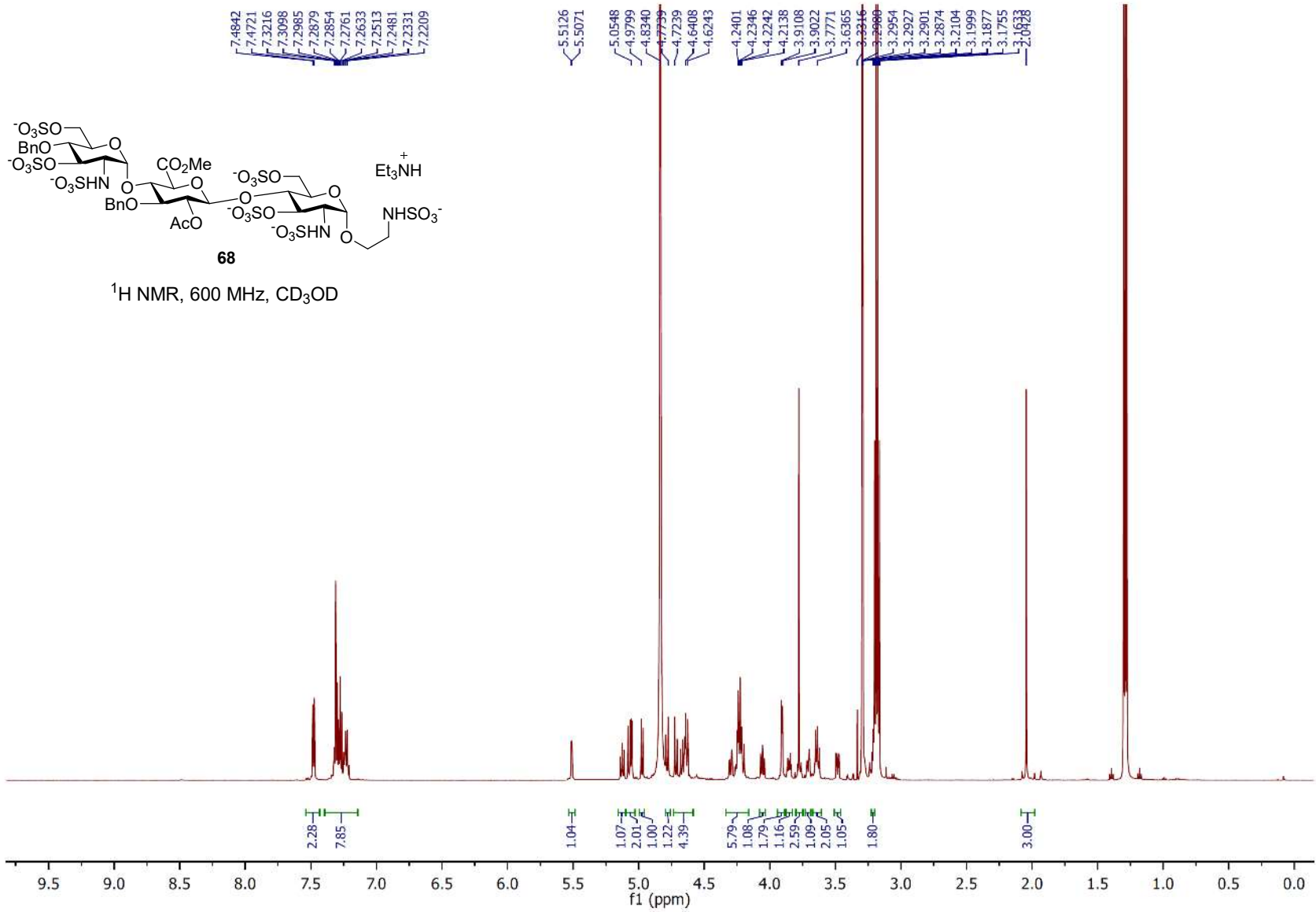


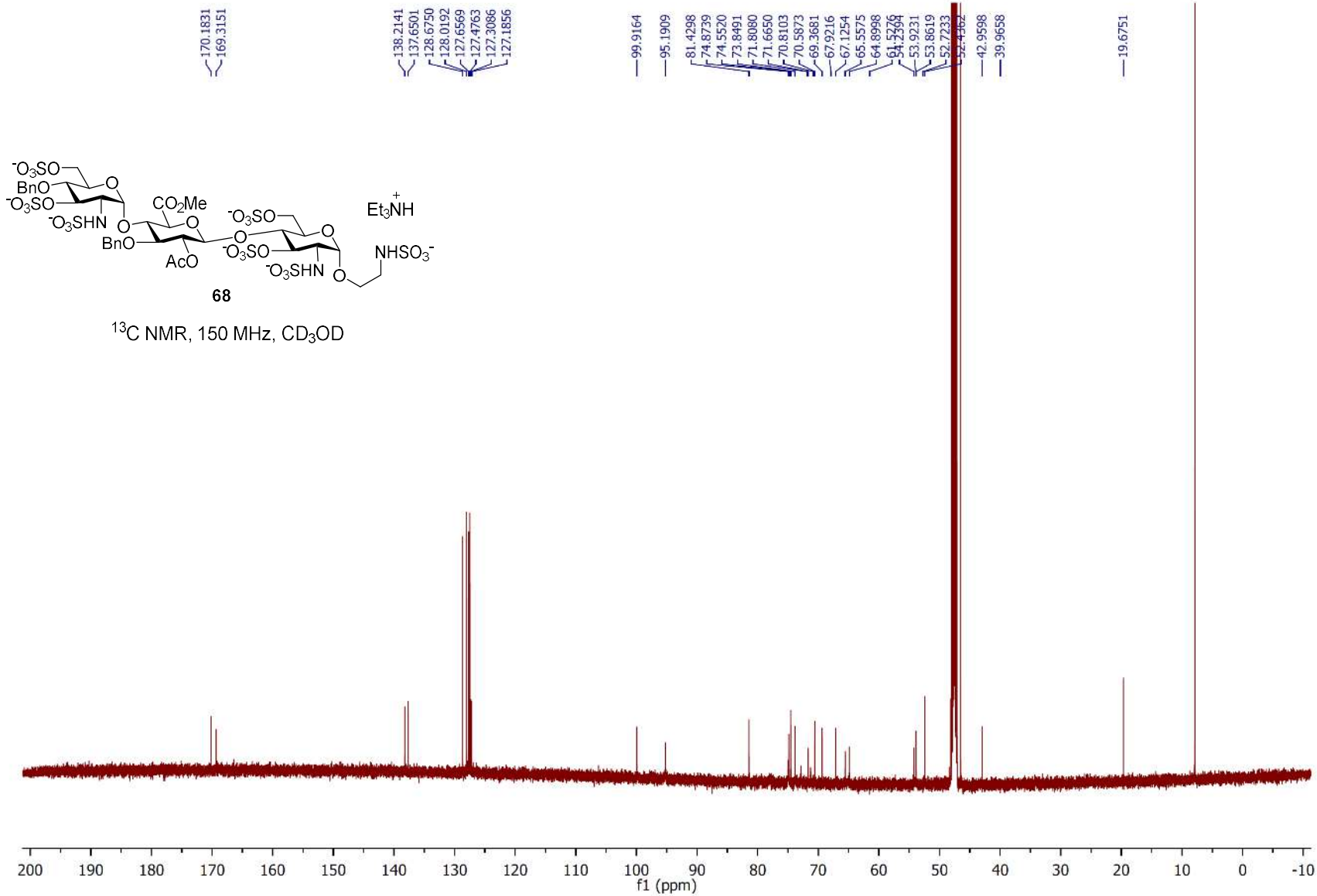
^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

