

Synthesis and Characterization of Oligodeoxyribonucleotides Modified with 2'-Amino- α -L-LNA Adenine Monomers: High-affinity Targeting of Single-Stranded DNA

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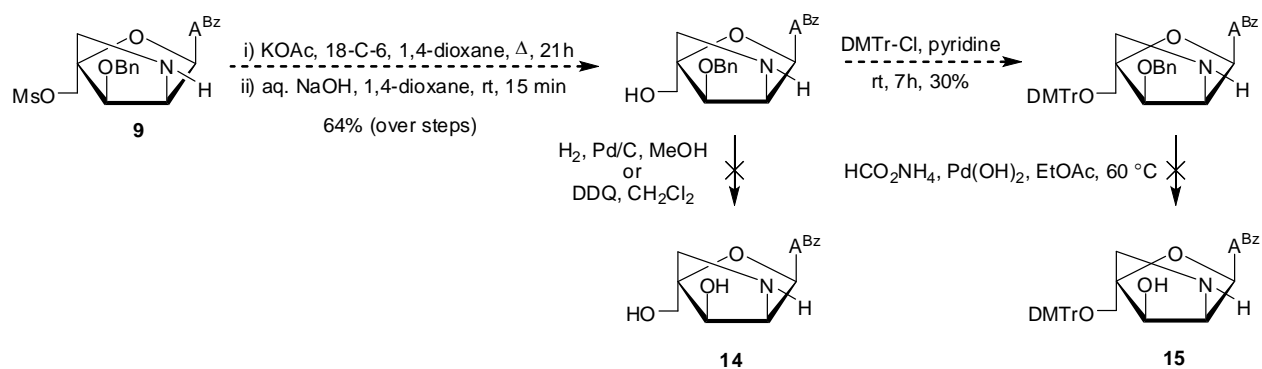
SUPPORTING INFORMATION

Table of contents

| | |
|--|-----|
| General experimental section | S2 |
| Additional attempted synthetic strategies toward key intermediates 14/15 (Scheme S1) | S3 |
| MS-data for modified ONs (Tables S1 and S2) | S4 |
| Representative thermal denaturation curves (Fig. S1) | S5 |
| DNA-selectivity of B1-B6 (Table S3) | S6 |
| Additional T _m data and discussion concerning mismatched duplexes (Table S4) | S7 |
| Representative absorption spectra involving X -modified ONs (Fig. S2) | S8 |
| Representative absorption spectra involving Z -modified ONs (Fig. S3) | S9 |
| Fluorescence emission spectra involving X -modified ONs (Fig. S4) | S10 |
| Fluorescence emission spectra involving Y -modified ONs (Fig. S5) | S11 |
| Fluorescence emission spectra of duplexes between Y1-Y6 and DNA (Fig. S6) | S12 |
| Fluorescence emission spectra involving Z -modified ONs (Fig. S7) | S13 |
| Fluorescence emission spectra of duplexes between X/Y/Z -modified ONs and matched/mismatched DNA targets (Figs. S8-S10) | S14 |
| NMR spectra of nucleosides x-y | S16 |

General experimental section. All solvents and reagents were obtained from commercial suppliers and used without further purification. Petroleum ether of the distillation range 60-80 °C was used. Anhydrous DMF and pyridine were used directly as obtained from commercial suppliers. Dichloromethane, 1,2-dichloroethane and *N,N'*-diisopropylethylamine were dried through storage over activated 4Å molecular sieves. Reactions were conducted under an atmosphere of argon whenever anhydrous solvents were used. All reactions were monitored by thin-layer chromatography (TLC) using silica gel coated plates with fluorescence indicator (SiO₂-60, F-254), which were visualized (a) under UV light, (b) by dipping in 5% concd. sulfuric acid in absolute ethanol (v/v) followed by heating, or (c) by dipping in a solution of molybdate phosphoric acid (12.5 g/L) and cerium(IV)sulfate (5 g/L) followed by heating. Silica gel column chromatography using moderate pressure (pressure ball) was performed using Silica gel 60 (particle size 0.040-0.063 mm). Evaporation of solvents was carried out under reduced pressure with a temperature not exceeding 45 °C. After column chromatography, appropriate fractions were pooled, evaporated, and dried at high vacuum for at least 8h to give products in high purity (>95% by 1D NMR techniques), unless stated otherwise. ¹H NMR and/or ¹³C NMR ascertained sample purity. ¹H NMR and ¹³C NMR spectra were recorded at either 500/125 MHz, or 300/75.5 MHz as specified. Chemical shifts are reported in parts per million (ppm) relative to tetramethylsilane or deuterated solvent as the internal standard (δ_{H} : CDCl₃ 7.26 ppm, DMSO-*d*₆ 2.50 ppm; δ_{C} : CDCl₃ 77.00 ppm, DMSO-*d*₆ 39.43 ppm). Exchangeable (ex) protons were identified through disappearance of signals upon D₂O addition. Assignments of NMR spectra are based on COSY, HSQC and DEPT and follow standard carbohydrate/nucleoside nomenclature. The carbon atom of C4 substituents is numbered C5" in nucleoside derivatives. Similar conventions apply for the corresponding hydrogen atoms. Quaternary carbons were not assigned

in ^{13}C NMR but their presence was verified through absence of signals in HSQC and DEPT. MALDI-HRMS were recorded in positive ion mode on a mass spectrometer using 2,5-dihydroxybenzoic acid or 3-hydroxypicolinic acid as a matrix and mixture of polyethylene glycol (PEG 600) and (PEG 1000) as internal calibration standards. ESI-HRMS were recorded in positive ion mode on a Q-TOF mass spectrometer using NaCl in MeCN:H₂O and PEG 600 and PEG 1000 as internal calibration standards.



Scheme S1. Additional attempted synthetic strategies toward key intermediates **14/15**. 18-C-6: 18-crown-6.

Table S1. MS-data for X/Y-modified ONs used in the current study.

| ONs | Sequence | Calc. m/z [M-H] | Found m/z [M-H] |
|-----------------------|---------------------------------------|-------------------|-------------------|
| X1 | 5'-GTG <u>X</u> TA TGC | 2995 | 2995 |
| X2 | 5'-GTG AT <u>X</u> TGC | 2995 | 2993 |
| X3 | 5'-GTG <u>X</u> <u>T</u> X TGC | 3236 | 3236 |
| X4 | 3'-CAC T <u>X</u> T ACG | 2924 | 2923 |
| X5 | 3'-CAC TAT <u>X</u> CG | 2924 | 2923 |
| X6 | 3'-CAC T <u>X</u> T <u>X</u> CG | 3165 | 3163 |
| Y1^a | 5'-GTG <u>Y</u> TA TGC | 3009 | 3008 |
| Y2 | 5'-GTG AT <u>Y</u> TGC | 3009 | 3009 |
| Y3 | 5'-GTG <u>Y</u> <u>T</u> <u>Y</u> TGC | 3264 | 3264 |
| Y4 | 3'-CAC T <u>Y</u> T ACG | 2937 | 2937 |
| Y5 | 3'-CAC TAT <u>Y</u> CG | 2937 | 2936 |
| Y6 | 3'-CAC T <u>Y</u> T <u>Y</u> CG | 3192 | 3192 |
| Y7^b | 3'-CAC T <u>Y</u> A ACG | 2947 | 2948 |
| Y8 | 3'-CAC T <u>Y</u> C ACG | 2923 | 2923 |
| Y9^c | 3'-CAC T <u>Y</u> G ACG | 2963 | 2962 |

Purity: ^a70%, ^b84% ^c75% purity.

Table S2. MS-data for X/Y-modified ONs used in the current study.

| ONs | Sequence | Calc. m/z [M] | Found m/z [M+H] |
|-----------------------|---------------------------------------|-----------------|-------------------|
| W1^a | 5'-GTG <u>W</u> TA TGC | 2780 | 2781 |
| W2^b | 5'-GTG AT <u>W</u> TGC | 2780 | 2781 |
| W3^c | 5'-GTG <u>W</u> <u>T</u> <u>W</u> TGC | 2807 | 2808 |
| W4^d | 3'-CAC T <u>W</u> T ACG | 2709 | 2710 |
| W5^e | 3'-CAC TAT <u>W</u> CG | 2709 | 2710 |
| W6^f | 3'-CAC T <u>W</u> T <u>W</u> CG | 2736 | 2737 |
| Z1 | 5'-GTG <u>Z</u> TA TGC | 3022 | 3023 |
| Z2 | 5'-GTG AT <u>Z</u> TGC | 3022 | 3023 |
| Z3 | 5'-GTG <u>Z</u> <u>T</u> <u>Z</u> TGC | 3291 | 3292 |
| Z4 | 3'-CAC T <u>Z</u> T ACG | 2951 | 2952 |
| Z5 | 3'-CAC TAT <u>Z</u> CG | 2951 | 2952 |
| Z6 | 3'-CAC T <u>Z</u> T <u>Z</u> CG | 3220 | 3221 |

Purity: ^a72%, ^b58%, ^c73%, ^d71%, ^e63%, ^f58% - we hypothesize that the low purities are due to the presence of 'skippers' (i.e., ONs without the W monomer), which arose due to inadequate capping during fabrication of W-modified ONs.

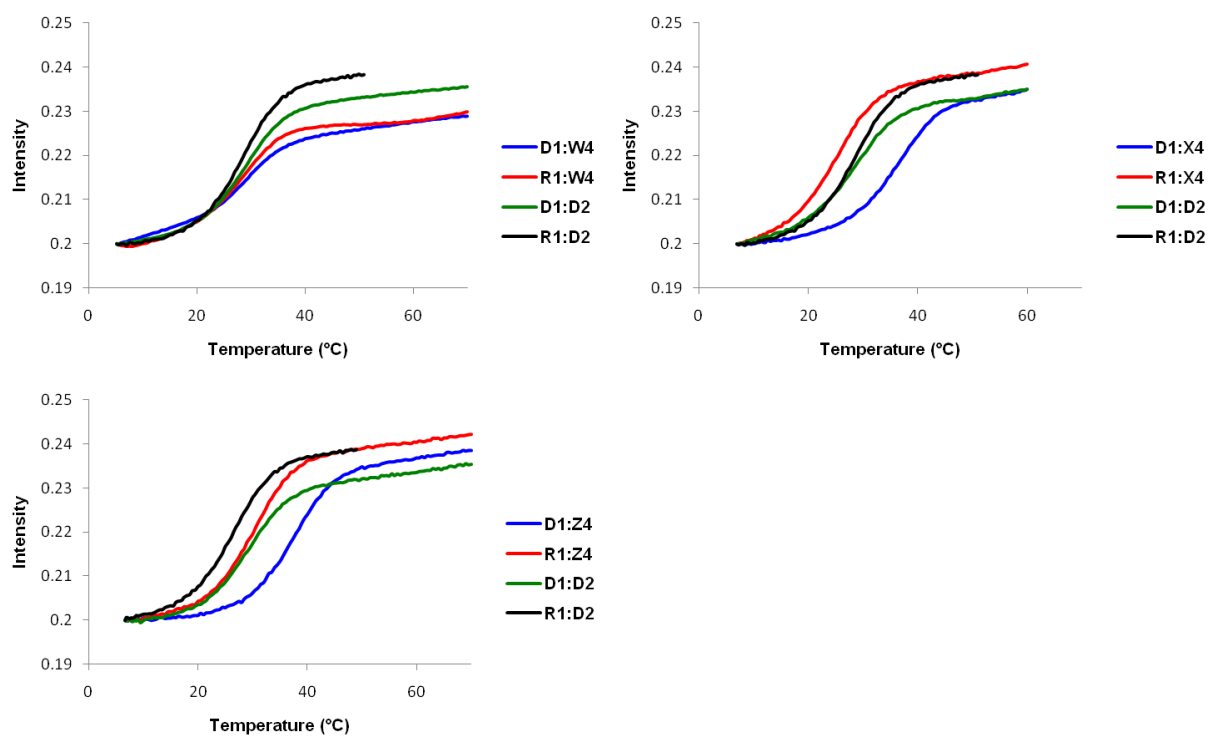


Figure S1. Representative thermal denaturation curves for modified and reference duplexes.

Table S3. DNA-selectivity of **B1-B6**.^a

| ON | Sequence | B = | $\Delta\Delta T_m$ (DNA-RNA)/°C | | | |
|-----------|---------------------------------|------------|---------------------------------|----------|----------|----------|
| | | | W | X | Y | Z |
| B1 | 5'-GTG <u>B</u> TA TGC | | -3.0 | +6.0 | +9.5 | +2.5 |
| B2 | 5'-GTG AT <u>B</u> TGC | | -2.0 | +6.0 | +9.0 | +3.0 |
| B3 | 5'-GTG <u>B</u> T <u>B</u> TGC | | -4.0 | +6.5 | +9.0 | +5.0 |
| B4 | 3'-CAC T <u>B</u> T ACG | | -4.5 | +7.0 | +9.0 | +1.0 |
| B5 | 3'-CAC TAT <u>B</u> CG | | -7.0 | +2.0 | +5.5 | -2.0 |
| B6 | 3'-CAC T <u>B</u> T <u>B</u> CG | | -9.0 | +5.0 | +6.5 | ±0.0 |

^a DNA selectivity defined as $\Delta\Delta T_m$ (DNA-RNA) = ΔT_m (vs DNA) - ΔT_m (vs RNA).

Additional discussion – mismatch discrimination of B3-series ONs. The specificity of ONs with two modifications positioned as next-nearest neighbors (**B3** series) was evaluated against DNA targets with a single central mismatched nucleotide opposite of the central thymidine (Table S4). **X3** and **Y3** display very poor binding specificity, whereas **Z3** displays binding specificity that is comparable to unmodified reference strand **D1**.

Table S4. Discrimination of mismatched DNA targets by **B3**-series and reference ONs.^a

| ON | Sequence | B = | DNA : 3'-CAC T BT ACG | | | |
|-----------|--------------------------------|------------|------------------------------|-----------------------------|-------|-------|
| | | | $T_m/^\circ\text{C}$ | $\Delta T_m/^\circ\text{C}$ | | |
| | | | A | C | G | T |
| D1 | 5'-GTG ATA TGC | | 27.5 | -16.5 | -9.5 | -17.0 |
| X3 | 5'-GTG <u>X</u> T <u>X</u> TGC | | 32.5 | +2.0 | +0.5 | +2.0 |
| Y3 | 5'-GTG <u>Y</u> T <u>Y</u> TGC | | 41.0 | -5.0 | -2.0 | -2.0 |
| Z3 | 5'-GTG <u>Z</u> T <u>Z</u> TGC | | 43.5 | -14.5 | -11.5 | -9.5 |

^a For conditions of thermal denaturation experiments, see Table 1. T_m 's of fully matched duplexes are shown in bold. ΔT_m = change in T_m relative to fully matched DNA:DNA duplex.

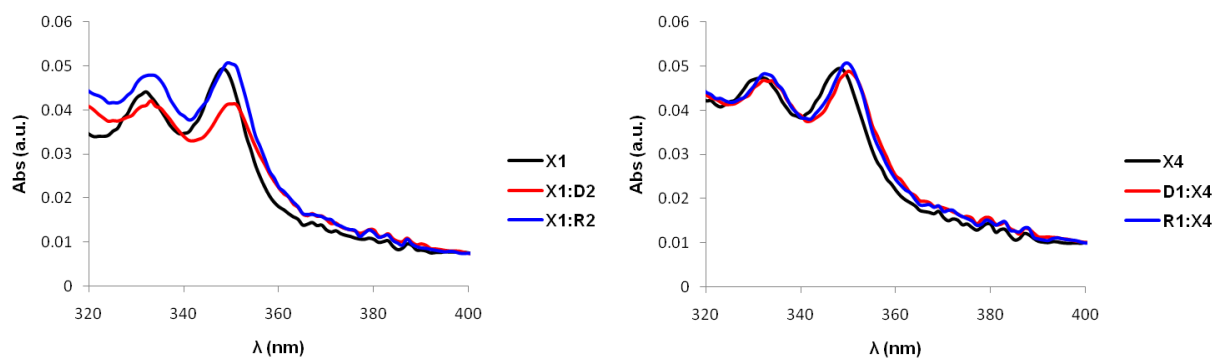


Figure S2. Representative absorption spectra of X-modified ONs and the corresponding duplexes with complementary DNA/RNA.

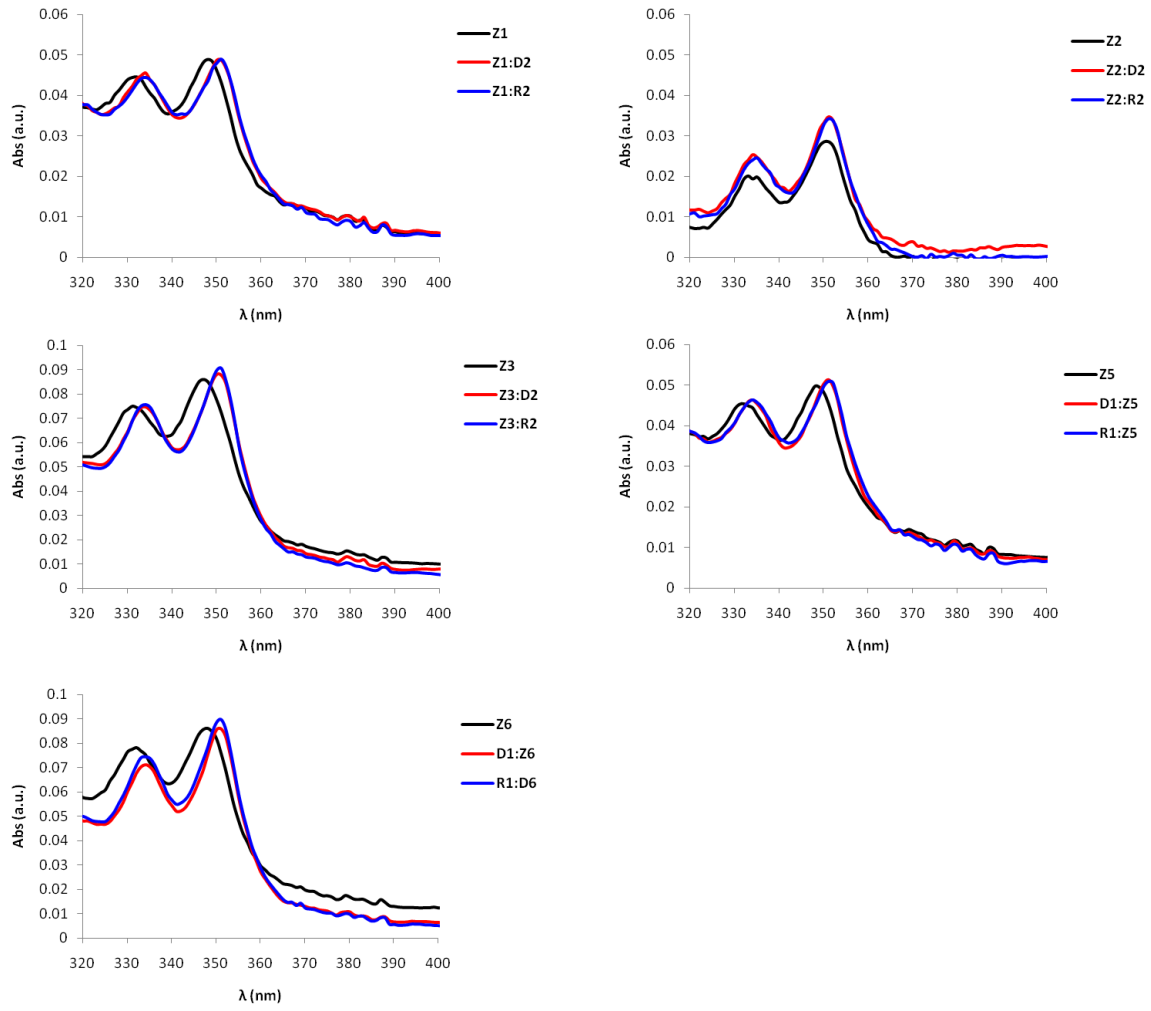


Figure S3. Representative absorption spectra of **Z**-modified ONs and the corresponding duplexes with complementary DNA/RNA.

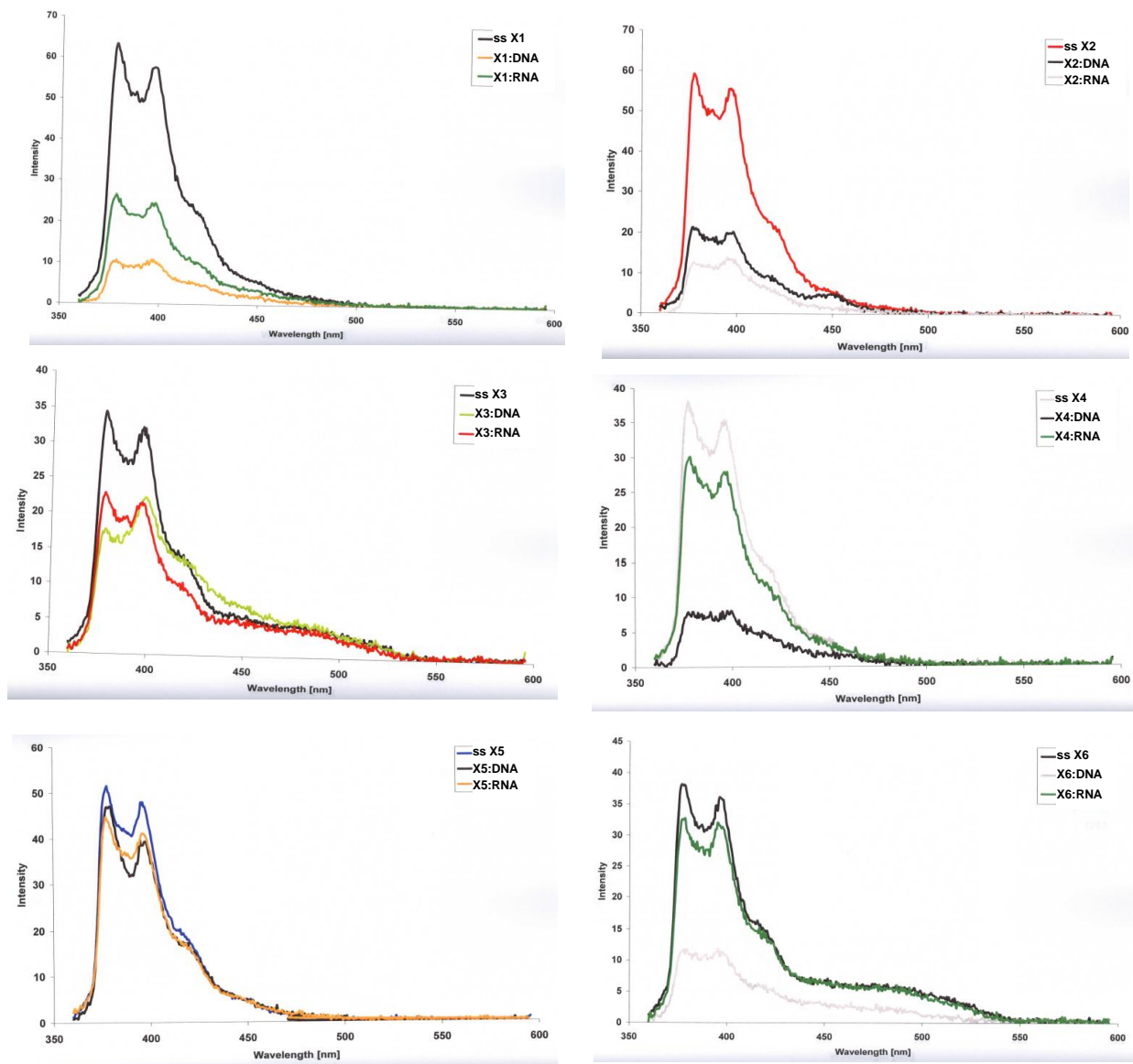


Figure S4. Steady-state fluorescence emission spectra of **X1-X6** in the presence of absence of complementary DNA/RNA. $T_{\text{exp}} = 5\text{ }^{\circ}\text{C}$; $\lambda_{\text{ex}} = 350\text{ nm}$; each ON used at $1\text{ }\mu\text{M}$ concentration in T_m buffer.

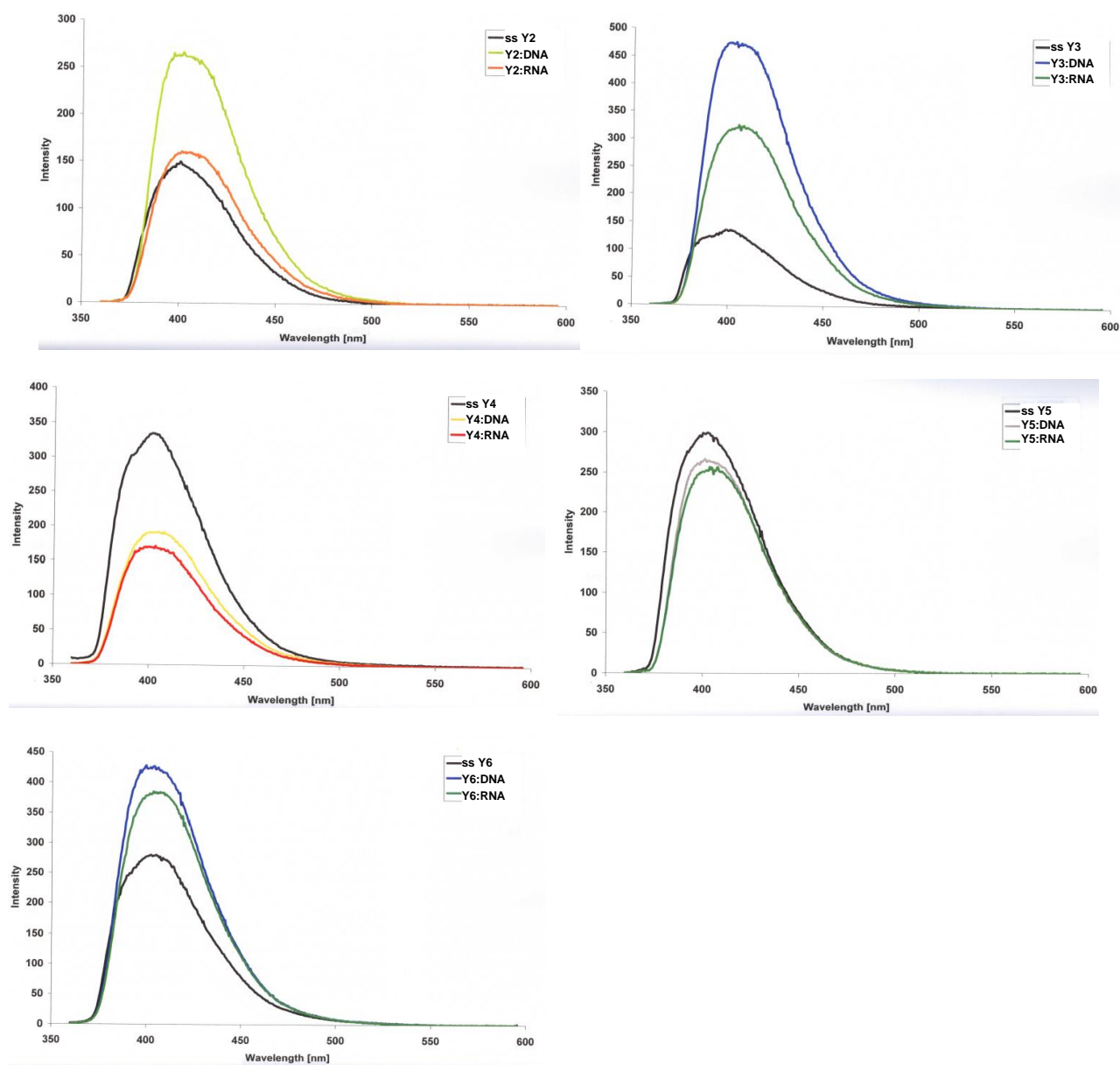


Figure S5. Steady-state fluorescence emission spectra of **Y1-Y6** in the presence and absence of complementary DNA/RNA. $T_{\text{exp}} = 5\text{ }^{\circ}\text{C}$; $\lambda_{\text{ex}} = 350\text{ nm}$; each ON used at $0.15\text{ }\mu\text{M}$ concentration in T_{m} buffer.

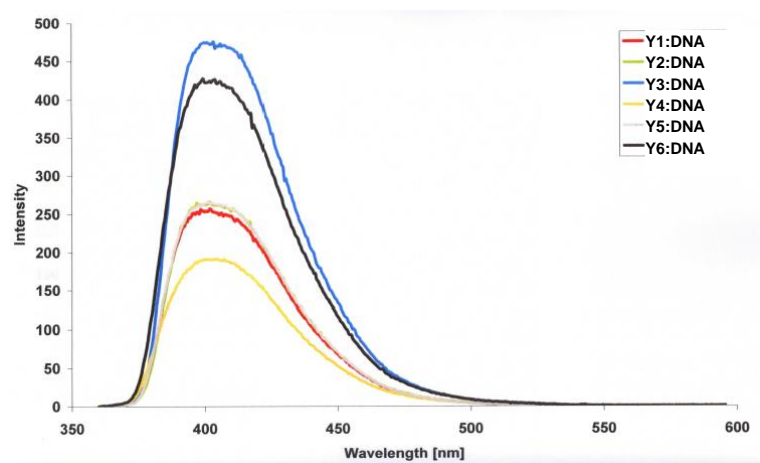


Figure S6. Steady-state fluorescence emission spectra of duplexes between **Y1-Y6** and complementary DNA. The spectra for **Y2:DNA** and **Y5:DNA** are overlapping. $T_{\text{exp}} = 5\text{ }^{\circ}\text{C}$; $\lambda_{\text{ex}} = 350\text{ nm}$; each ON used at $0.15\text{ }\mu\text{M}$ concentration in T_m buffer.

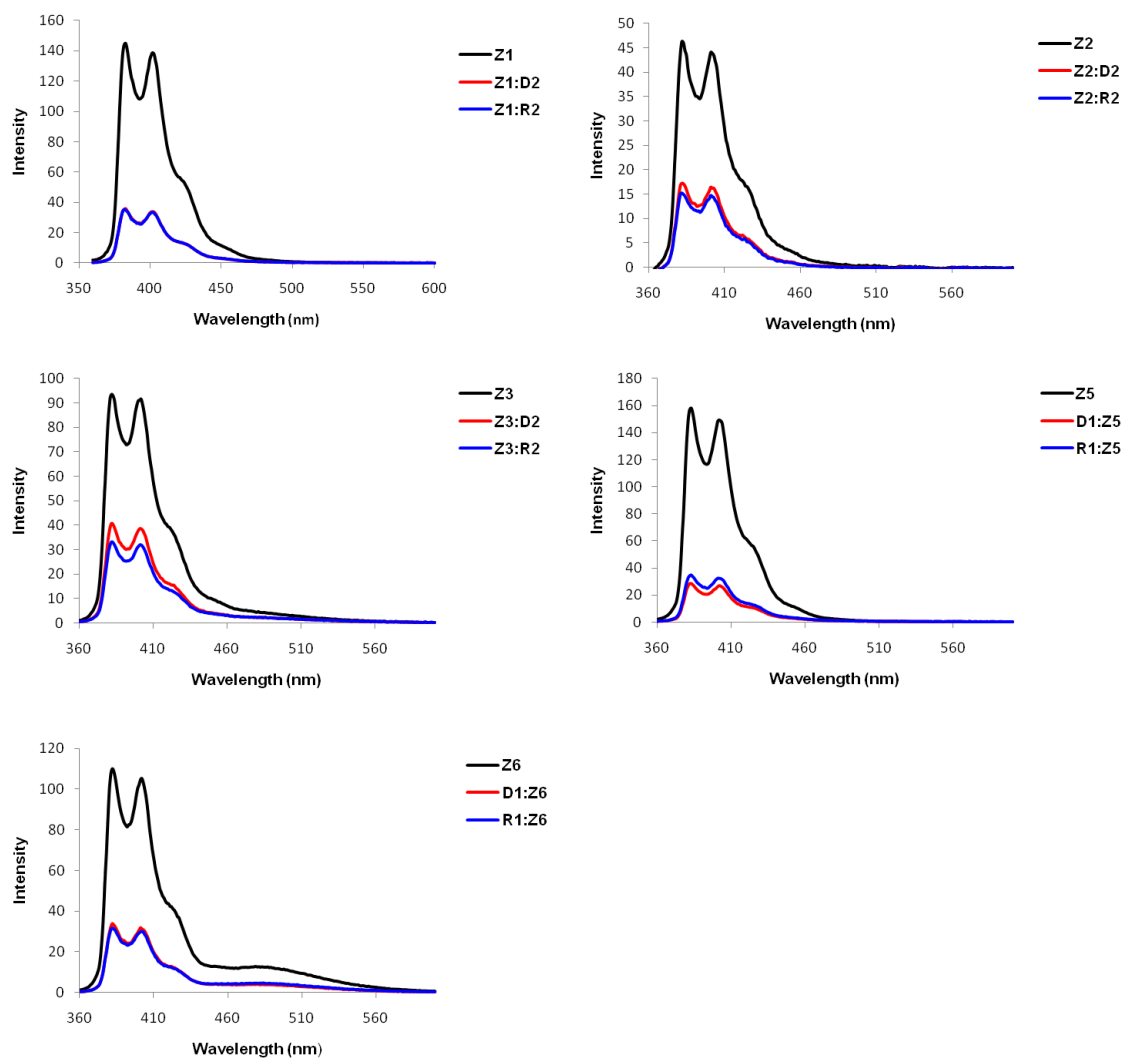


Figure S7. Steady-state fluorescence emission spectra of **Z**-modified ONs in the presence or absence of complementary DNA/RNA. $T_{\text{exp}} = 5 \text{ }^{\circ}\text{C}$; $\lambda_{\text{ex}} = 350 \text{ nm}$; each ON used at $1 \text{ } \mu\text{M}$ concentration in T_{m} buffer.

Additional discussion – mismatch discrimination via fluorescence. Probes **X4/Y4/Z4** were evaluated as probes for potential discrimination of single nucleotide polymorphisms (SNPs). Thus, these probes were hybridized with DNA strands with mismatched nucleotides opposite of the **X-Z** monomers. Although differences in fluorescence emission are observed, the differences are too small to be practically useful (Fig. S8-S10).

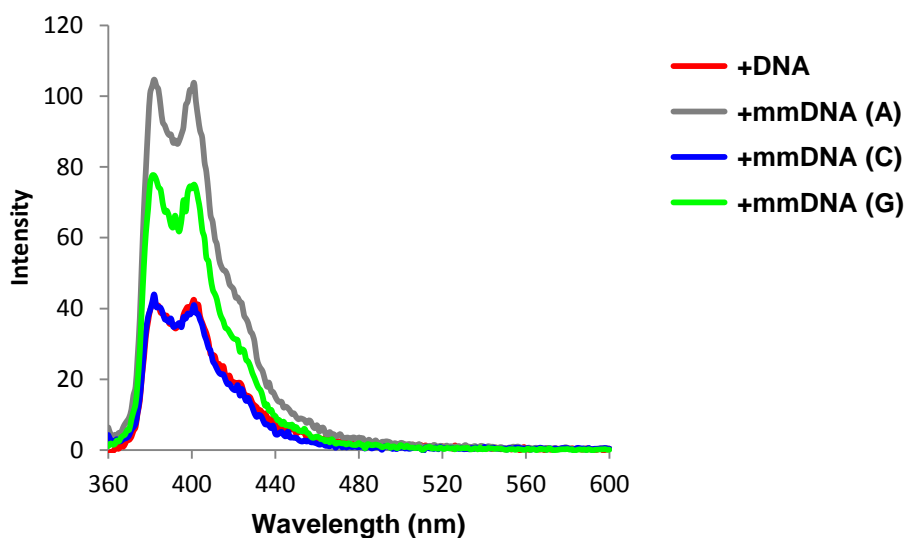


Figure S8. Steady-state fluorescence emission spectra of duplexes between **X4** and matched or mismatched DNA targets (mismatched nucleotide listed in parenthesis). Spectra were recorded at 5 °C using $\lambda_{\text{ex}} = 350$ nm and 1 μM concentration of each ON.

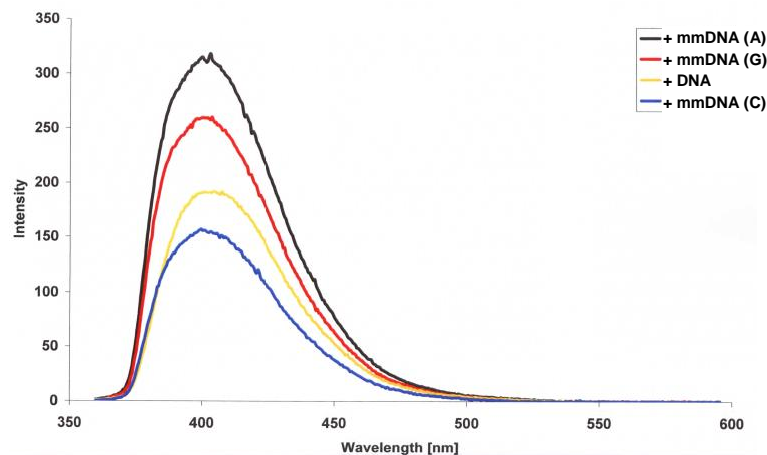


Figure S9. Steady-state fluorescence emission spectra of duplexes between **Y4** and matched or mismatched DNA targets (mismatched nucleotide listed in parenthesis). Spectra were recorded at 5 °C using $\lambda_{\text{ex}} = 350$ nm and 0.15 μM concentration of each ON.