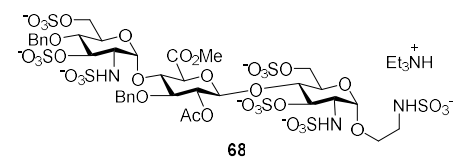




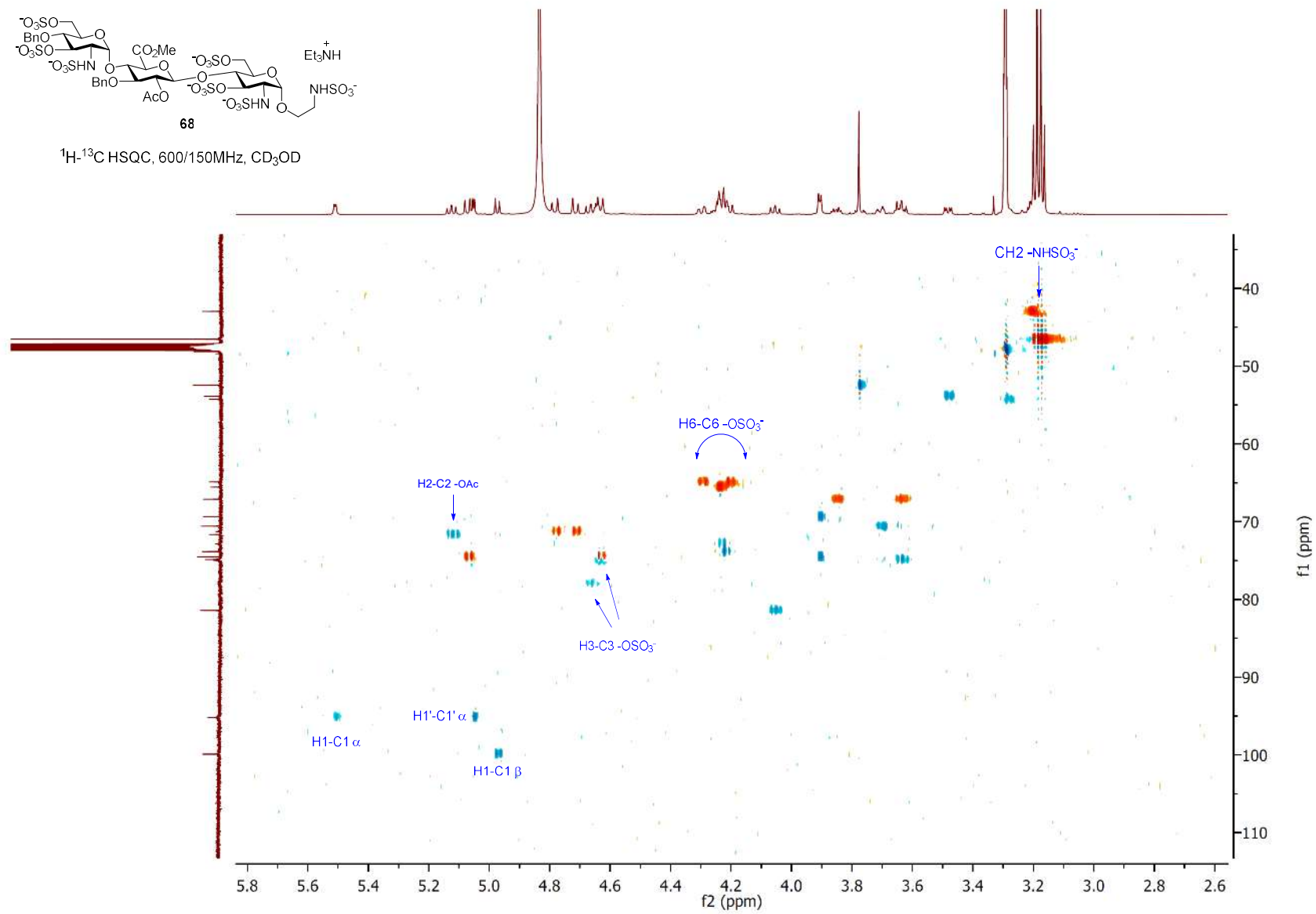


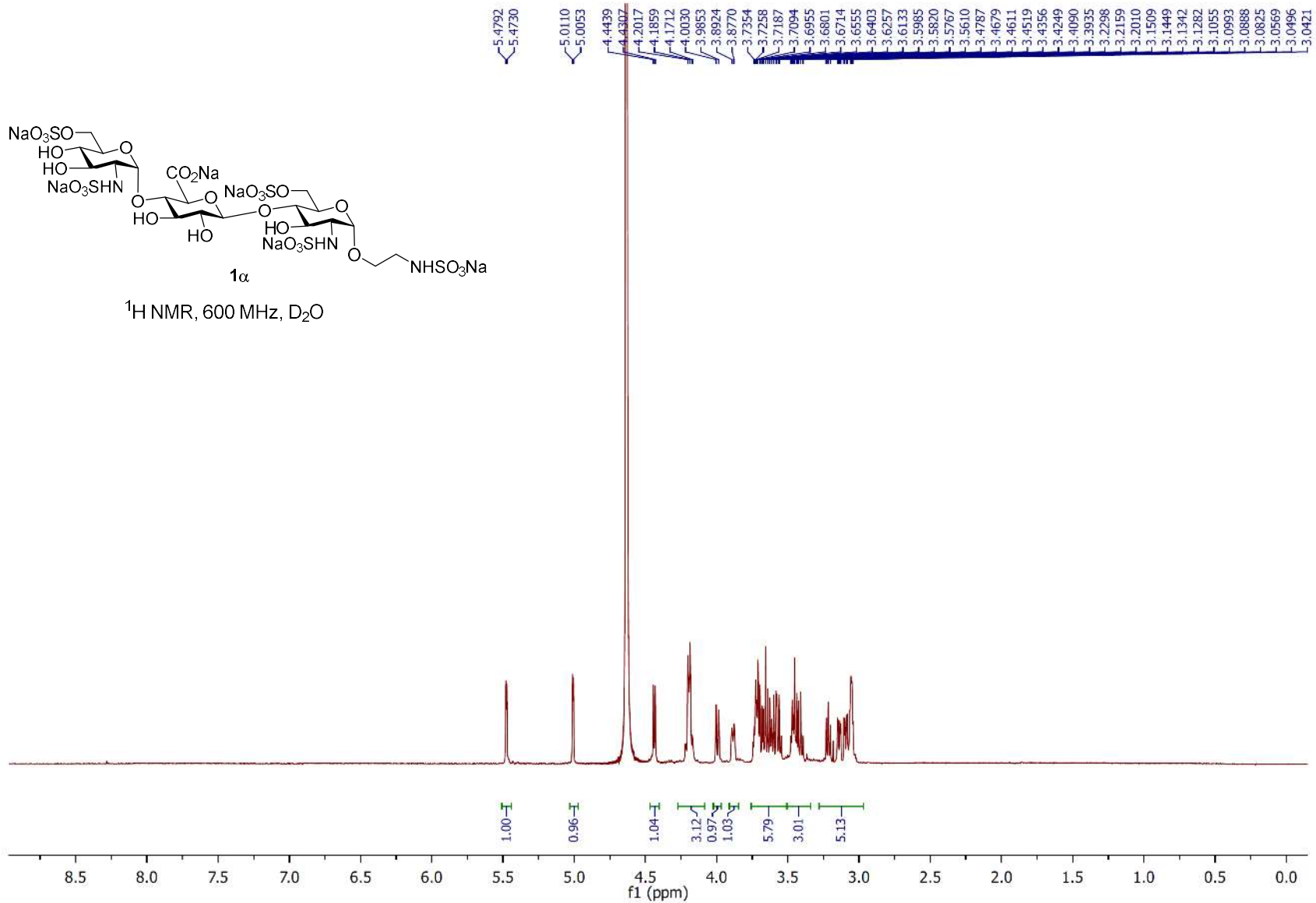


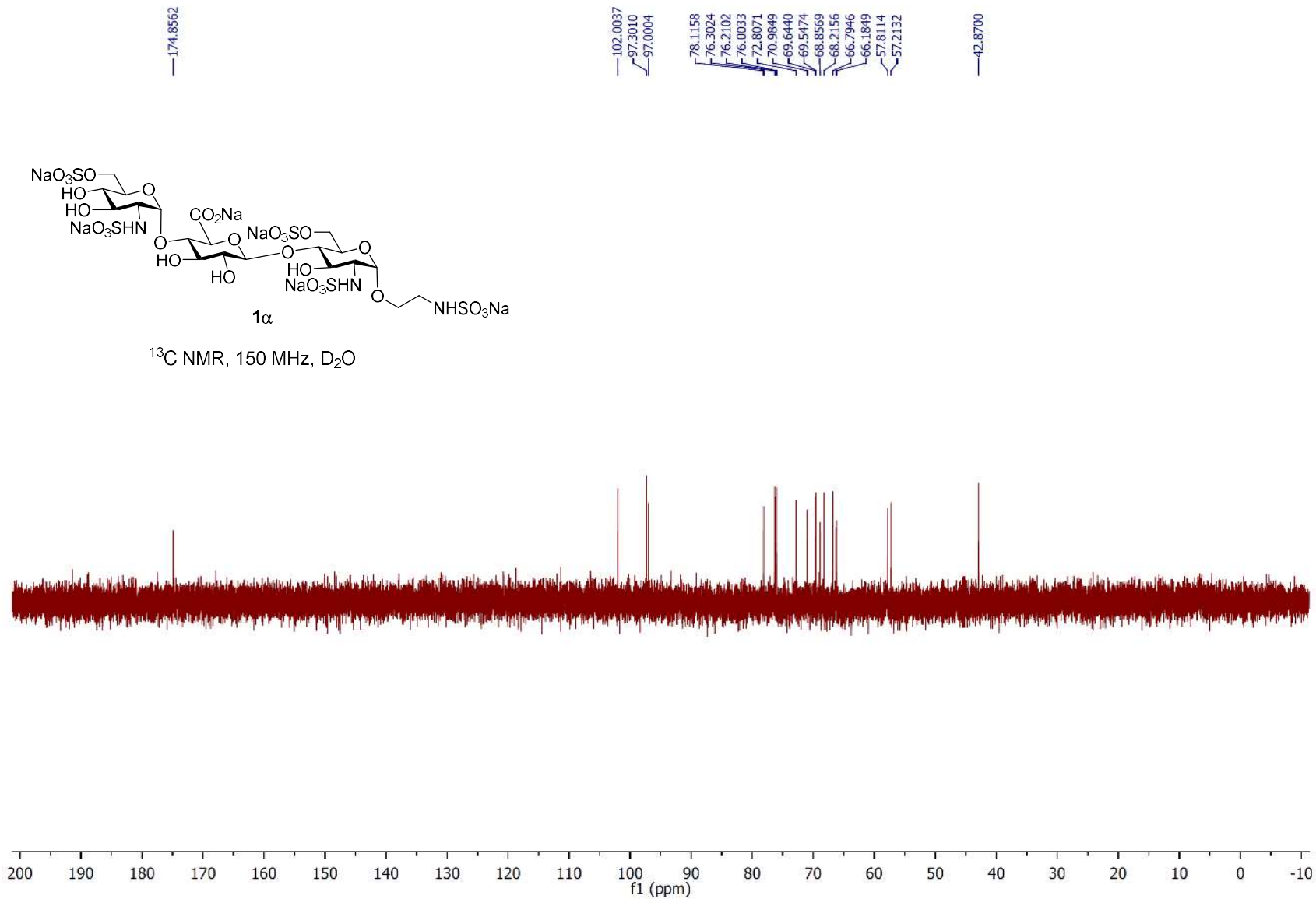


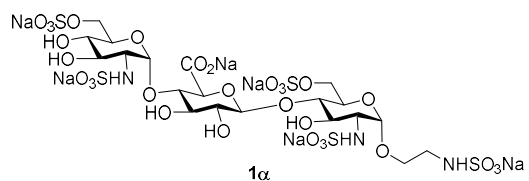


^1H - ^{13}C HSQC, 600/150MHz, CD_3OD

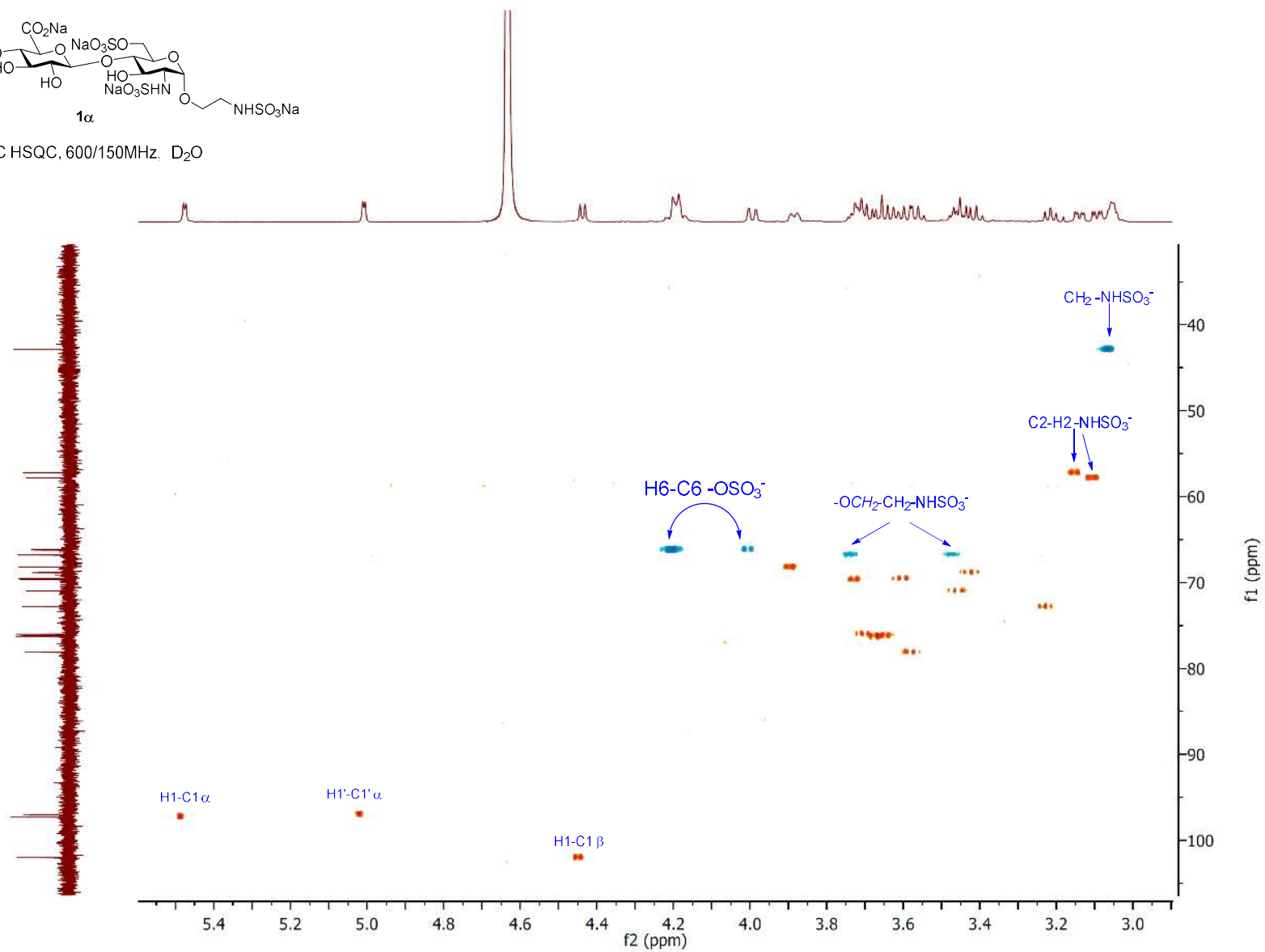


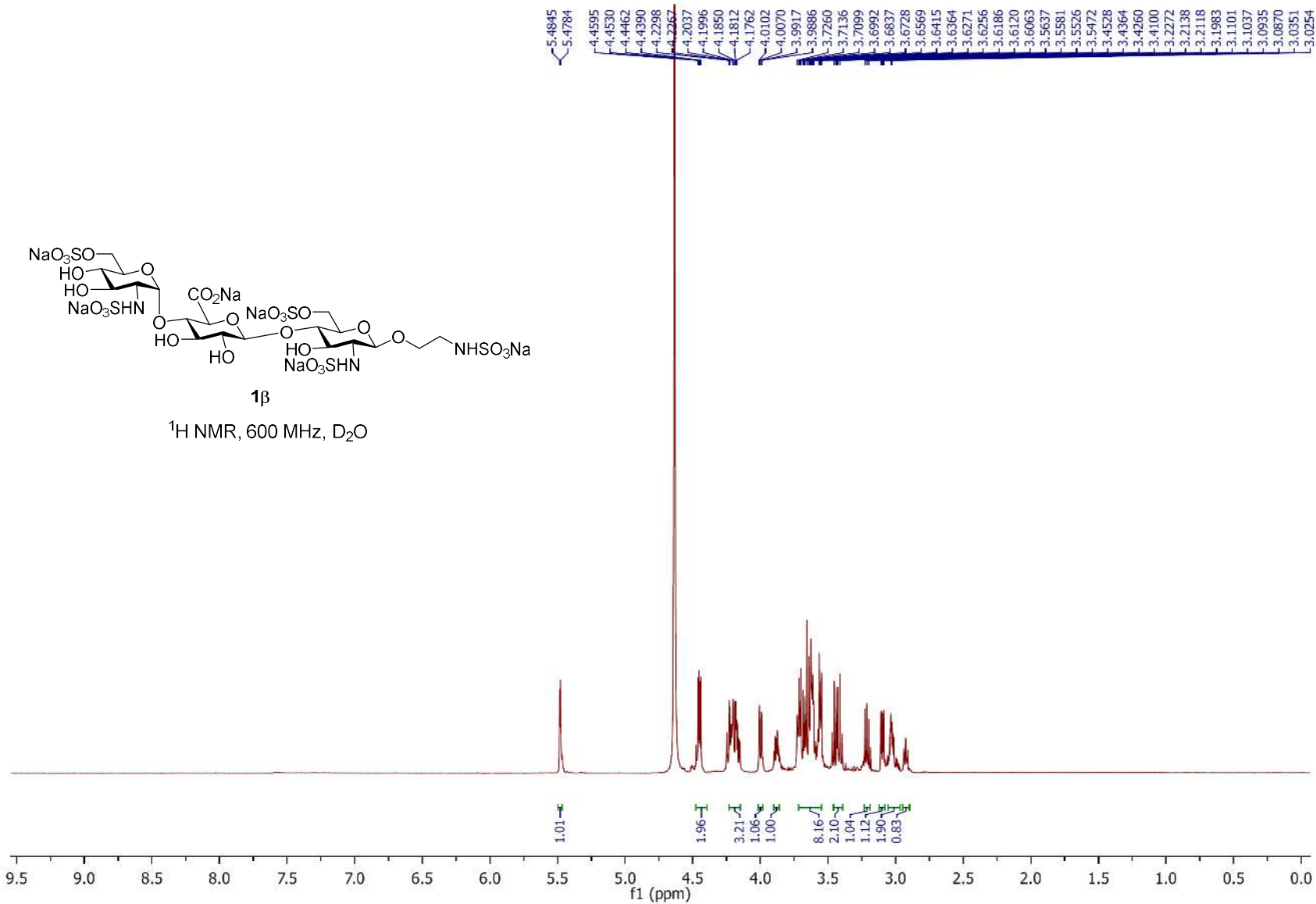


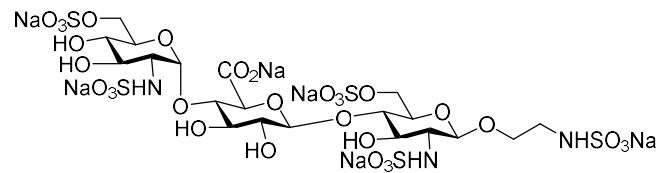




^1H - ^{13}C HSQC, 600/150MHz, D₂O

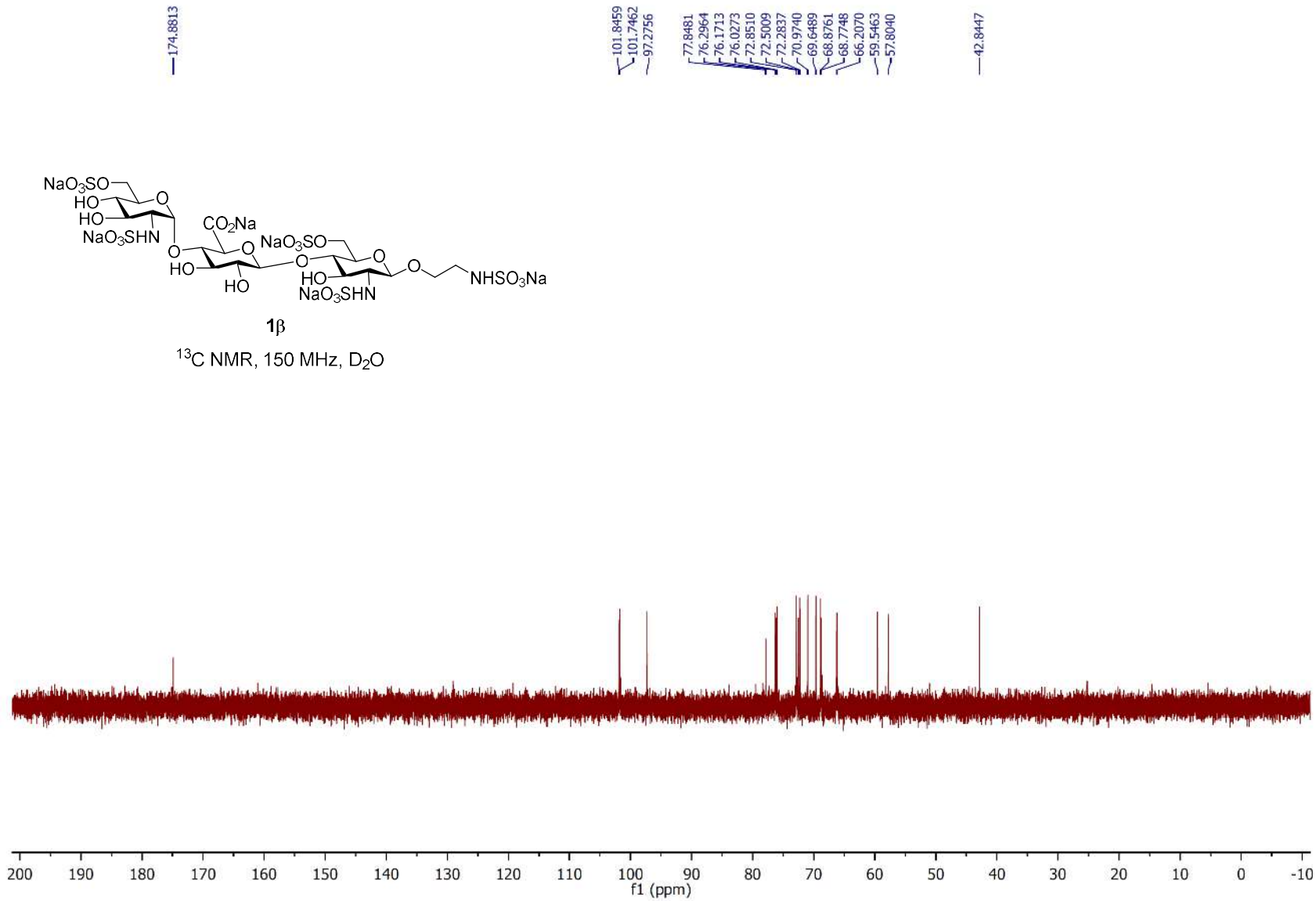


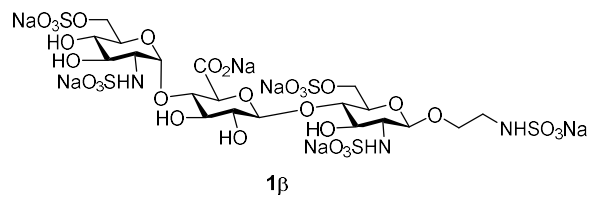




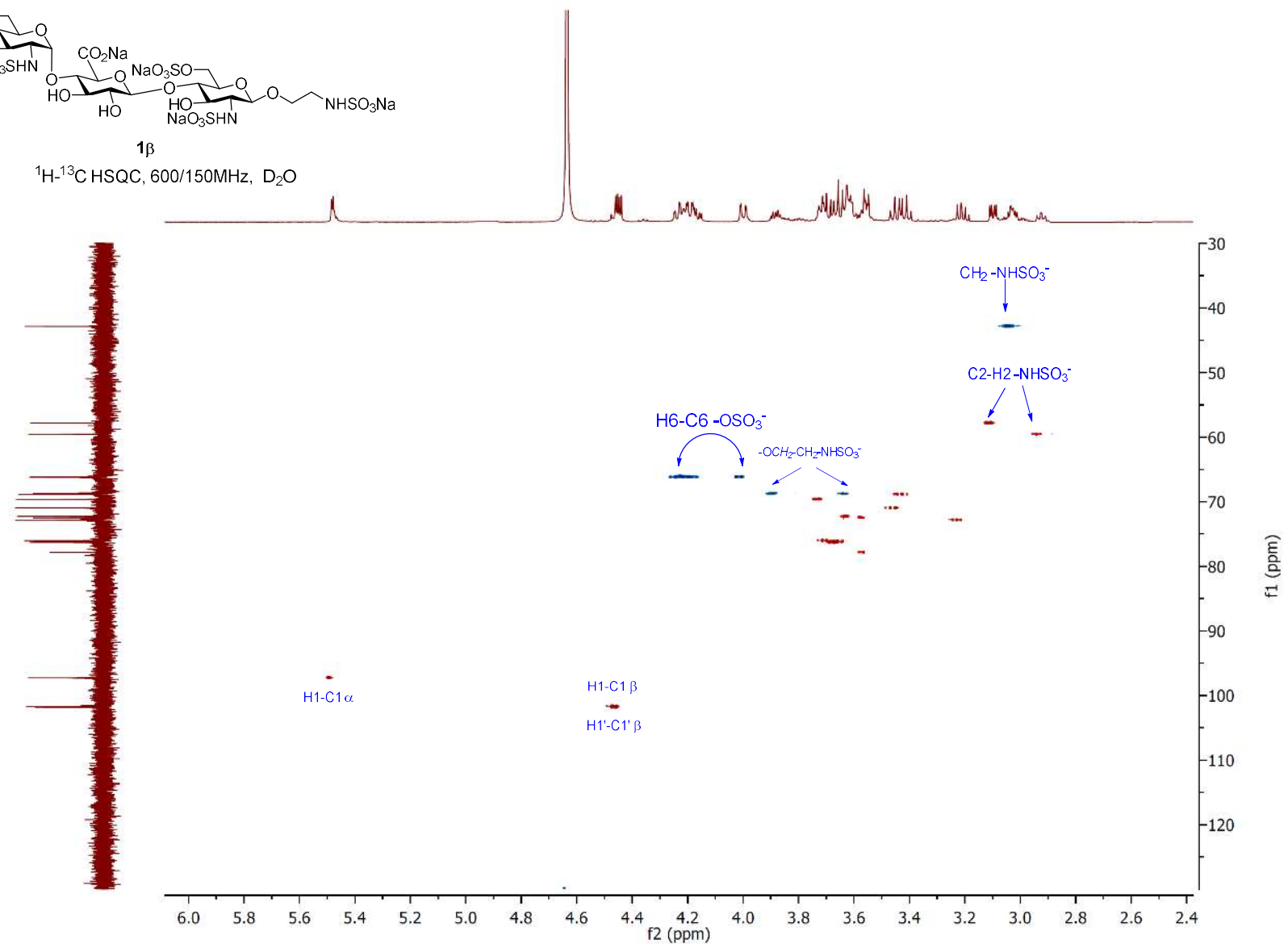
1β

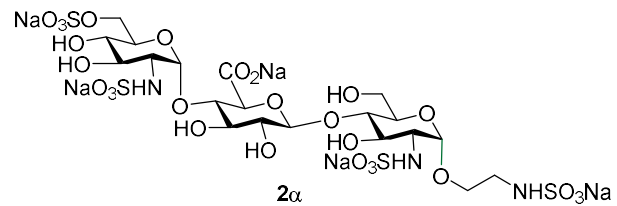
¹³C NMR, 150 MHz, D₂O



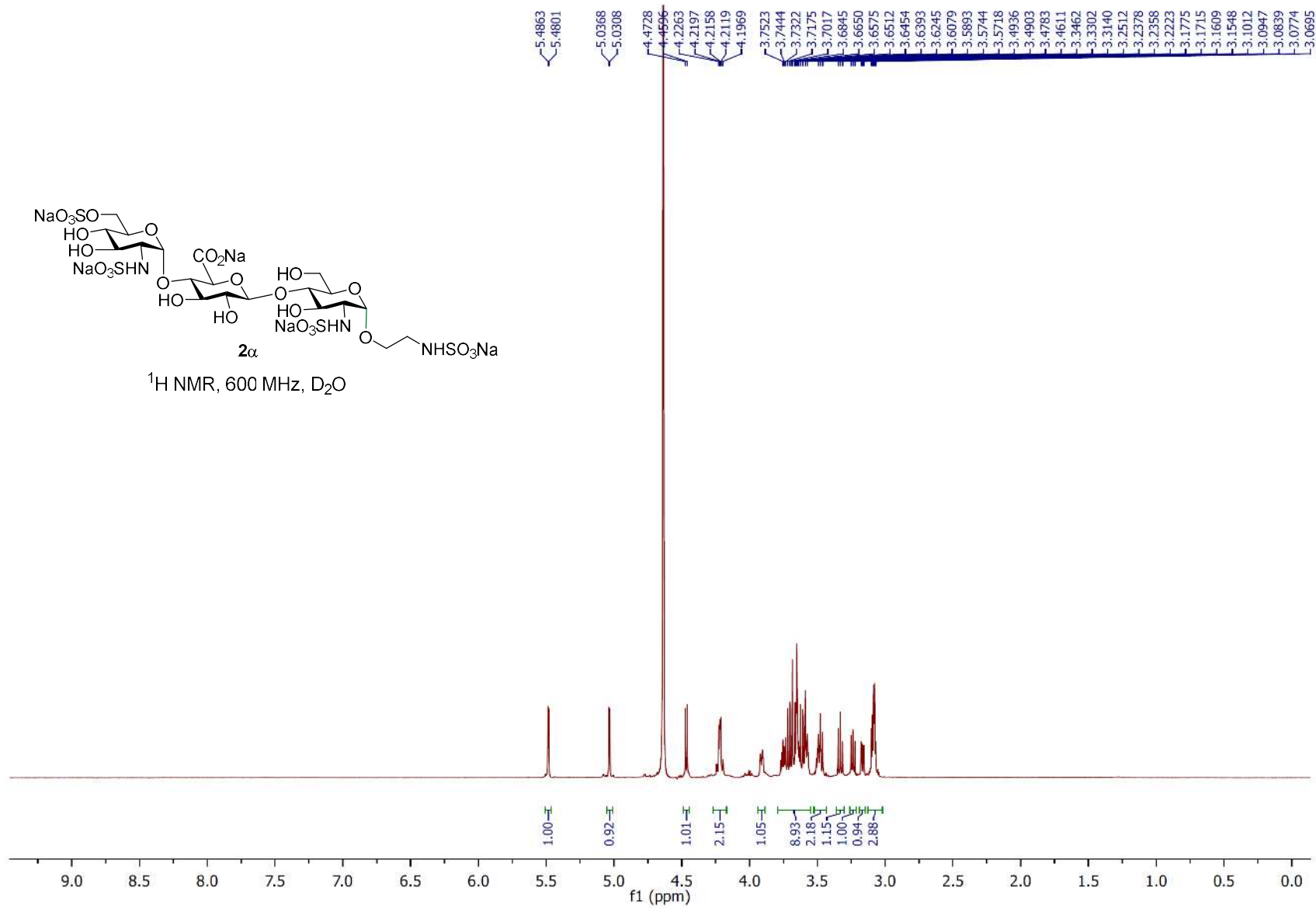


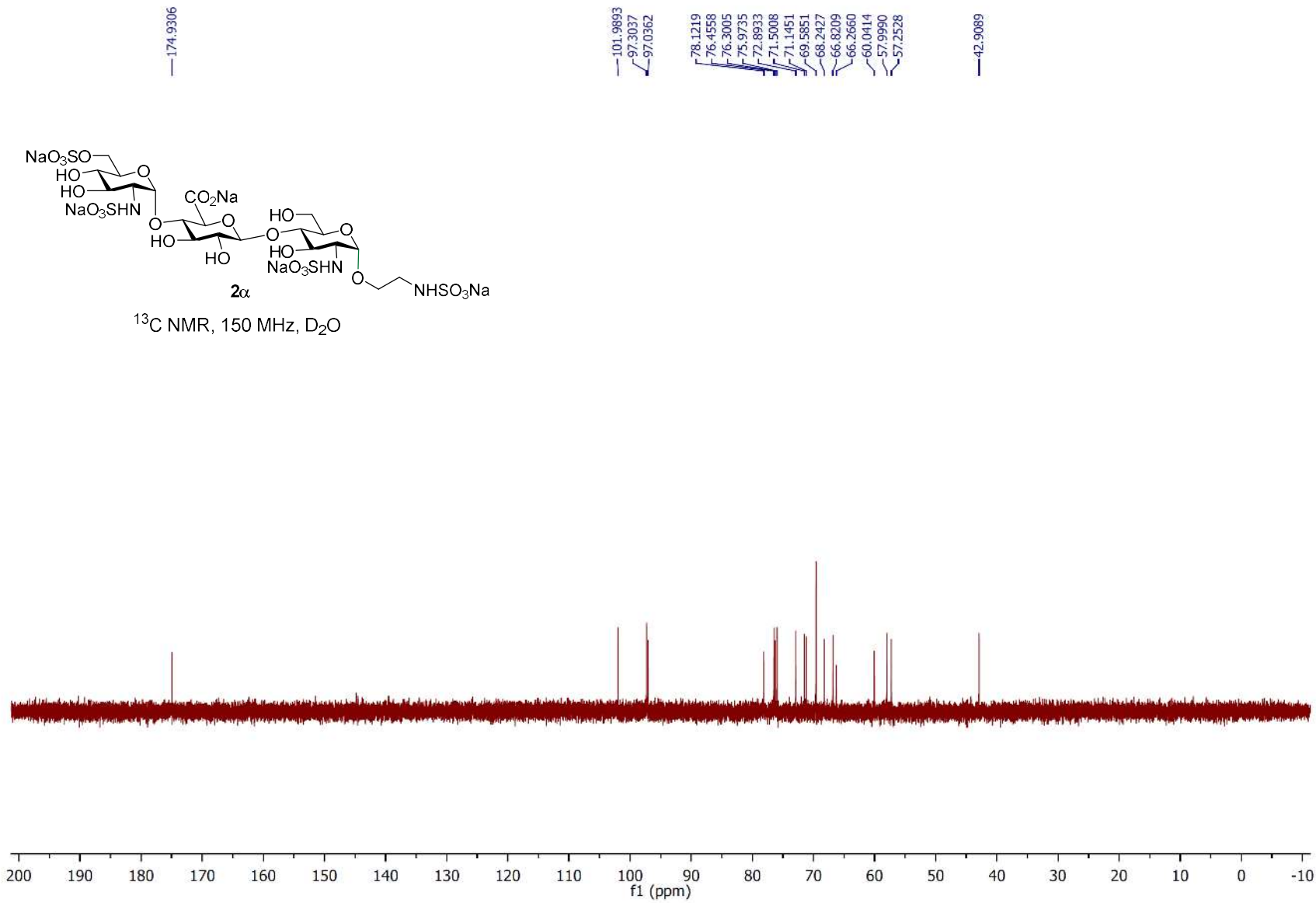
^1H - ^{13}C HSQC, 600/150MHz, D_2O

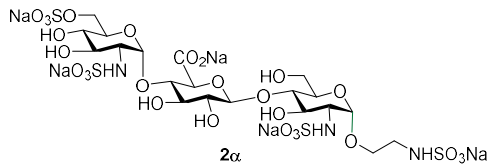




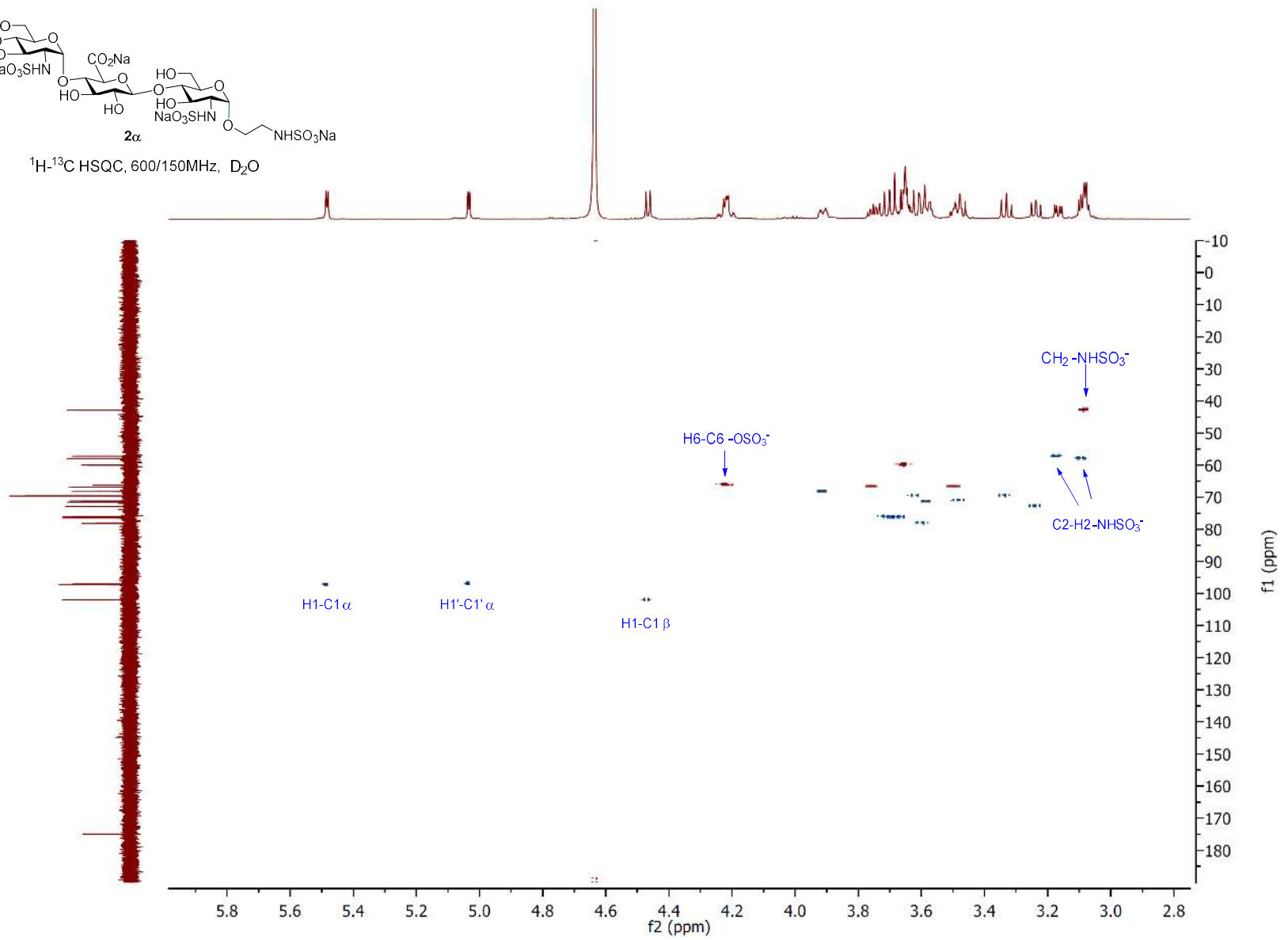