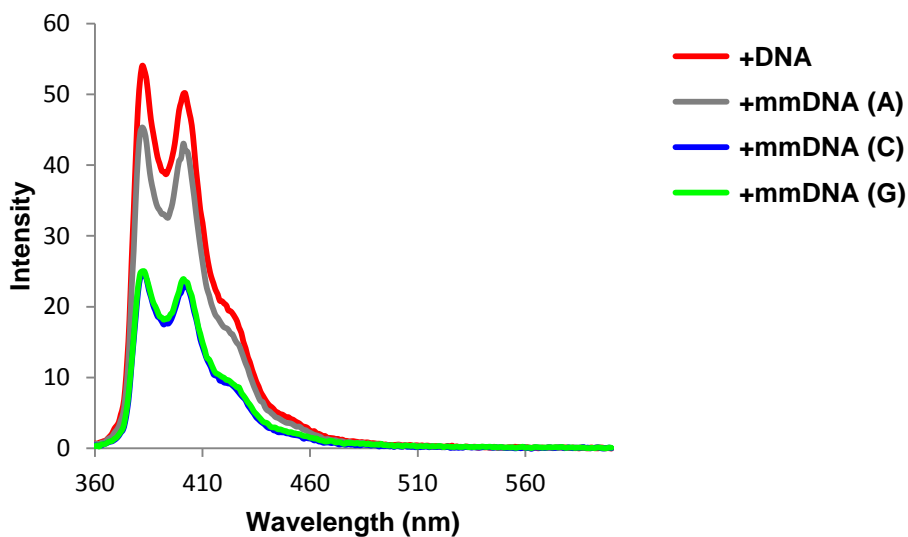
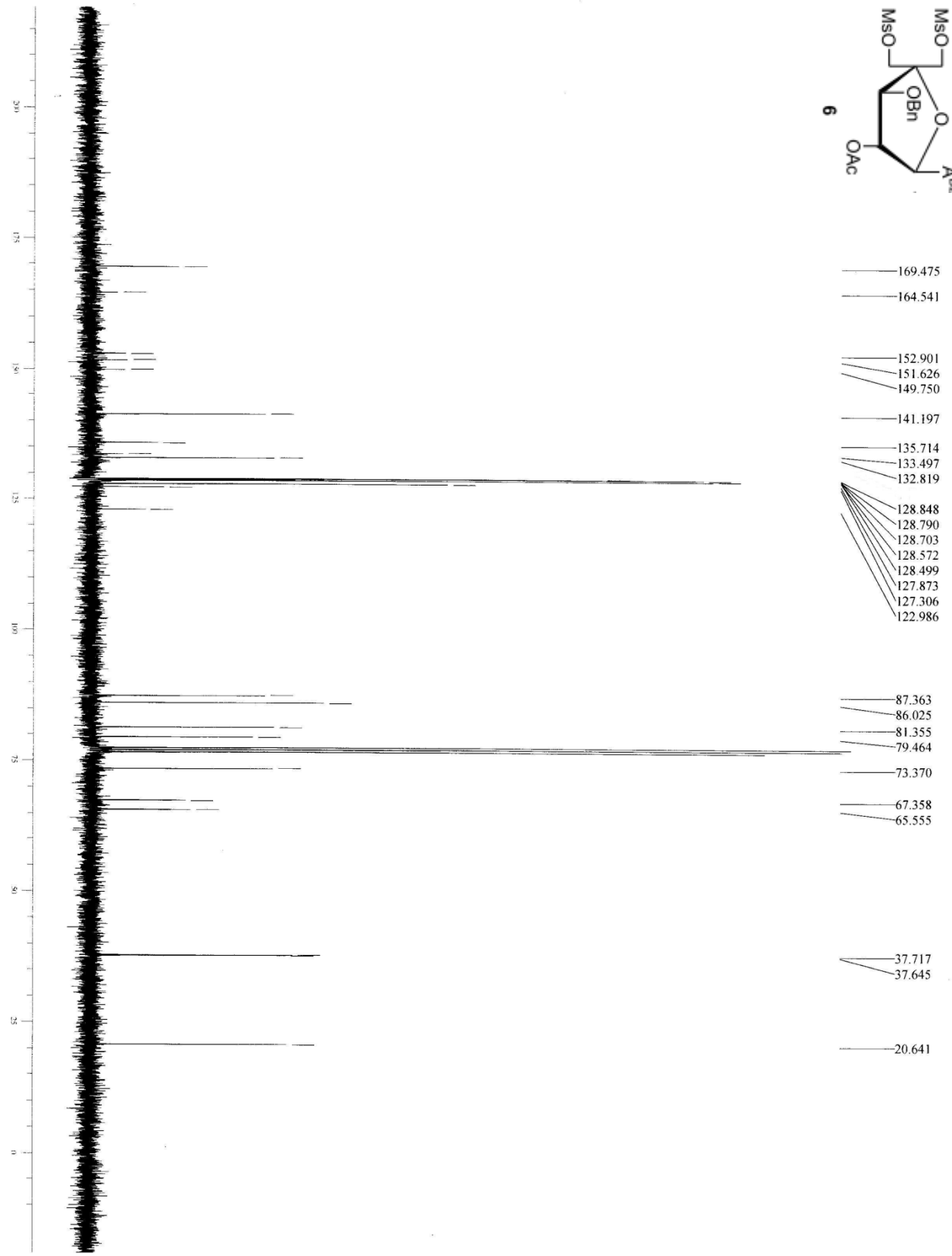
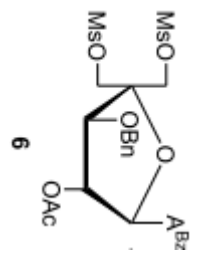
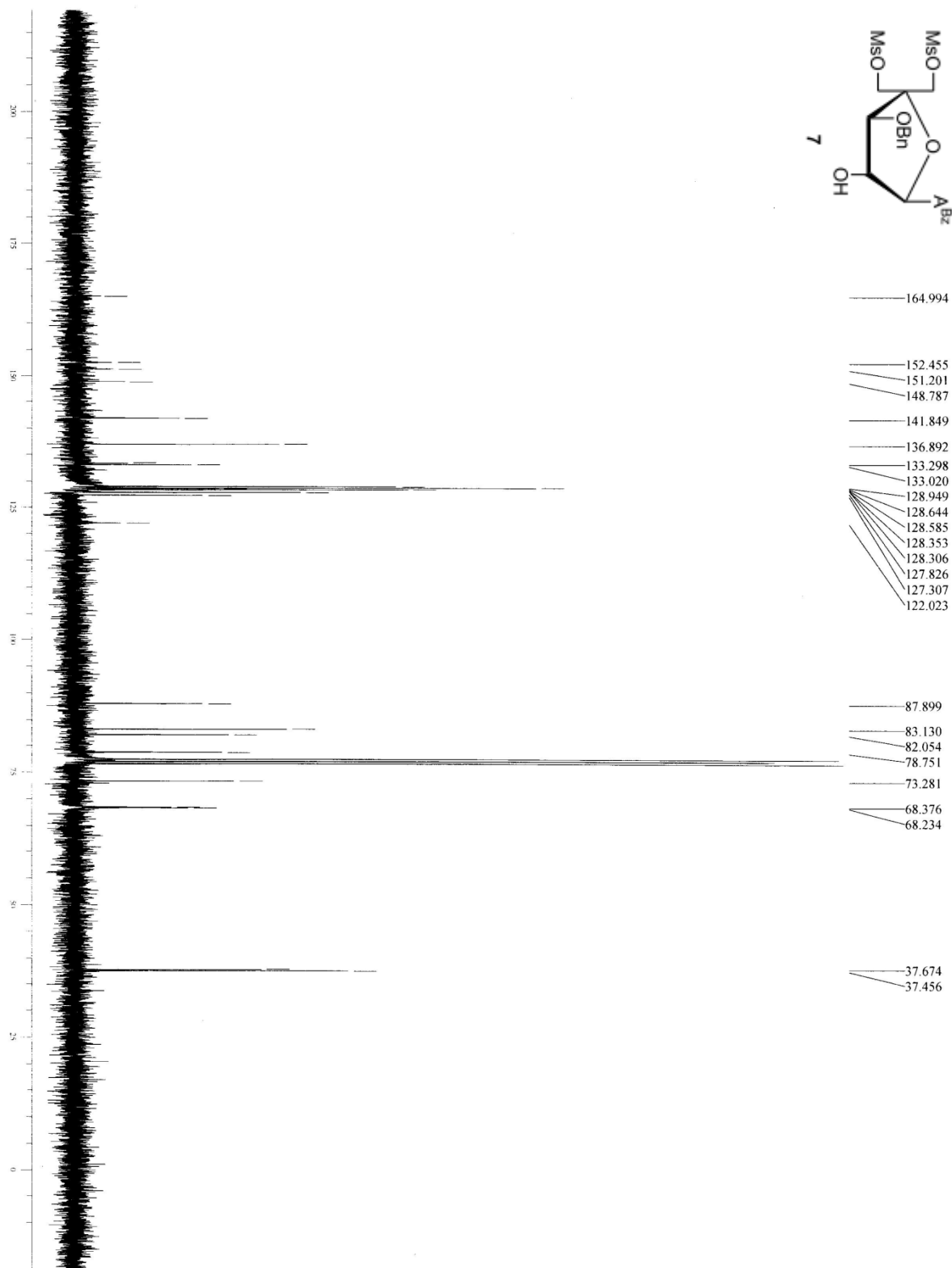
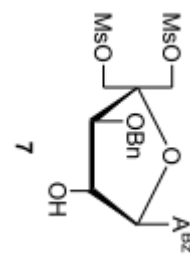
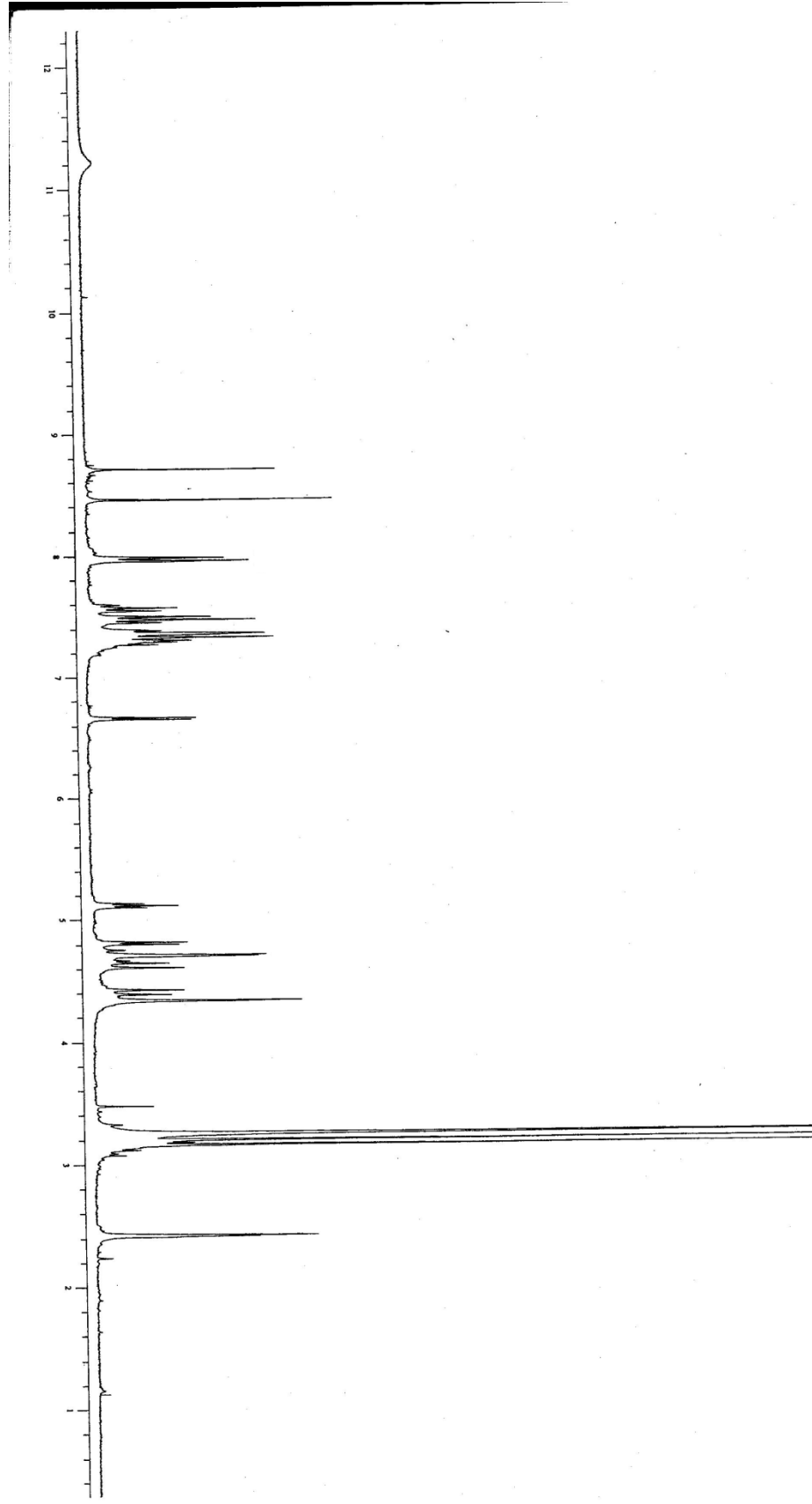
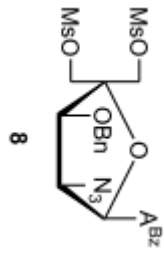
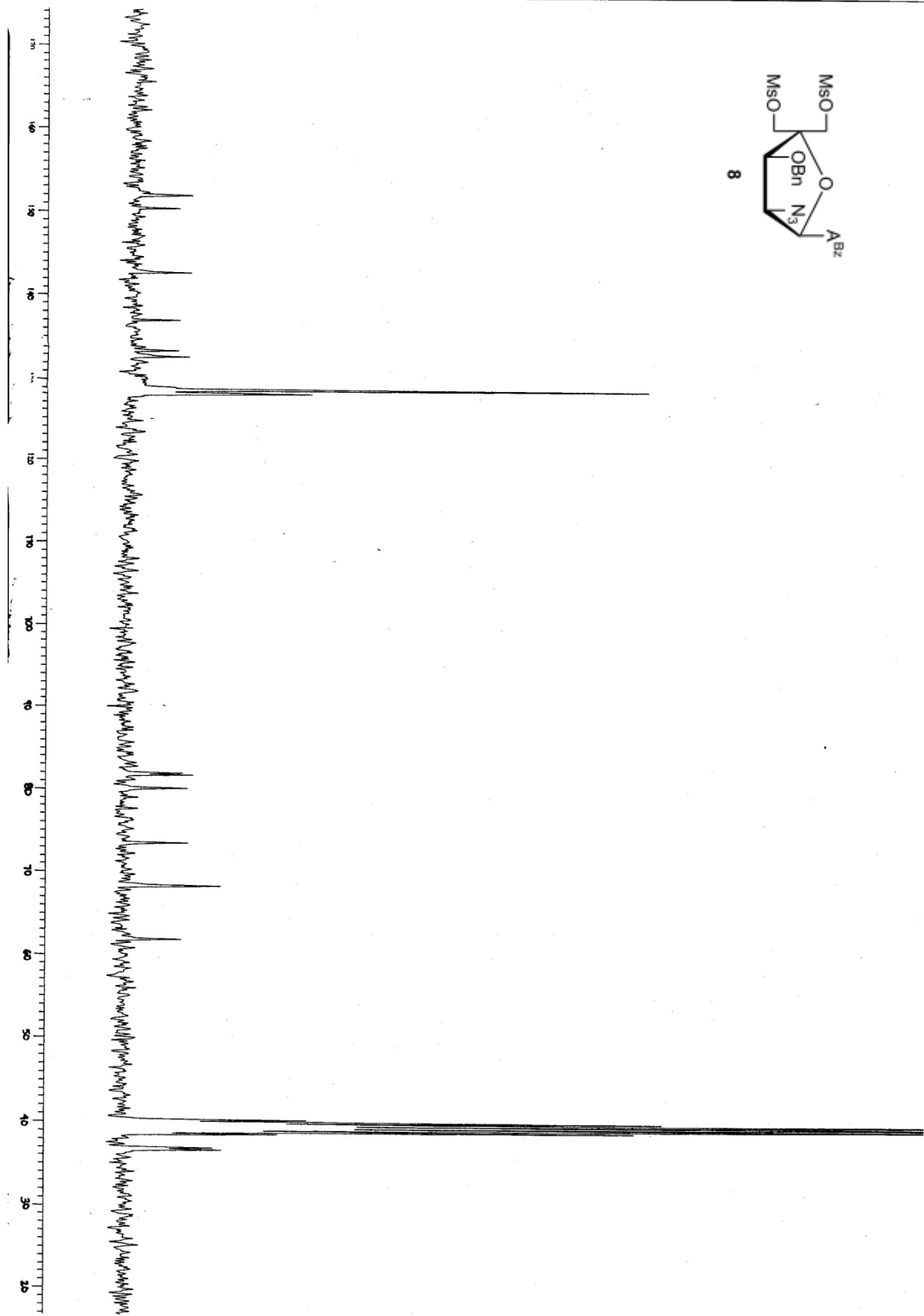
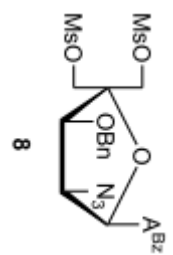


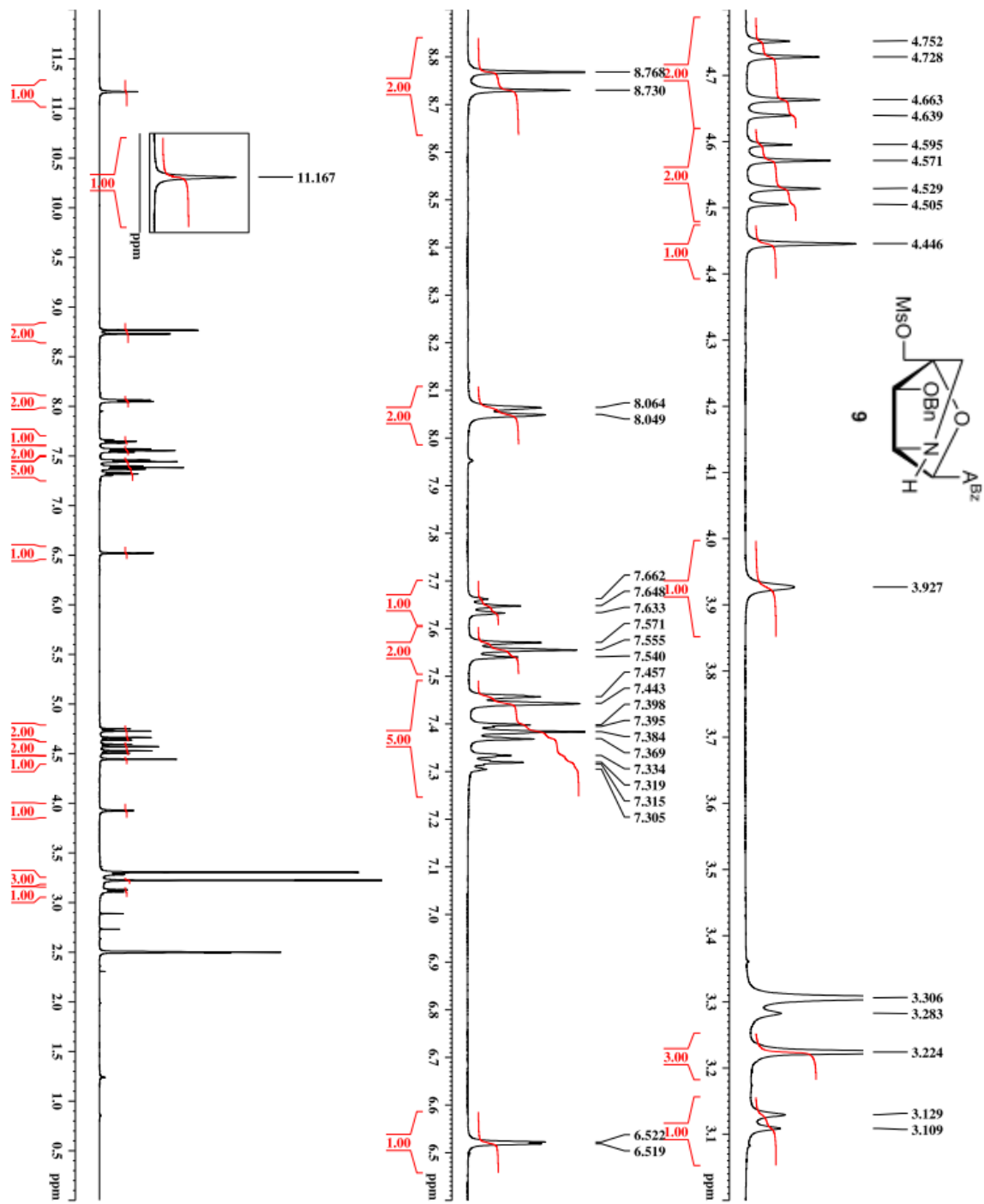
Figure S10. Steady-state fluorescence emission spectra of duplexes between **Z4** and matched or mismatched DNA targets (mismatched nucleotide listed in parenthesis). Spectra were recorded at 5 °C using $\lambda_{\text{ex}} = 350$ nm and 1 μM concentration of each ON.

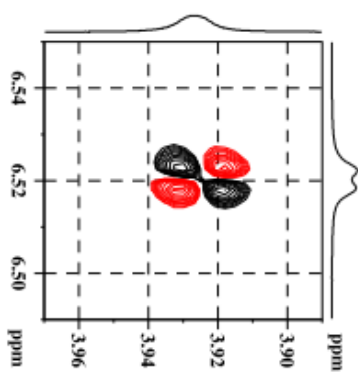
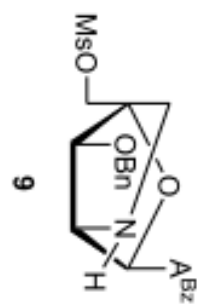
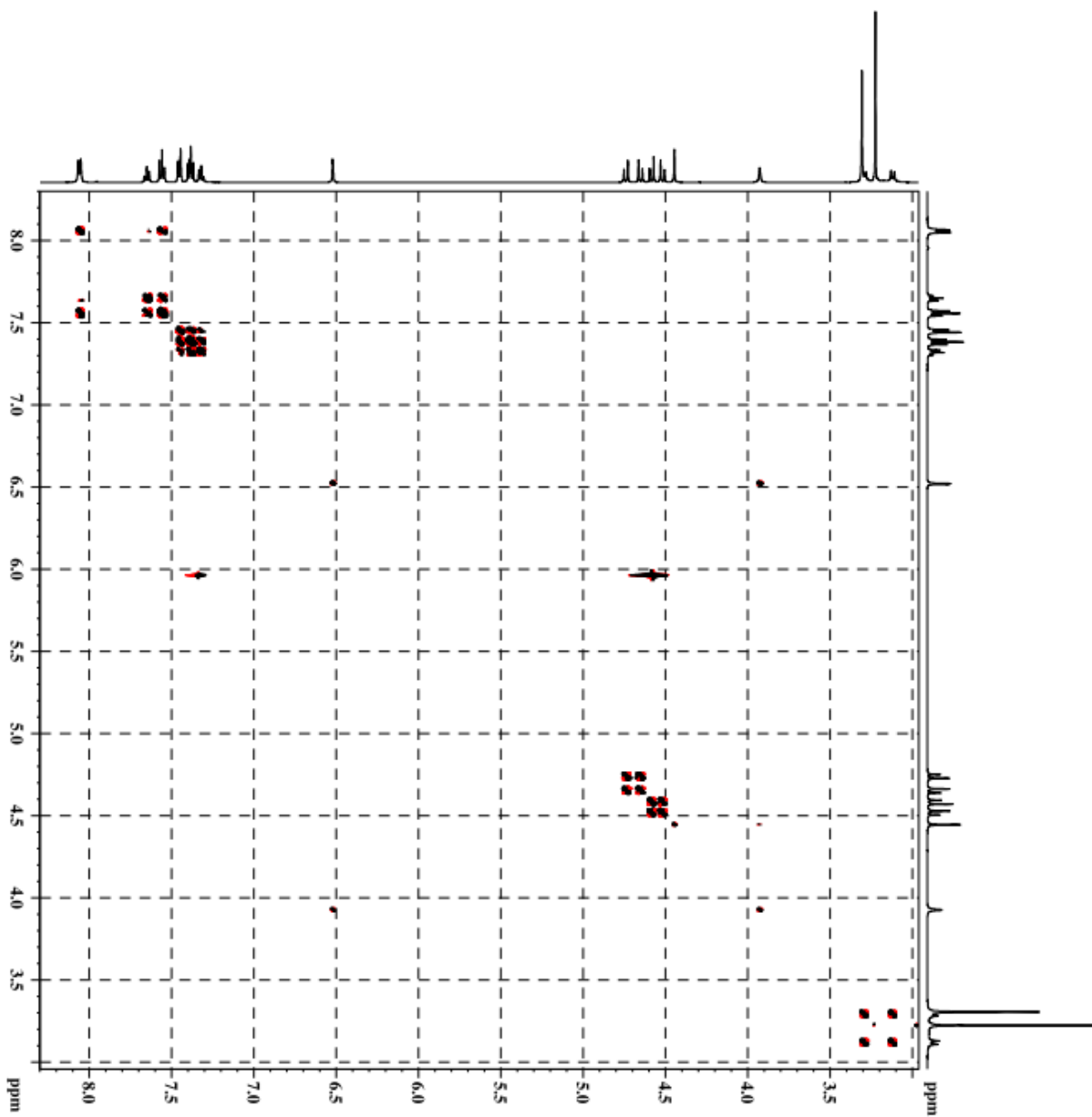


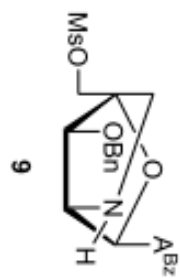
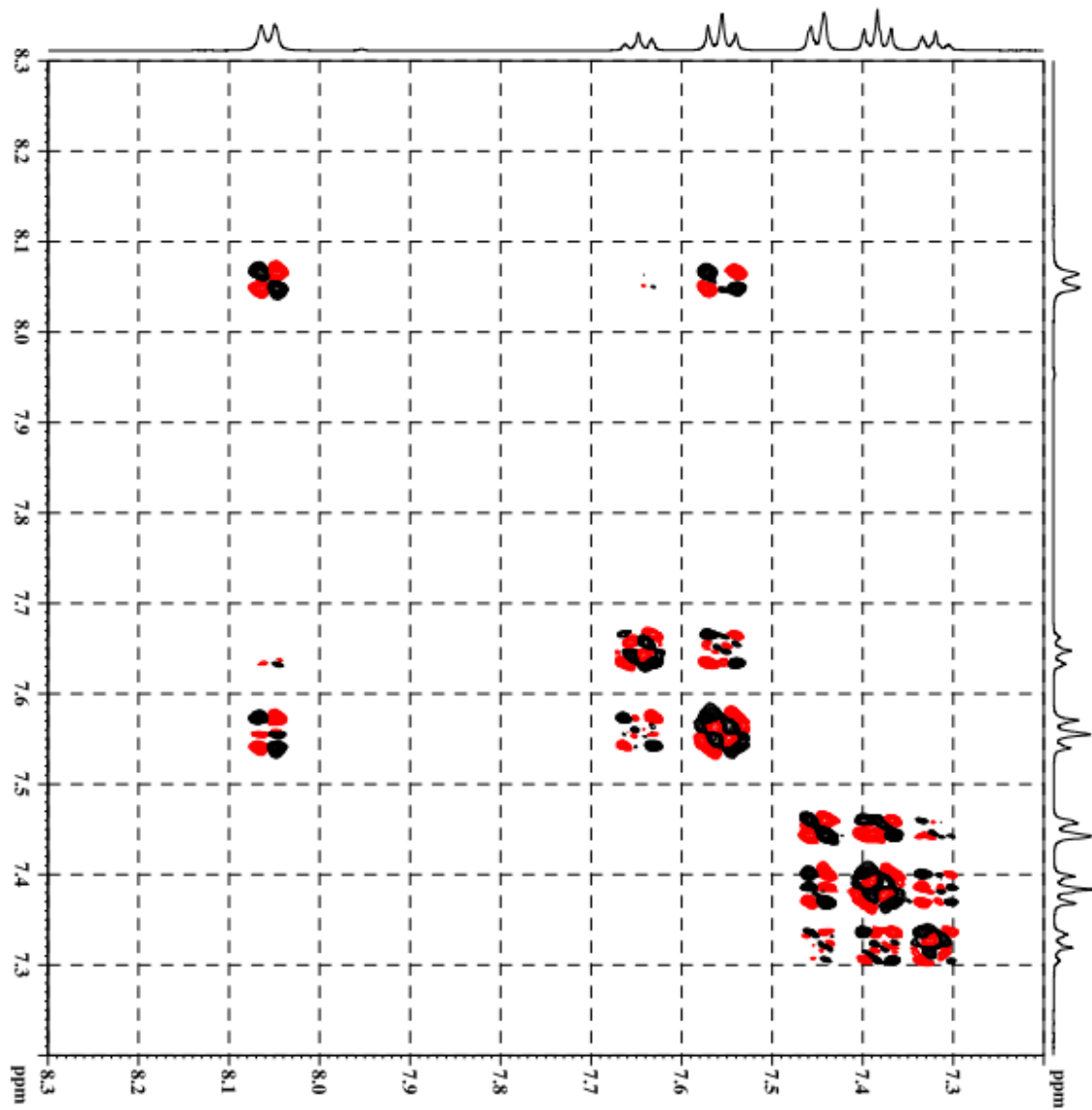