^1H NMR, 600 MHz, D_2O

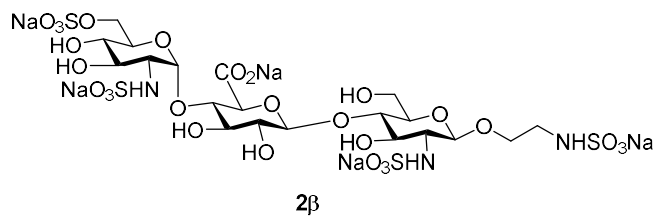




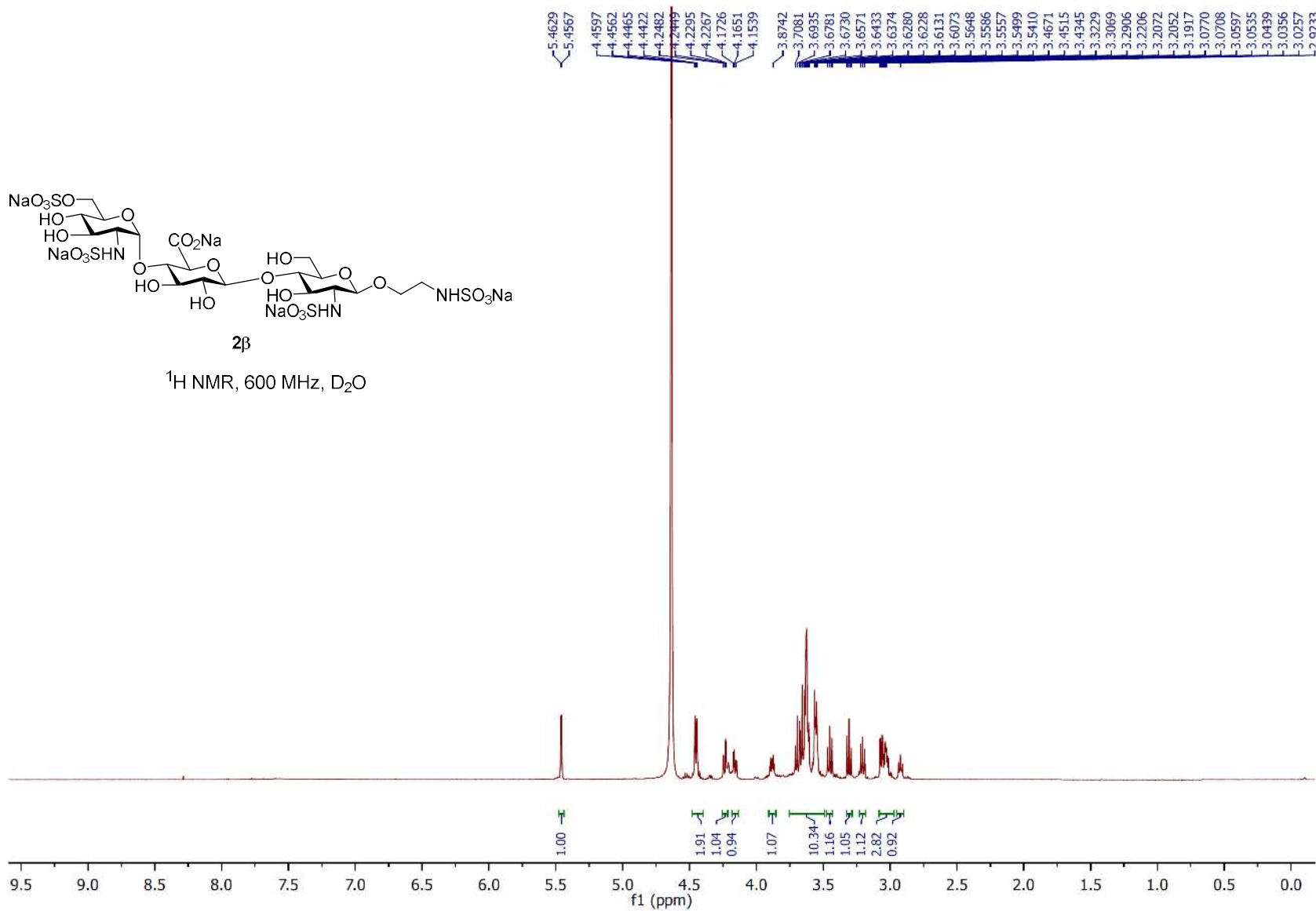


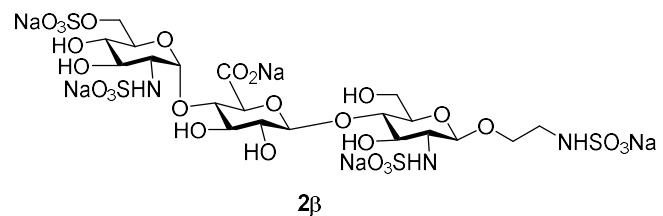
^1H - ^{13}C HSQC, 600/150MHz, D_2O





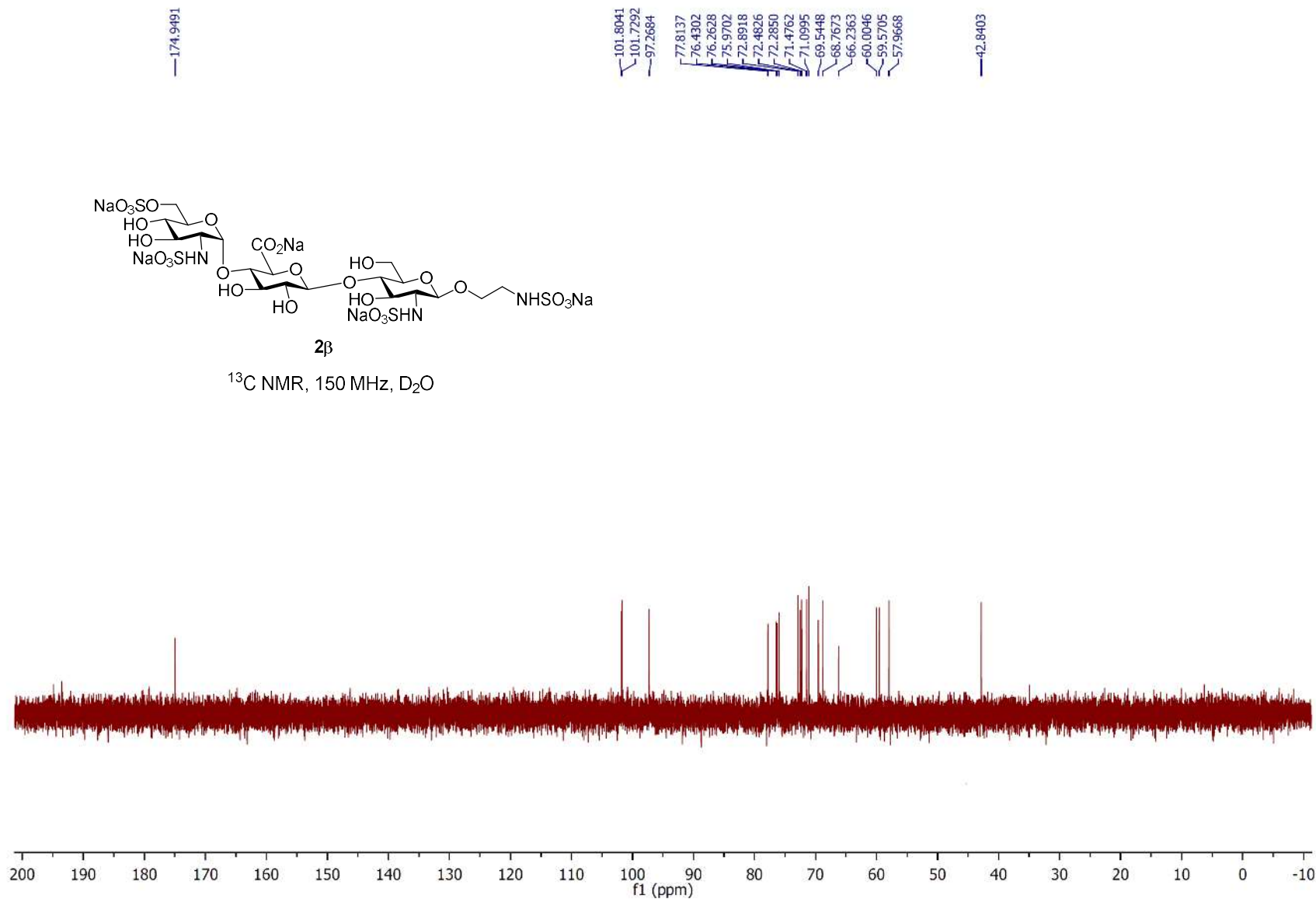
¹H NMR, 600 MHz, D₂O

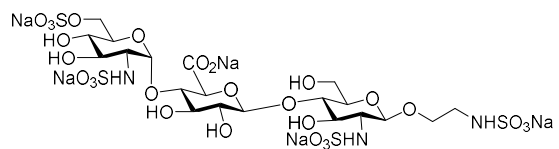




2β

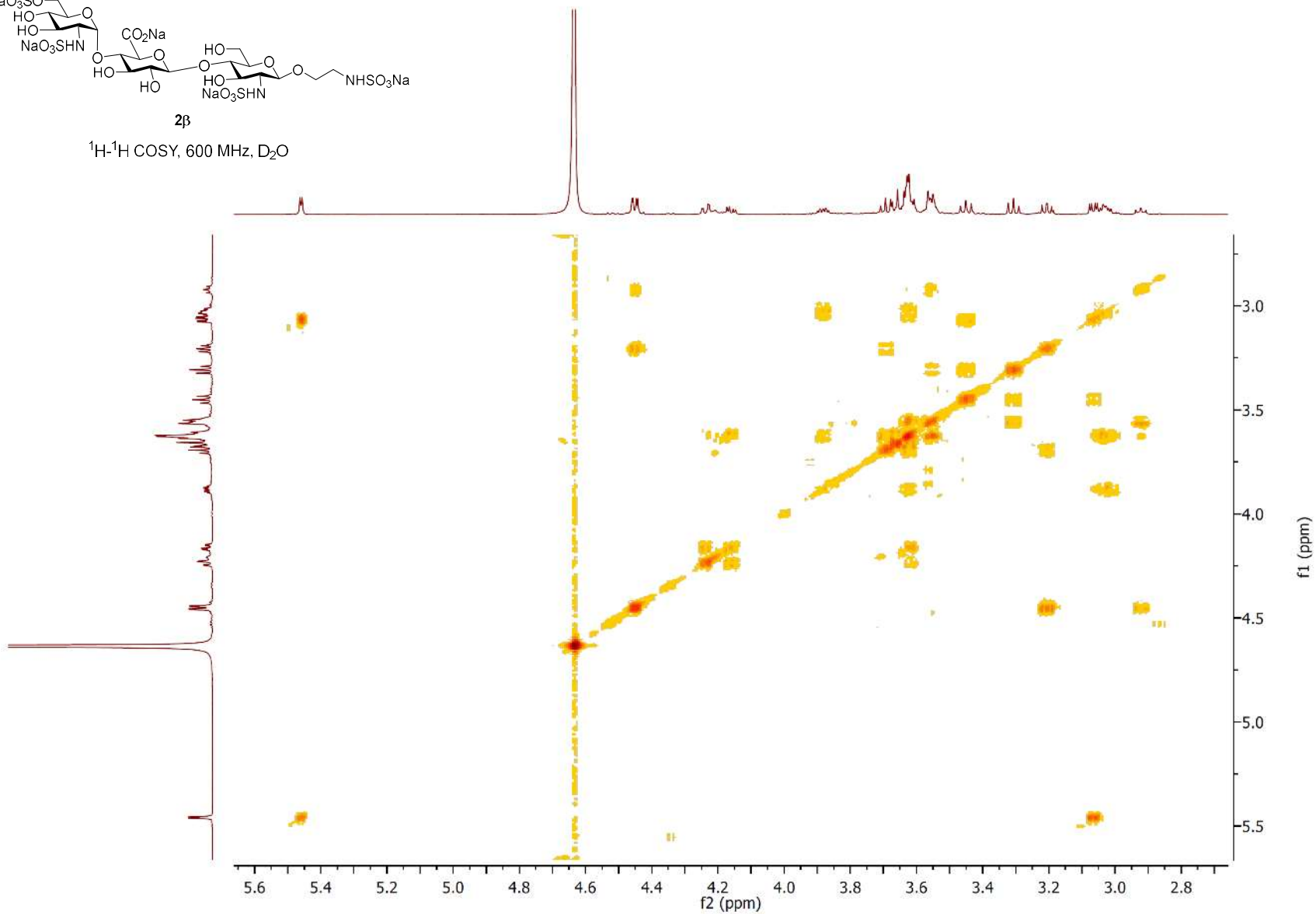
^{13}C NMR, 150 MHz, D_2O

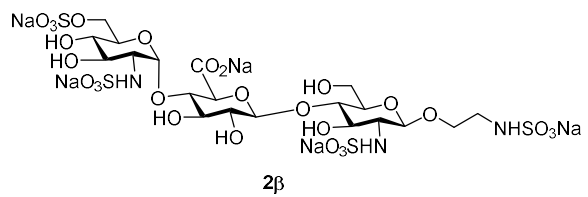




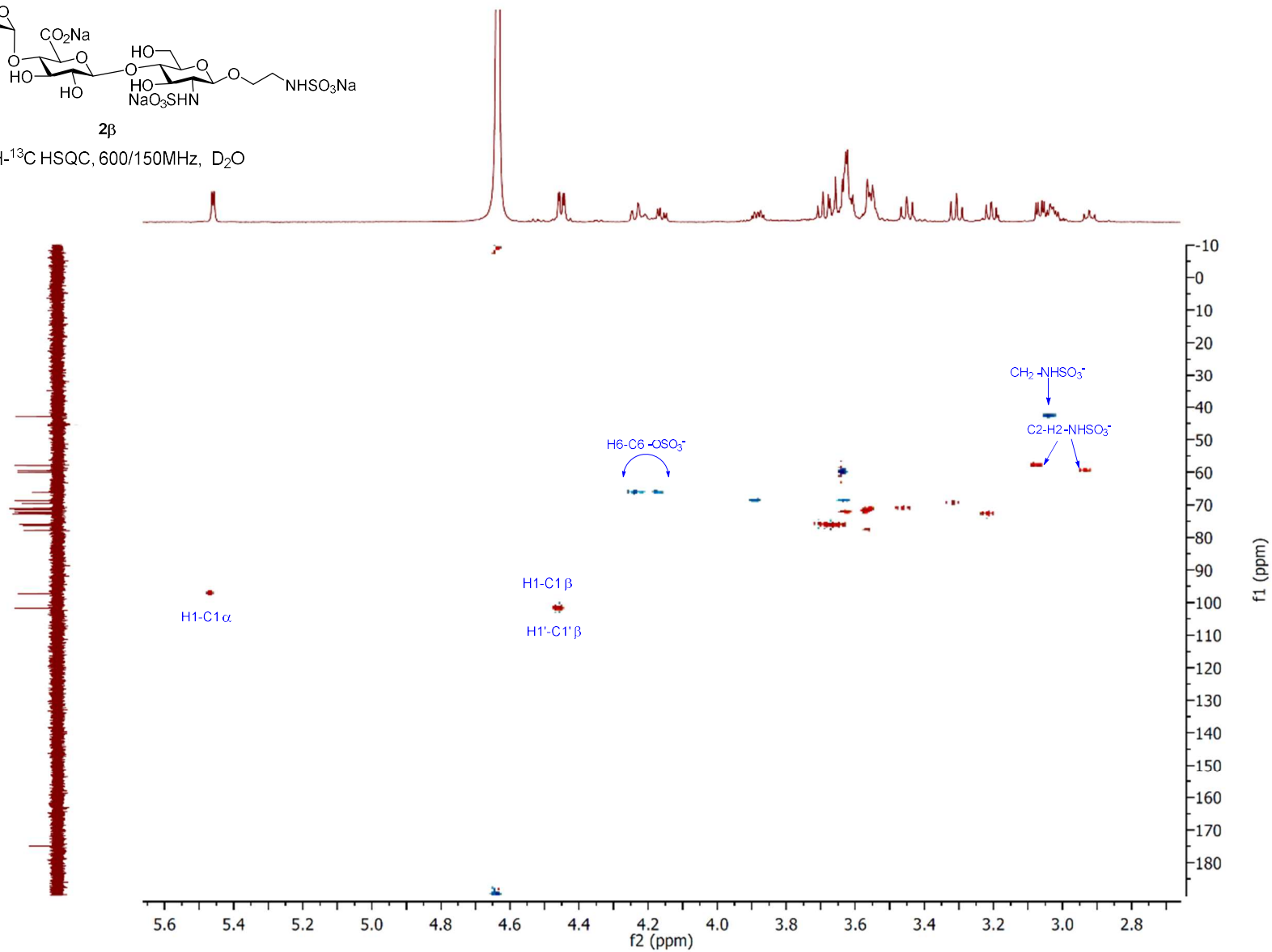
2 β

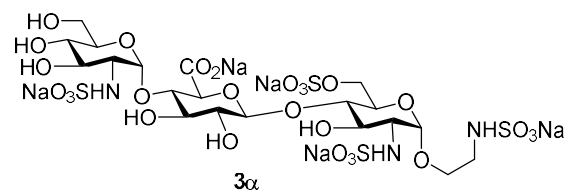
^1H - ^1H COSY, 600 MHz, D₂O



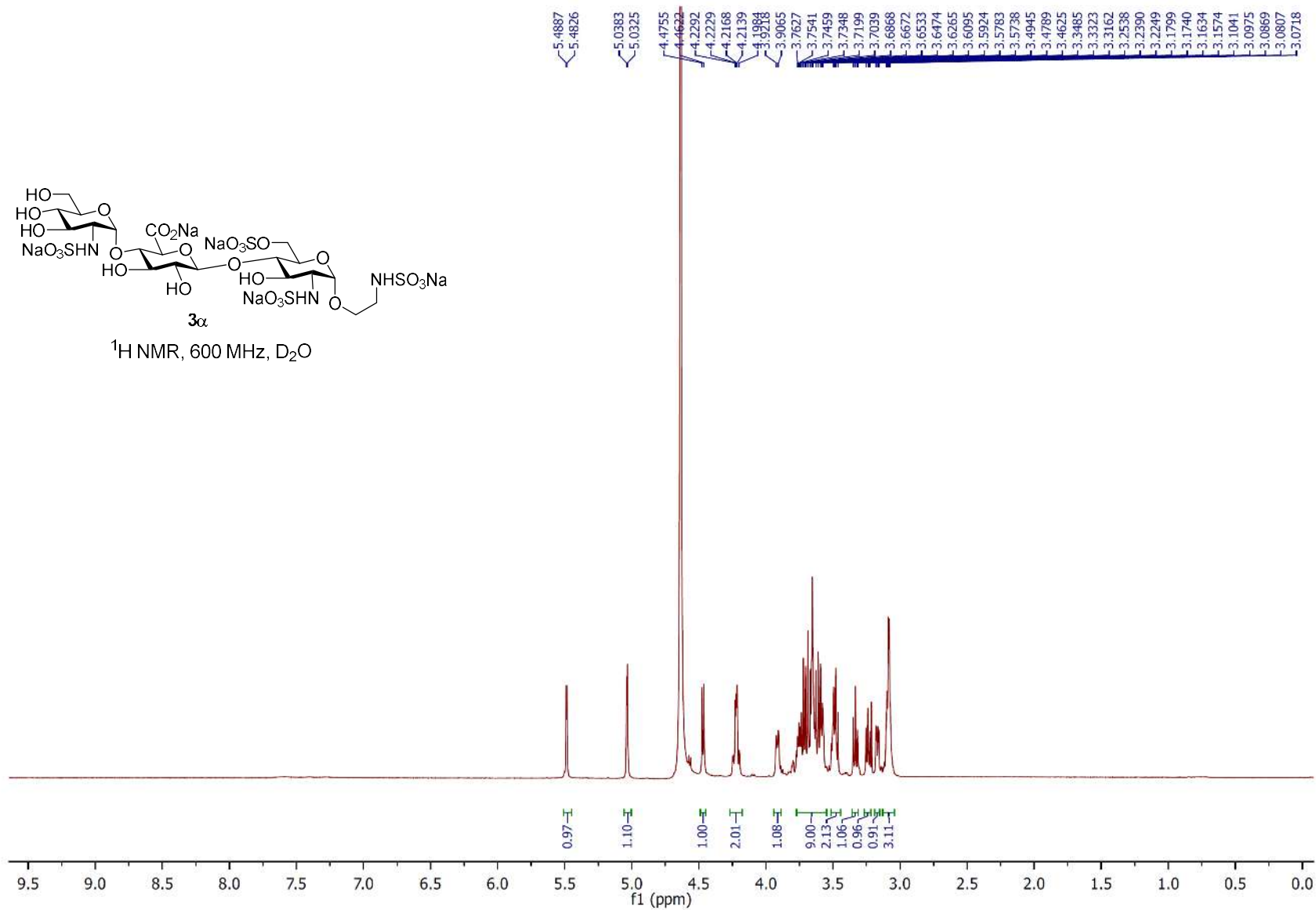


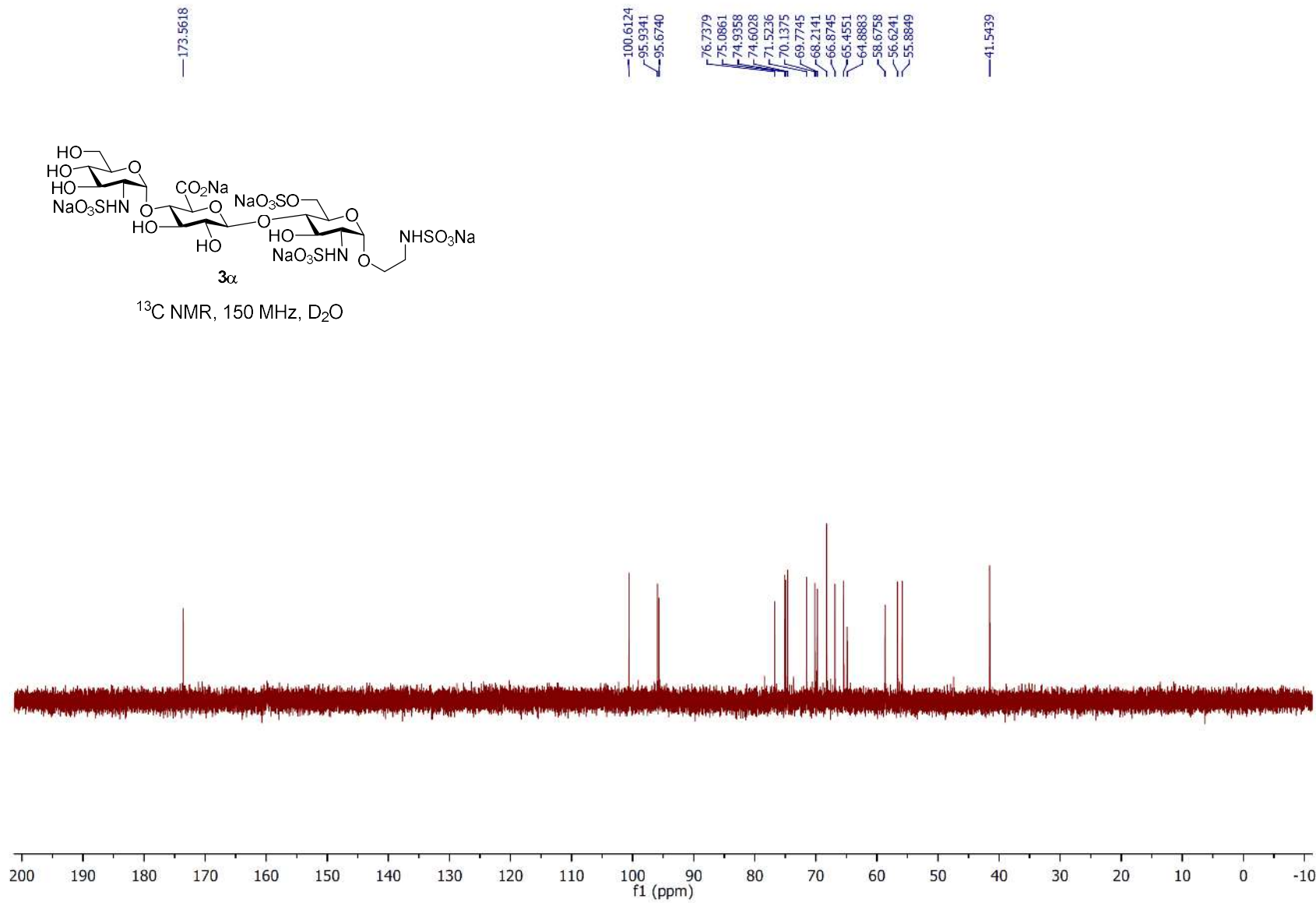
^1H - ^{13}C HSQC, 600/150MHz, D_2O

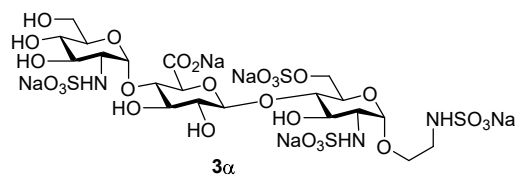




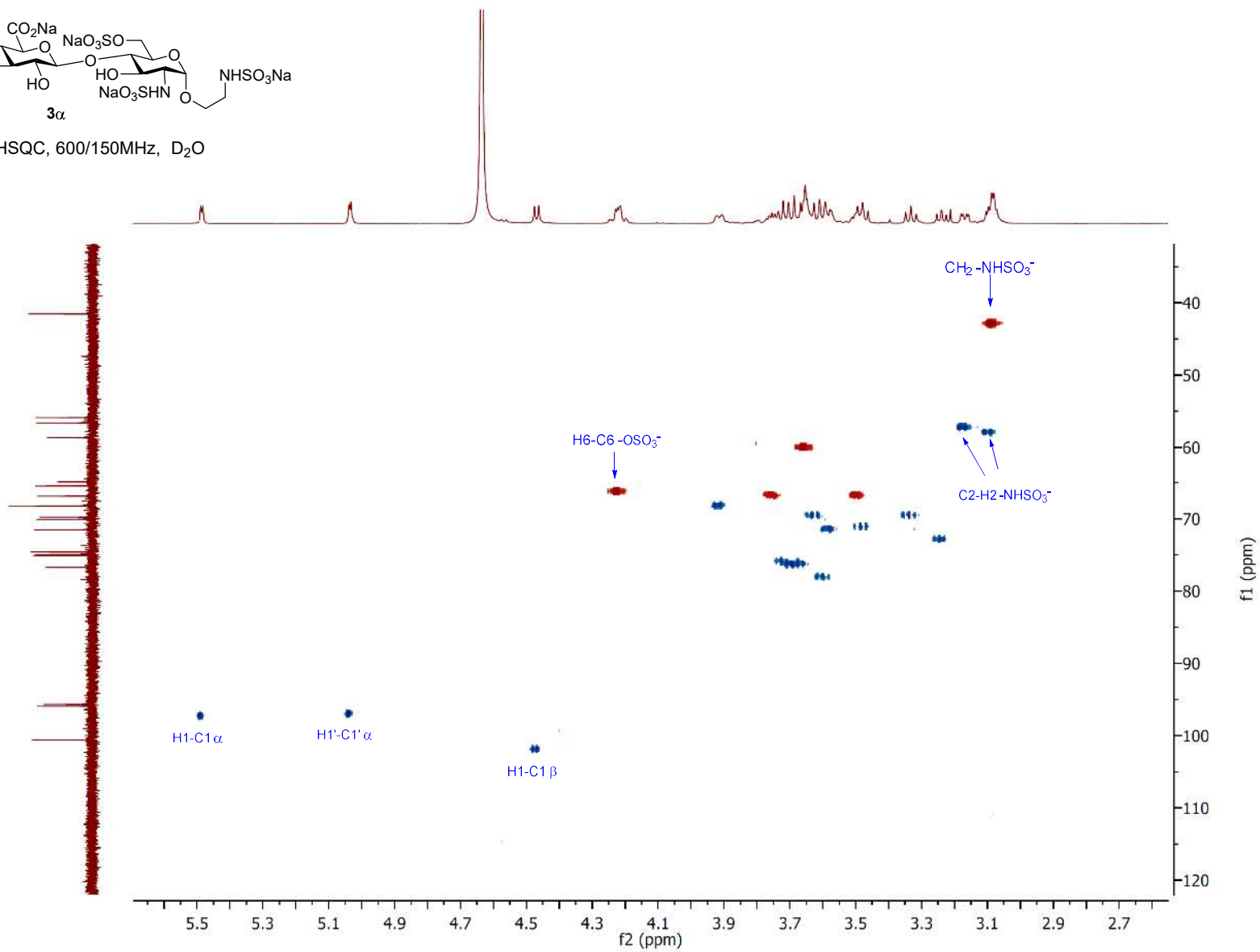
¹H NMR, 600 MHz, D₂O

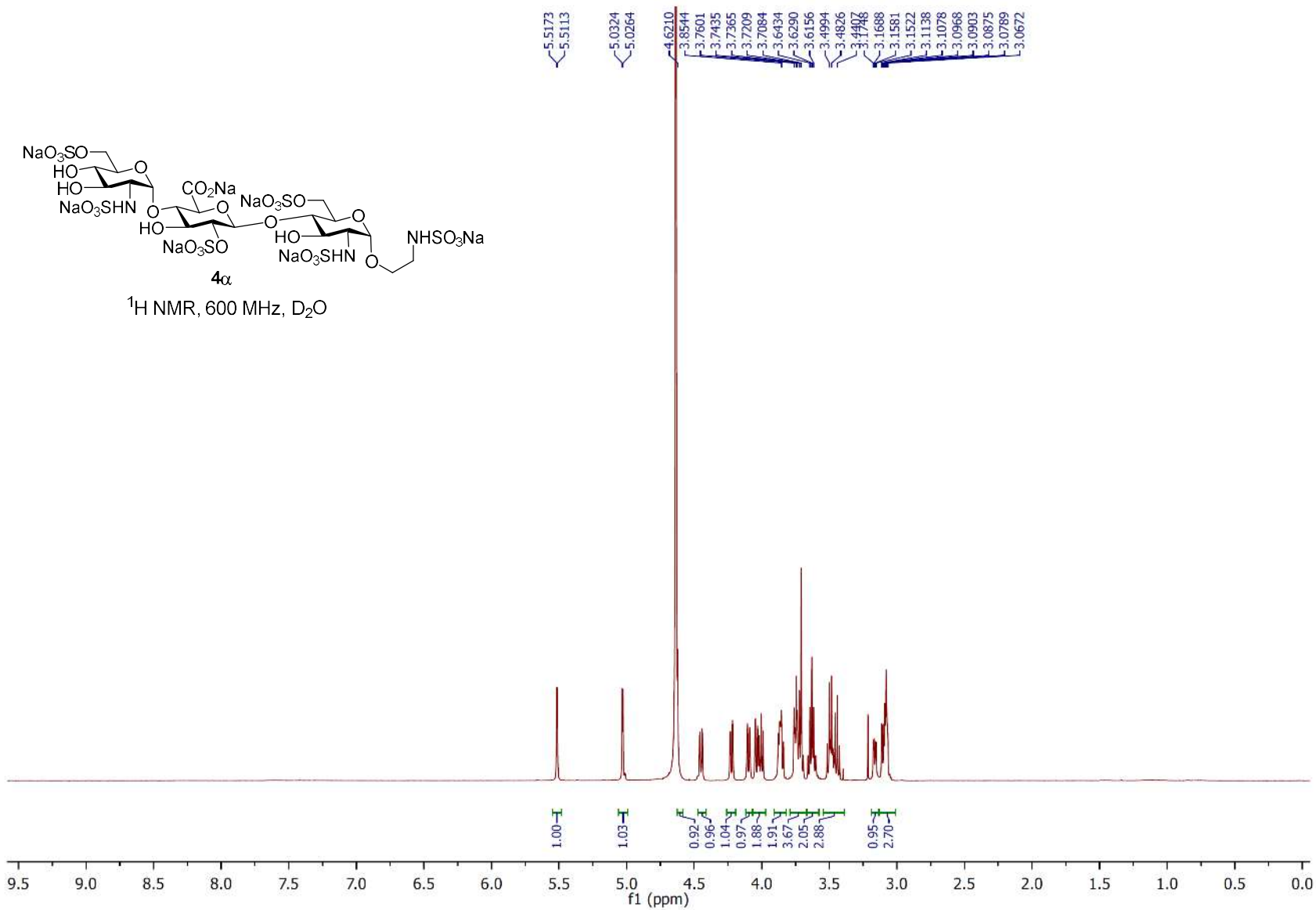


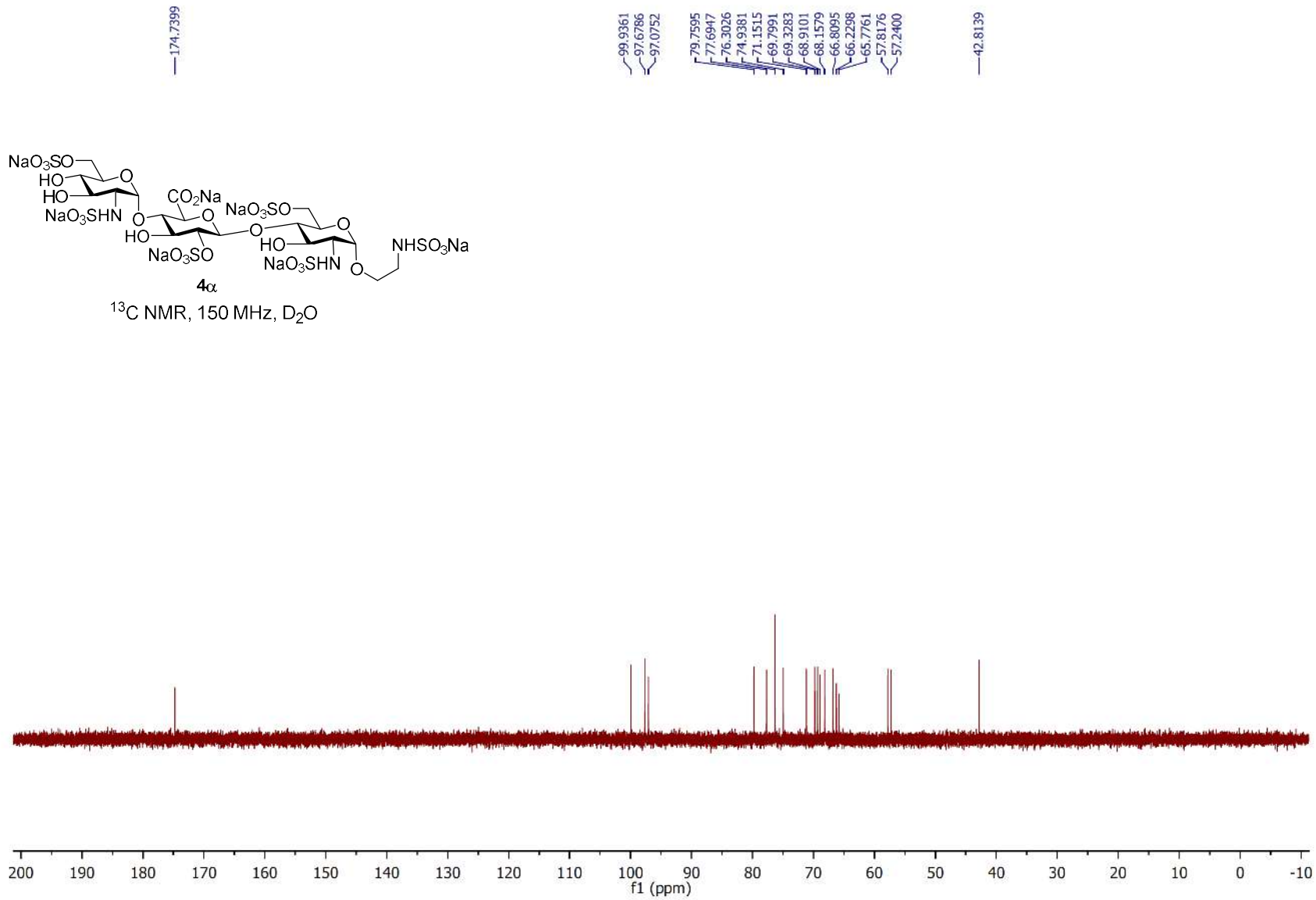