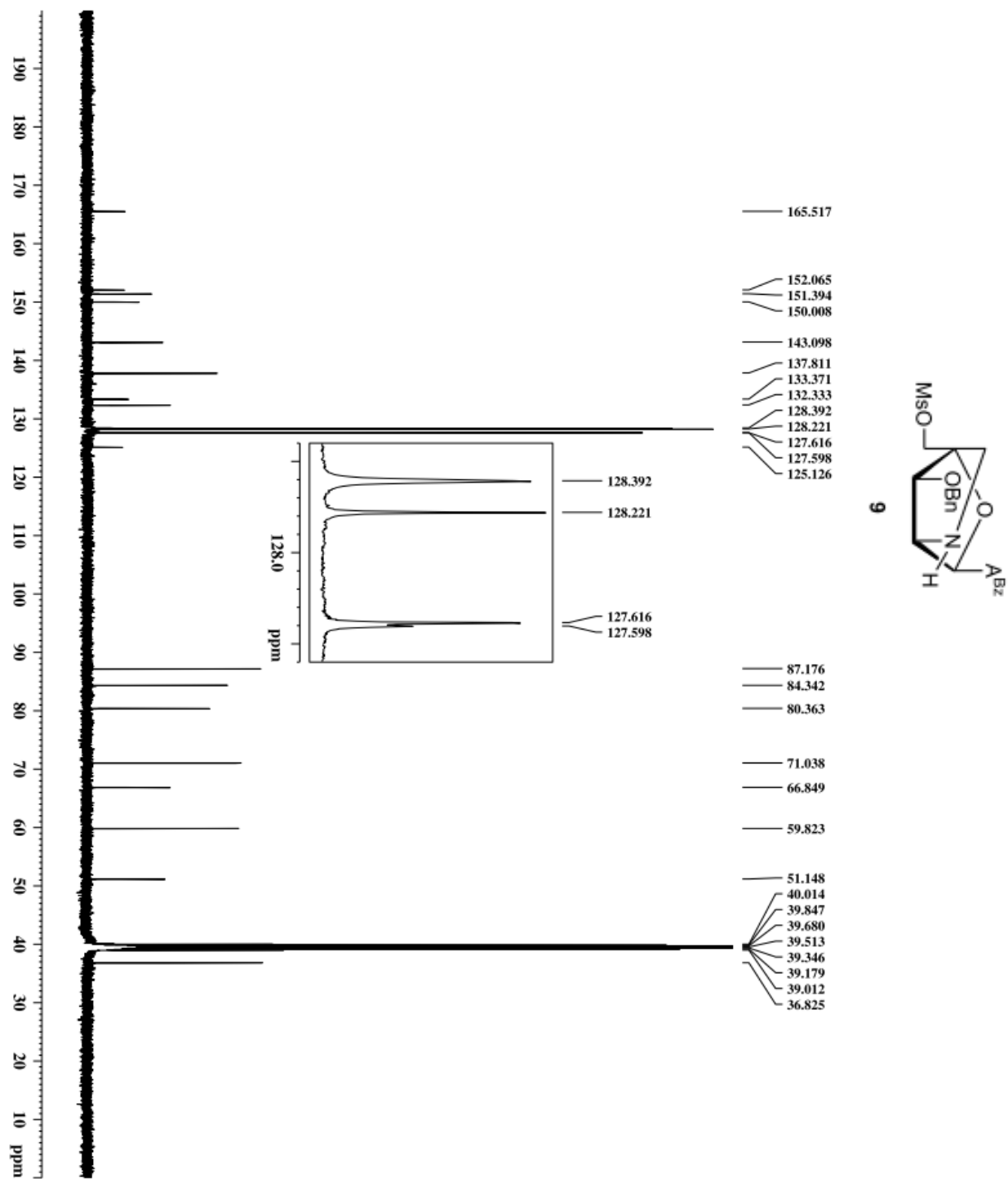


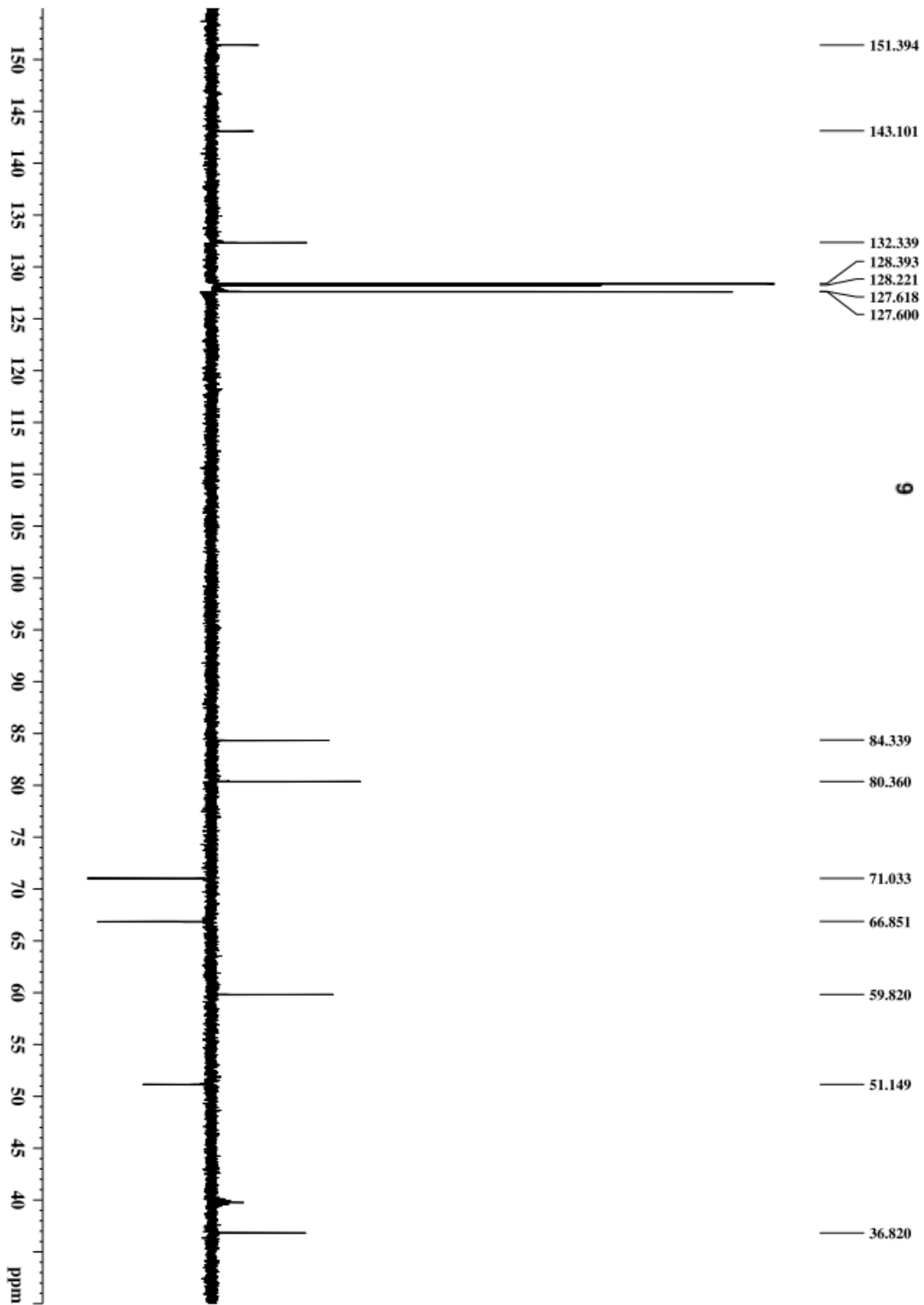


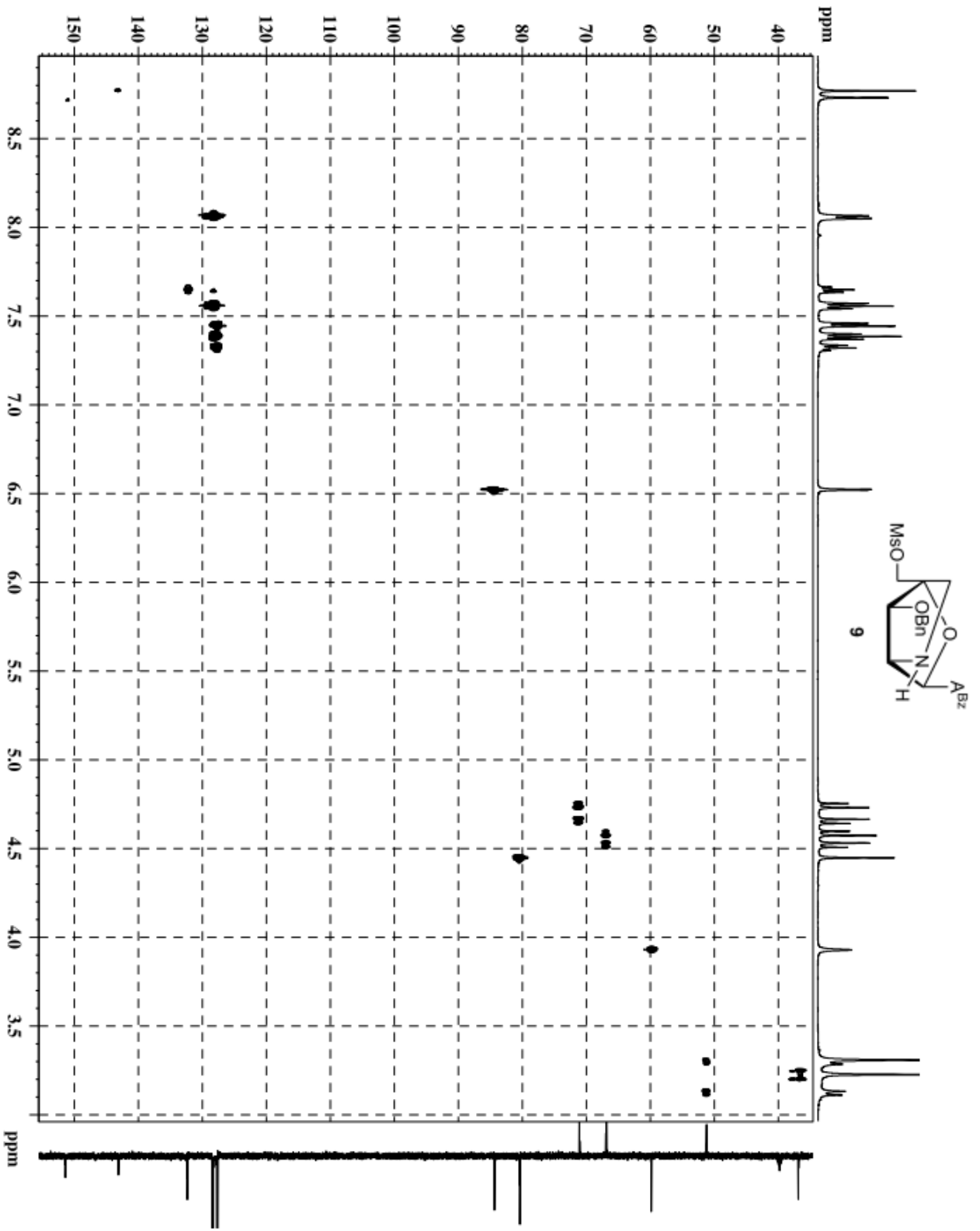


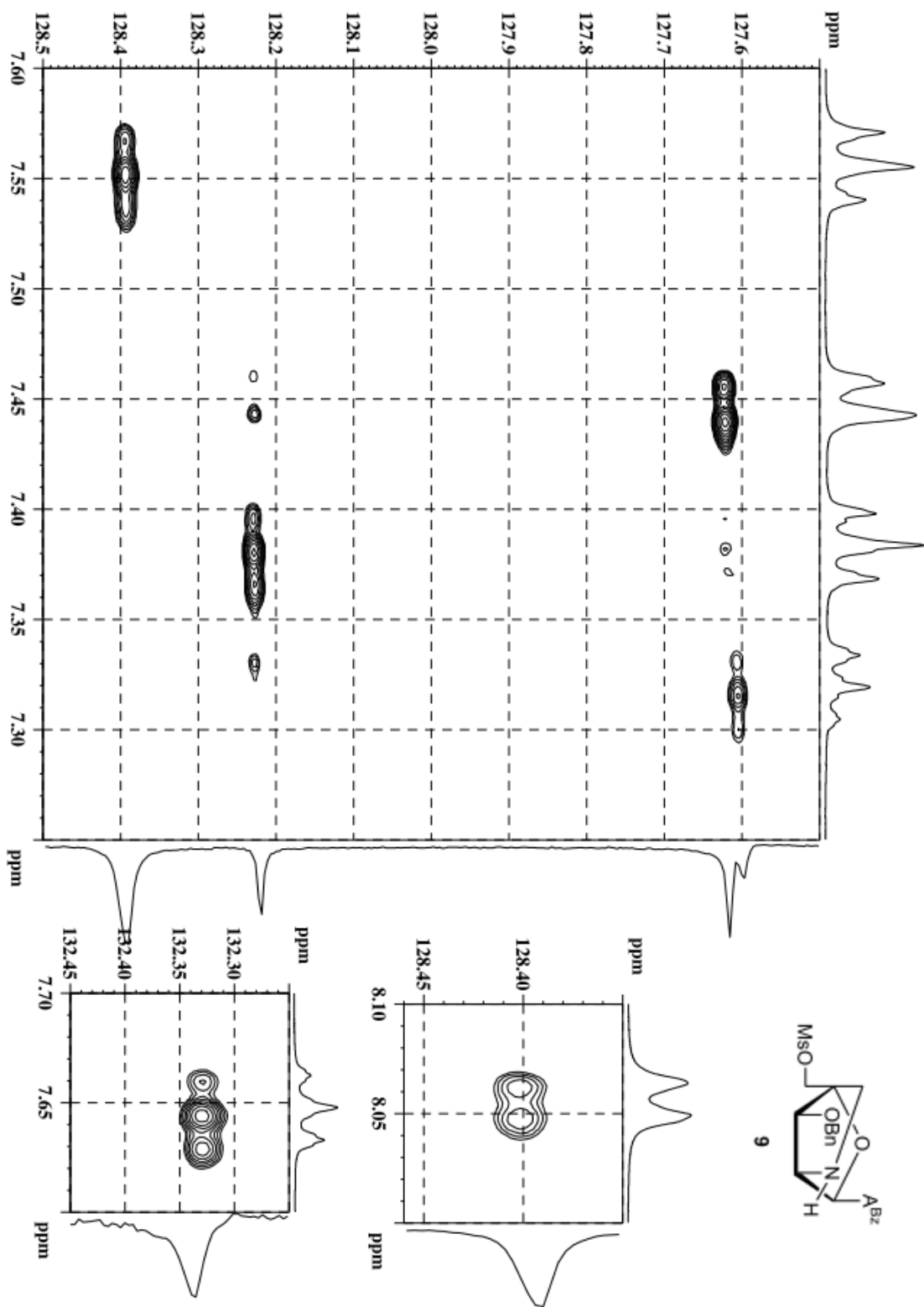


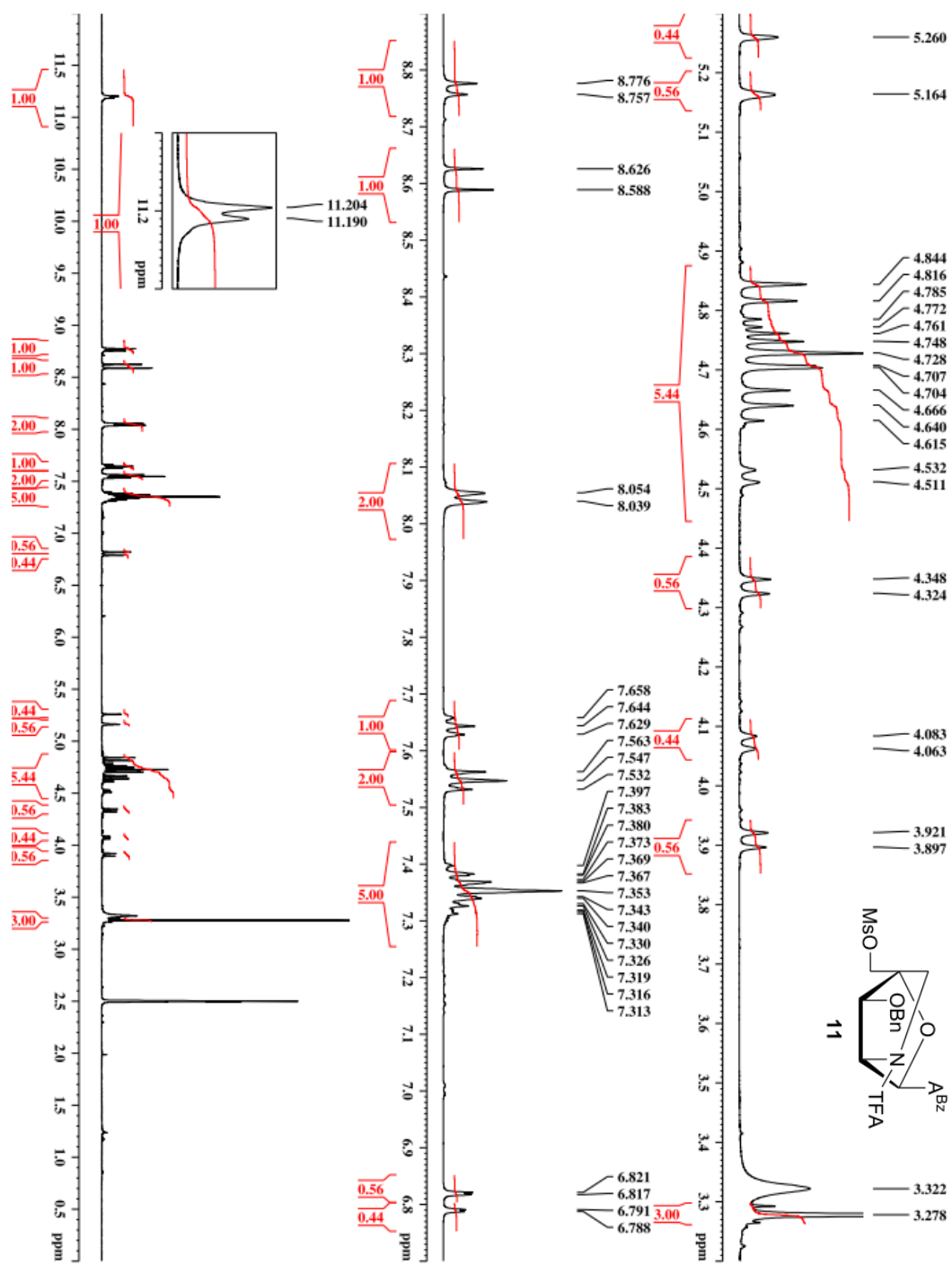


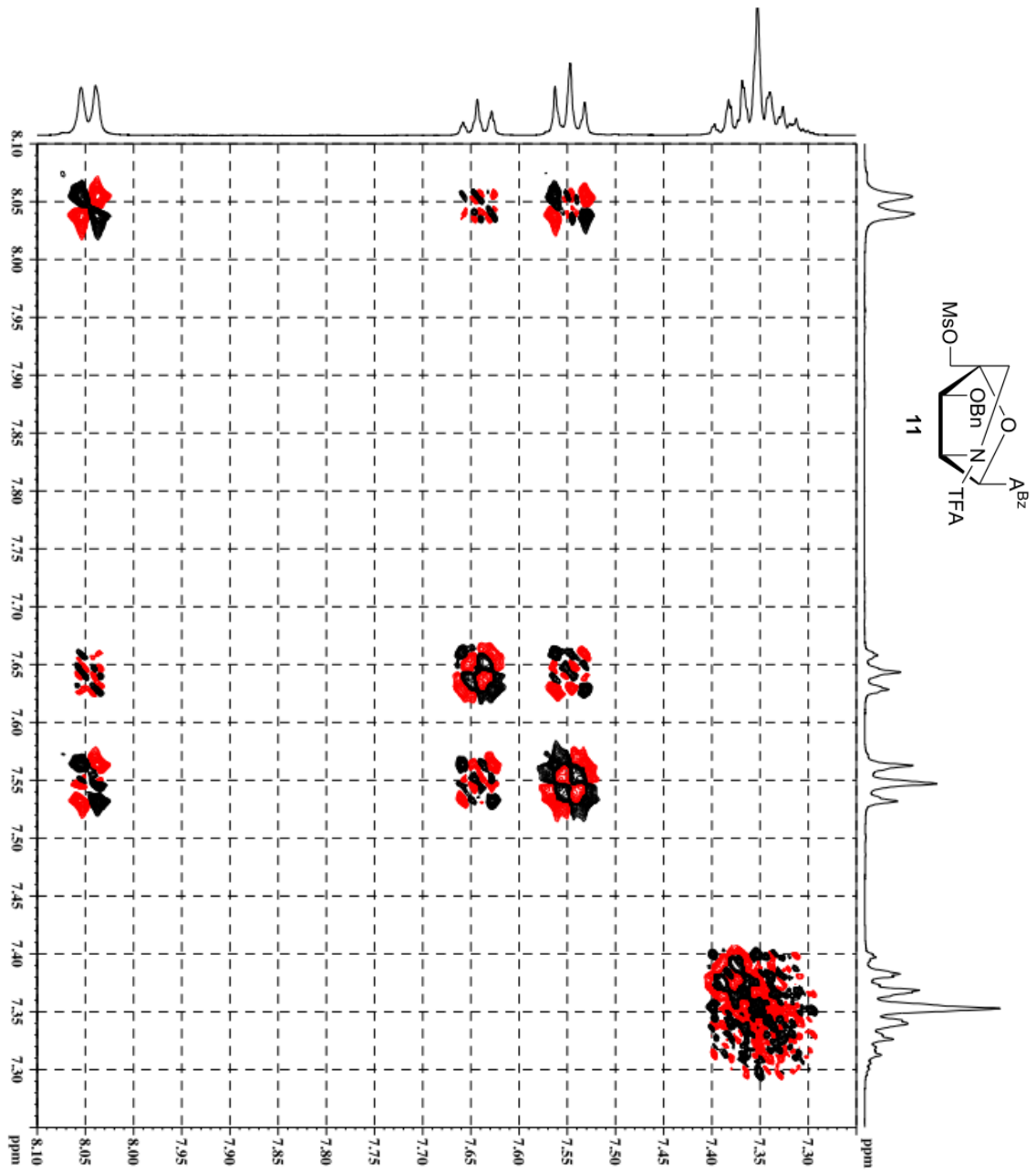


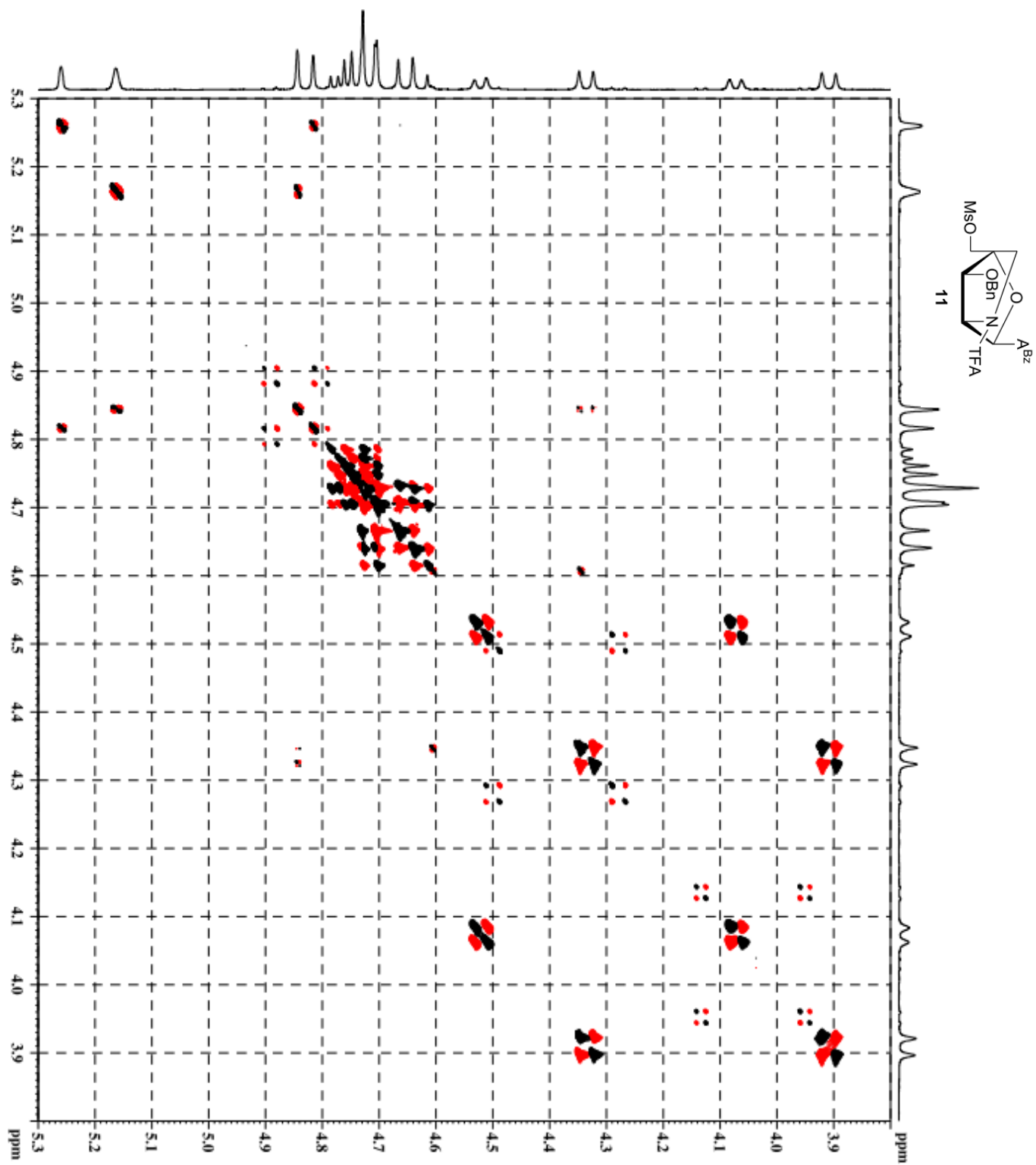


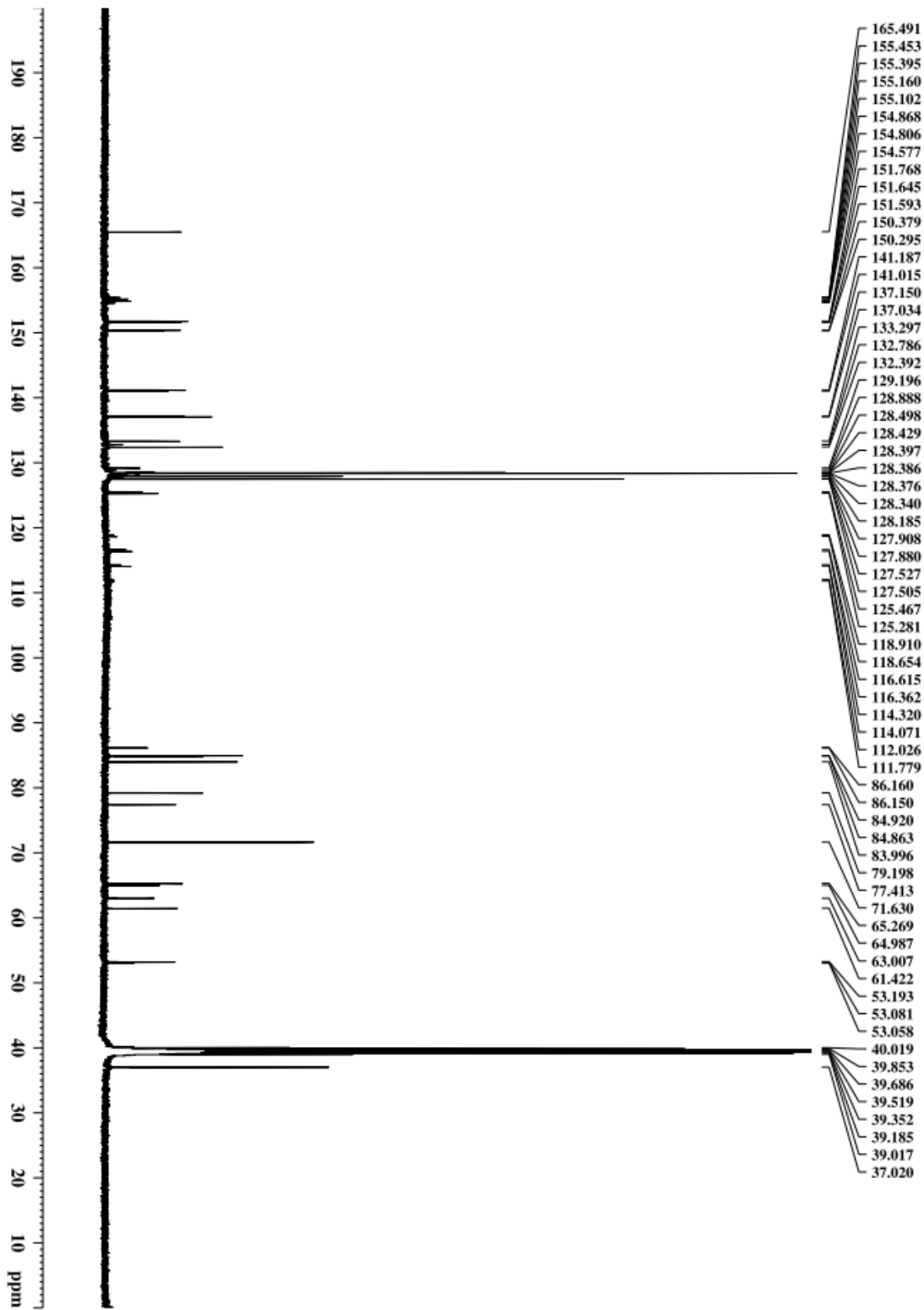


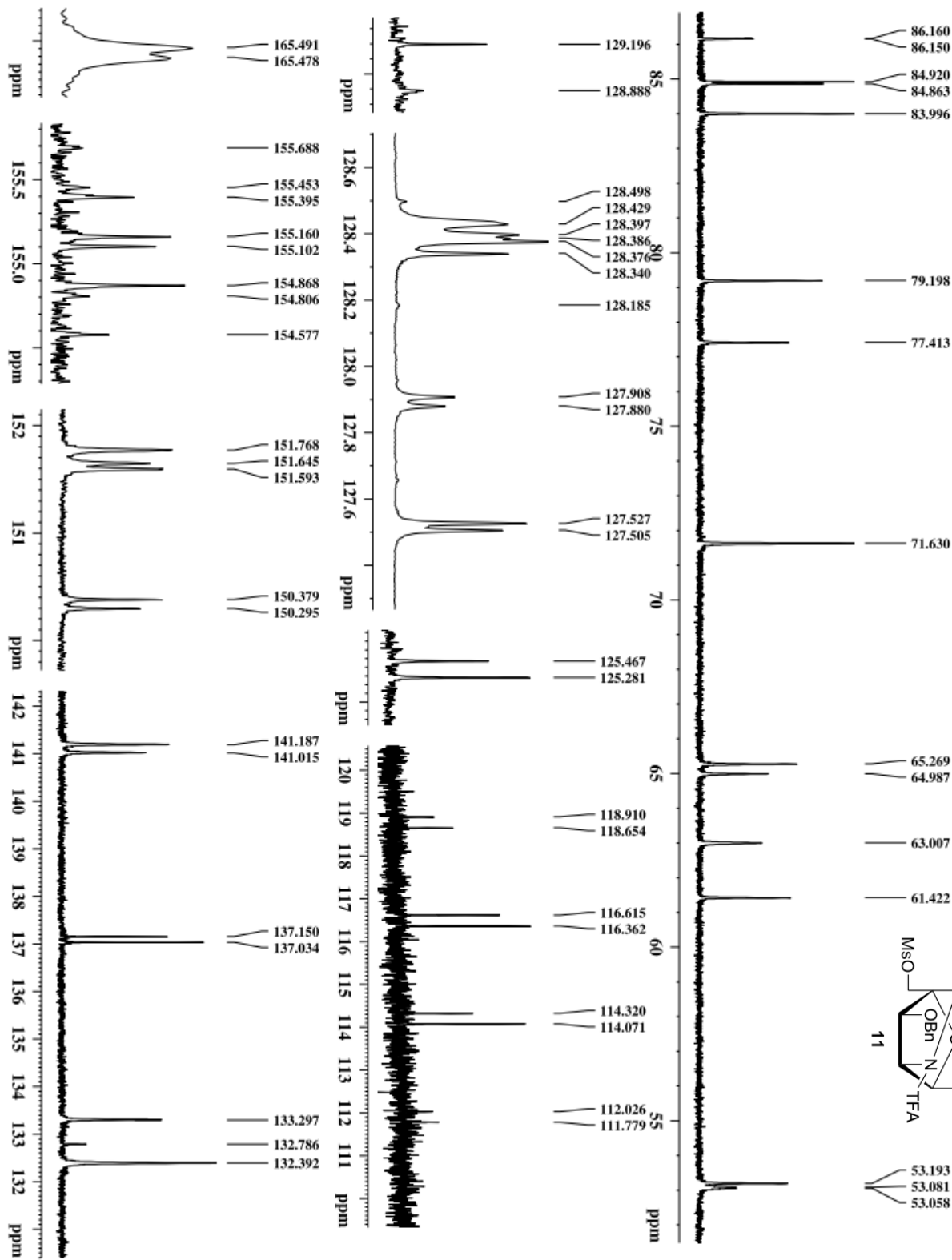


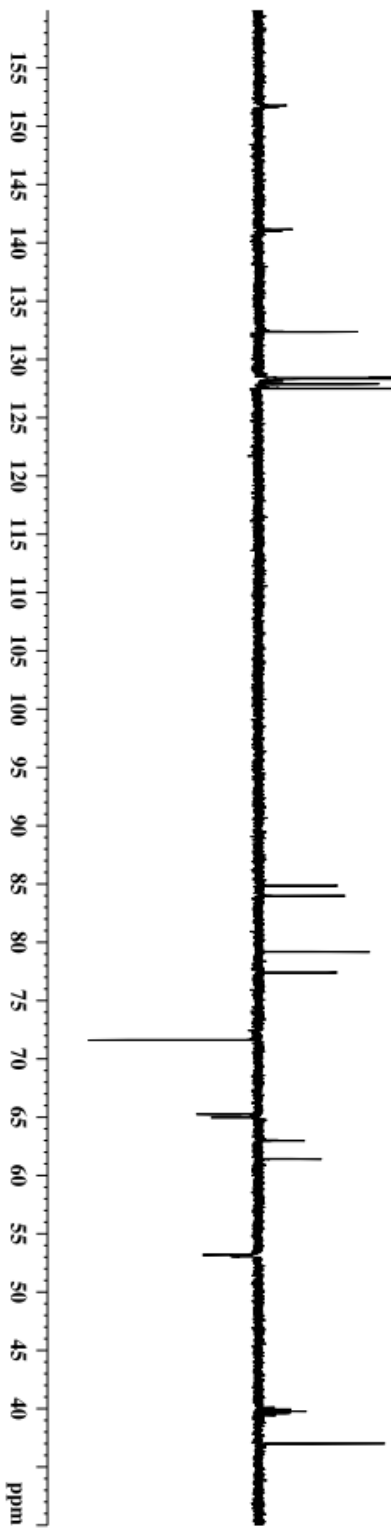
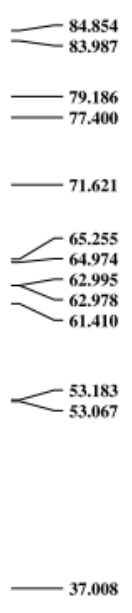
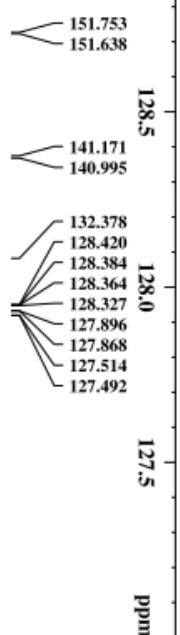
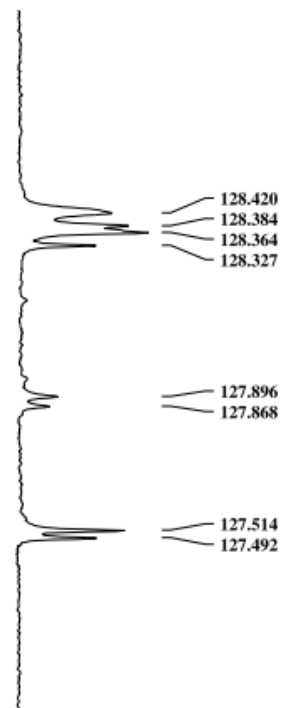
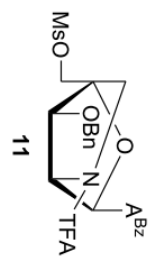


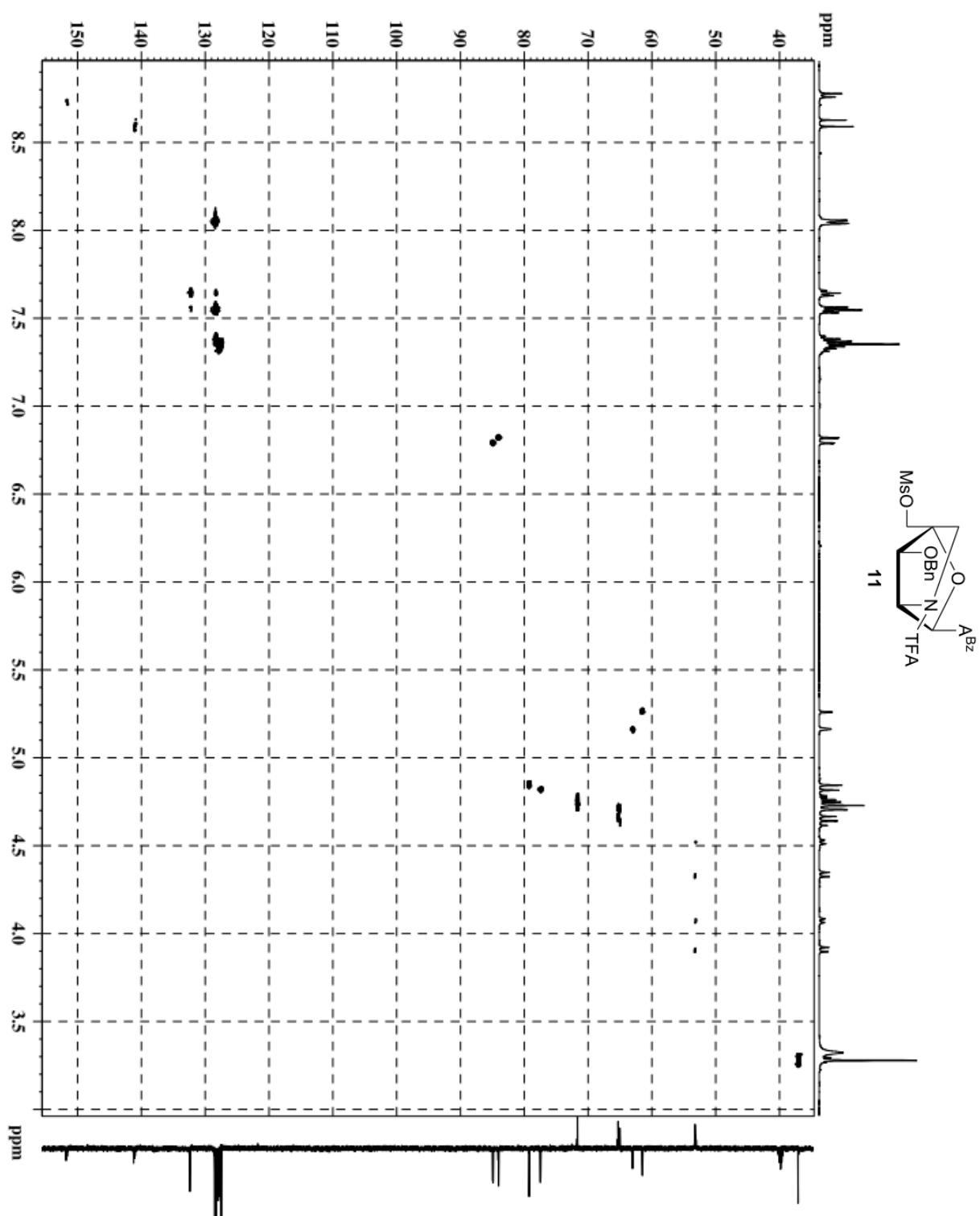


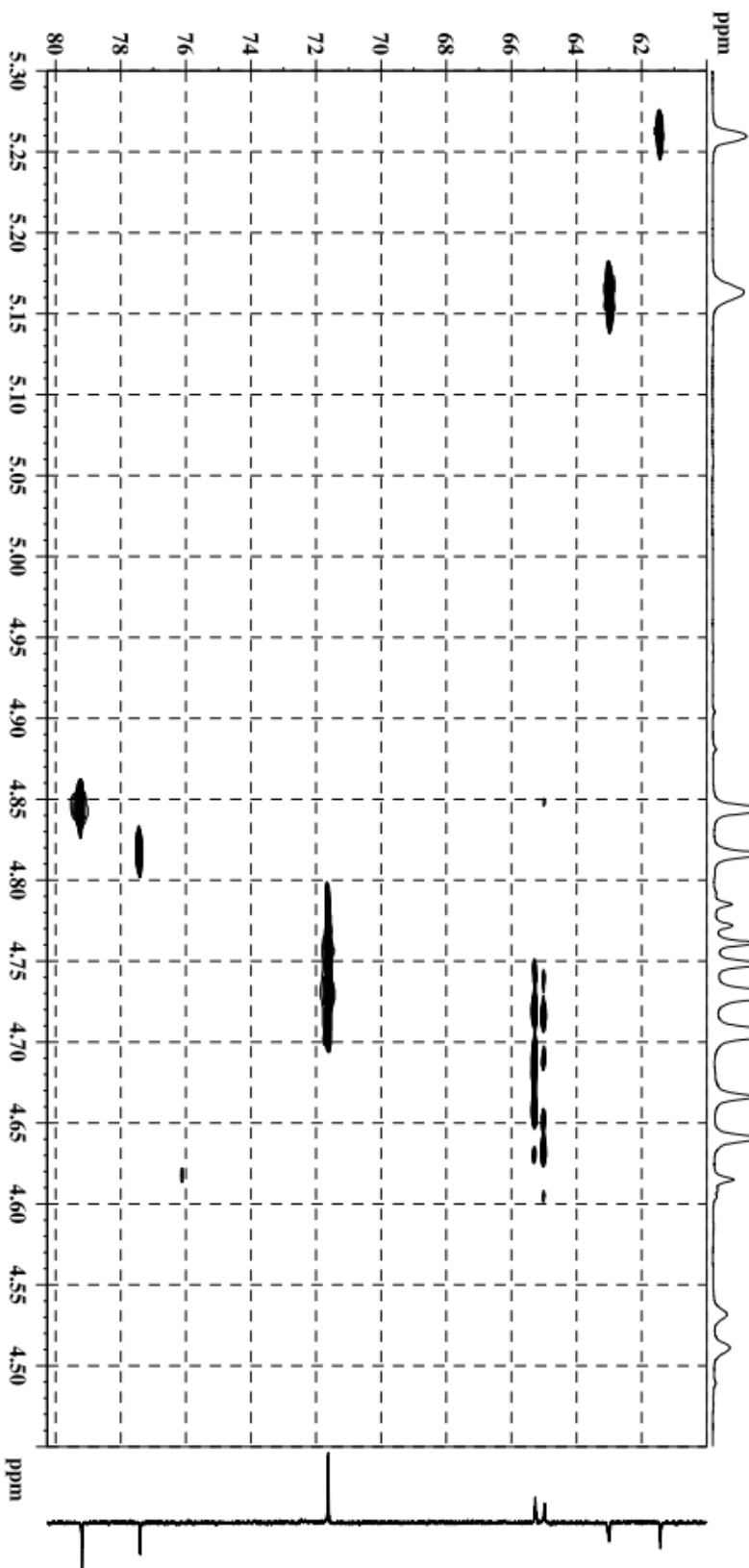
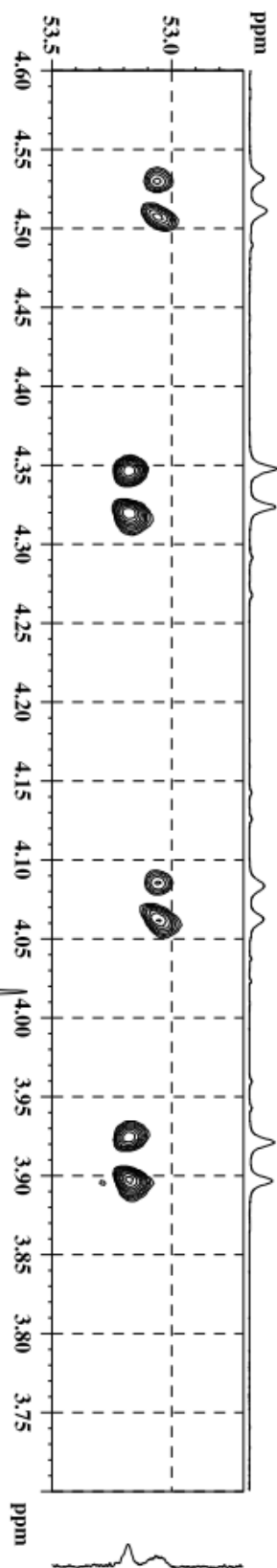
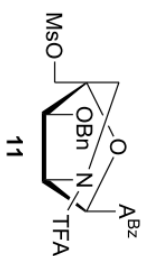


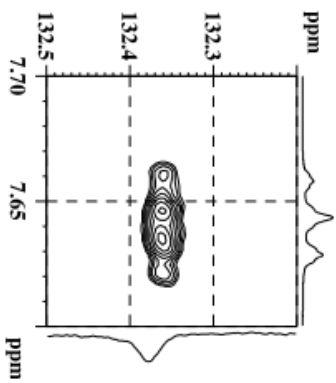
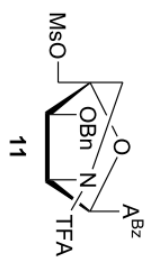
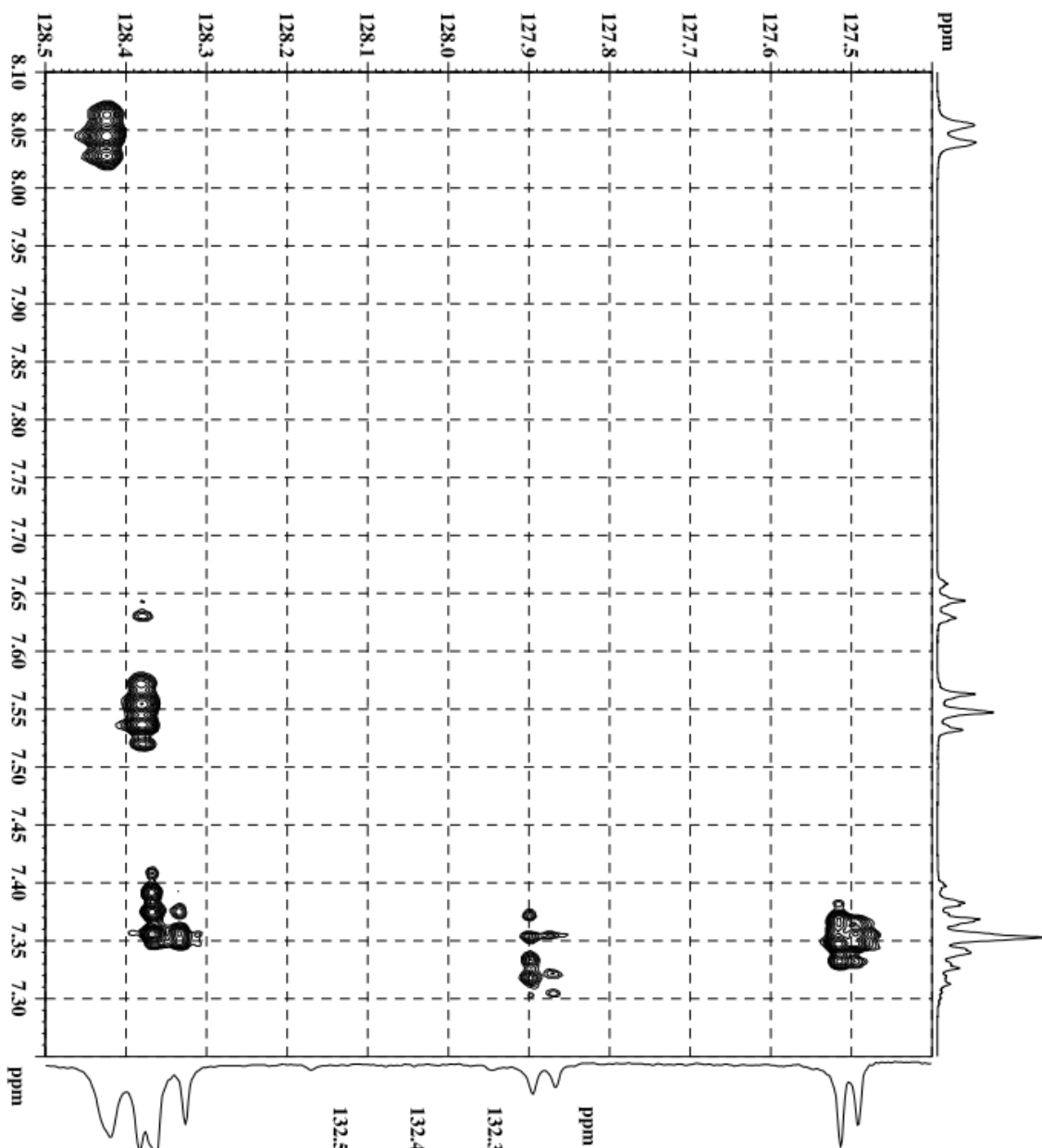