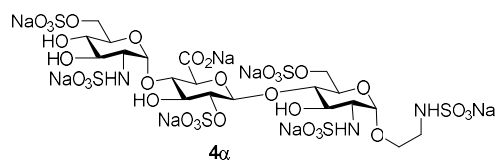


^1H - ^{13}C HSQC, 600/150MHz, D₂O

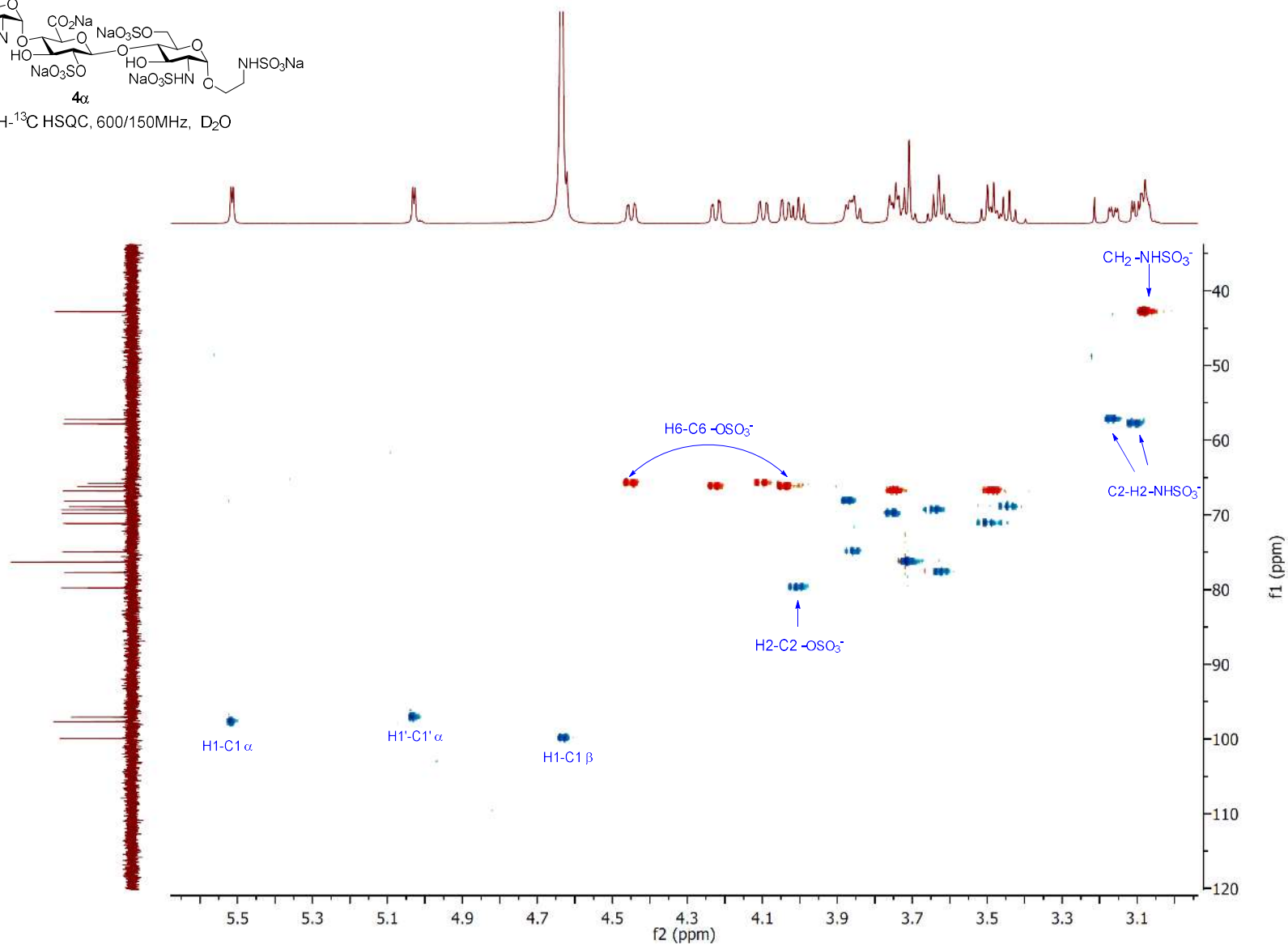


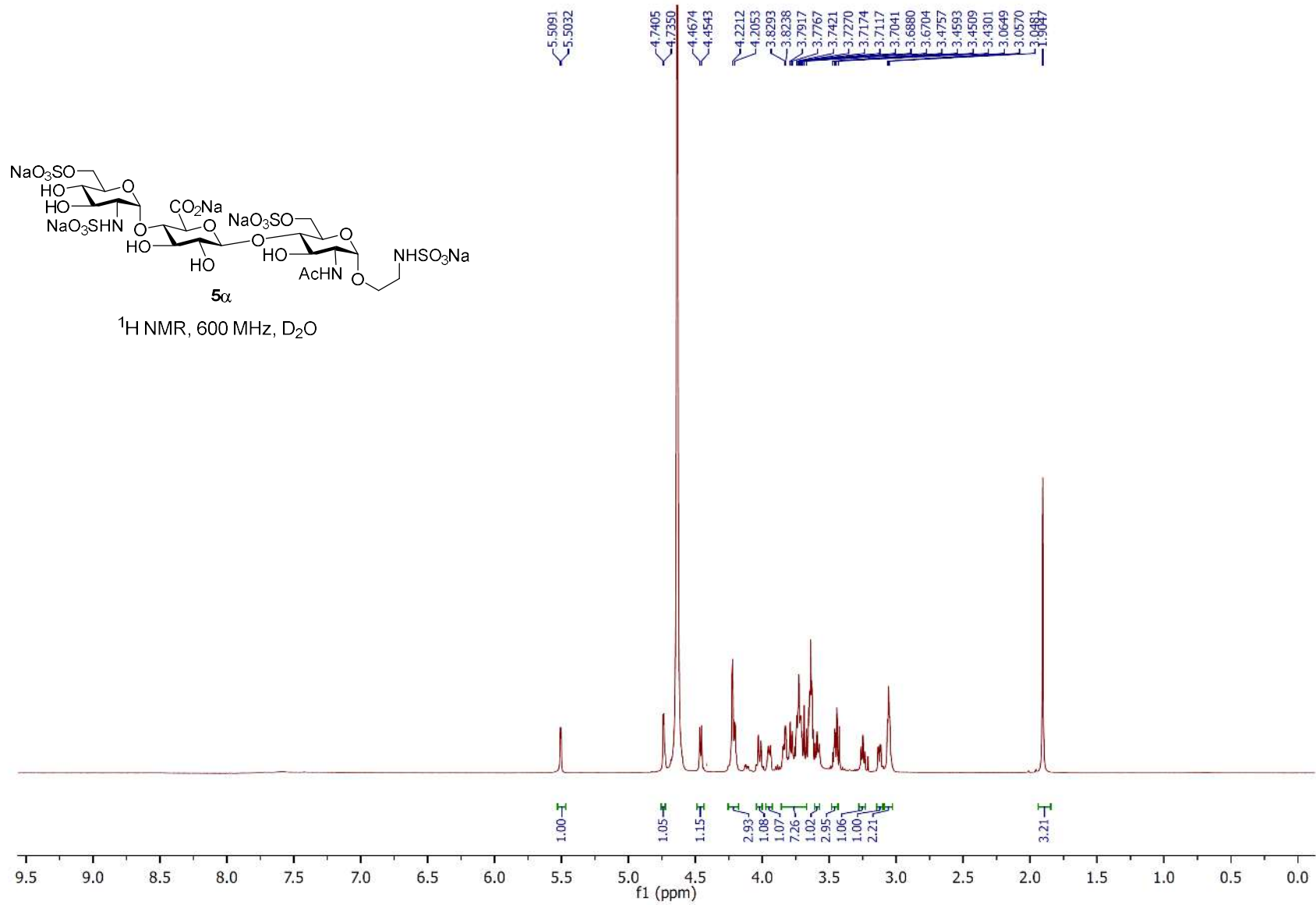






^1H - ^{13}C HSQC, 600/150MHz, D_2O





174.7443
174.3234

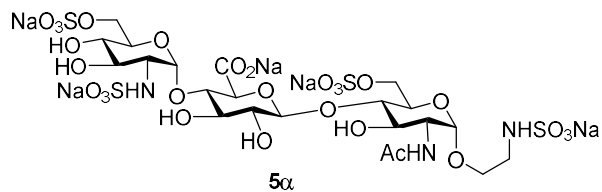
102.1017
97.2904
96.8323

78.4094
76.2726
76.1342
76.0070
72.8358
71.0144
69.6629
69.3771
68.8985
68.4860
66.7041
66.2526
57.8184