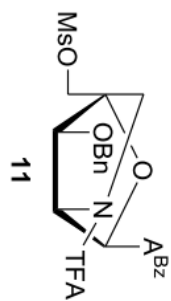
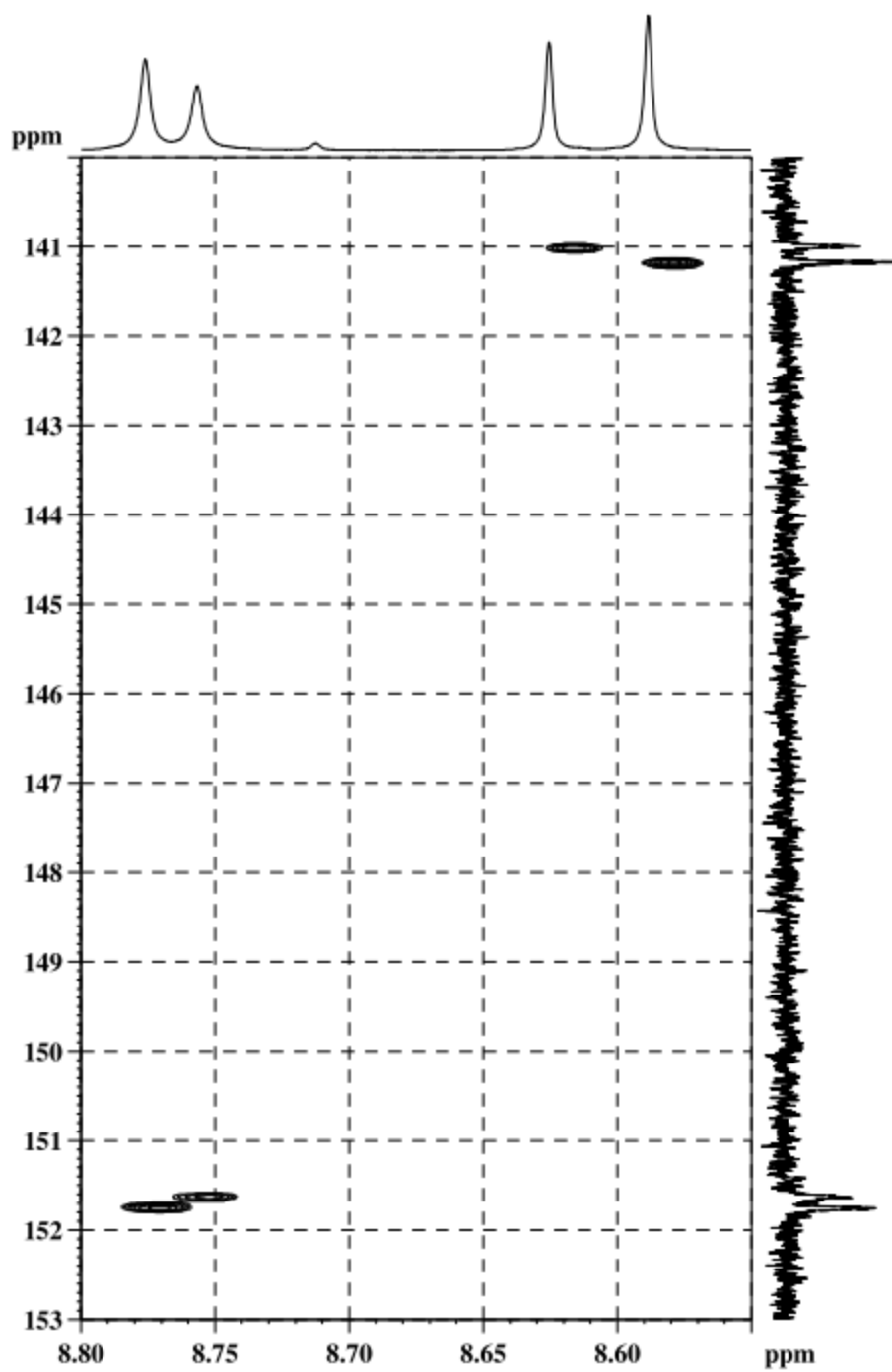


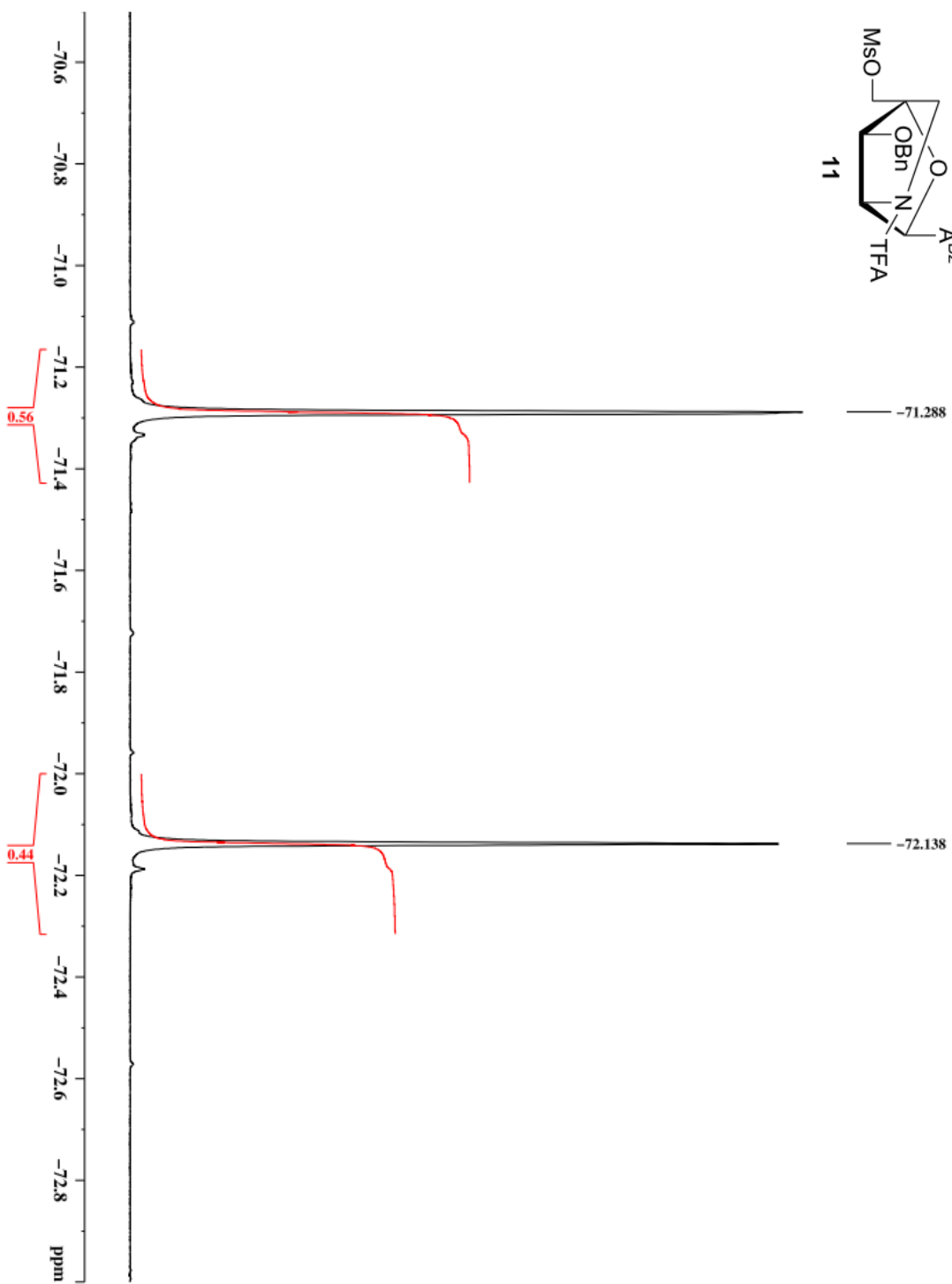
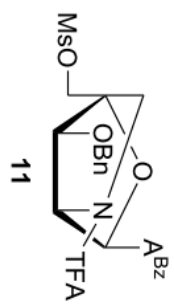


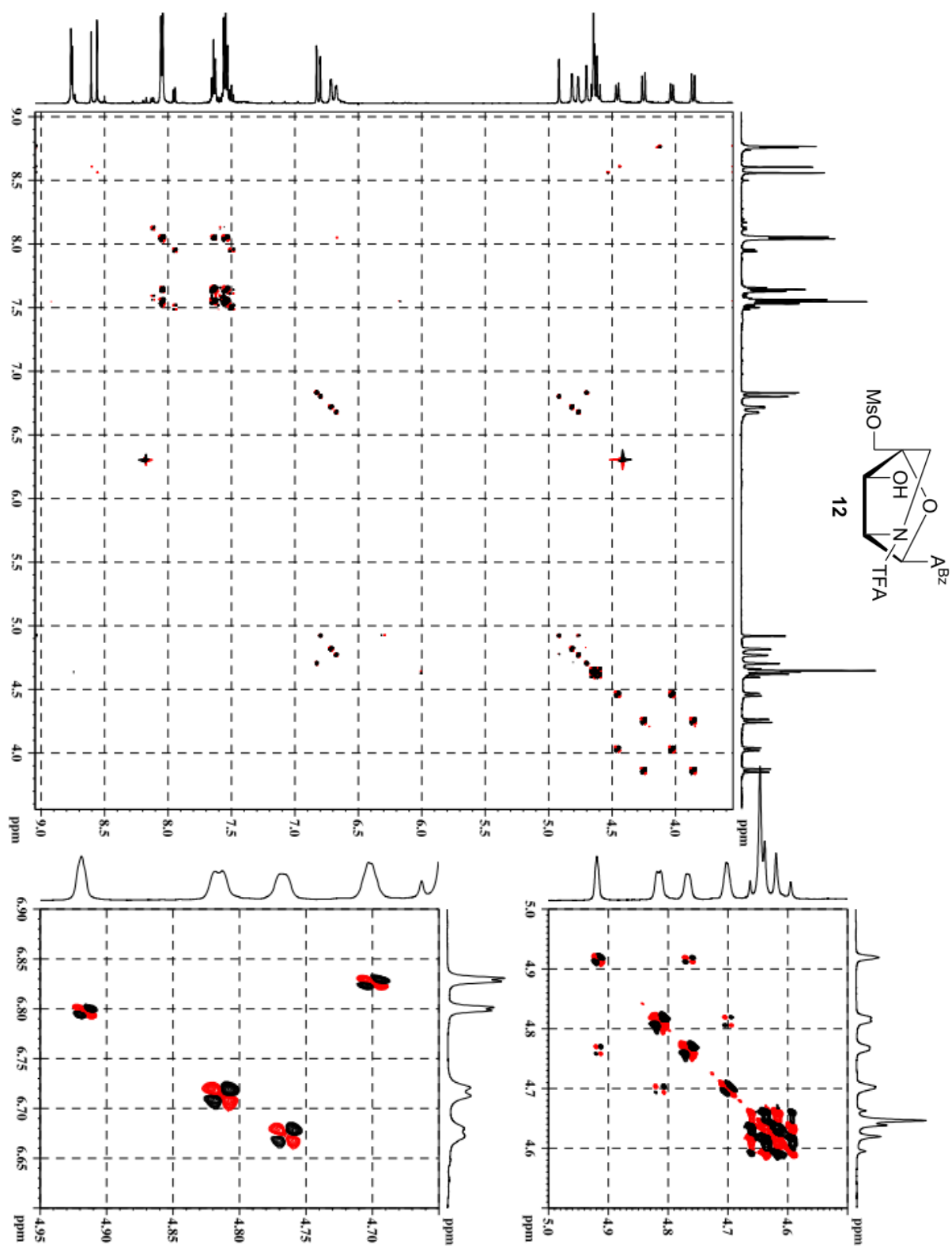


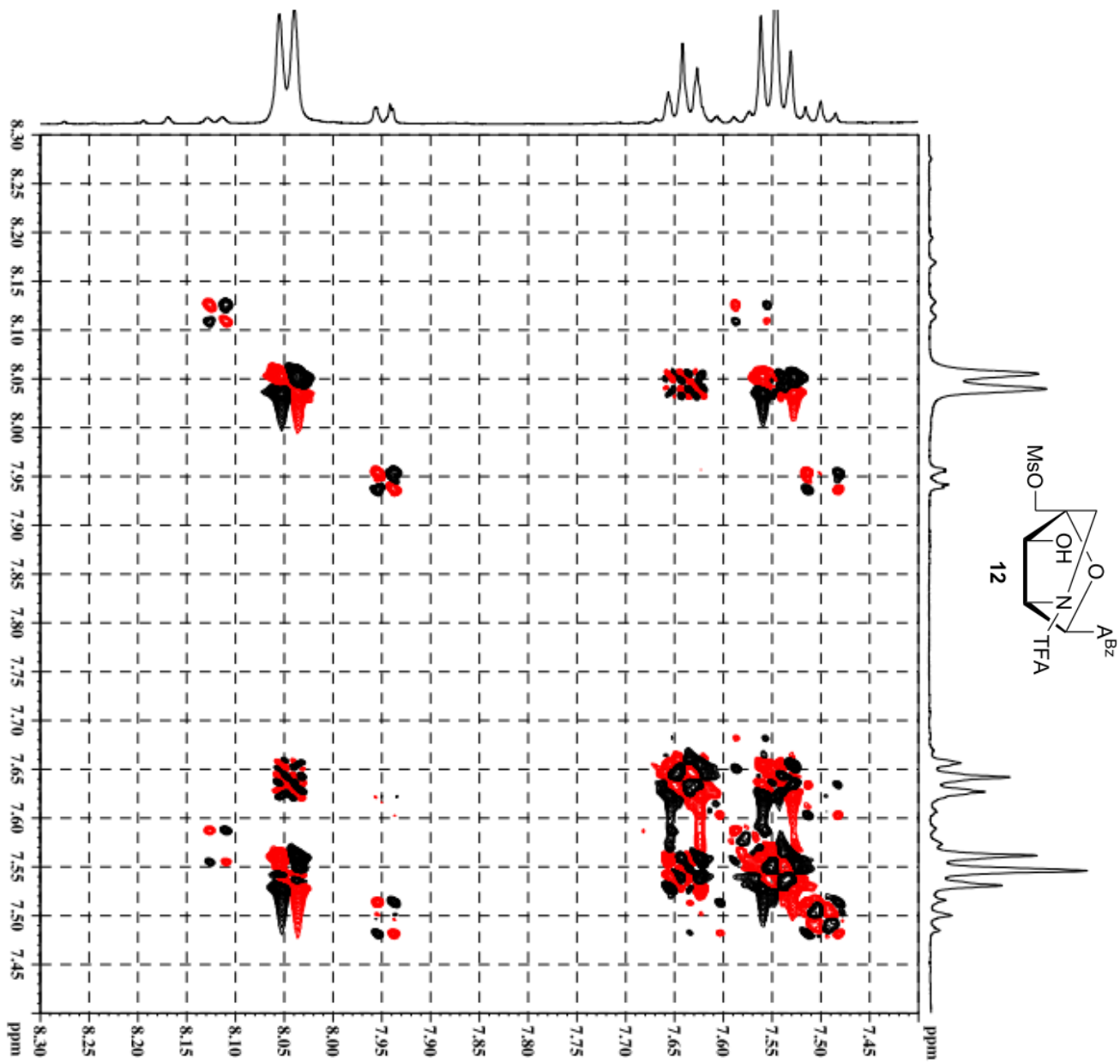


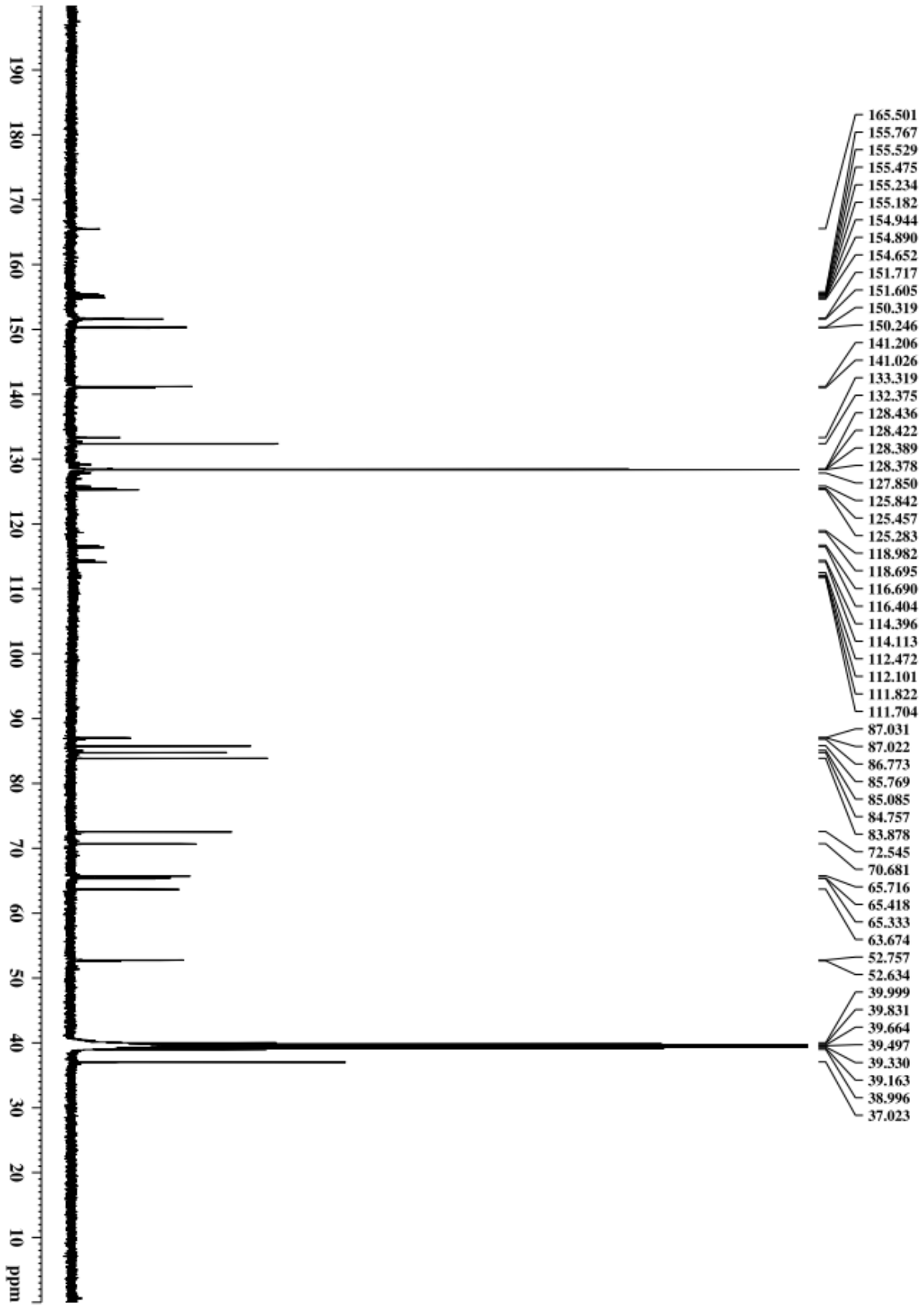
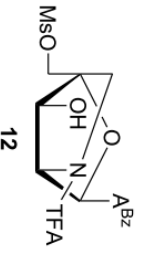


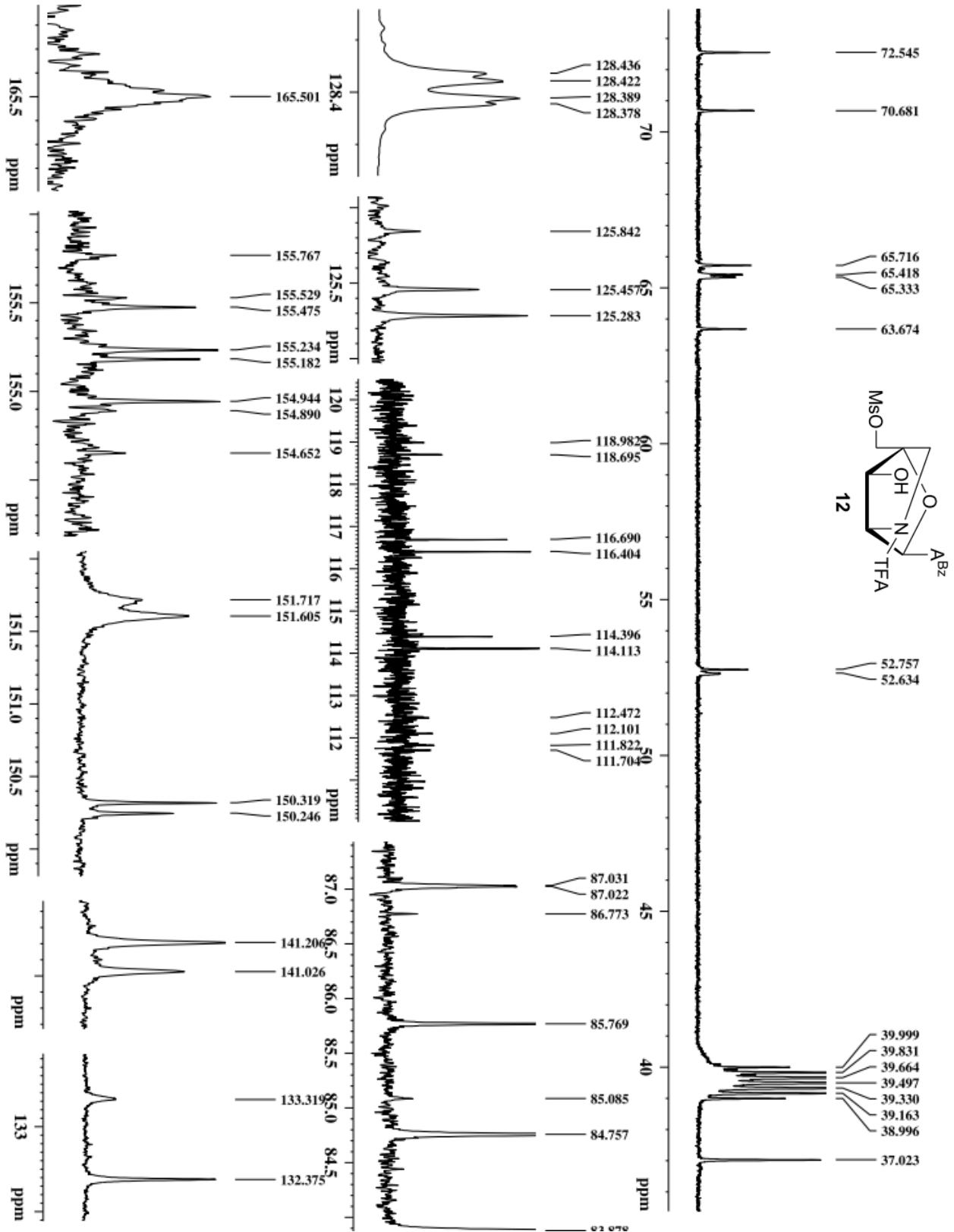


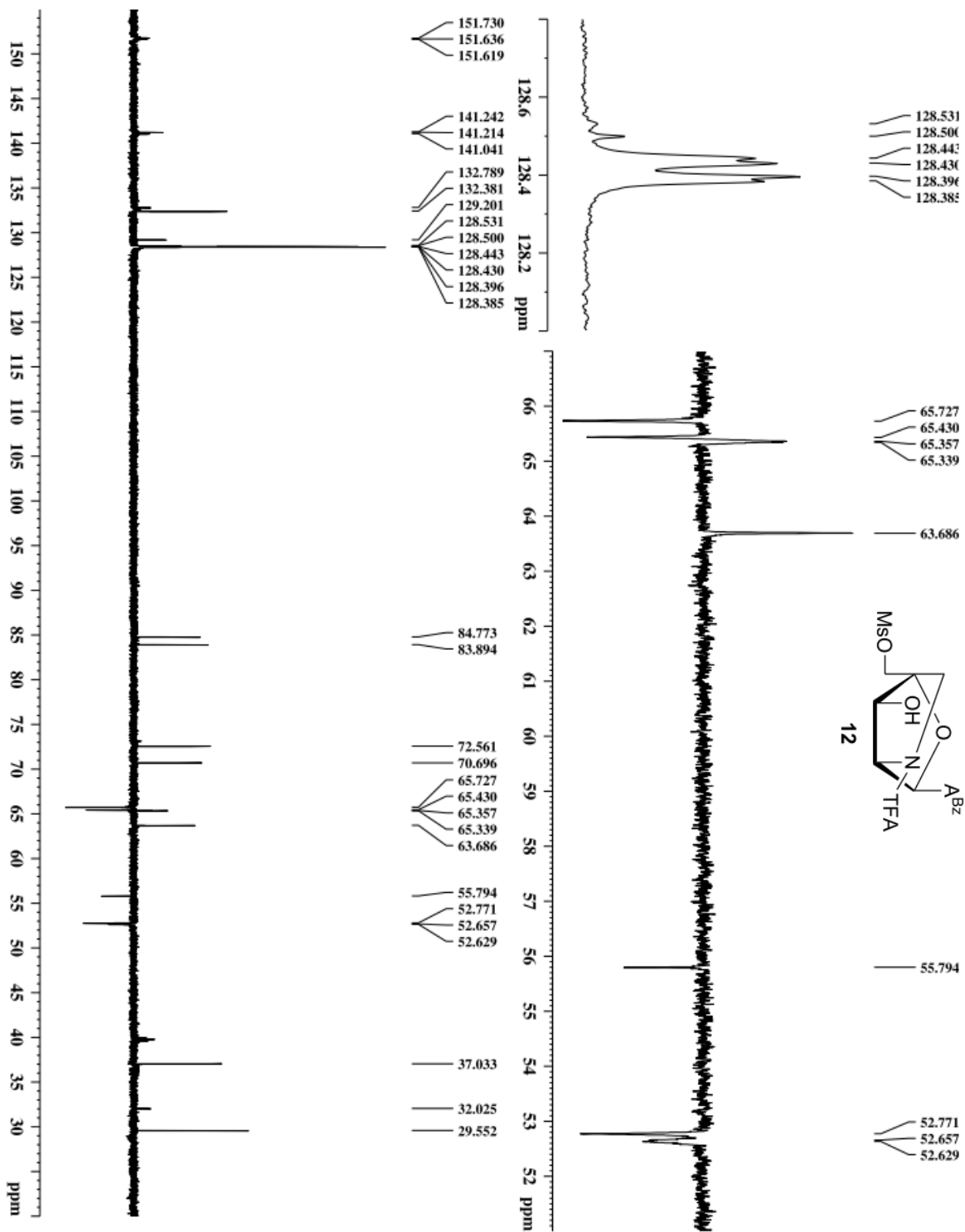


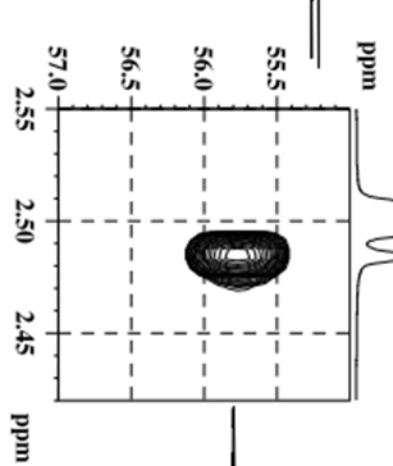
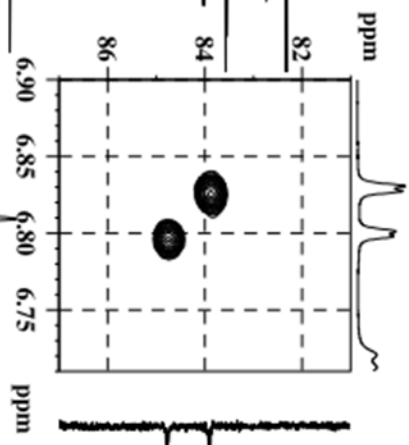
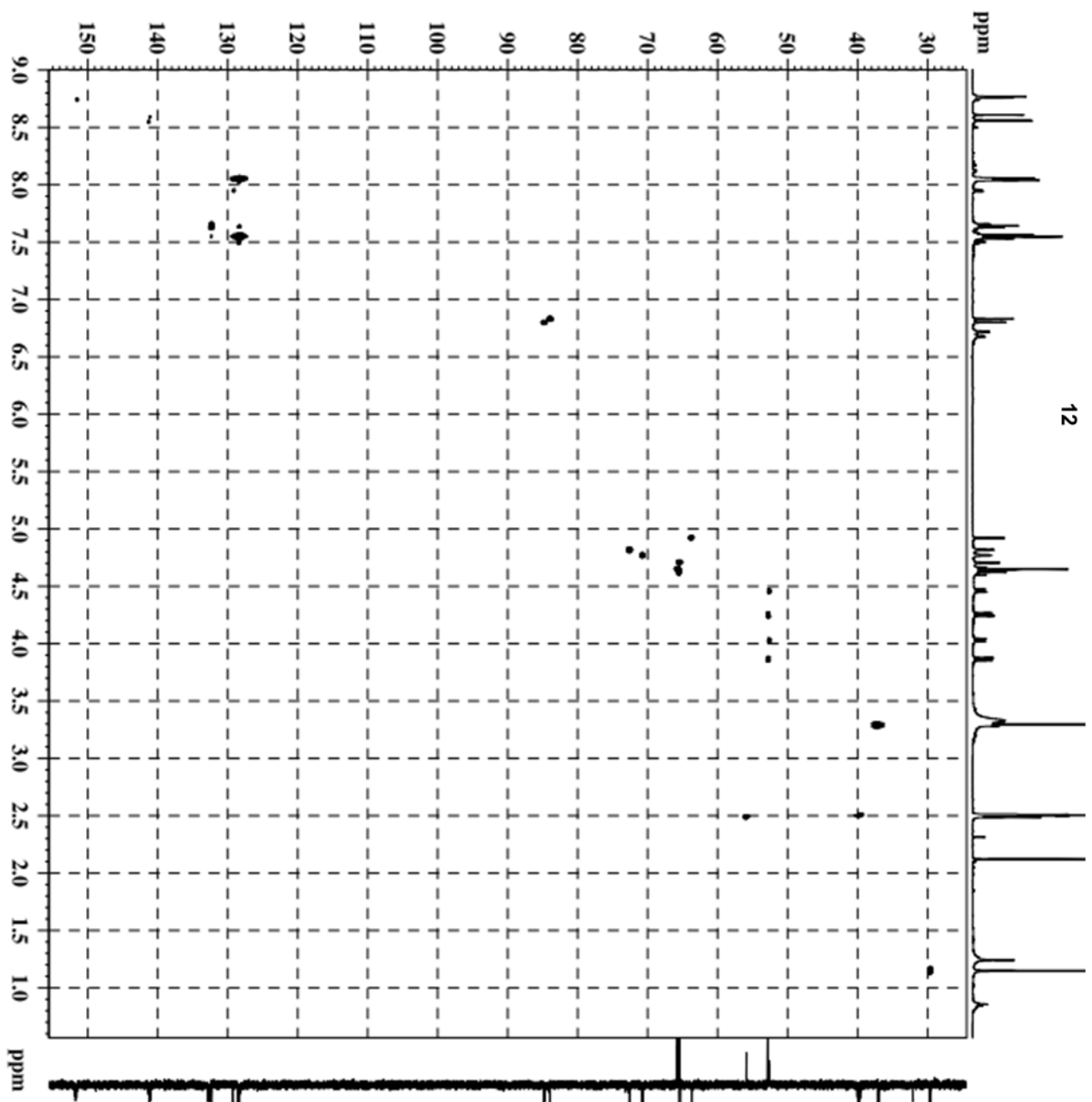
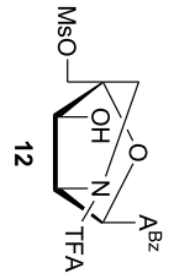


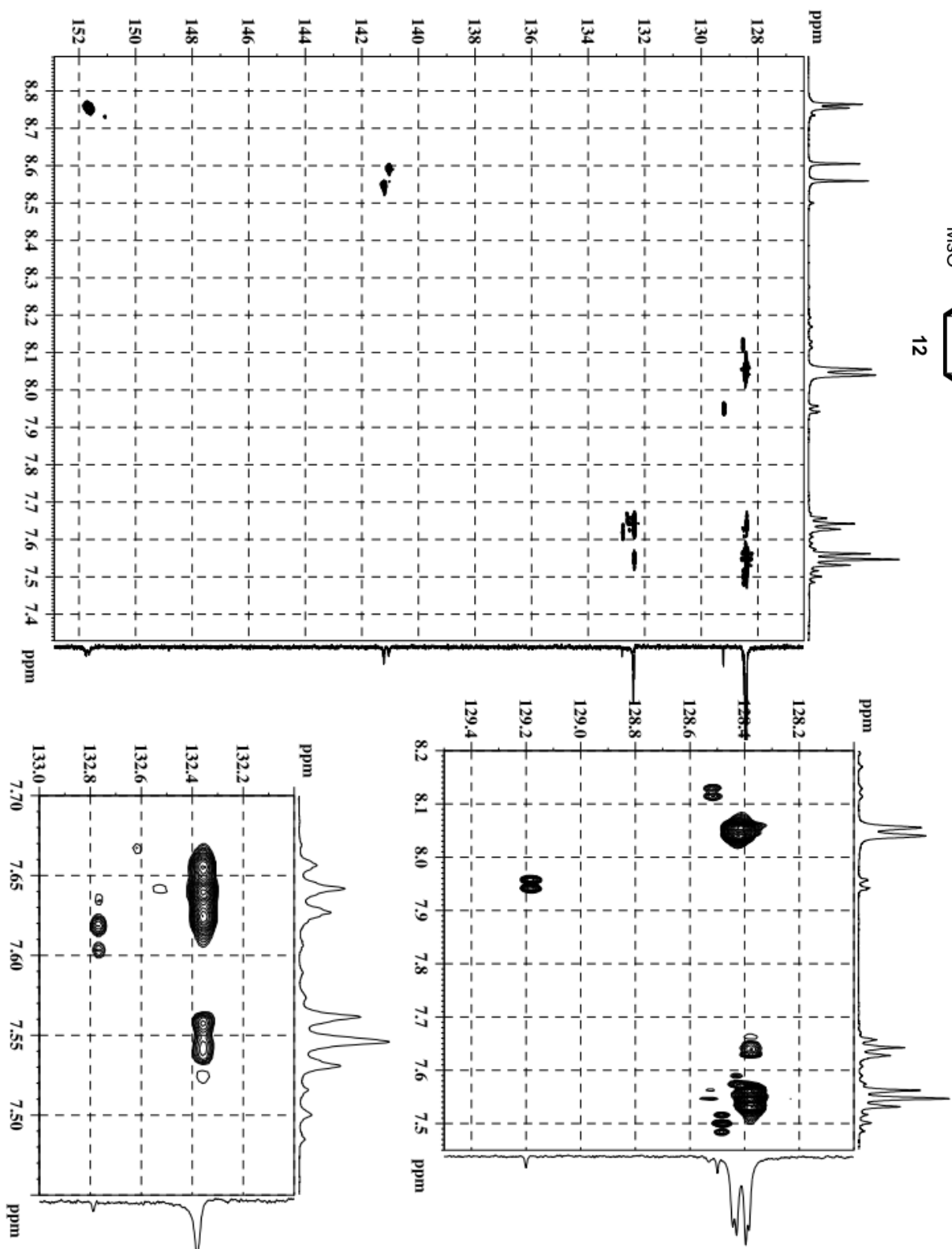
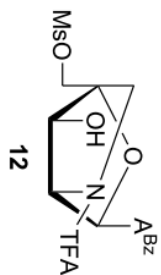


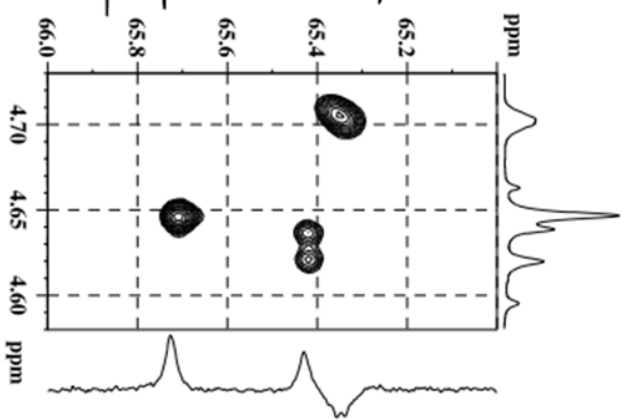
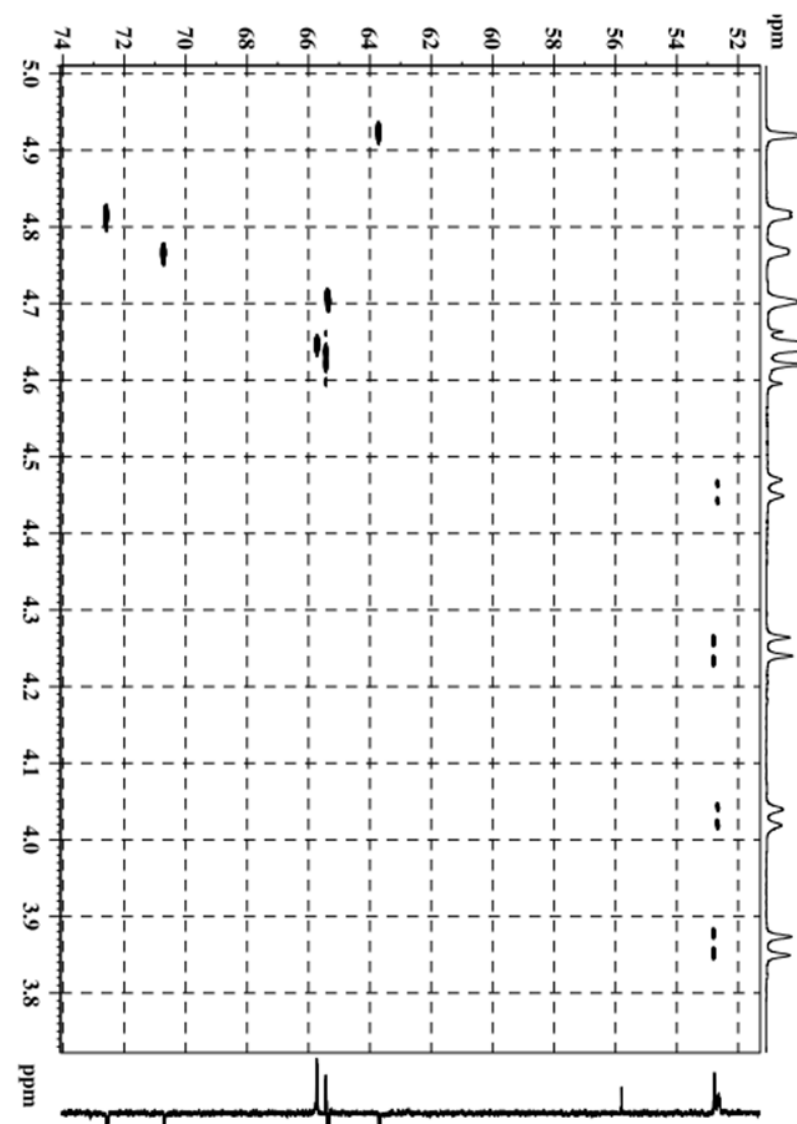
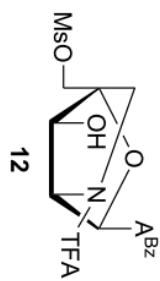
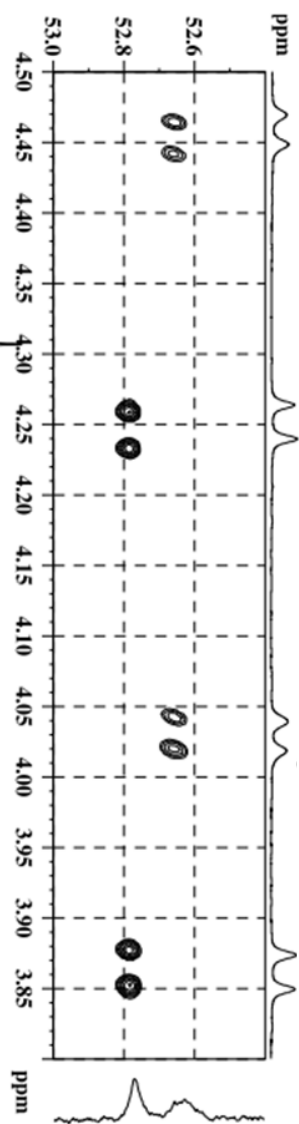


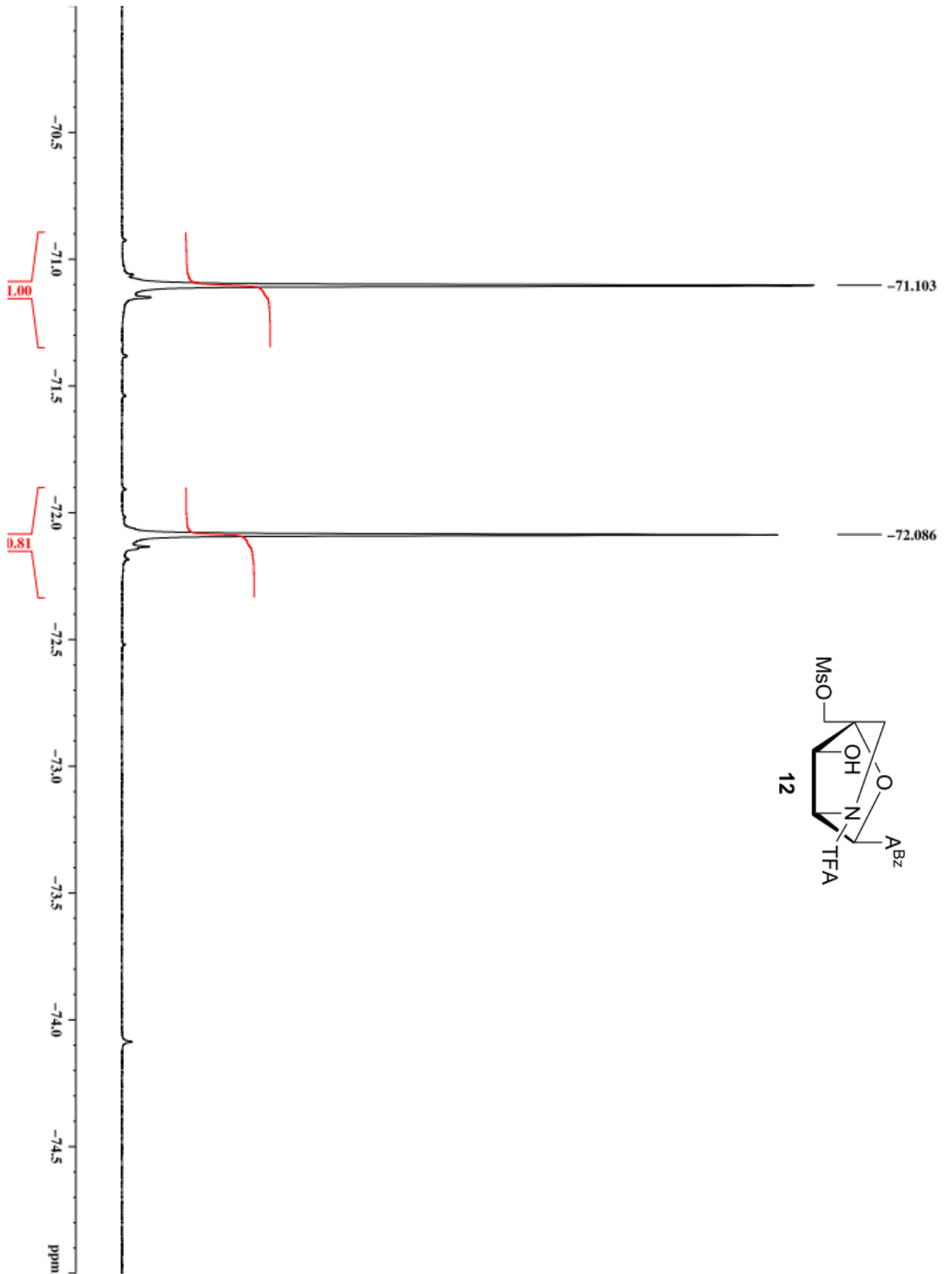


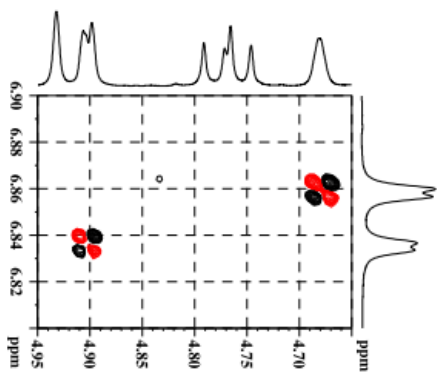
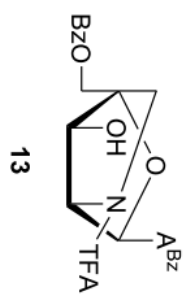
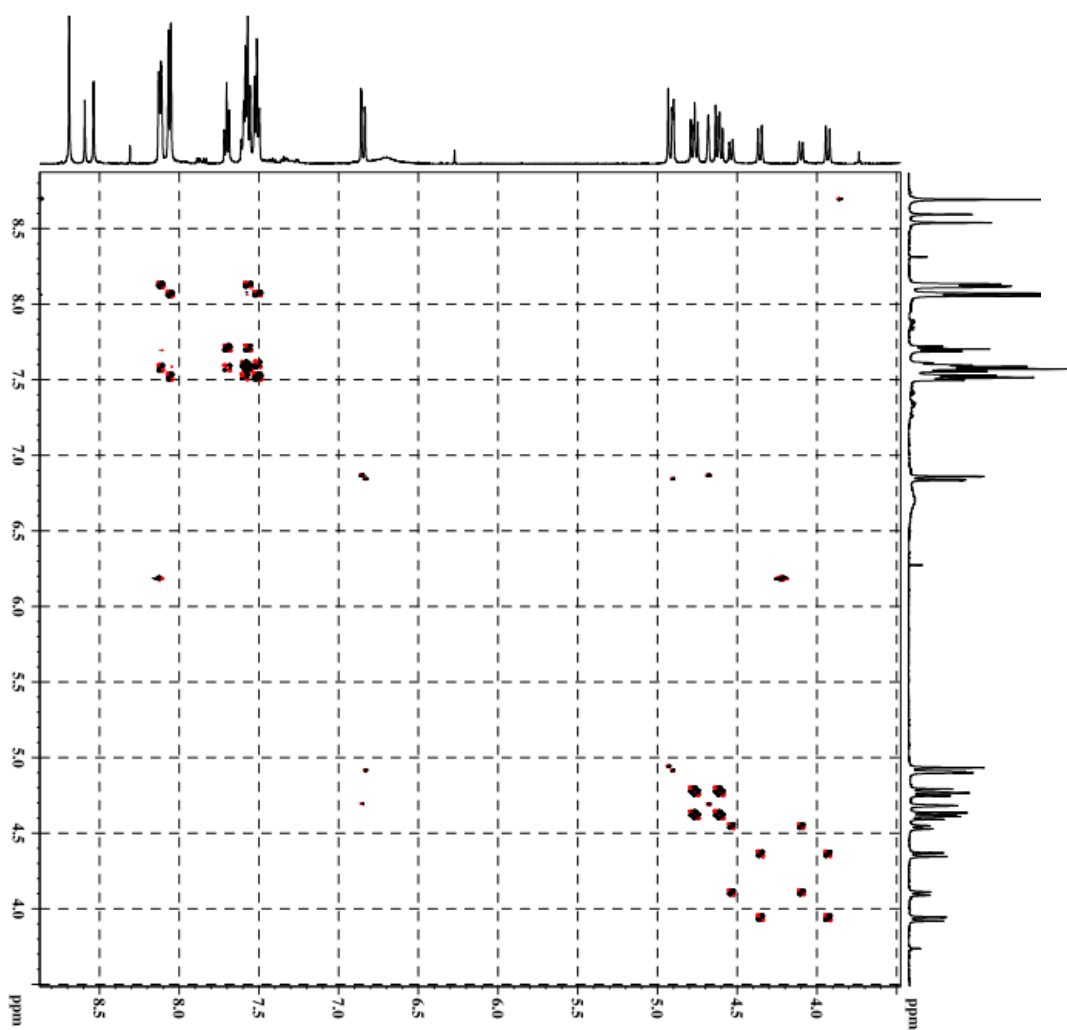


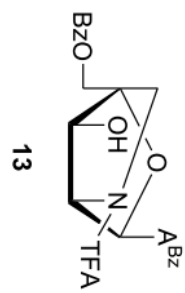
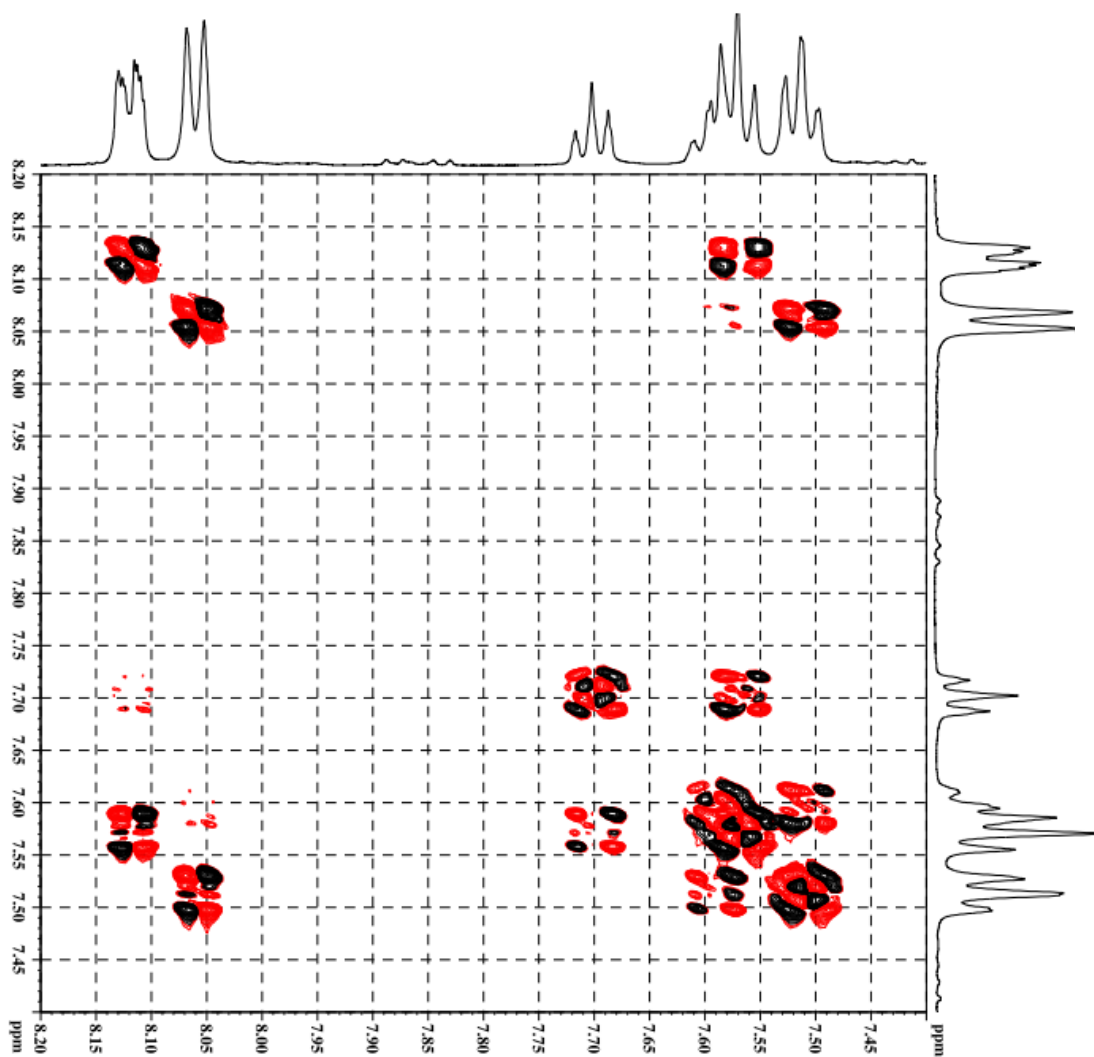


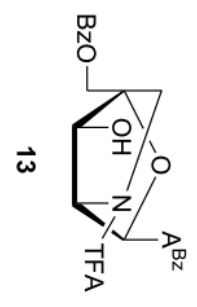
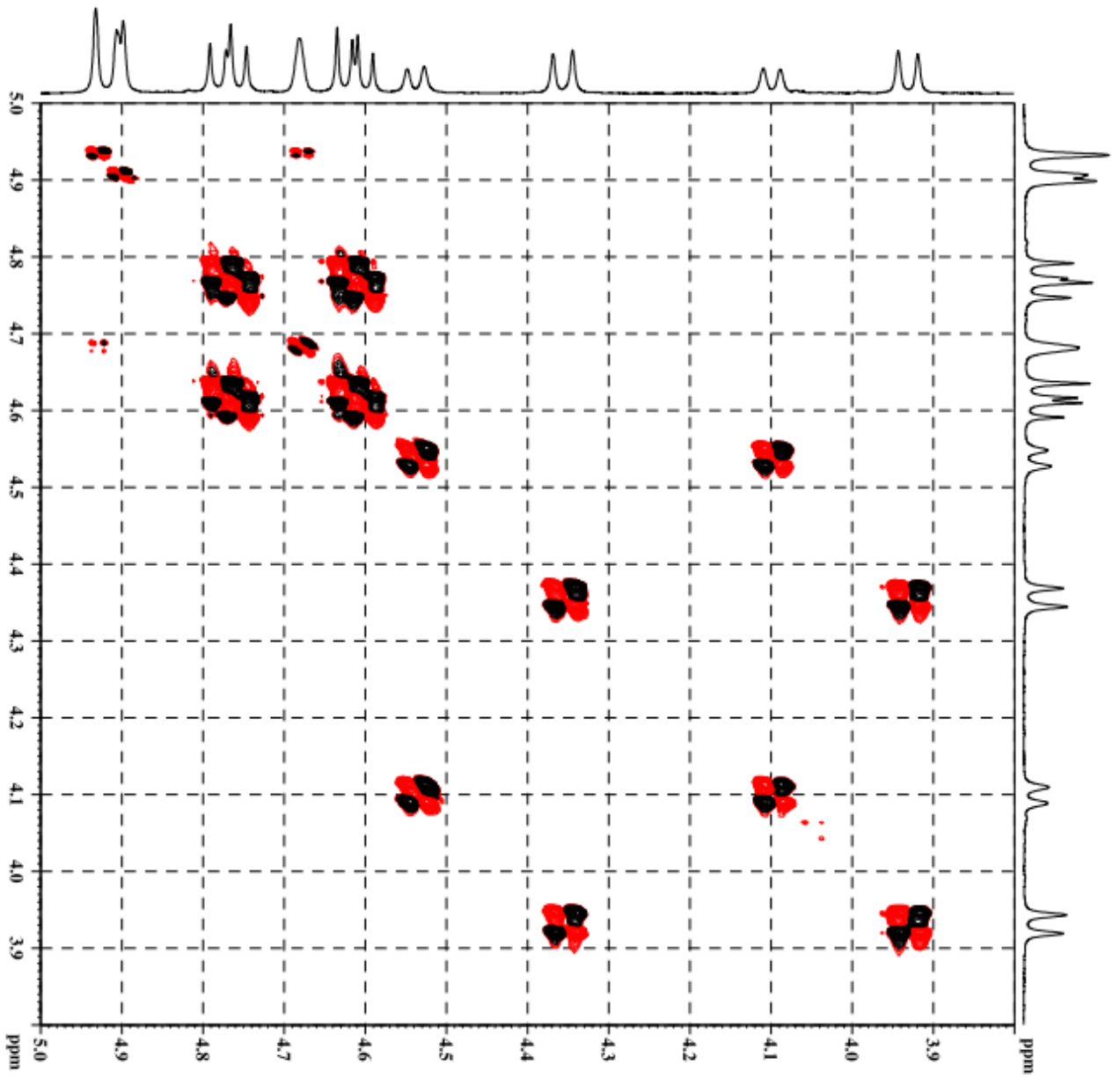


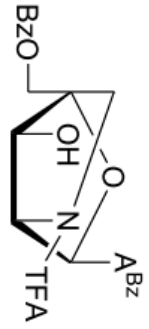




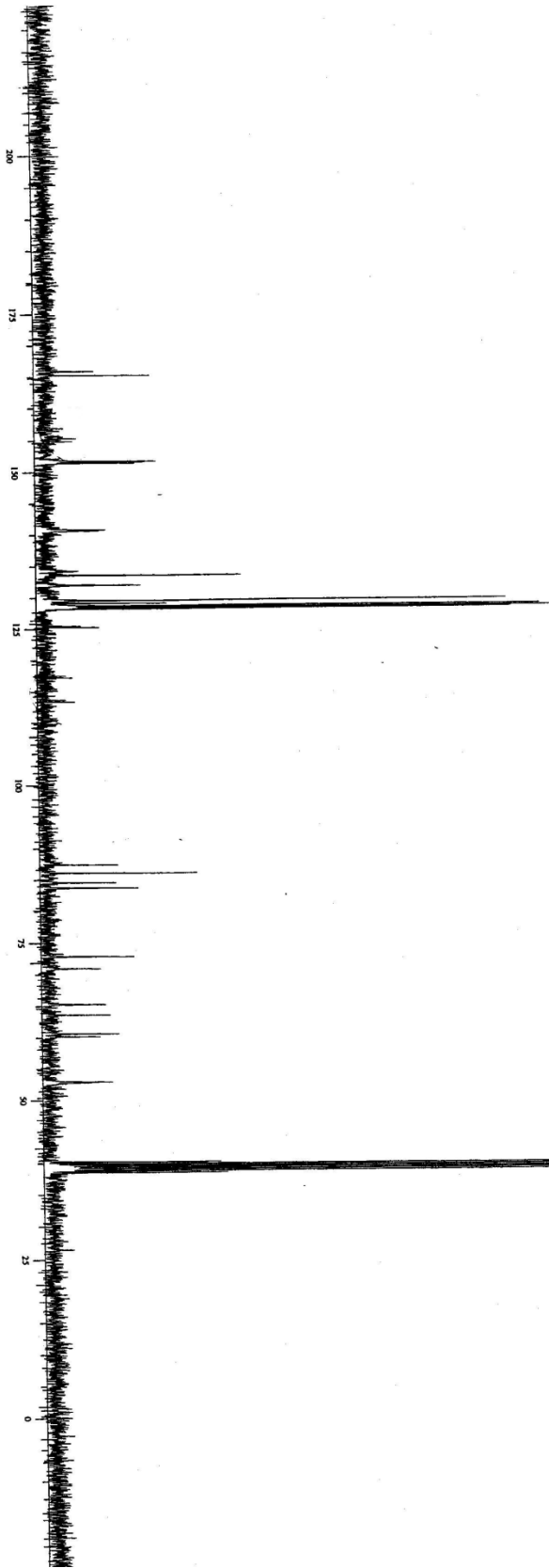


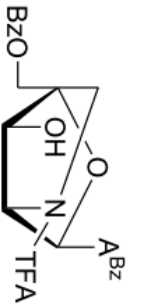




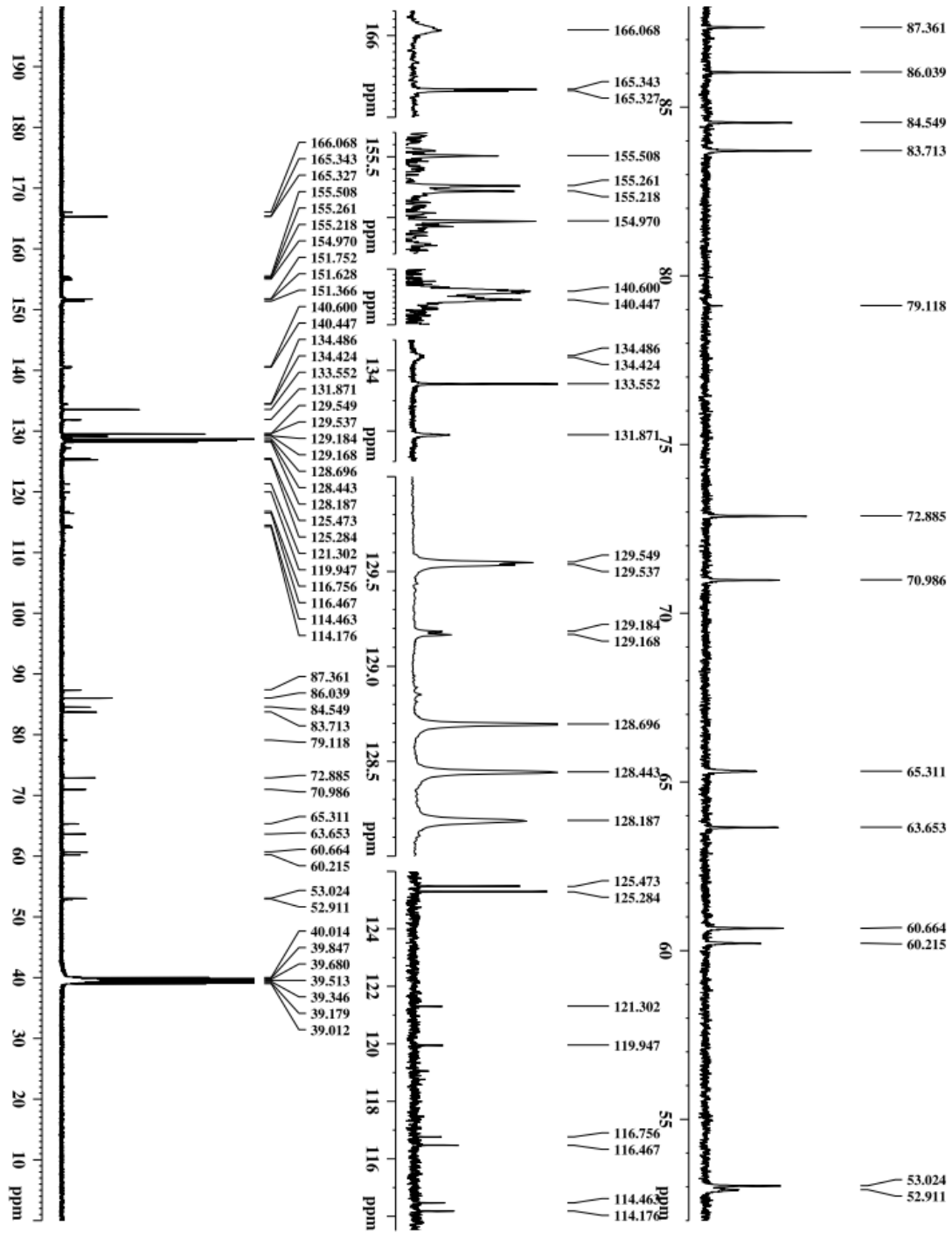


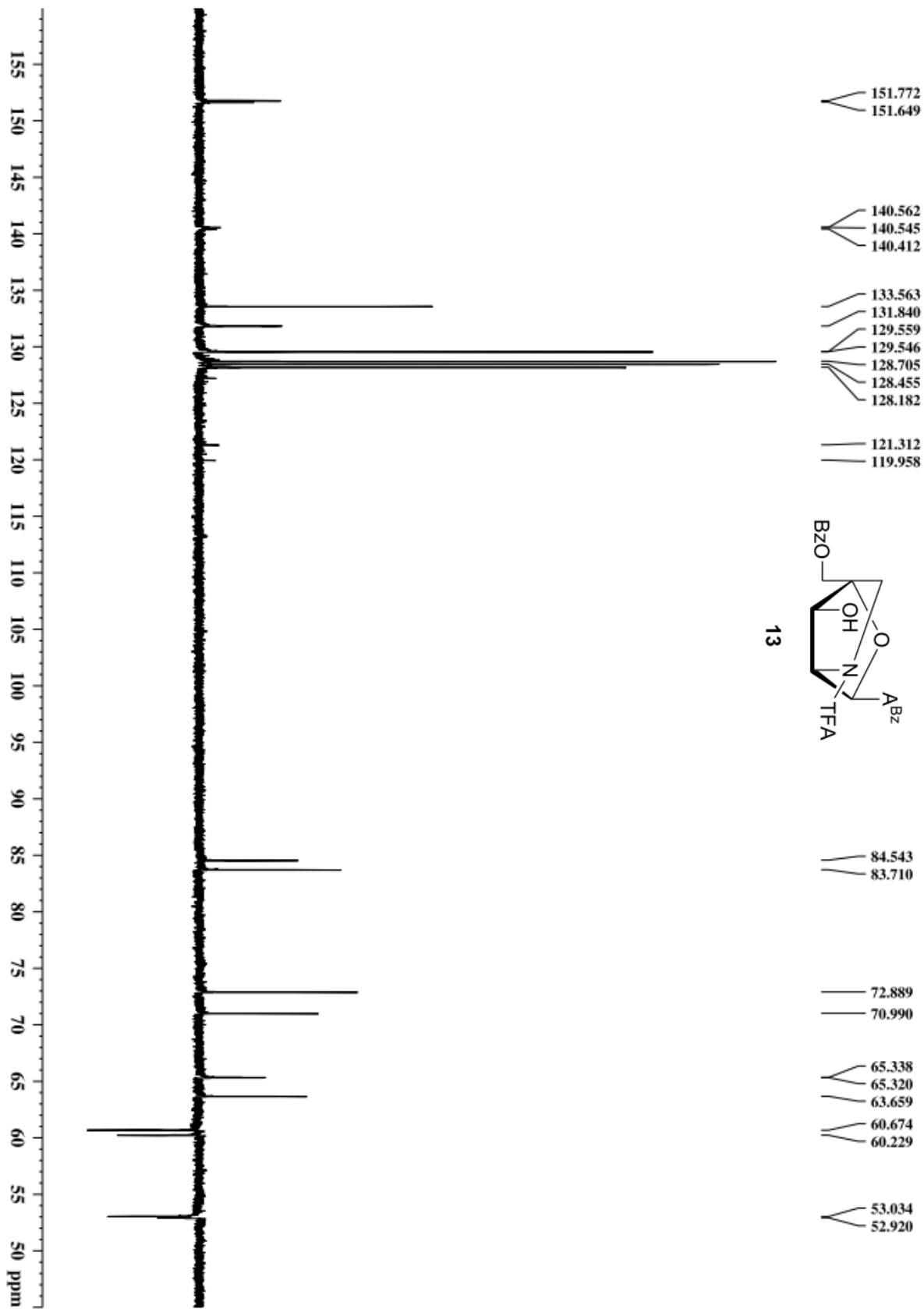
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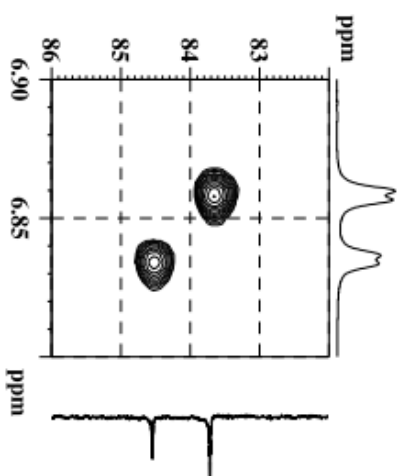
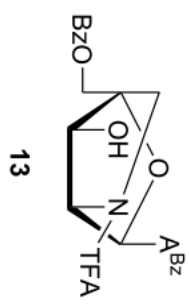
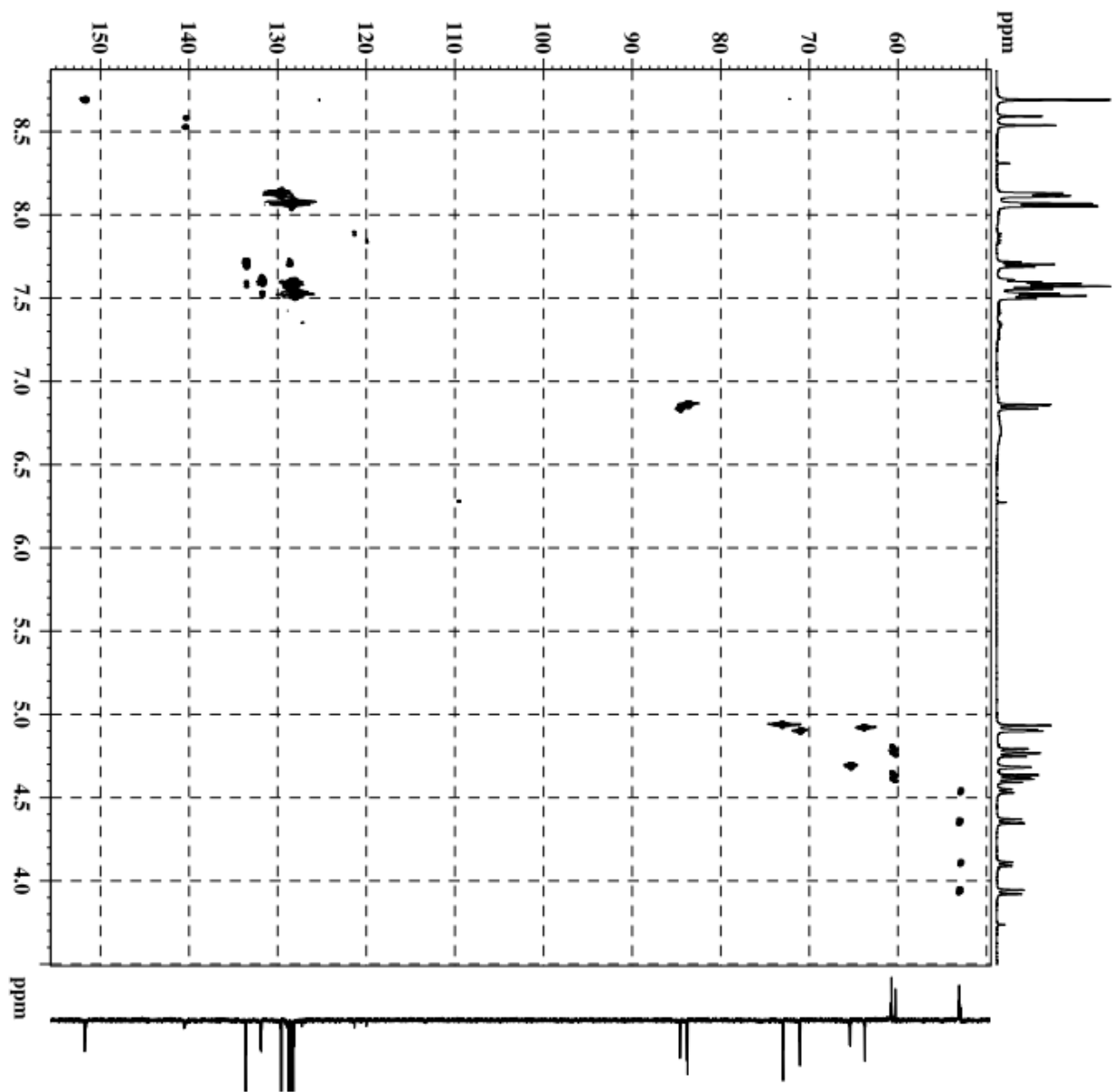


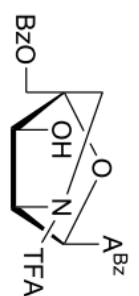
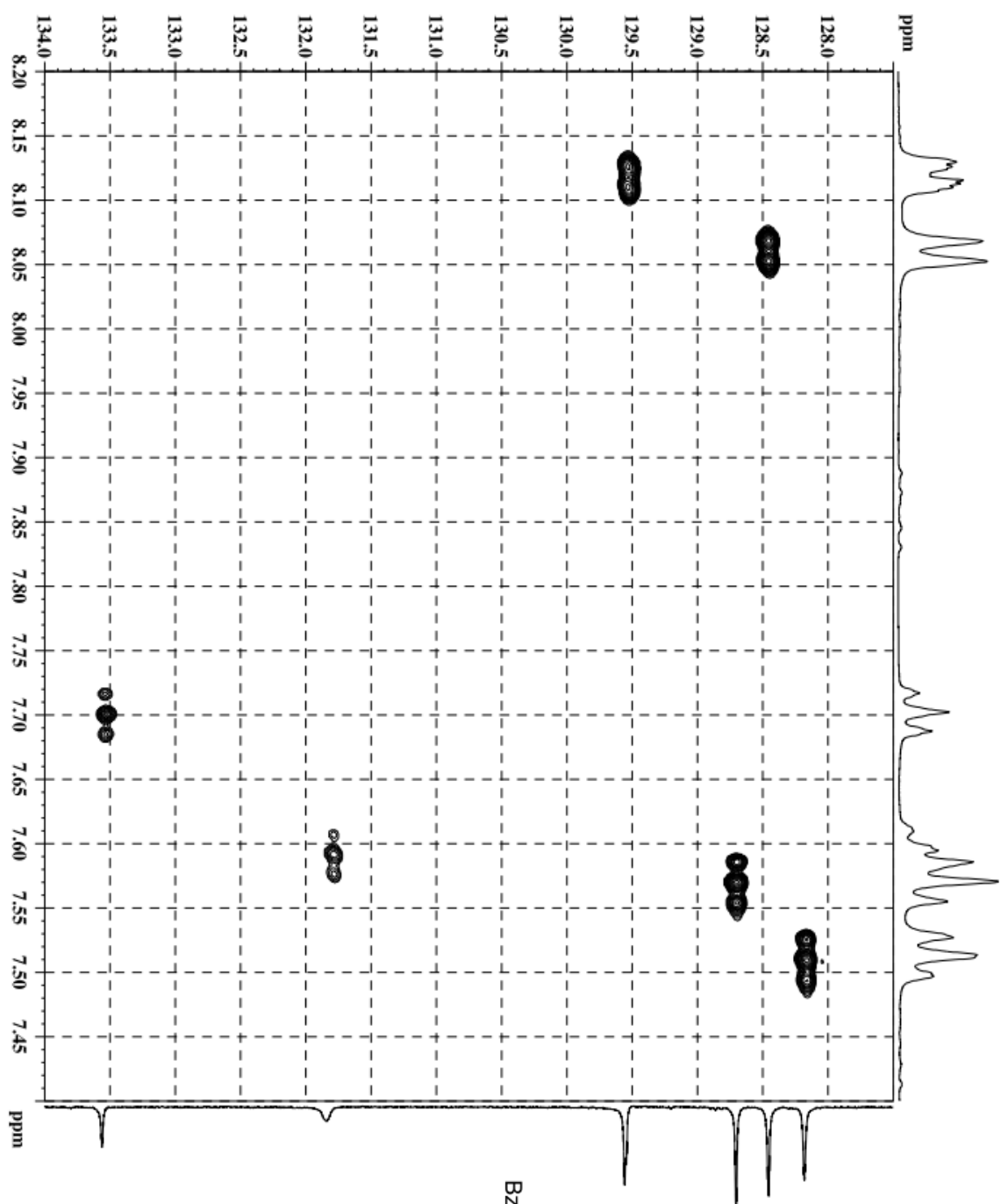