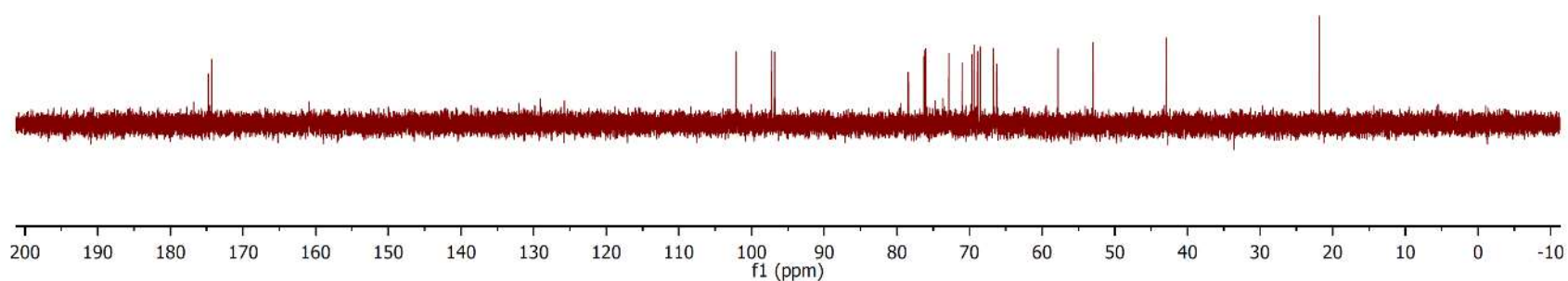
52.9789

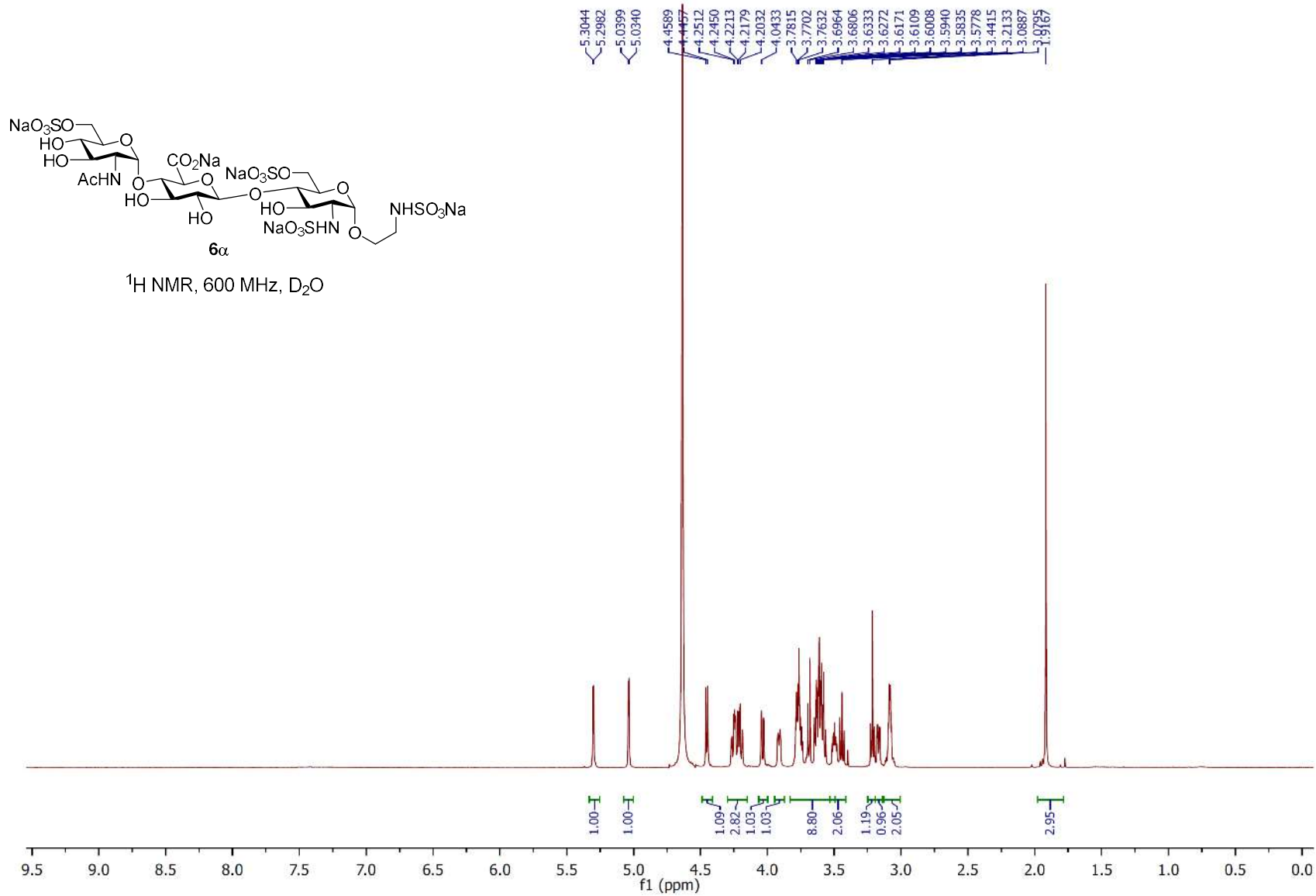
42.9011

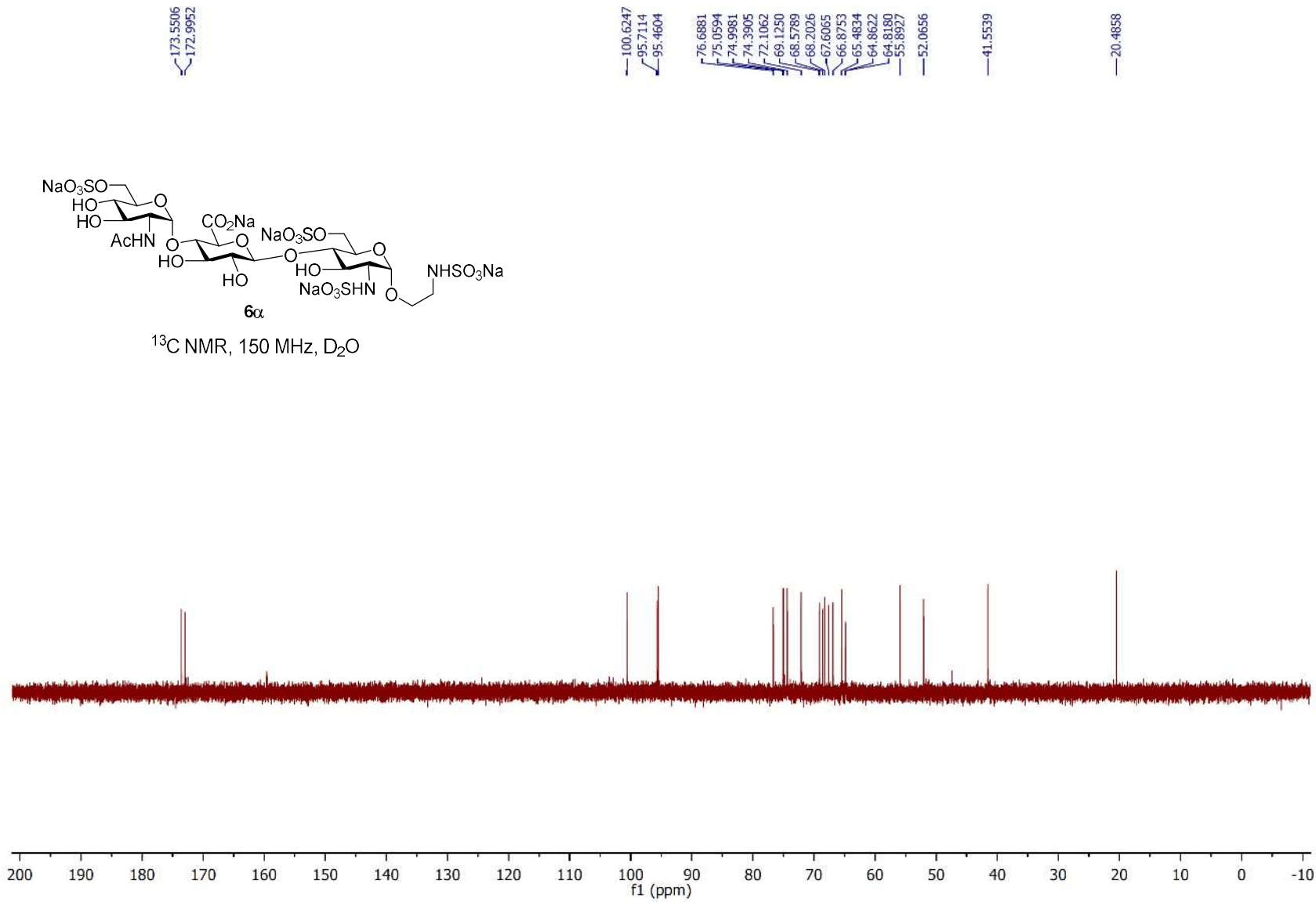
21.8361

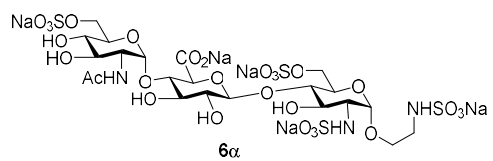


¹³C NMR, 150 MHz, D₂O

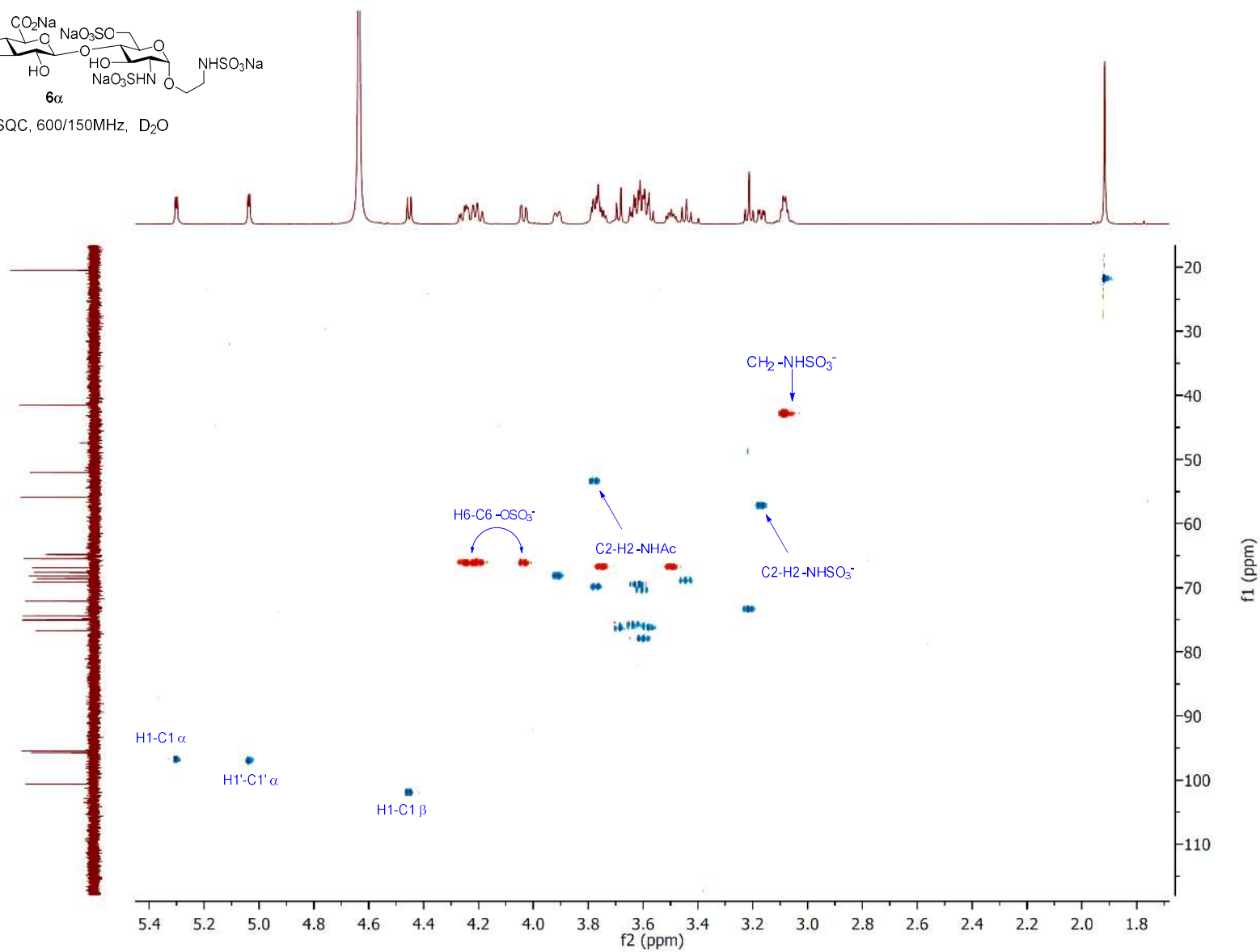


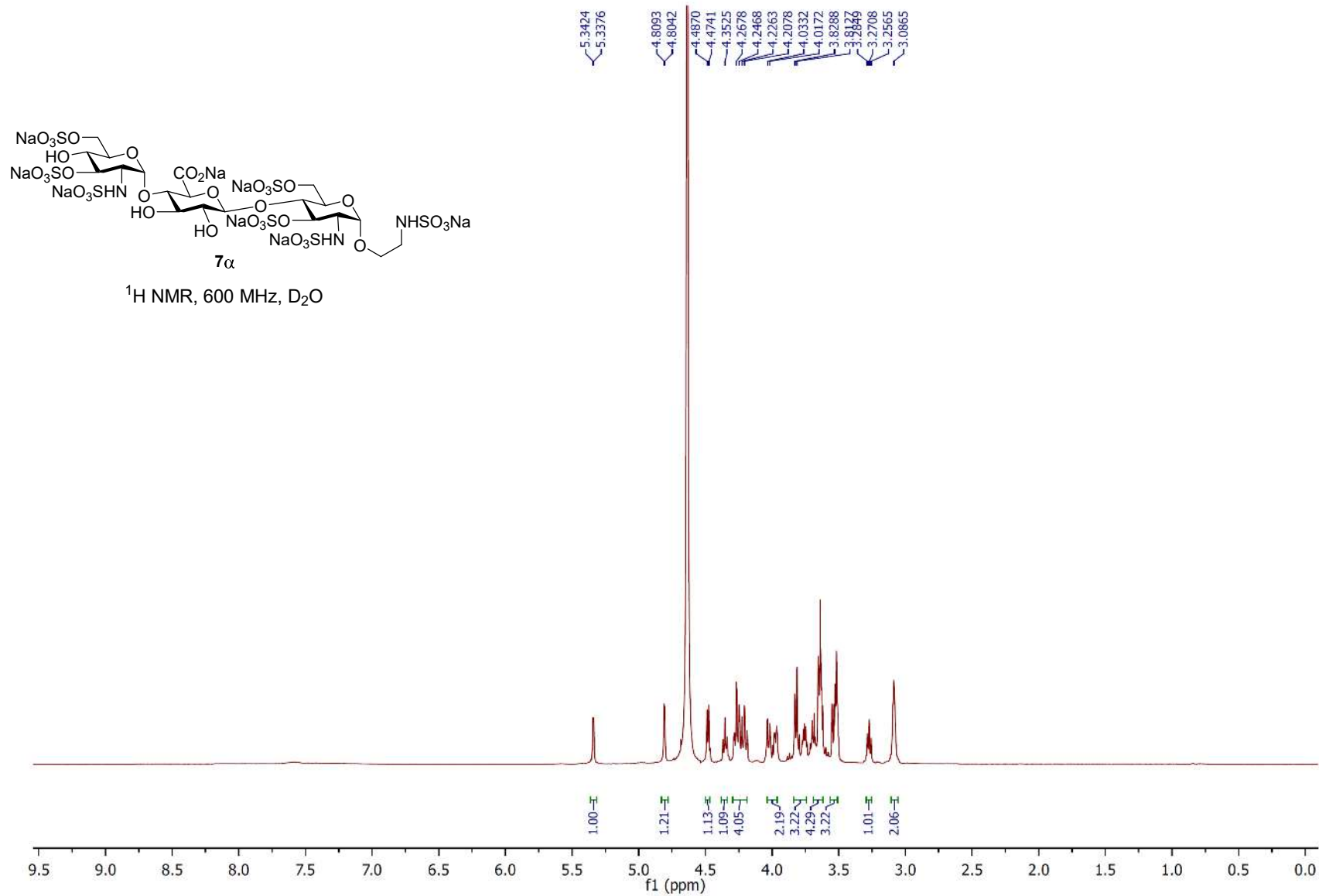


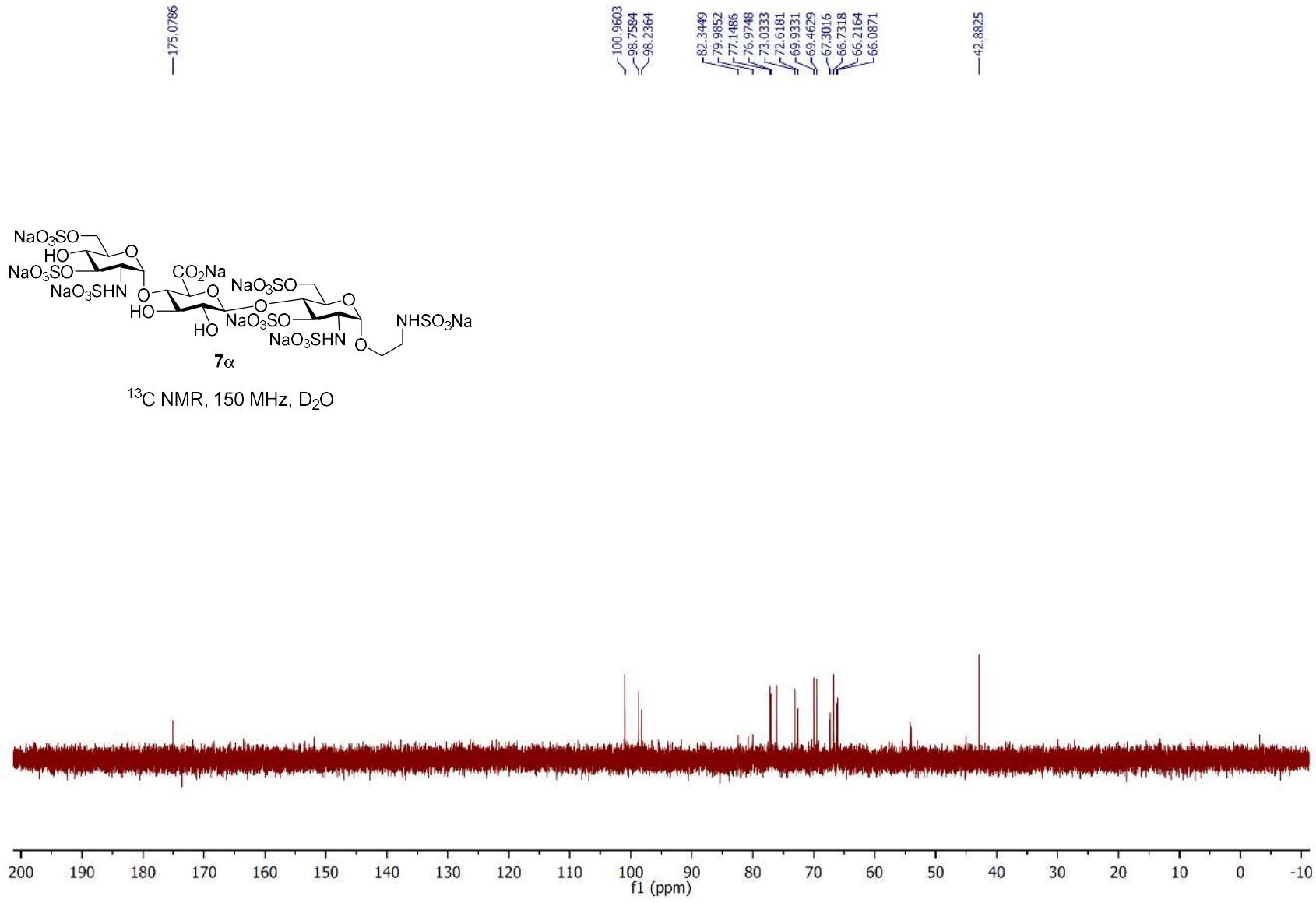


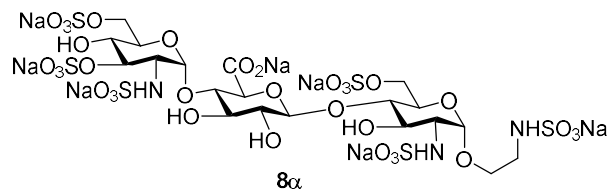


^1H - ^{13}C HSQC, 600/150MHz, D₂O