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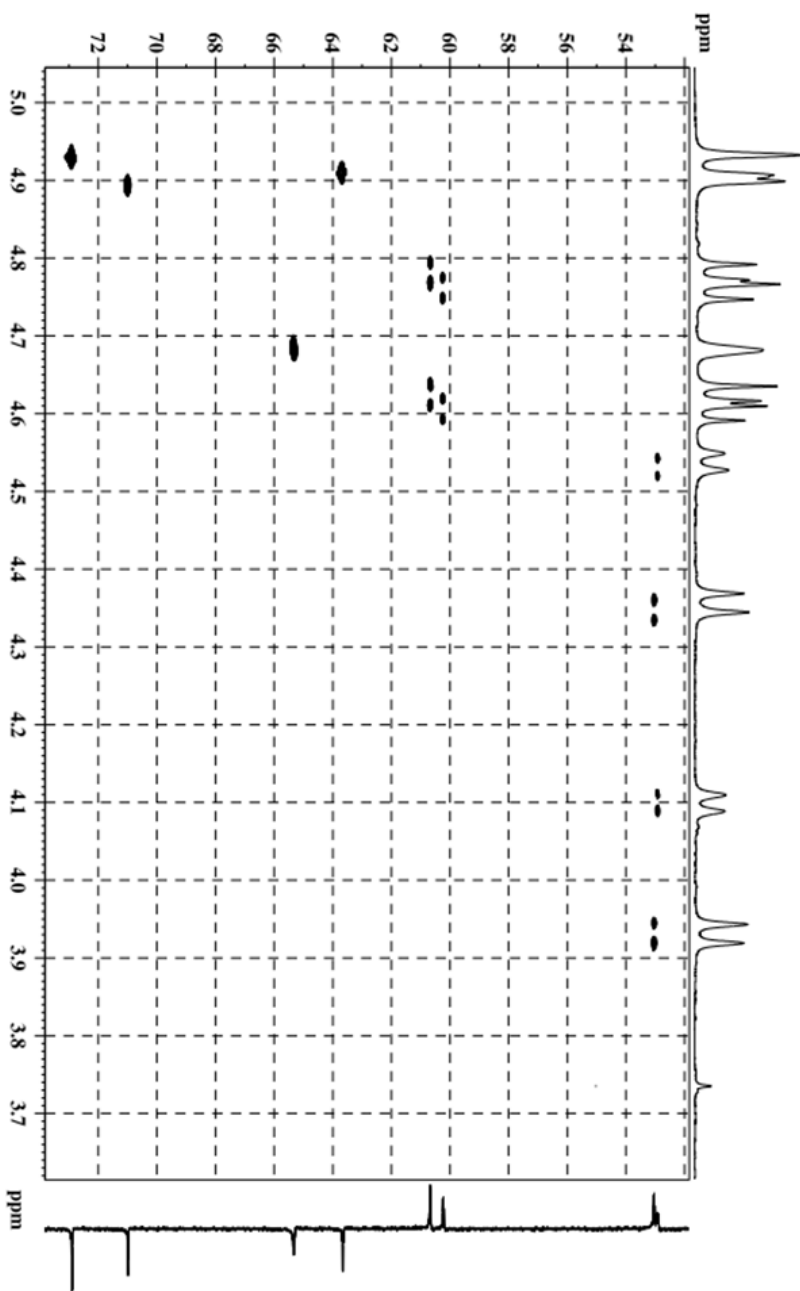
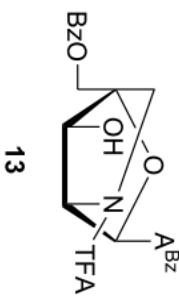
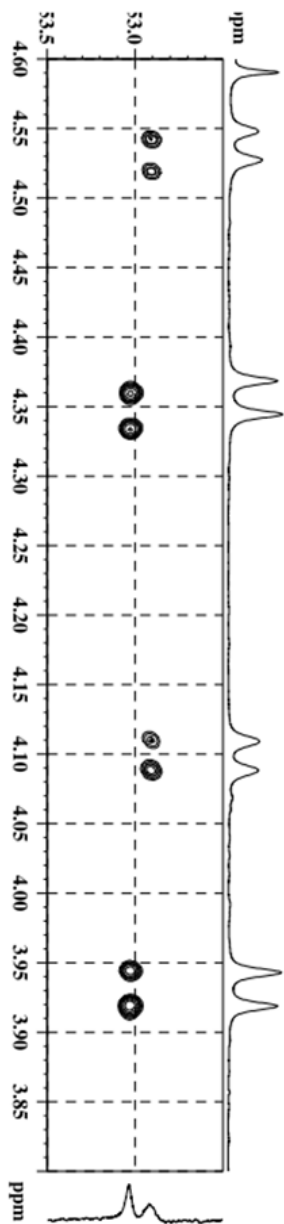


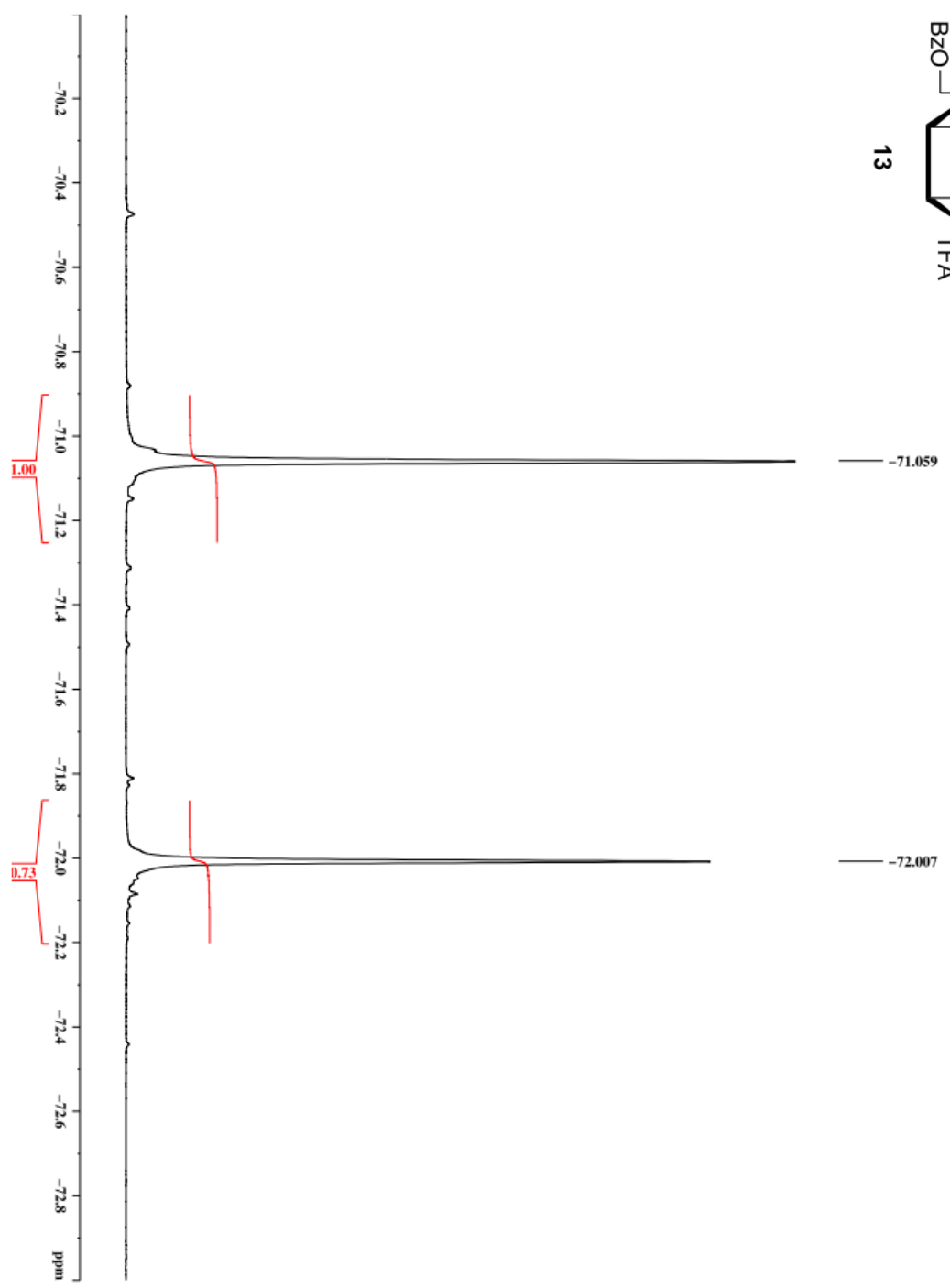
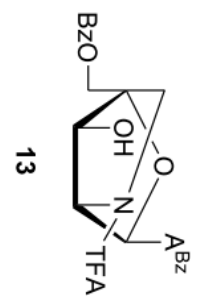


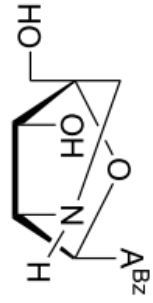




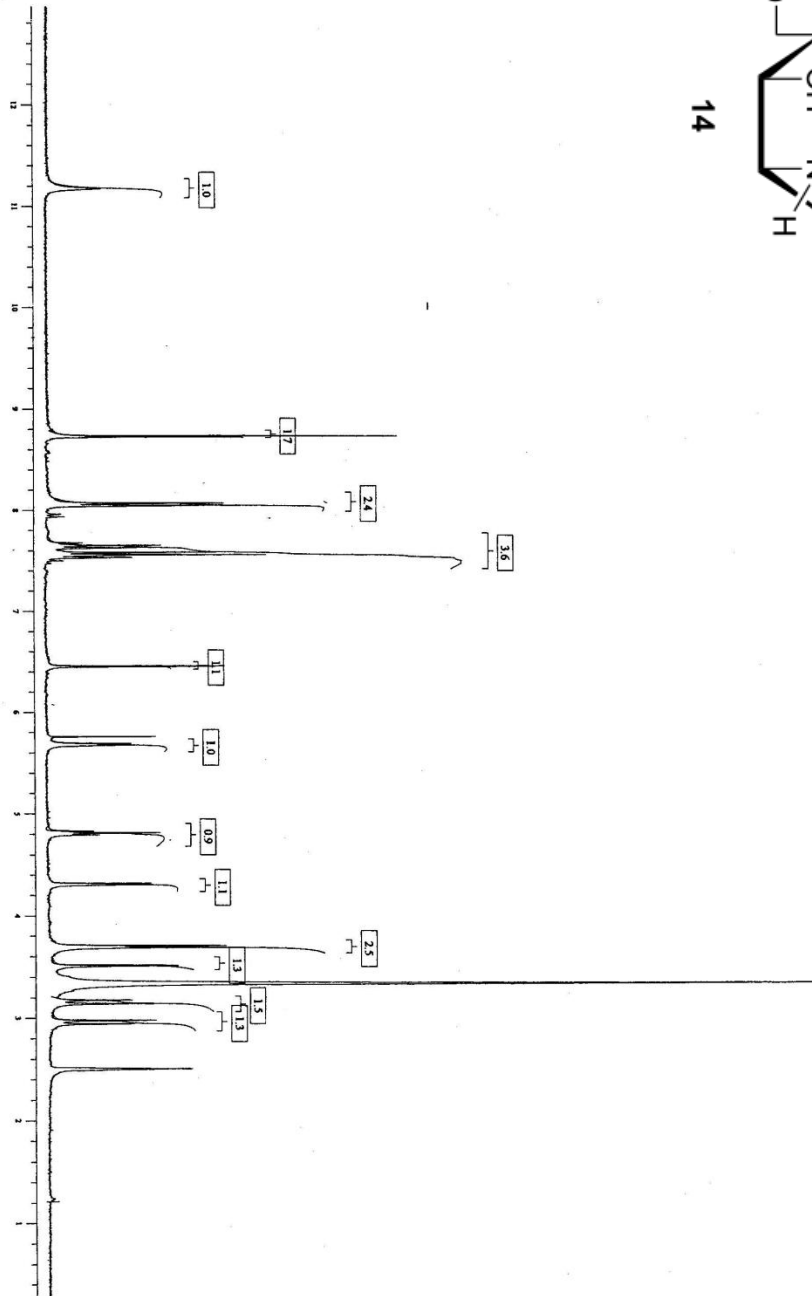
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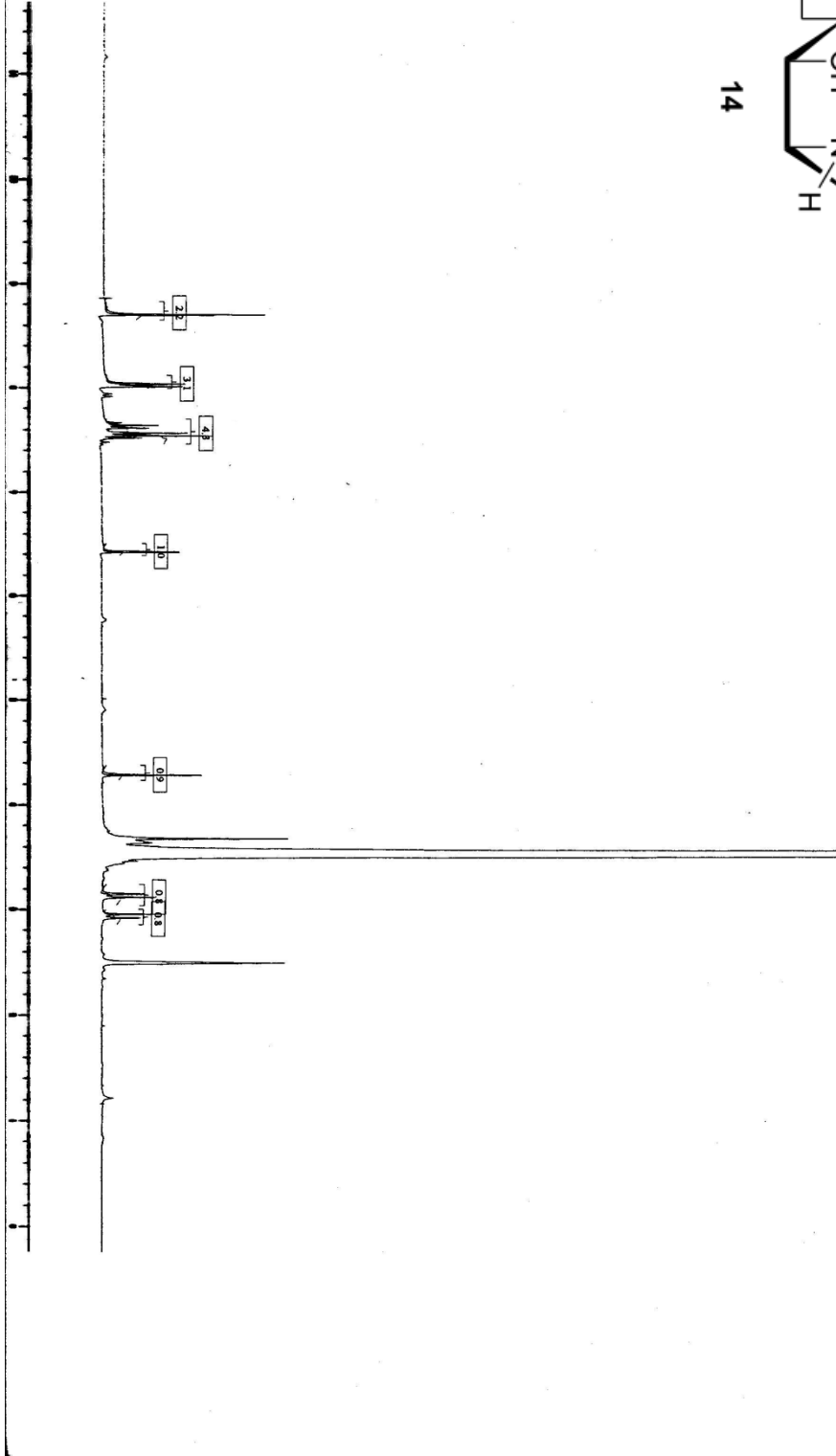
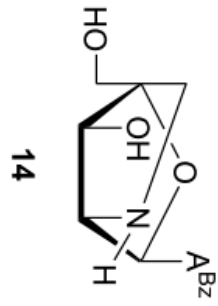


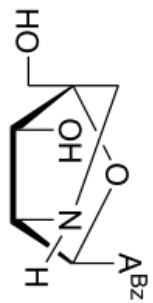


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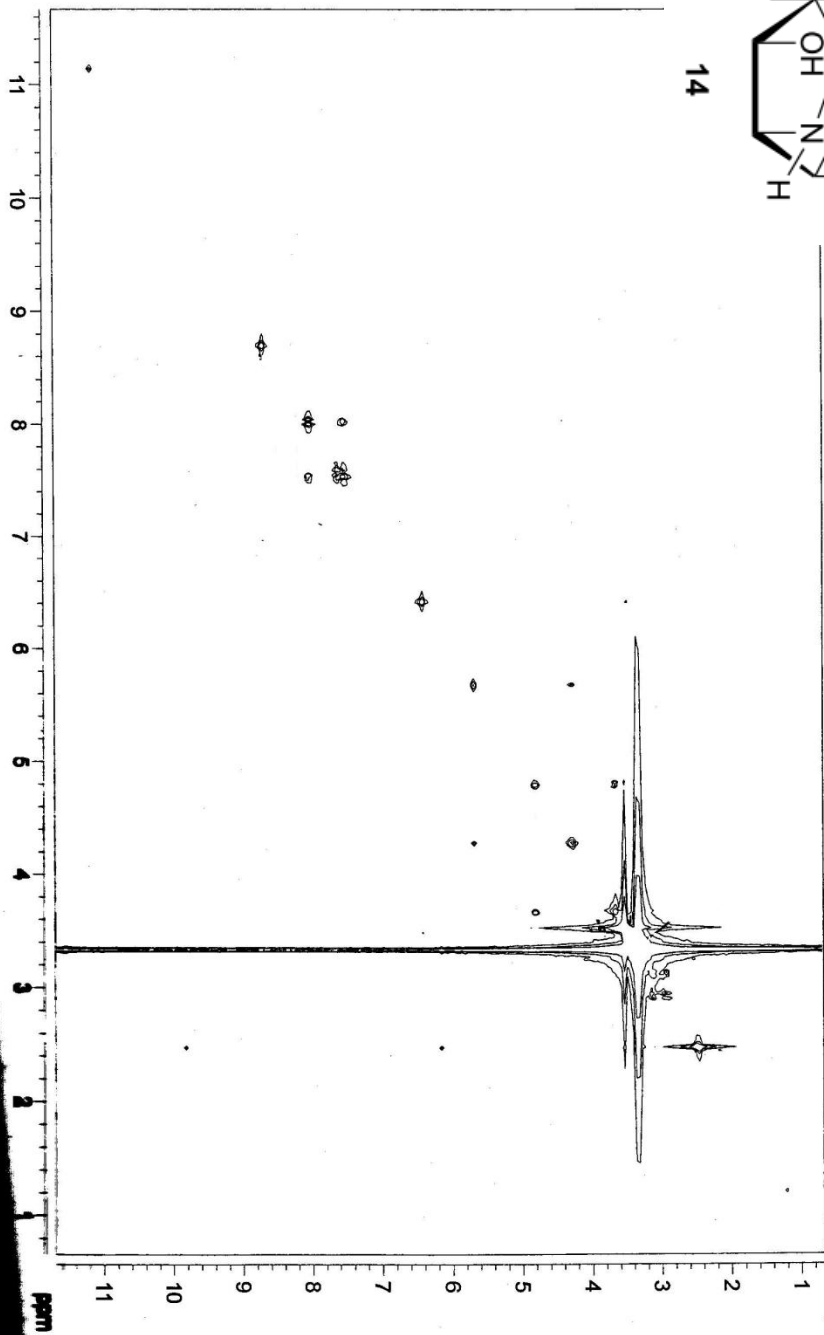


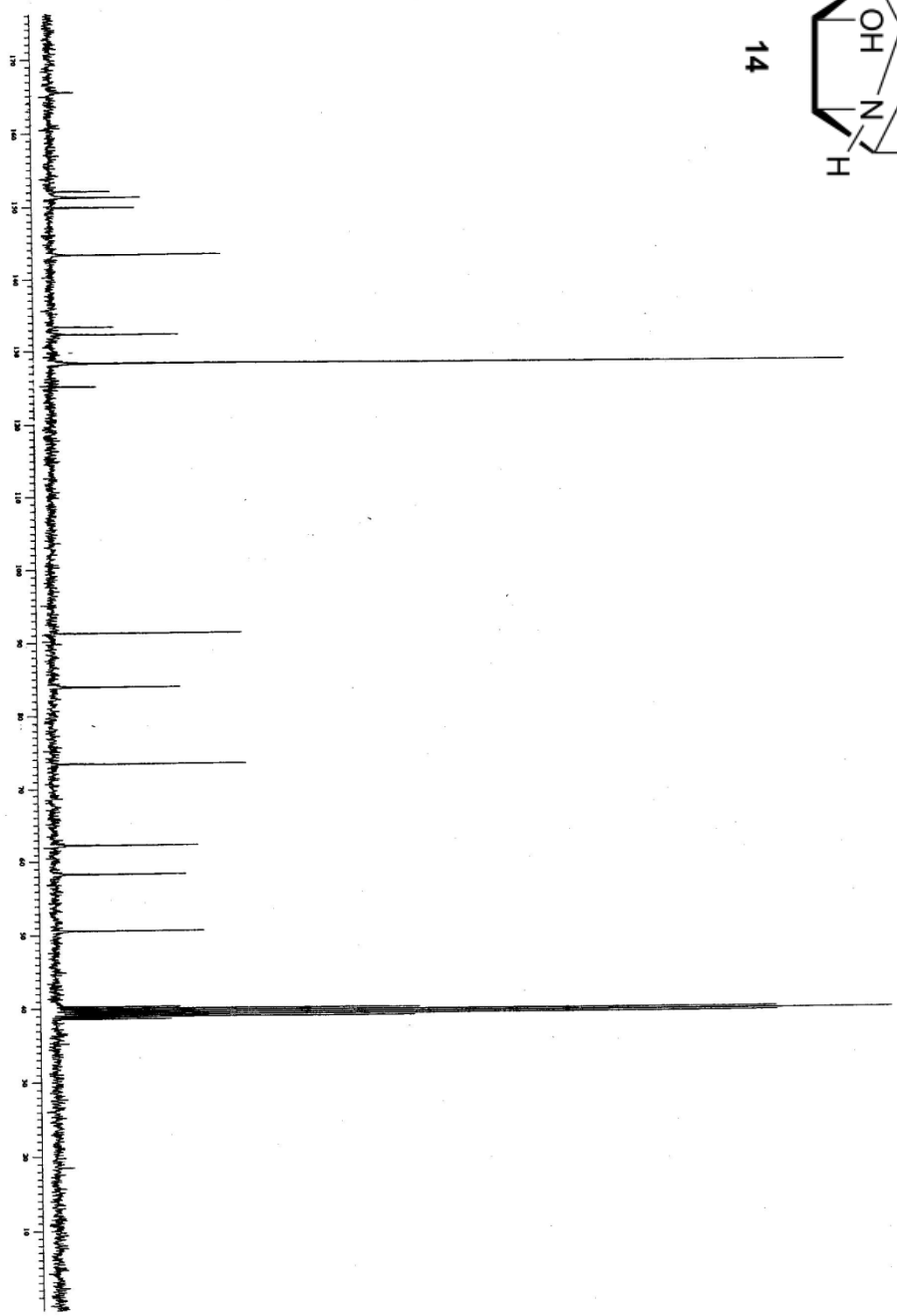
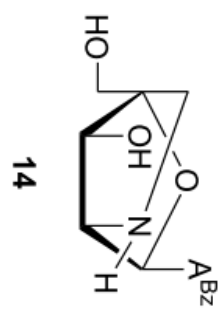
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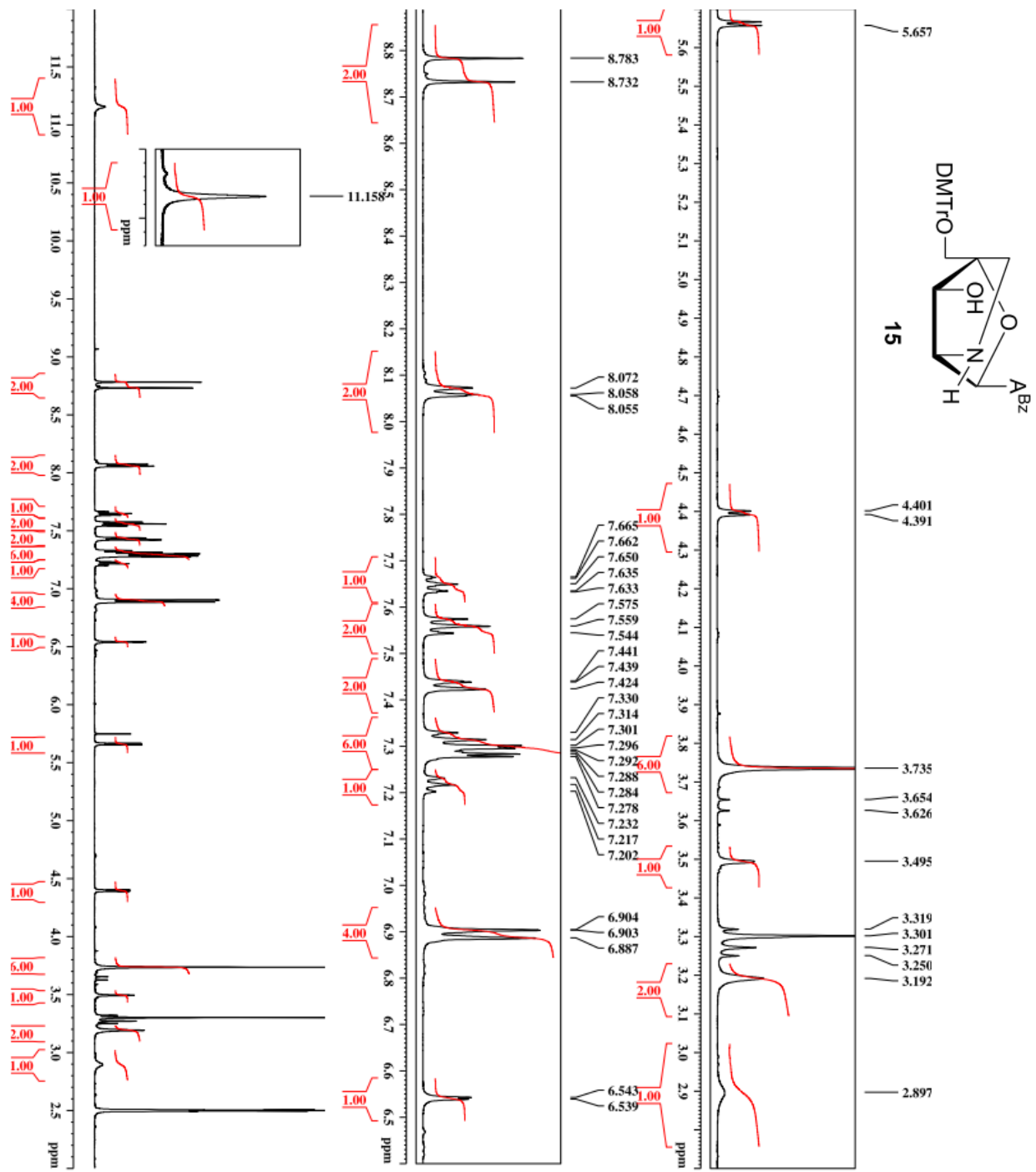


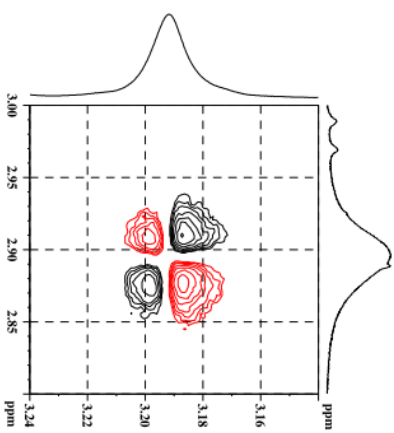
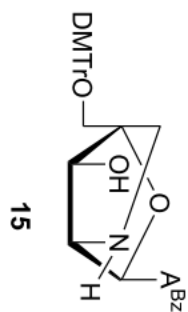
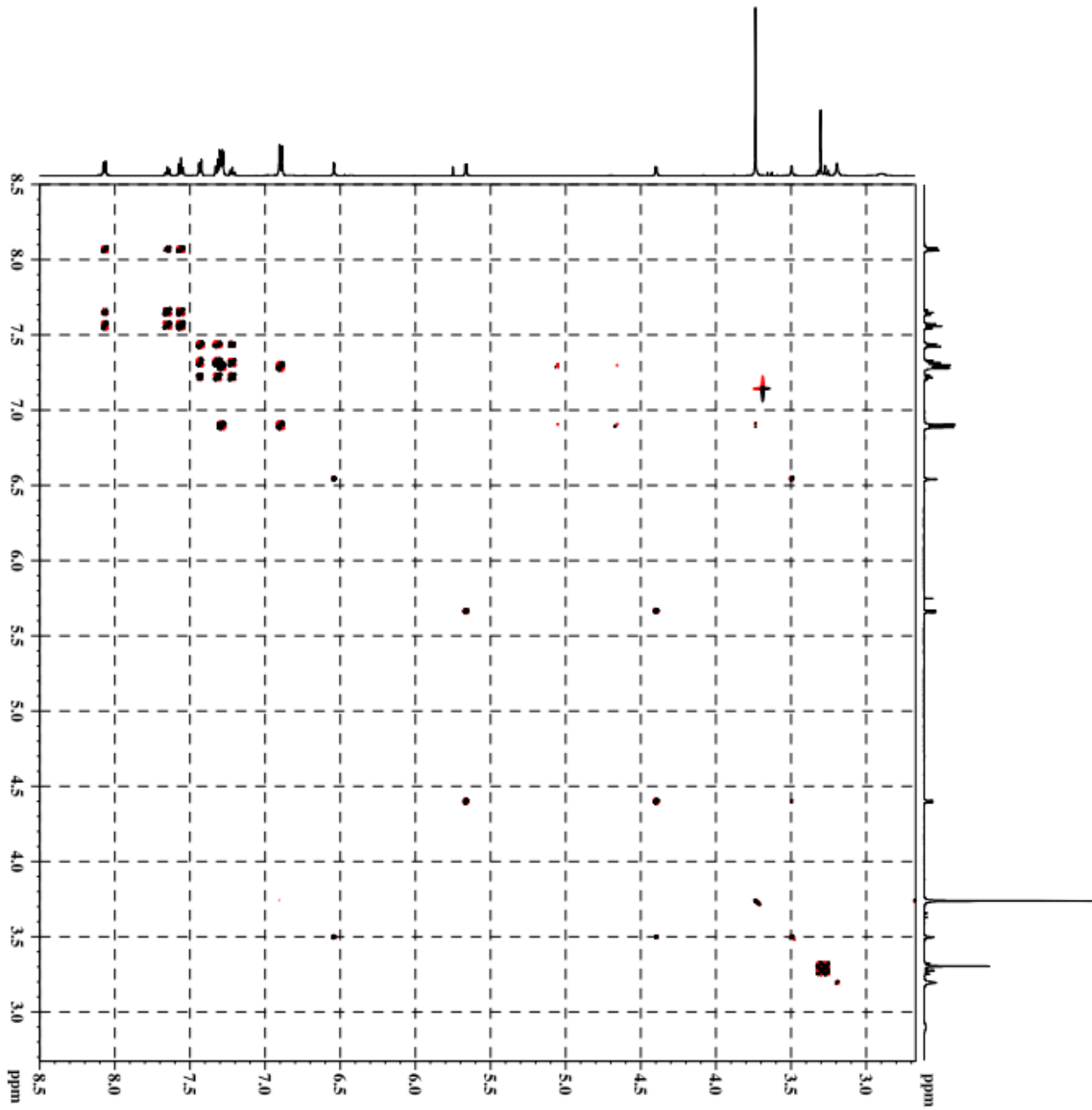


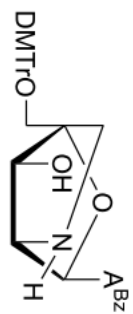
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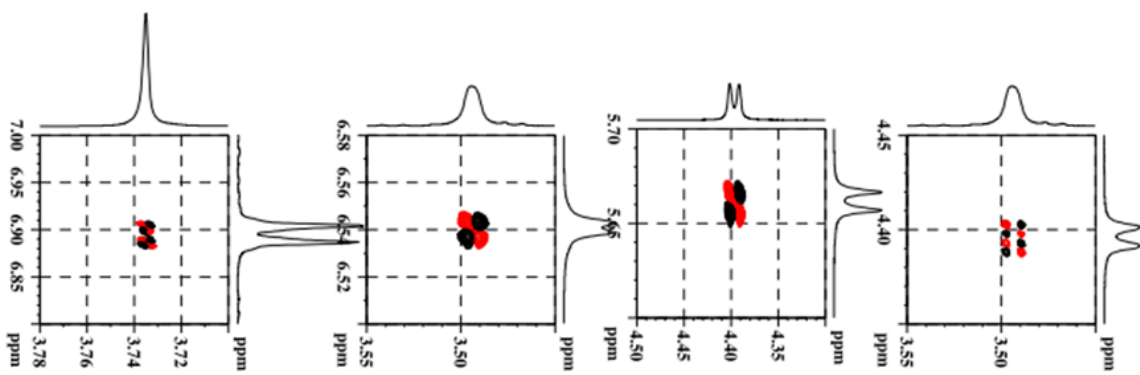
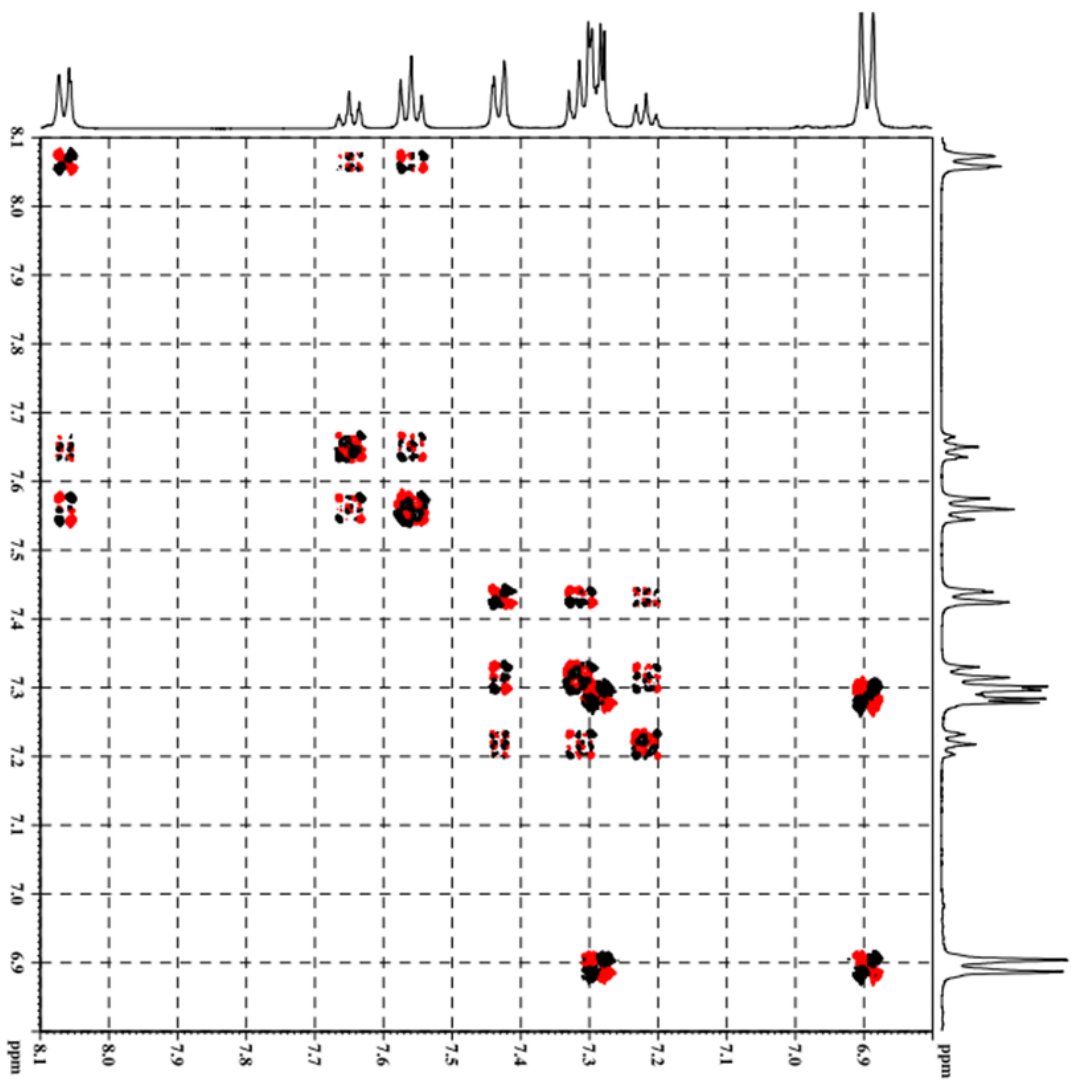


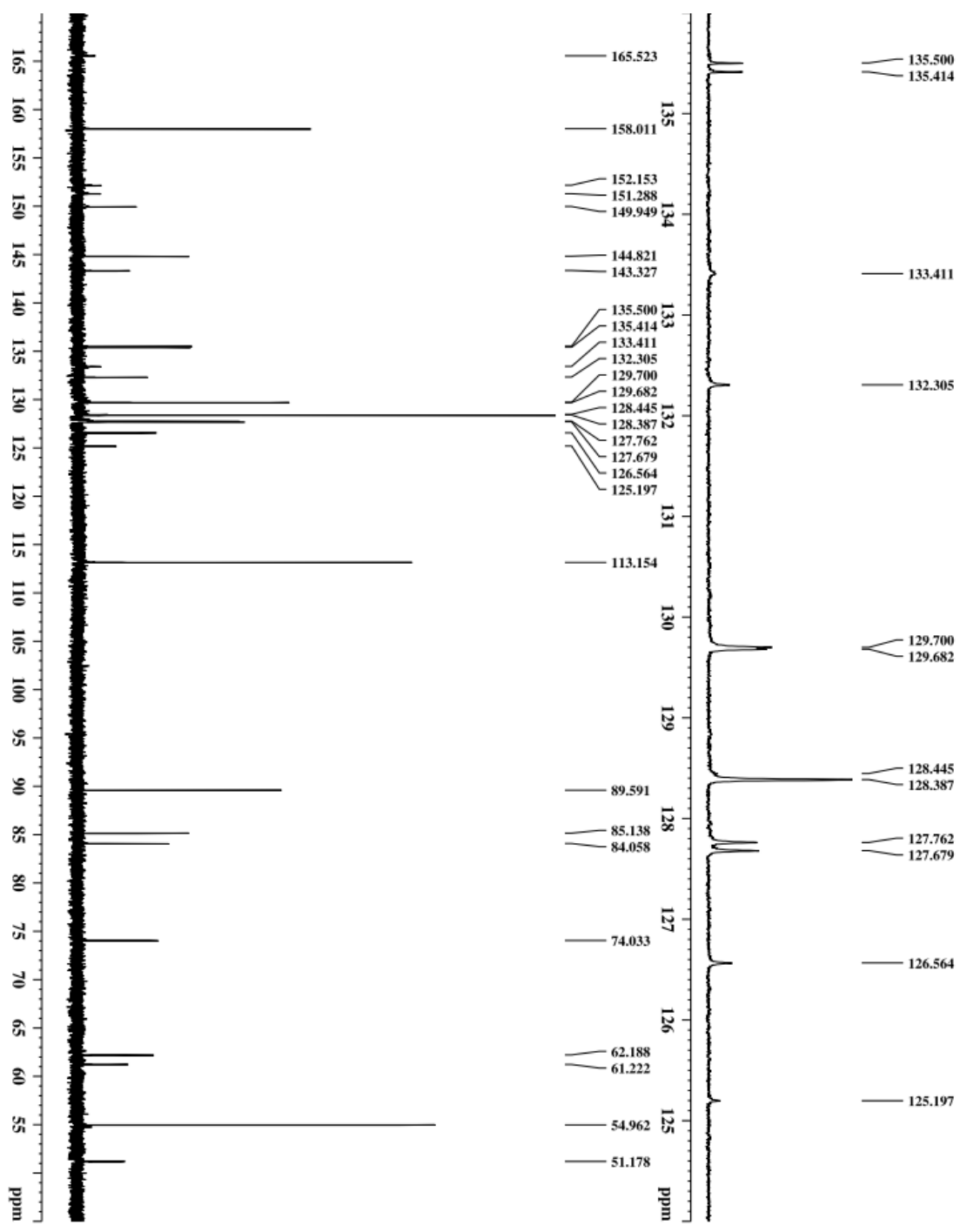
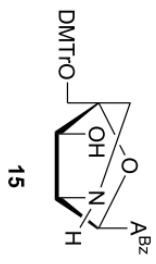


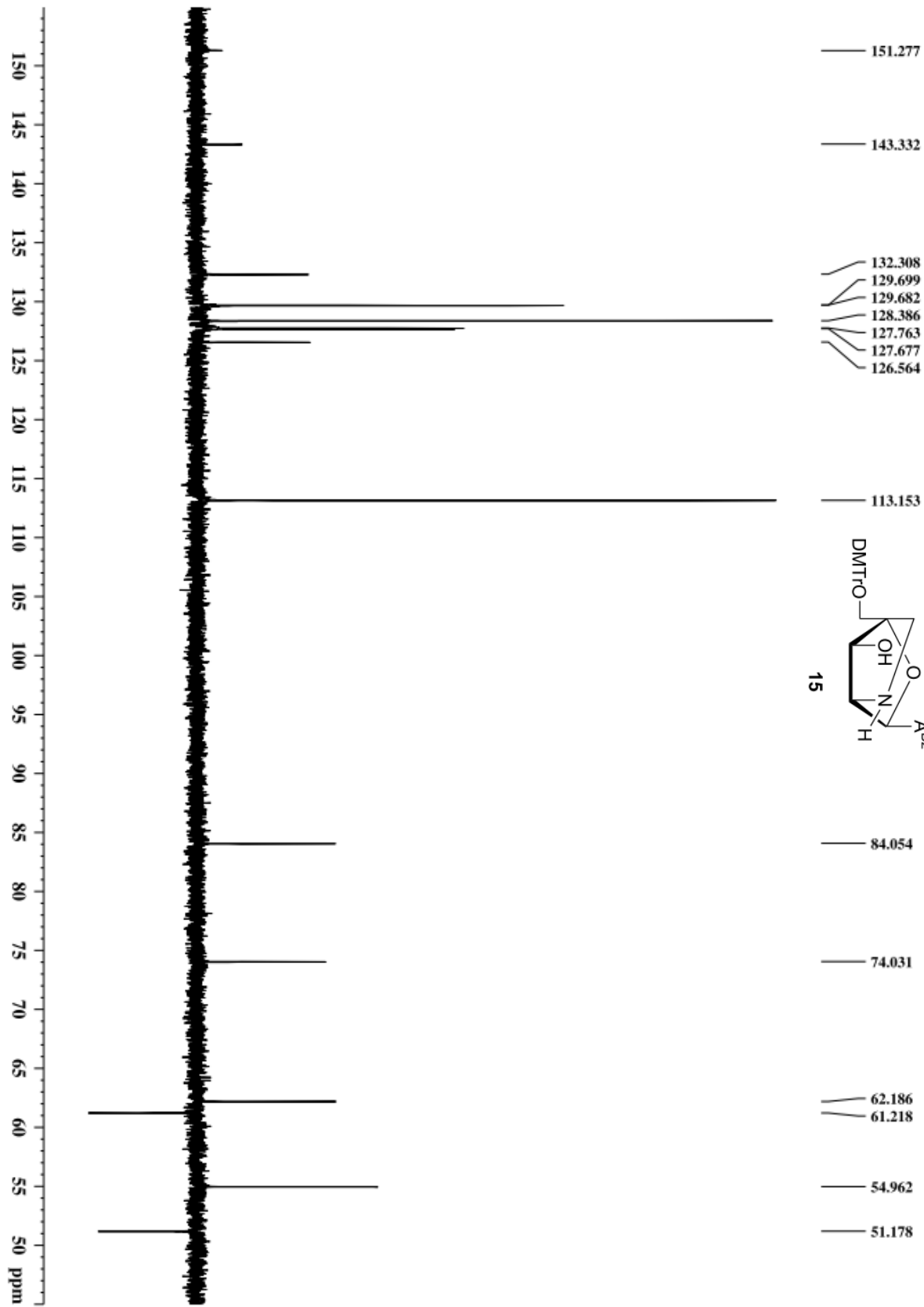


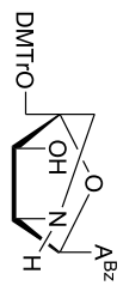


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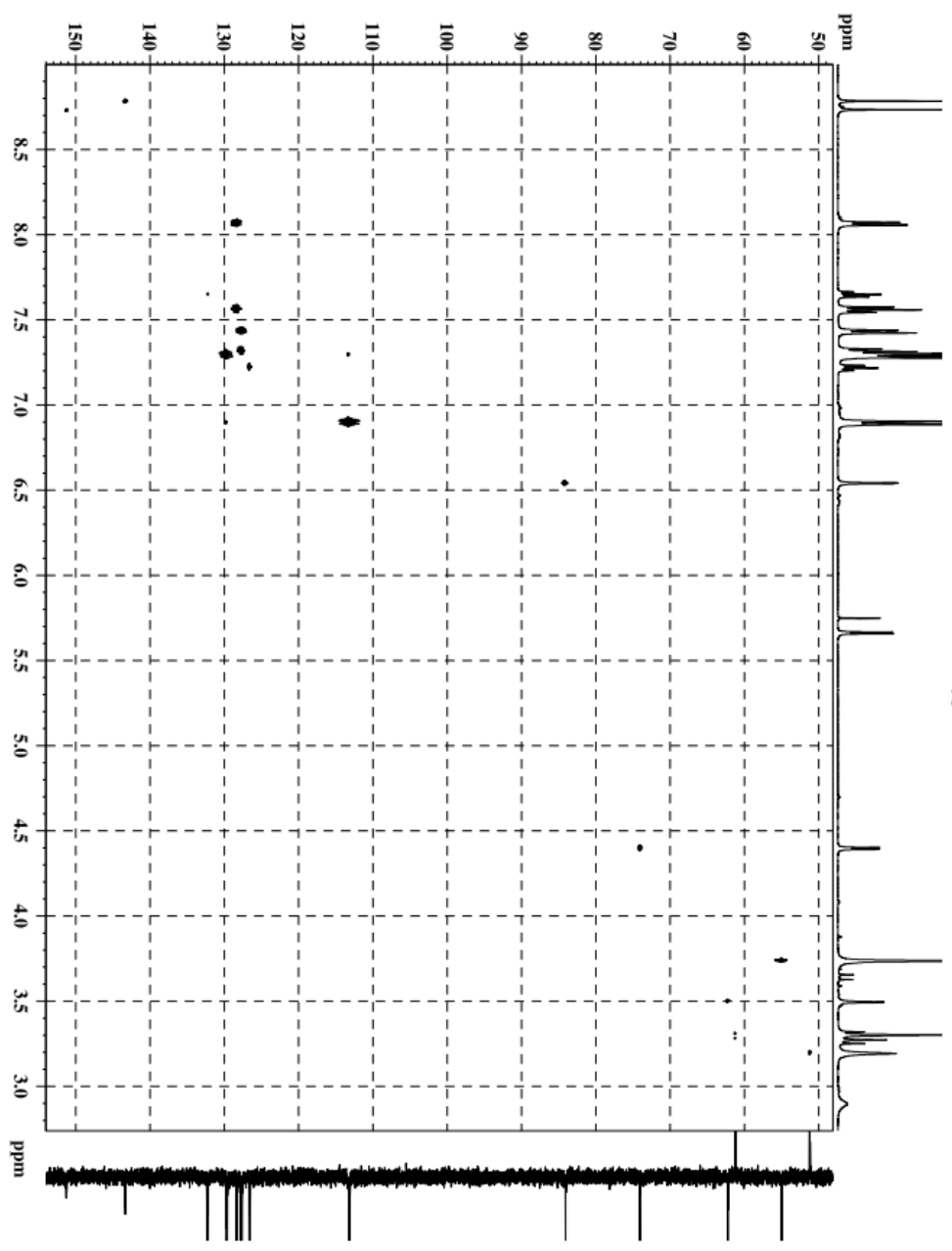


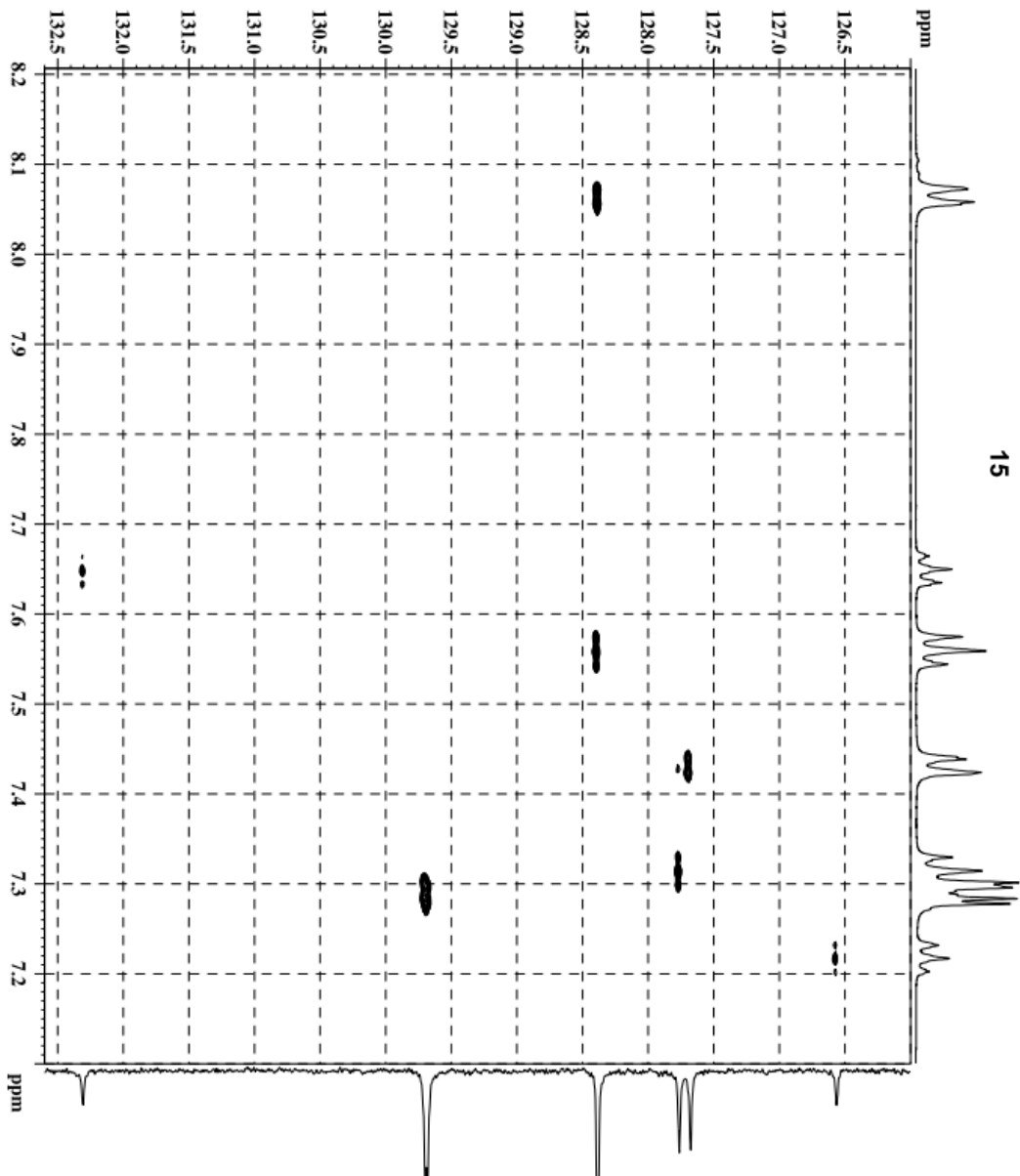
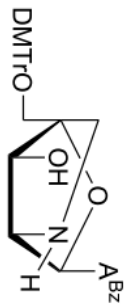


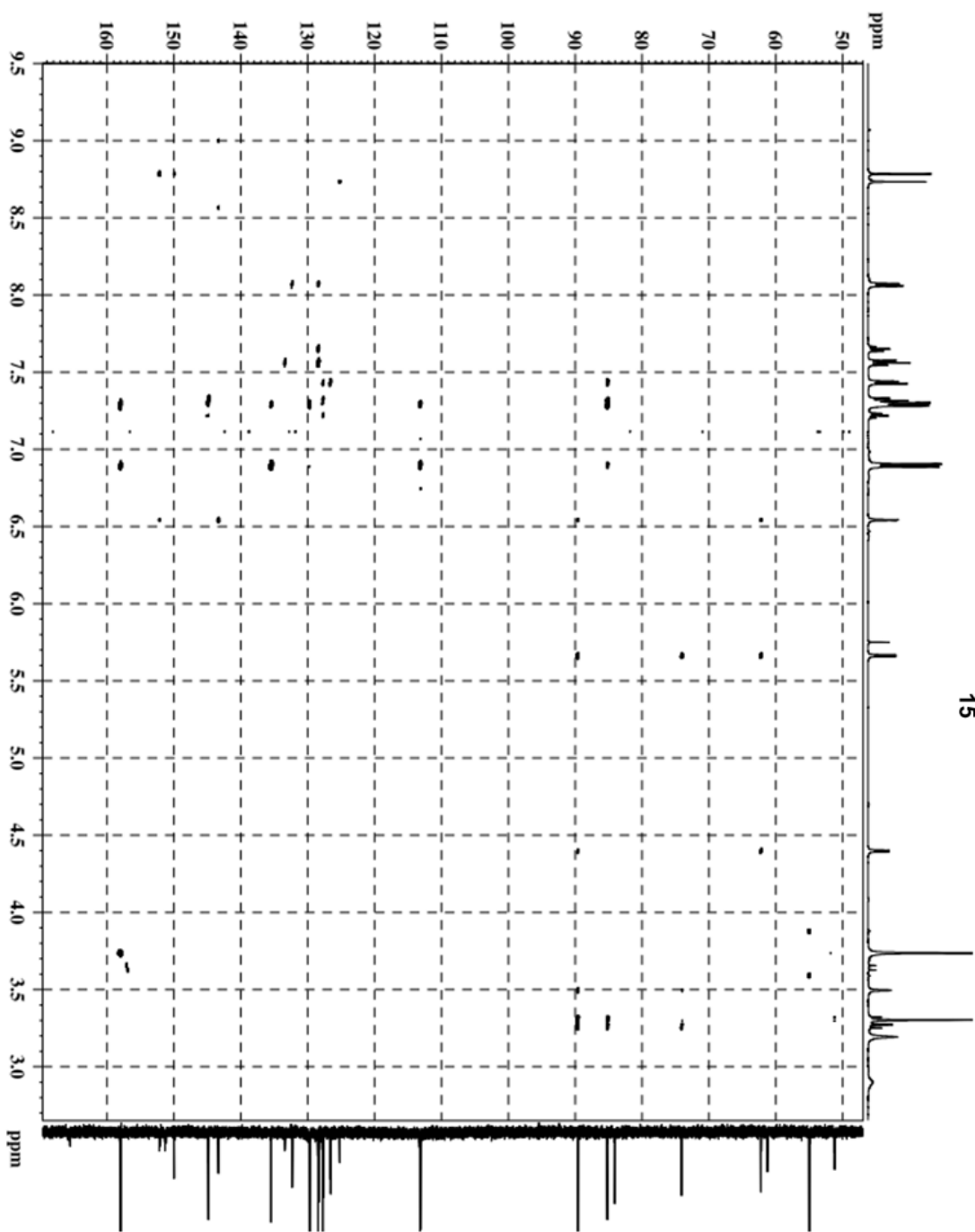
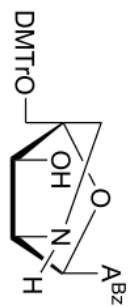


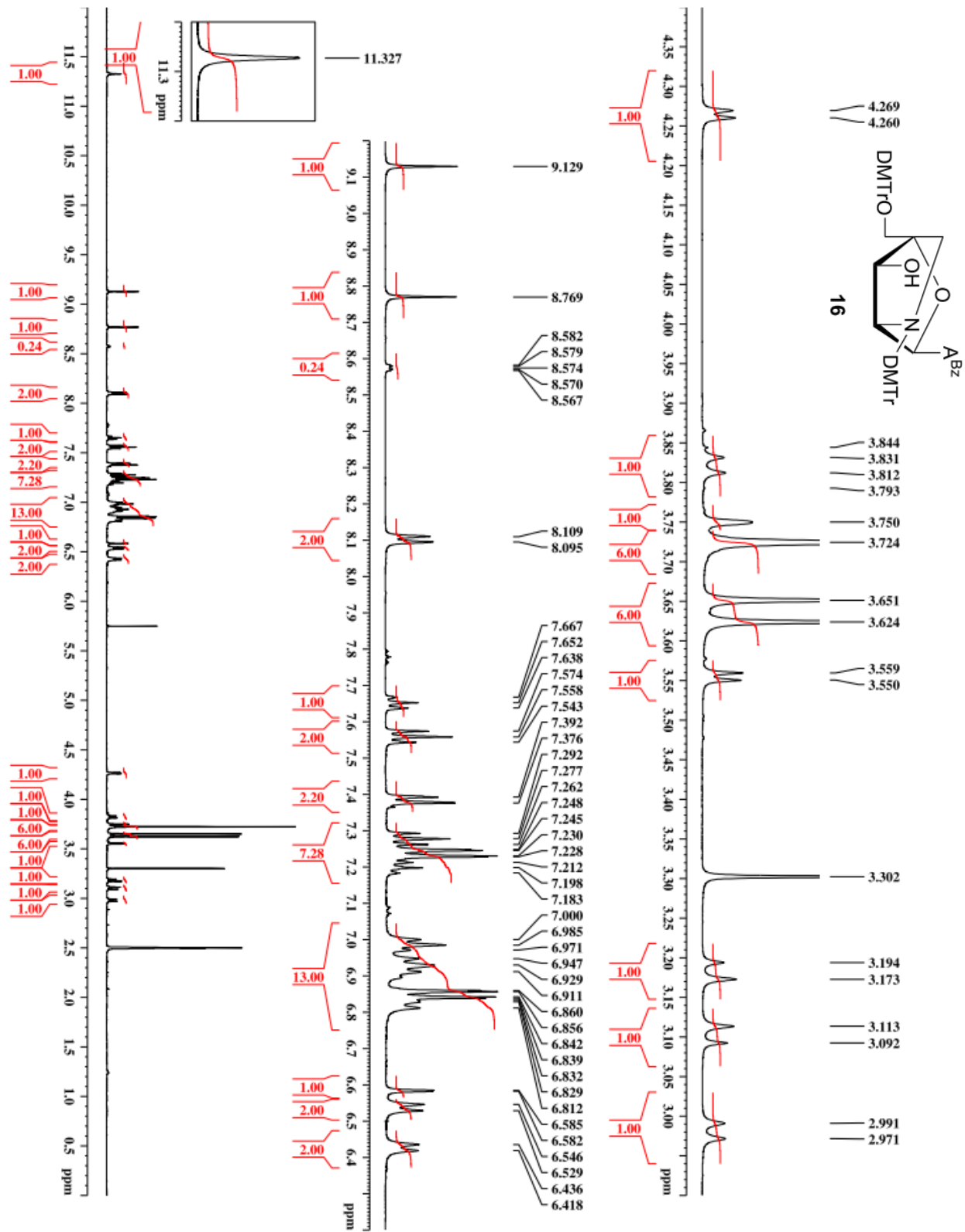


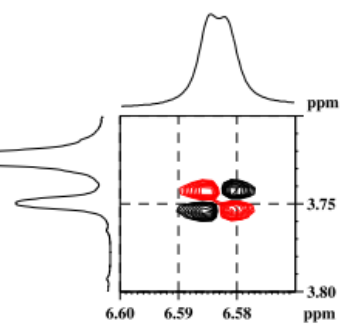
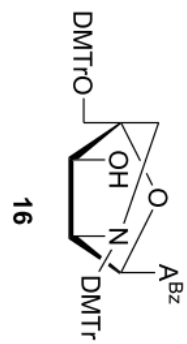
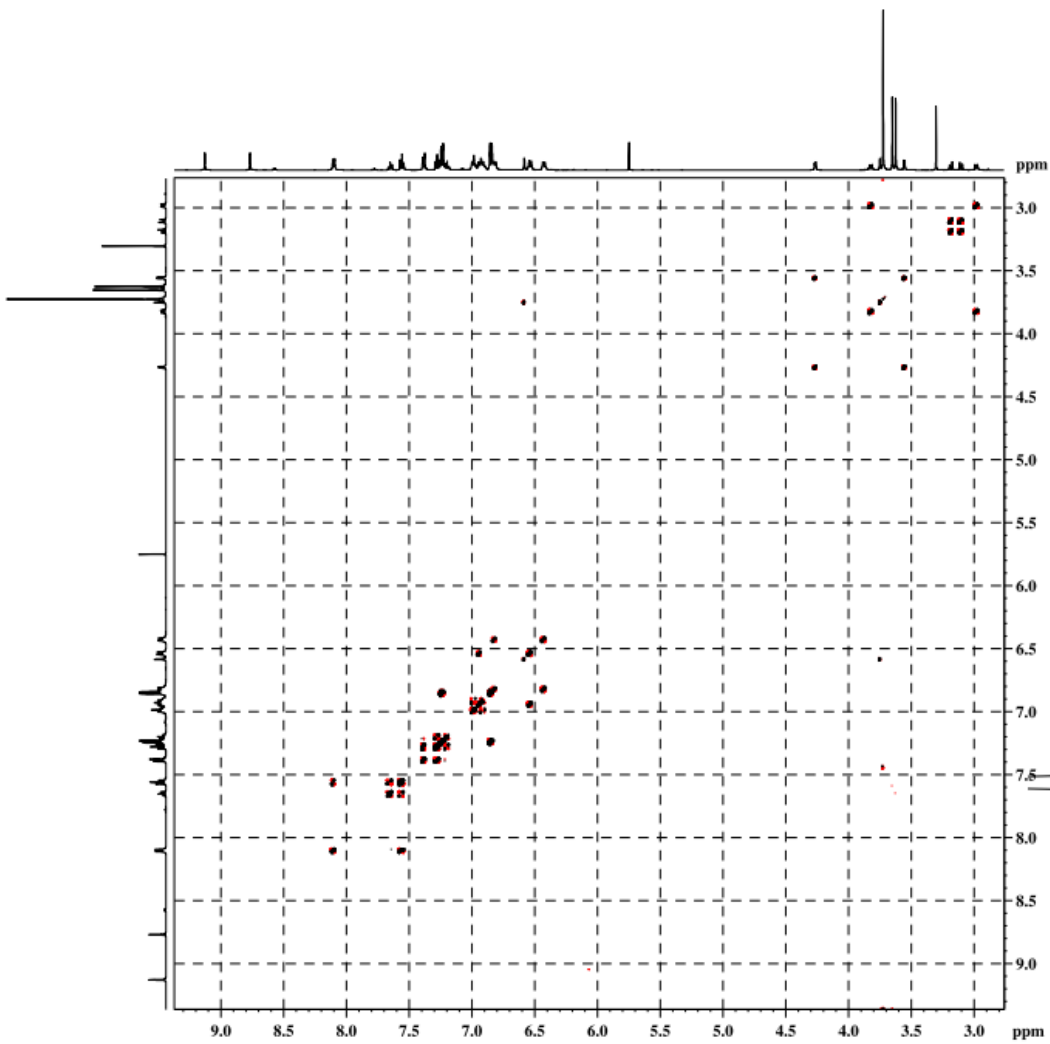
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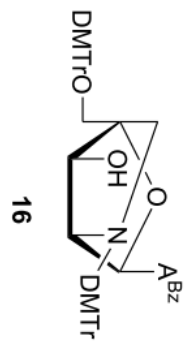
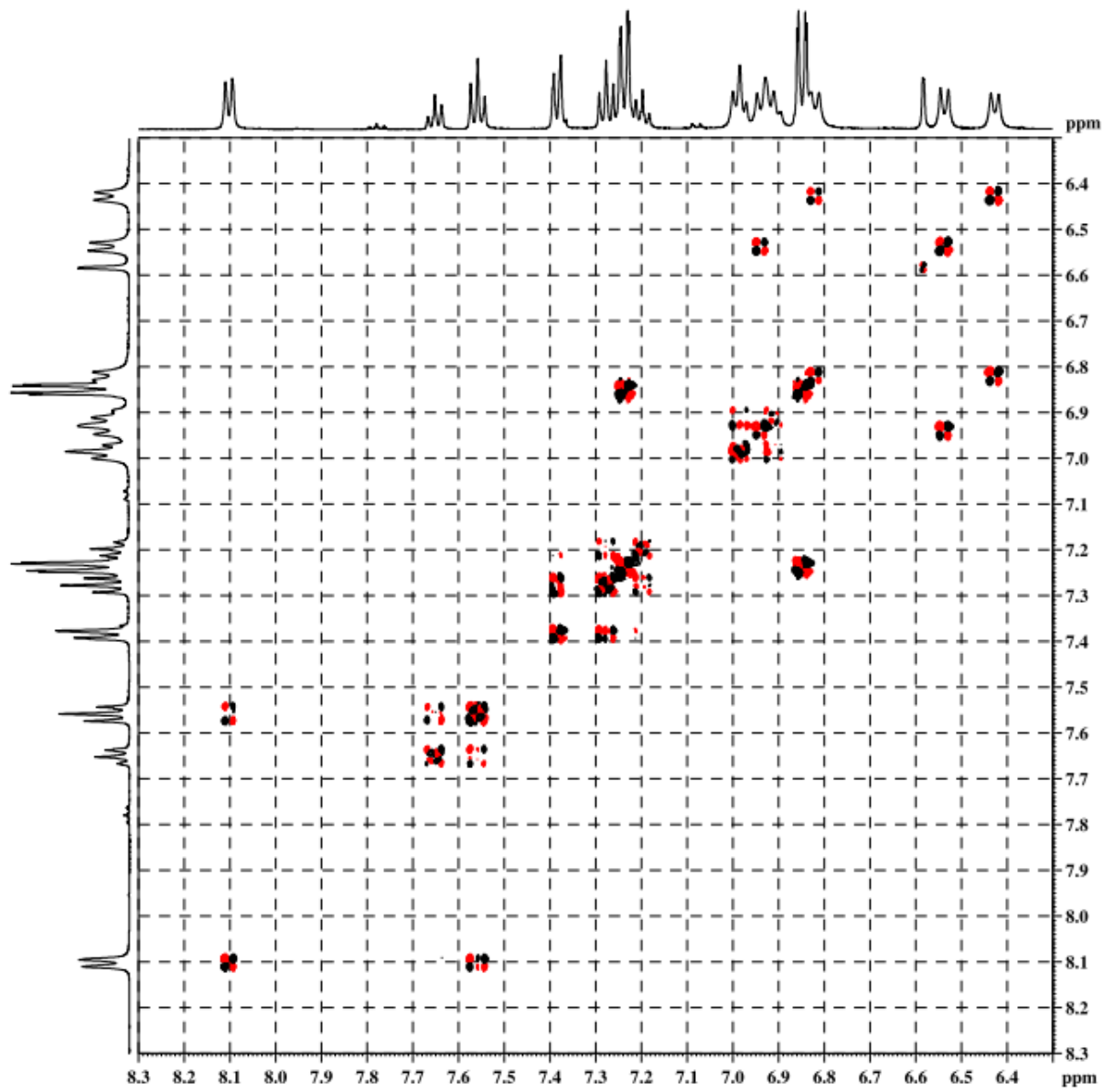


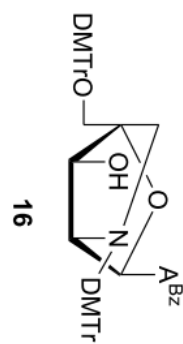
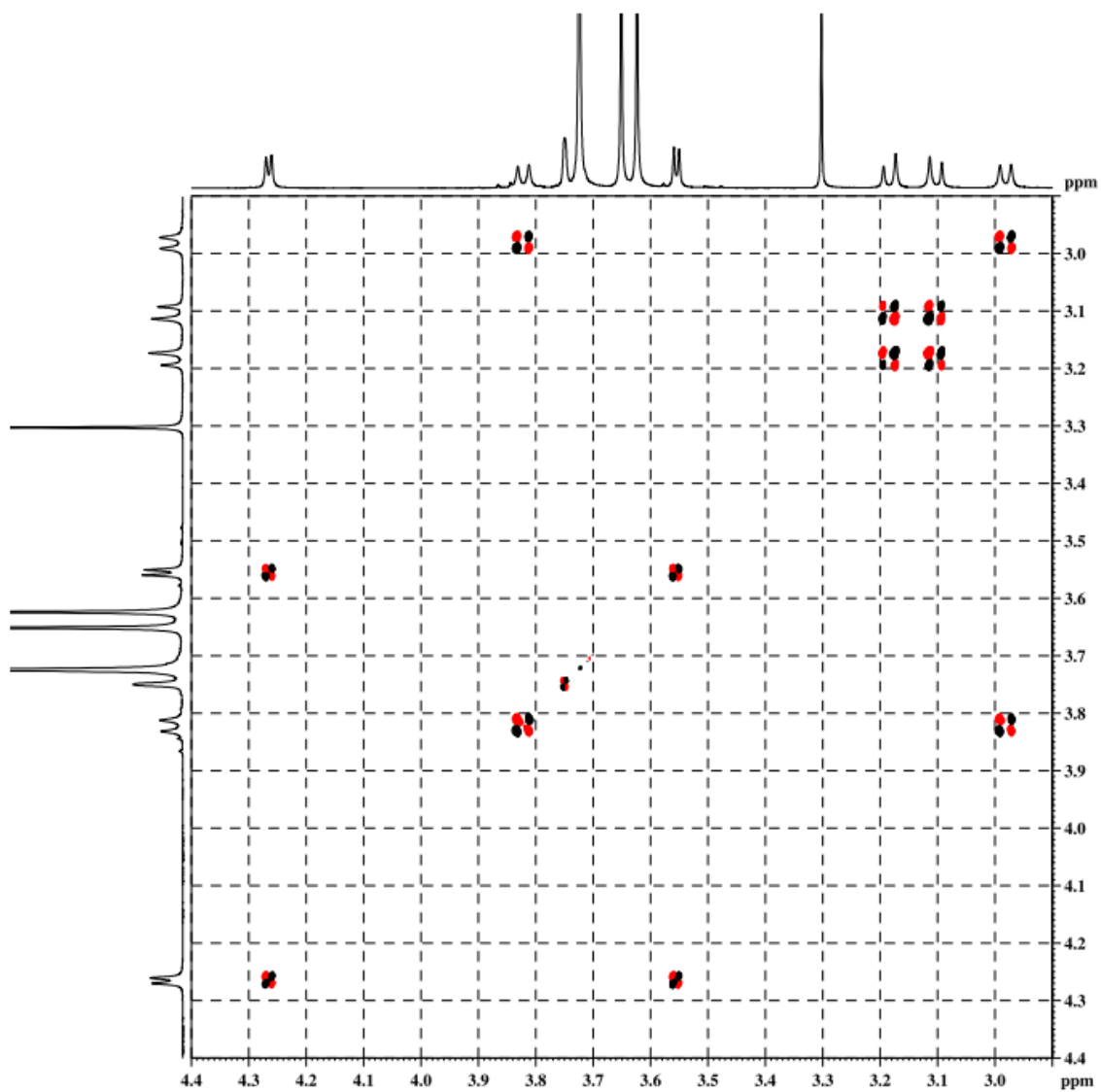