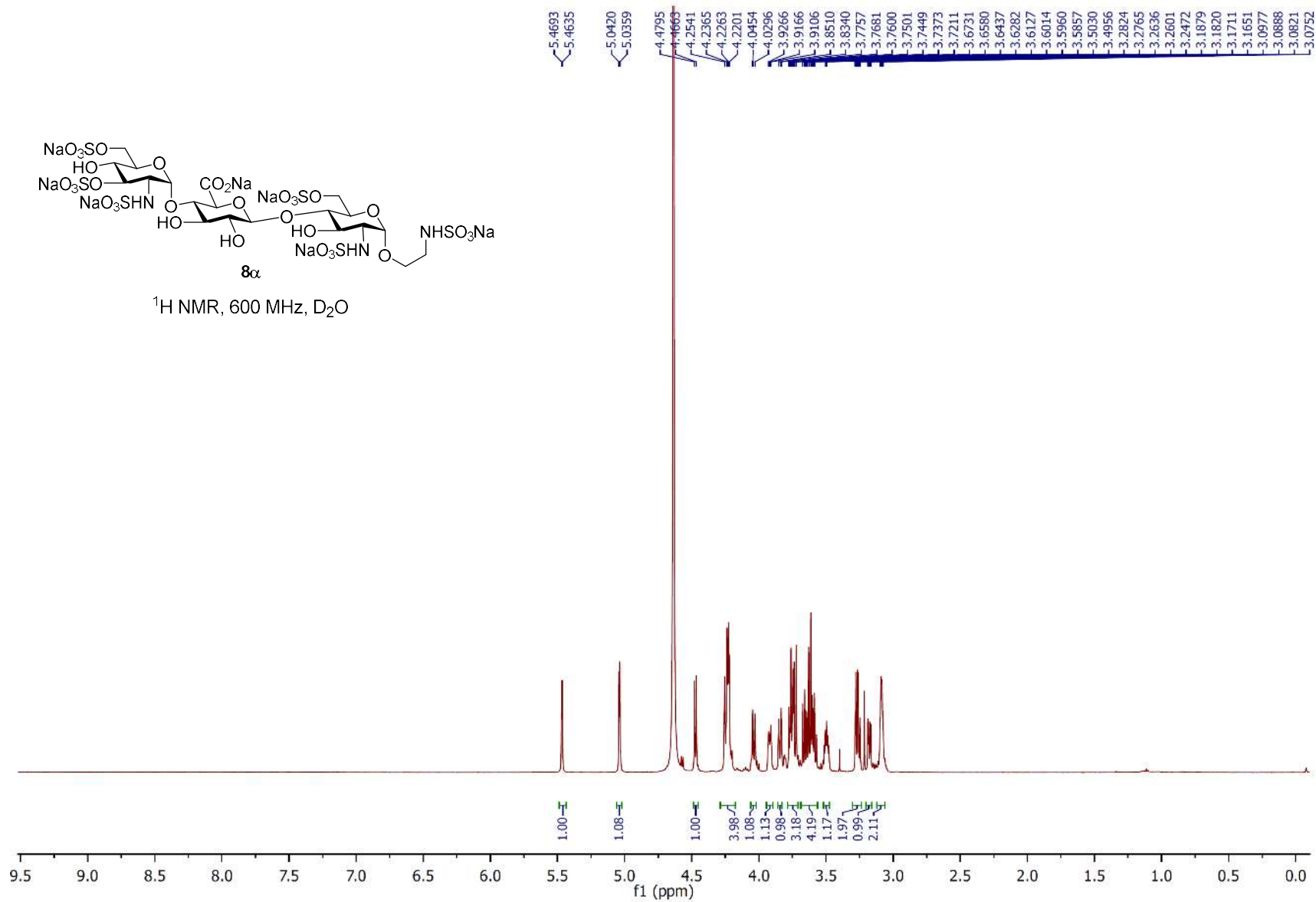


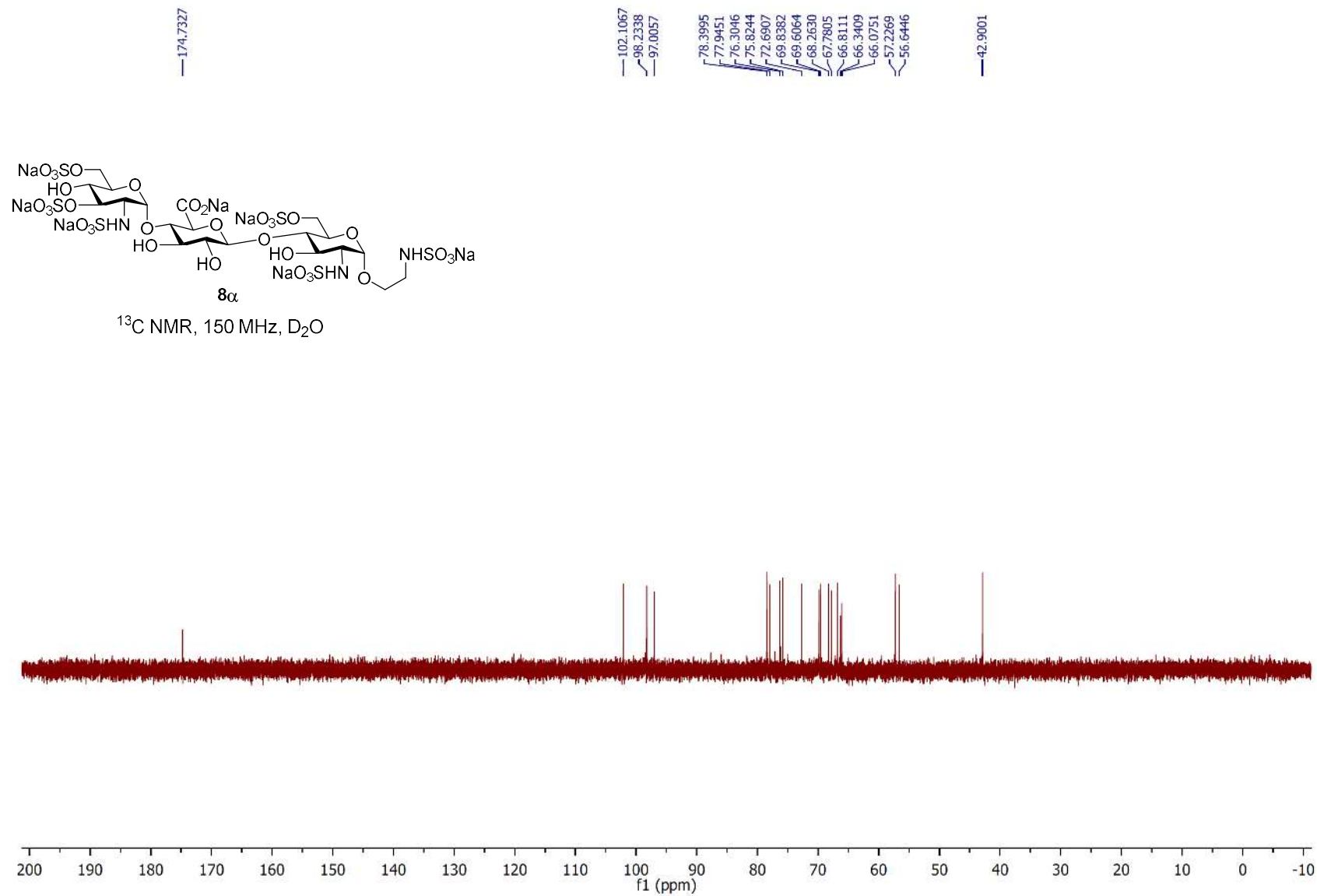


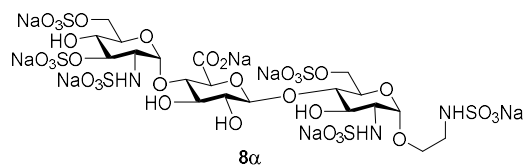




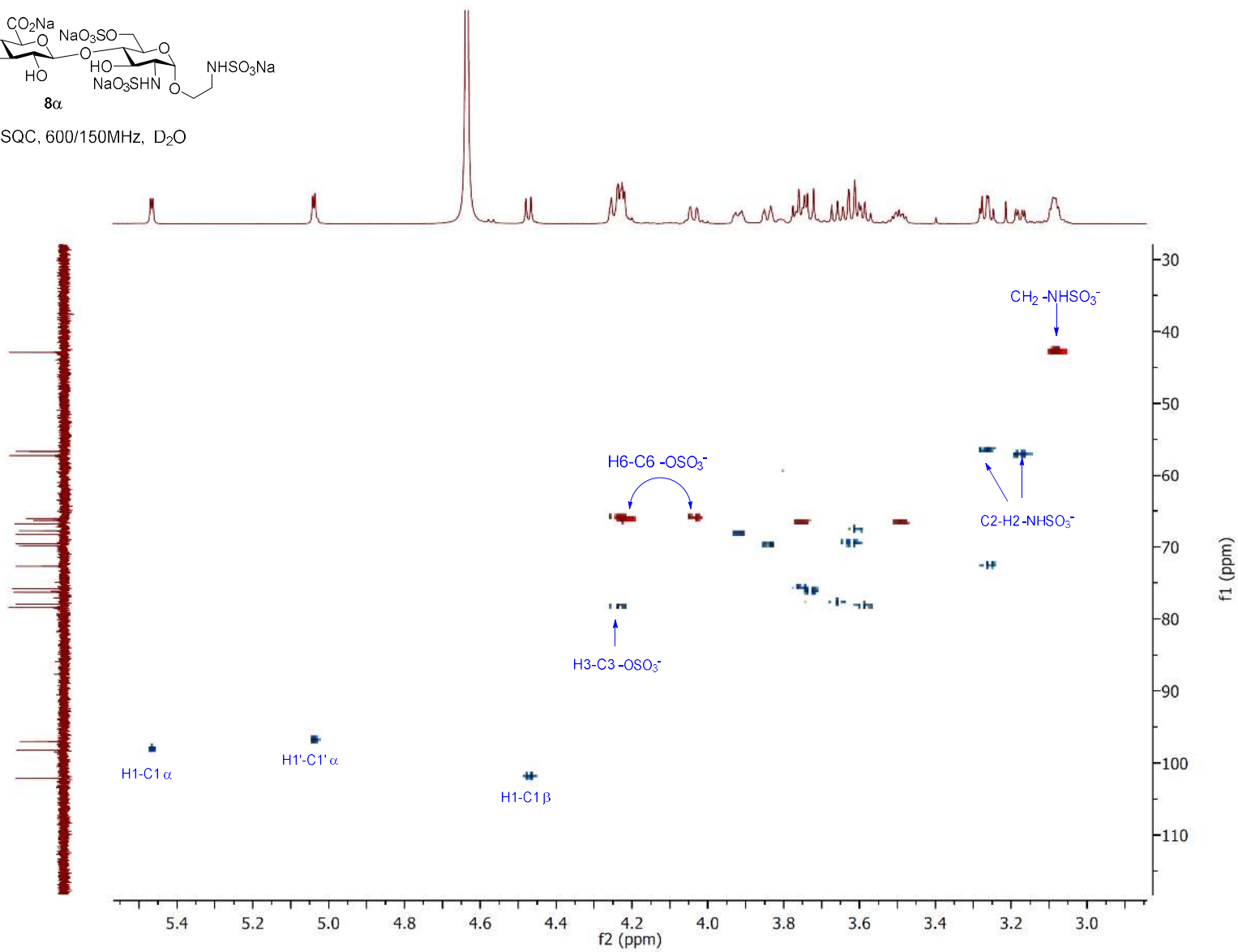
^1H NMR, 600 MHz, D_2O

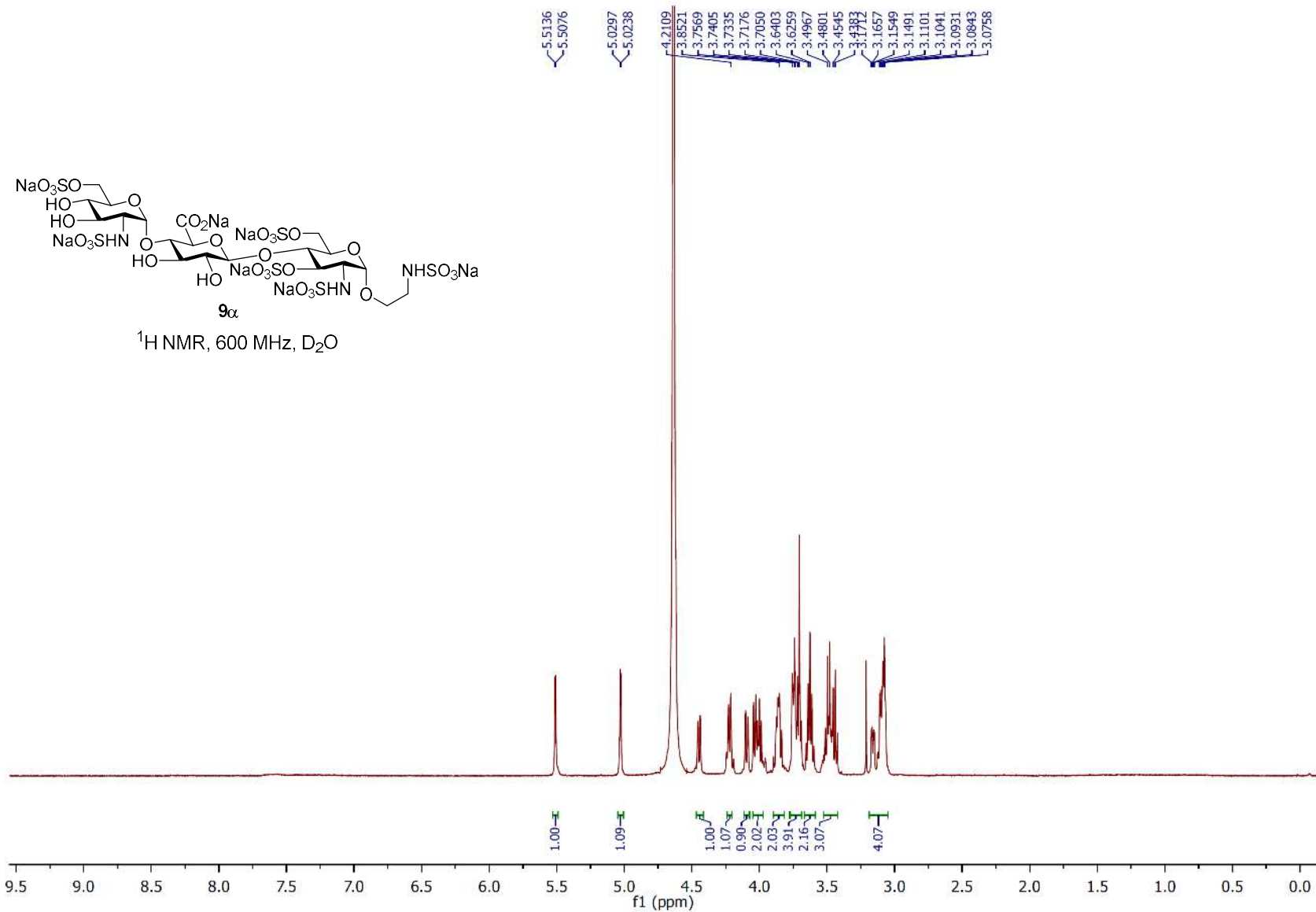


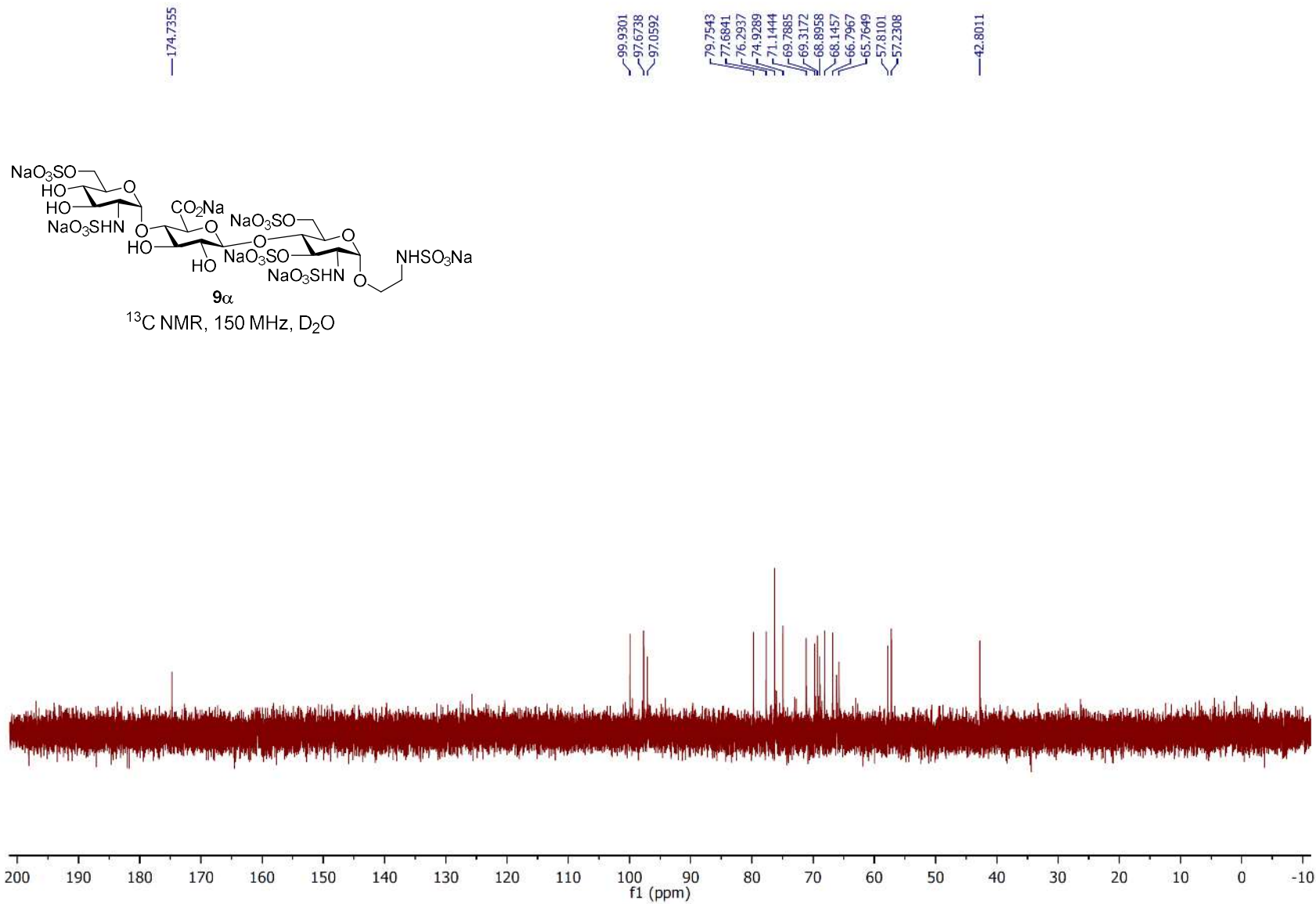


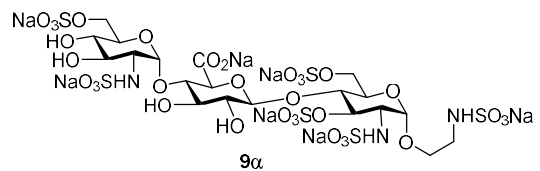


^1H - ^{13}C HSQC, 600/150MHz, D_2O









^1H - ^{13}C HSQC, 600/150MHz, D_2O