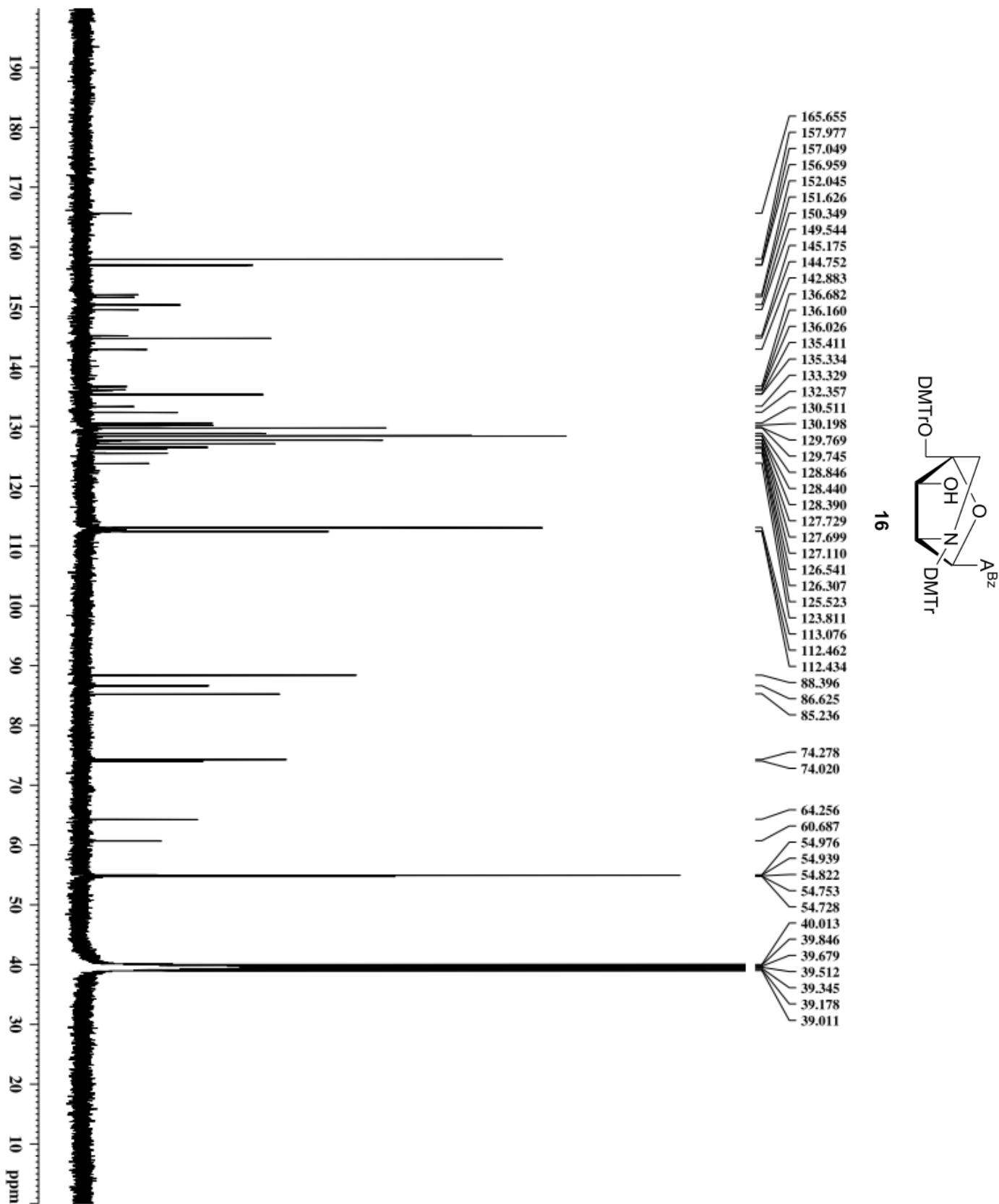


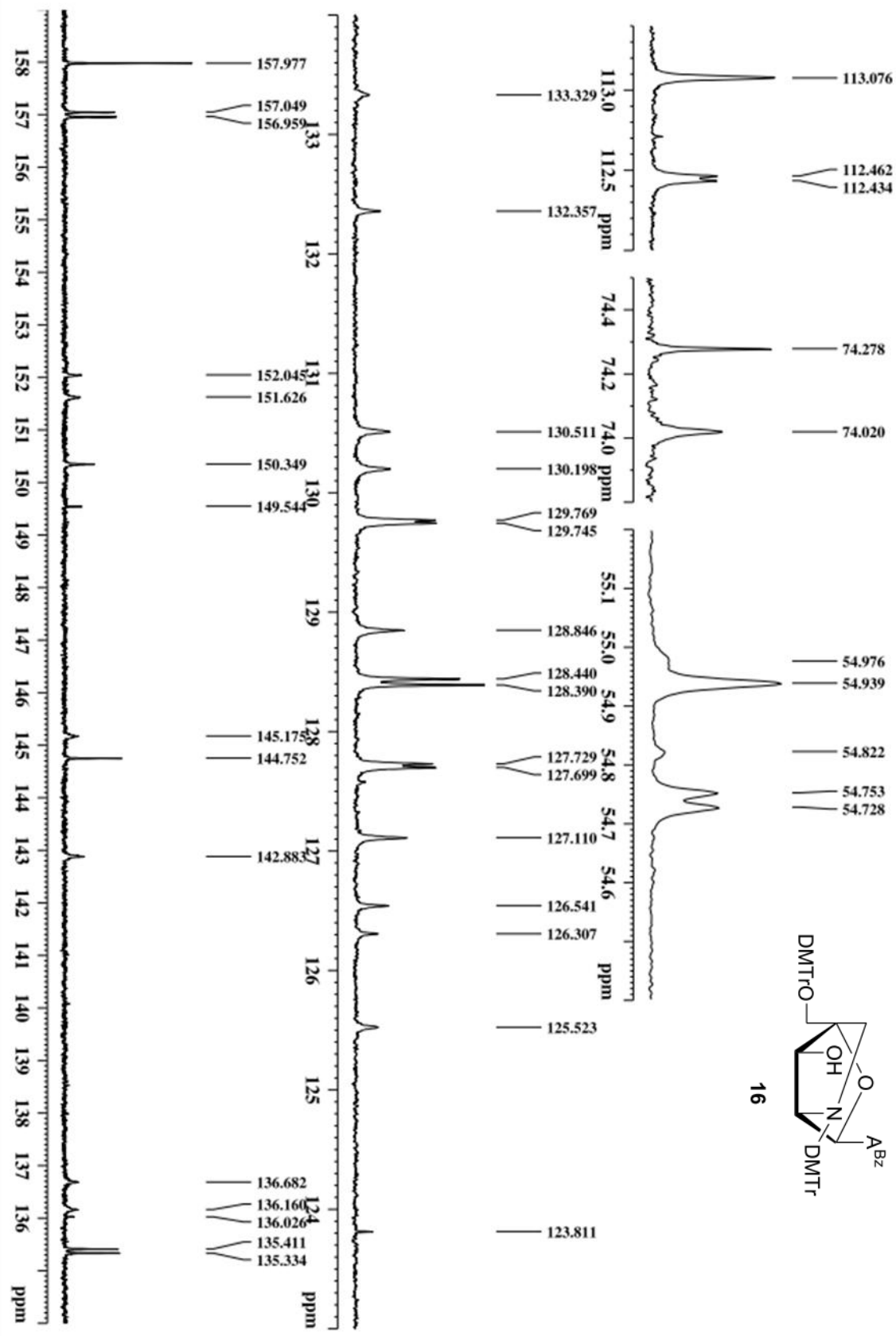


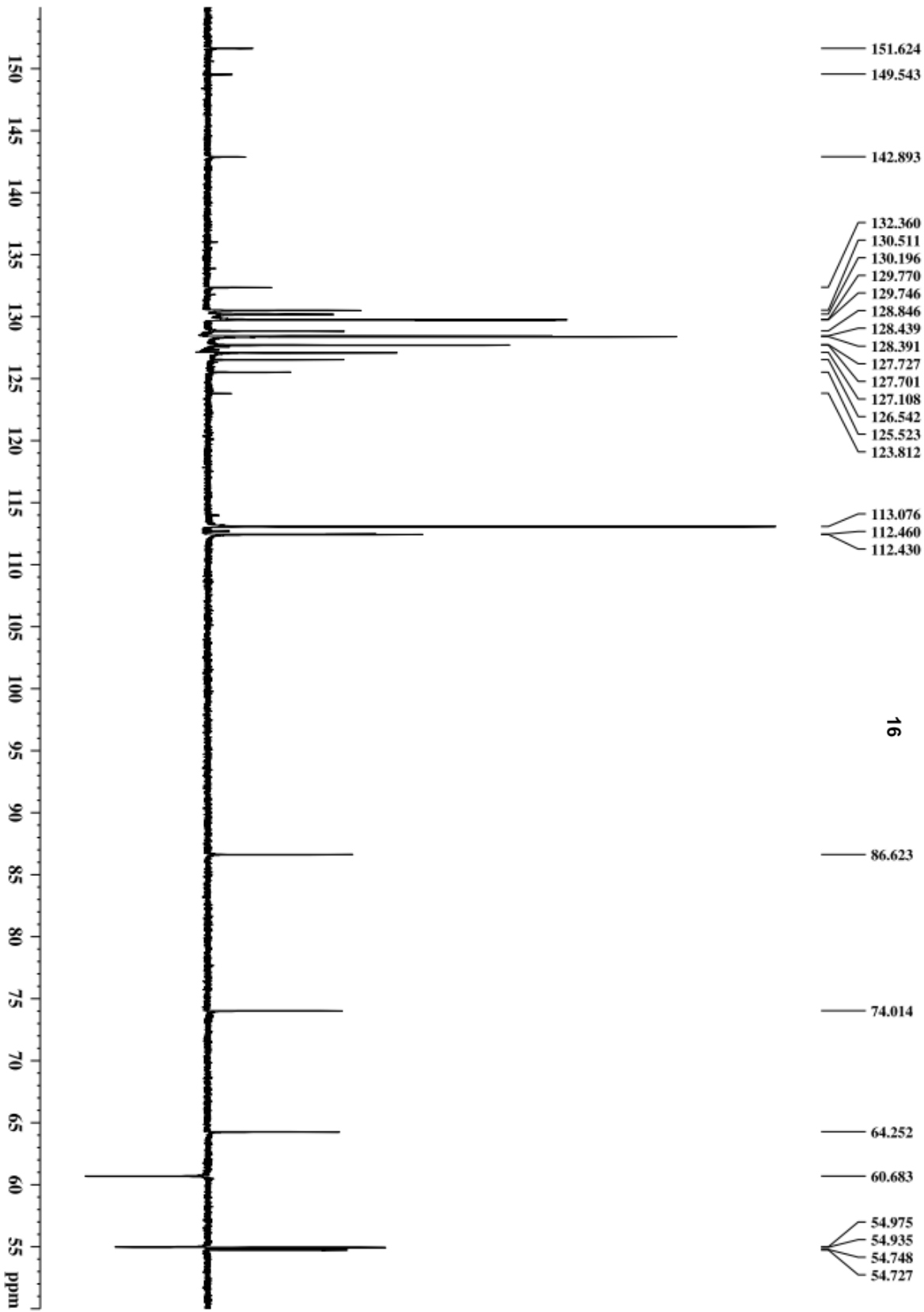


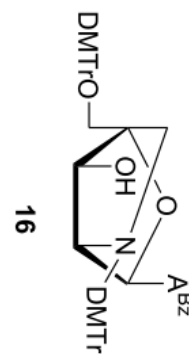
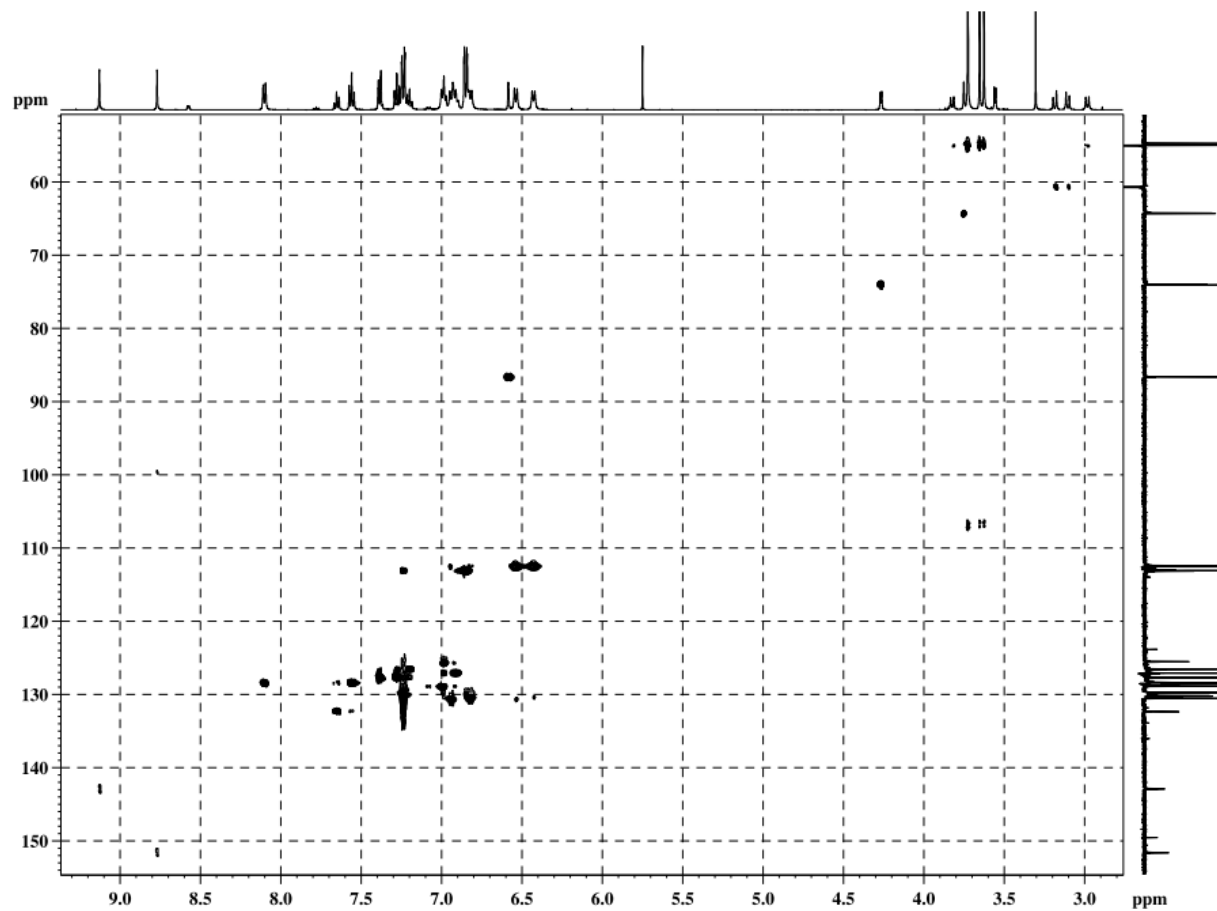


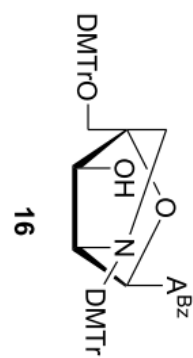
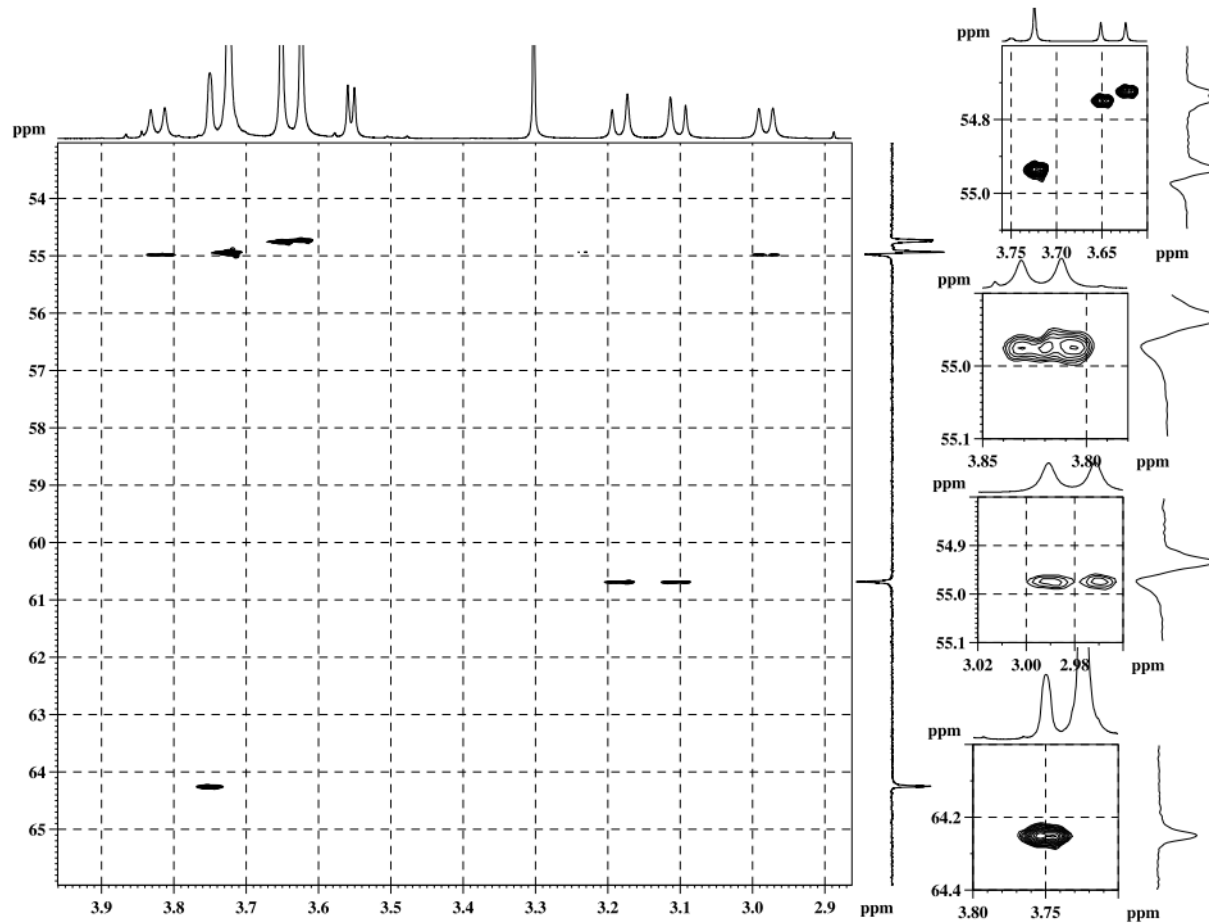


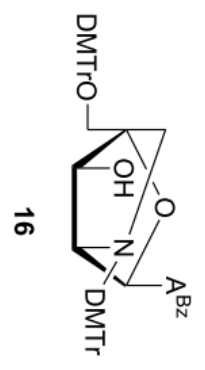
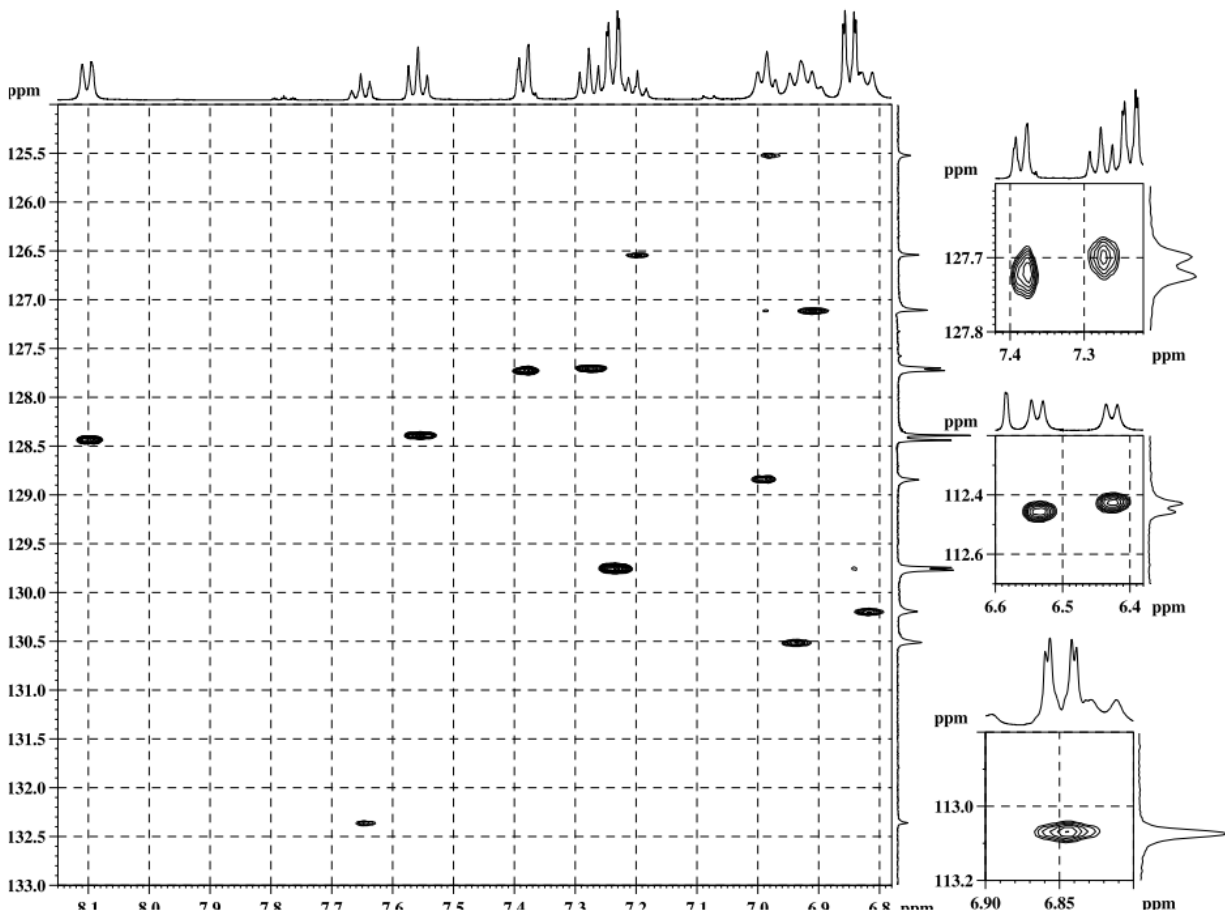


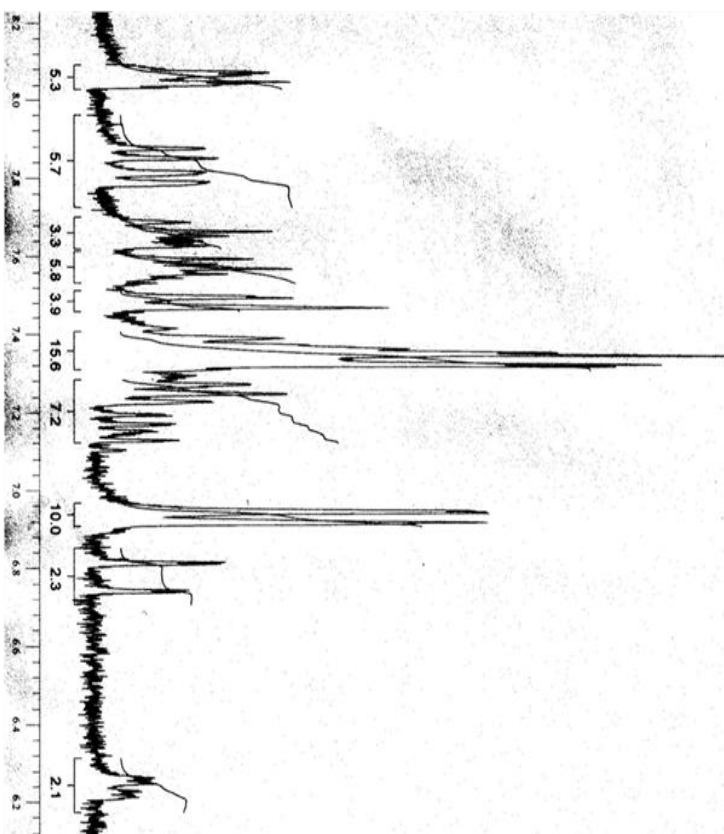
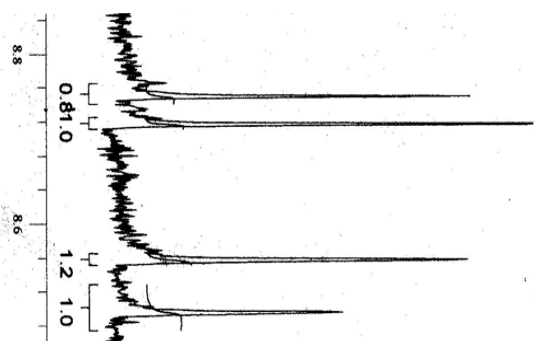
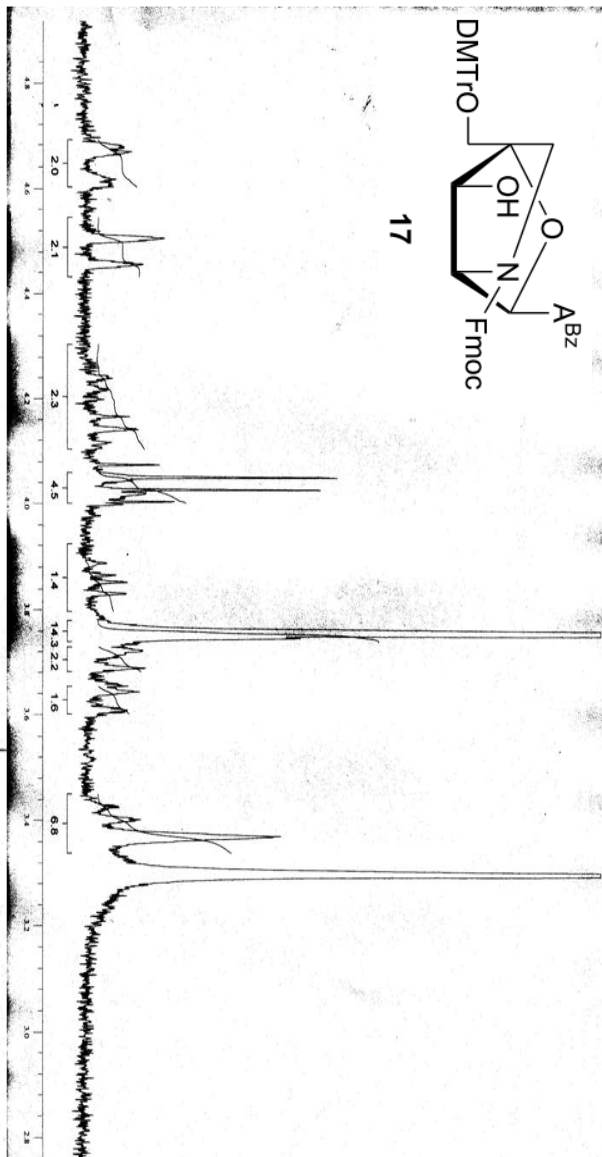
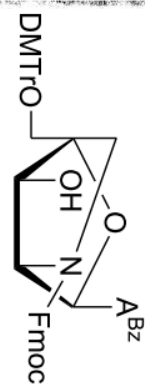


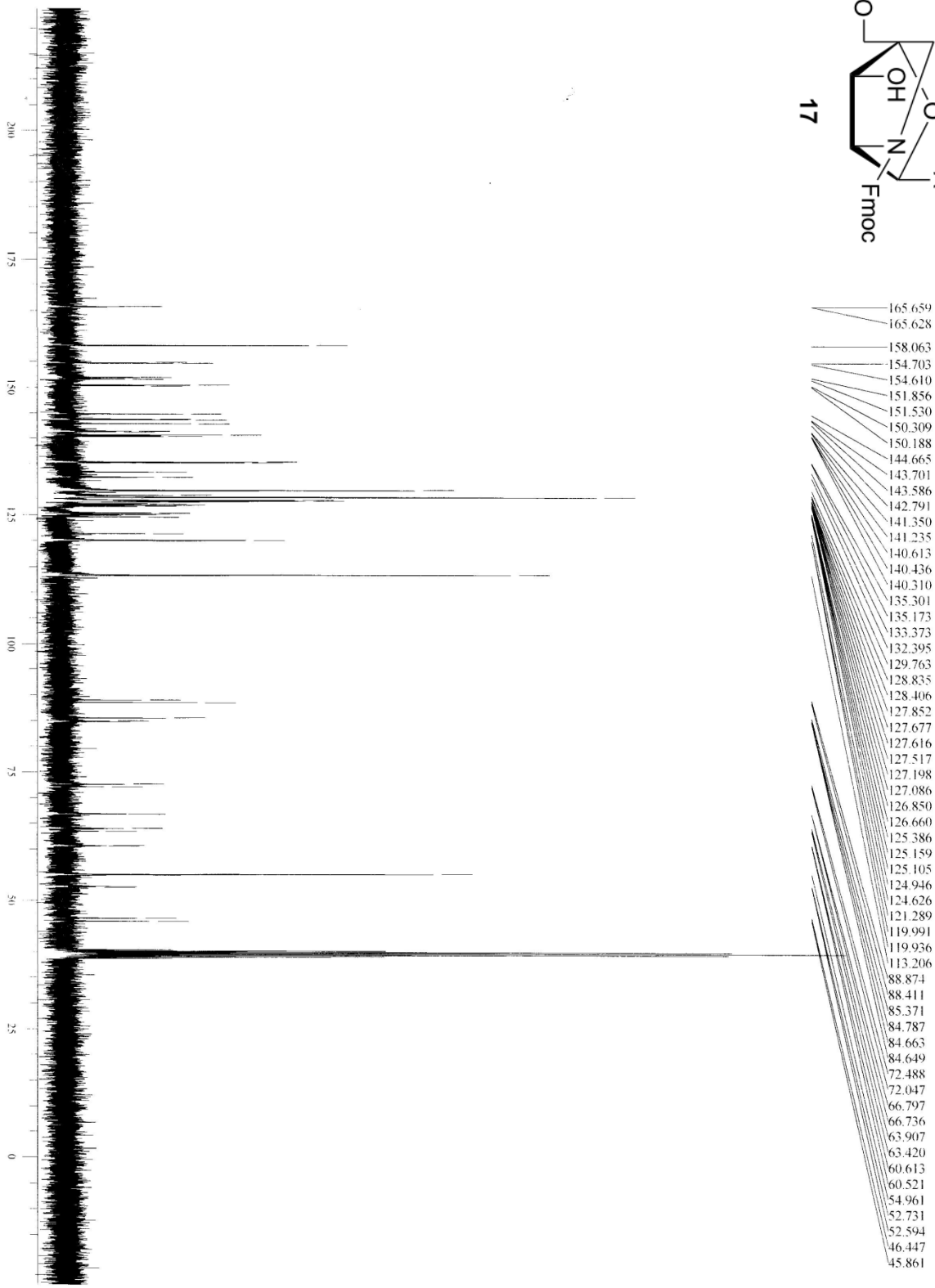
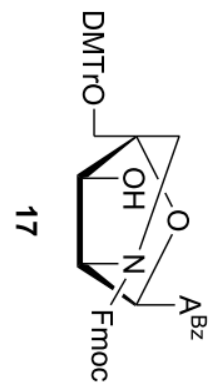


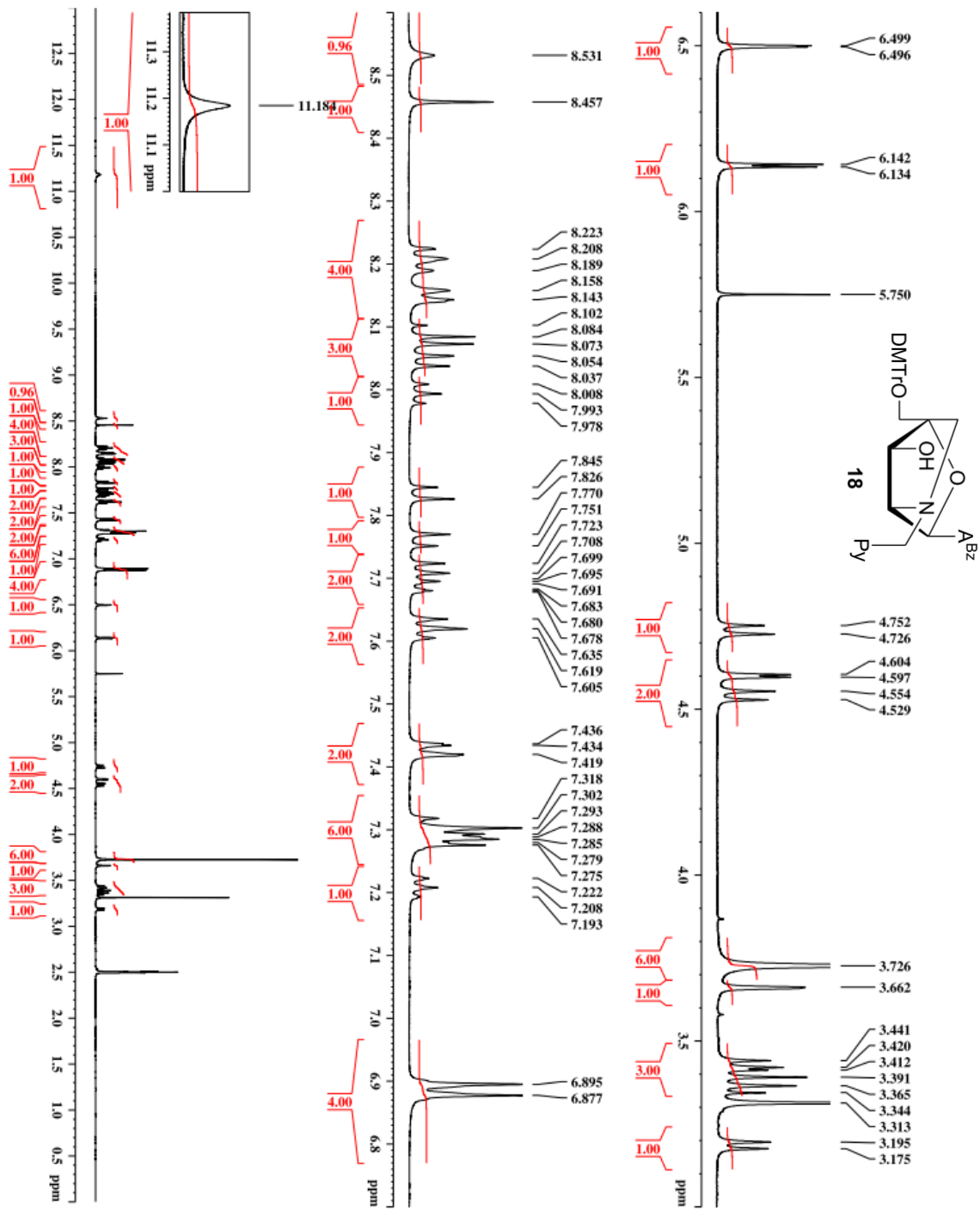


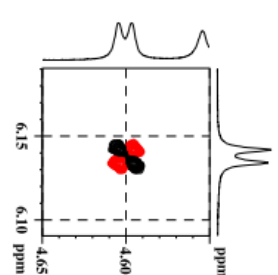
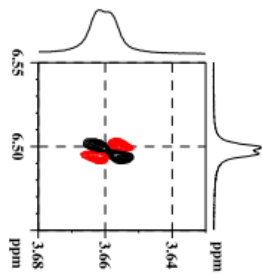
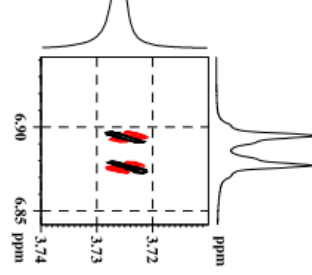
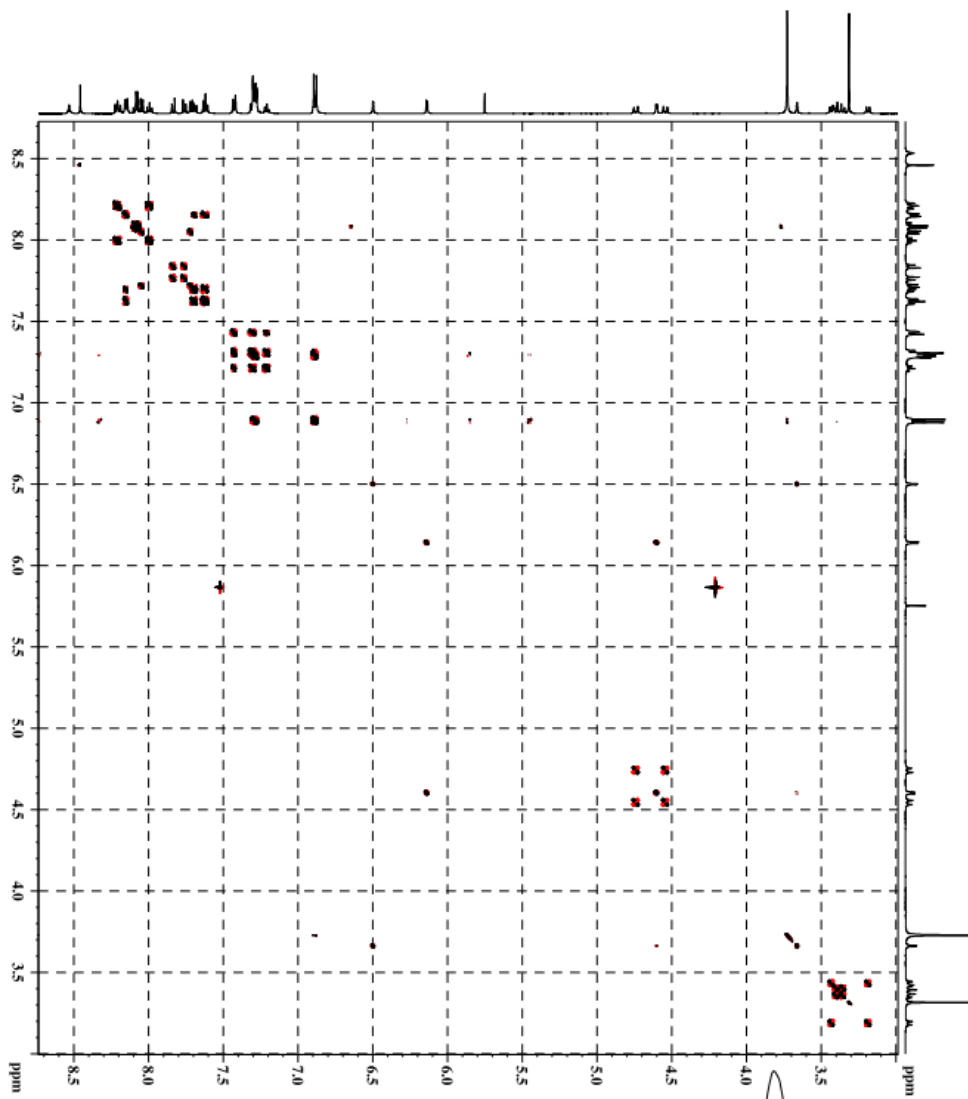
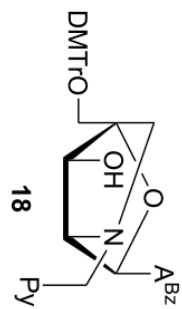


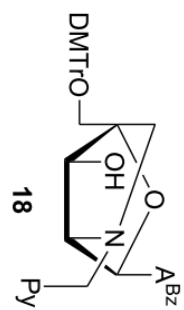
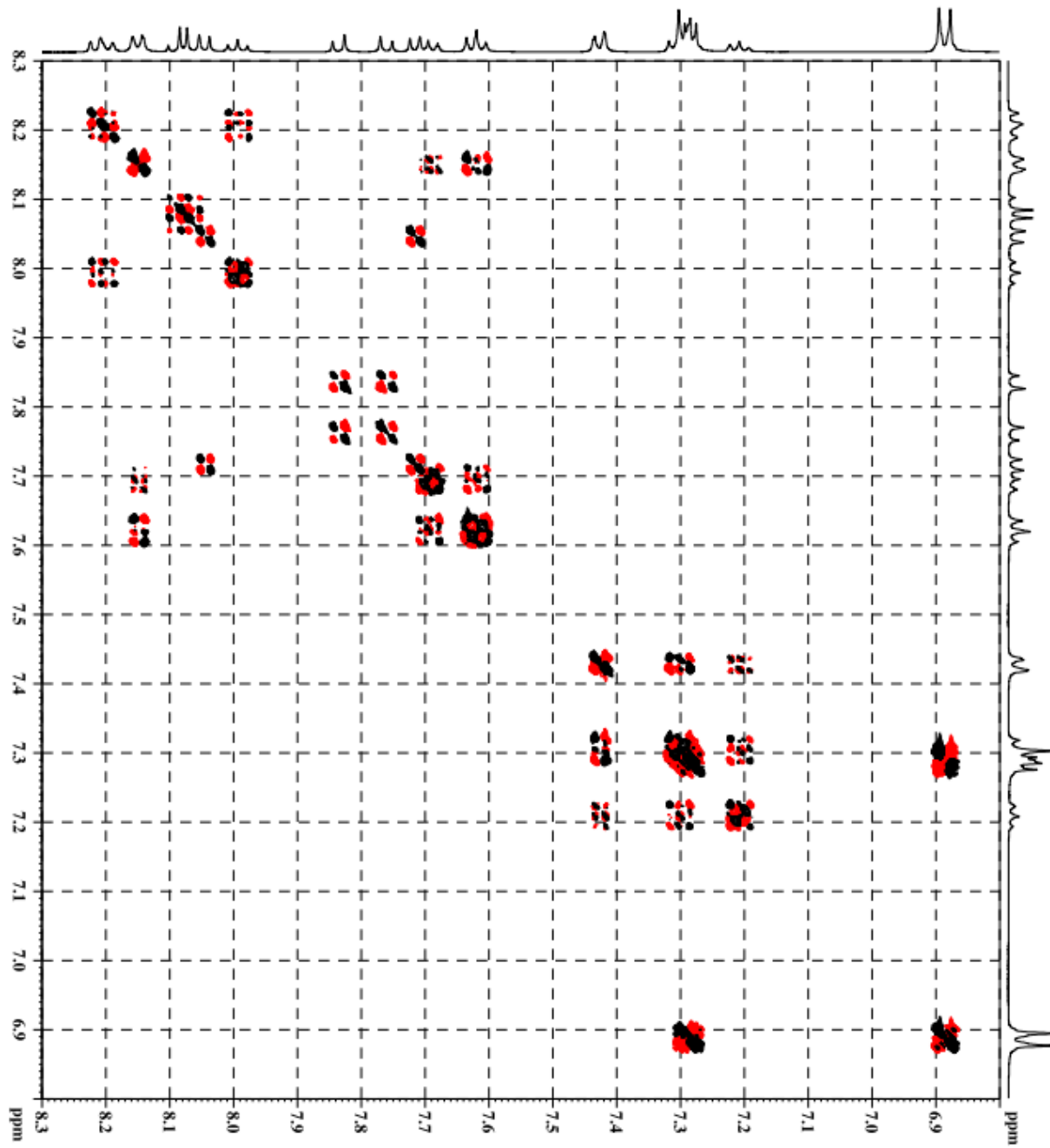


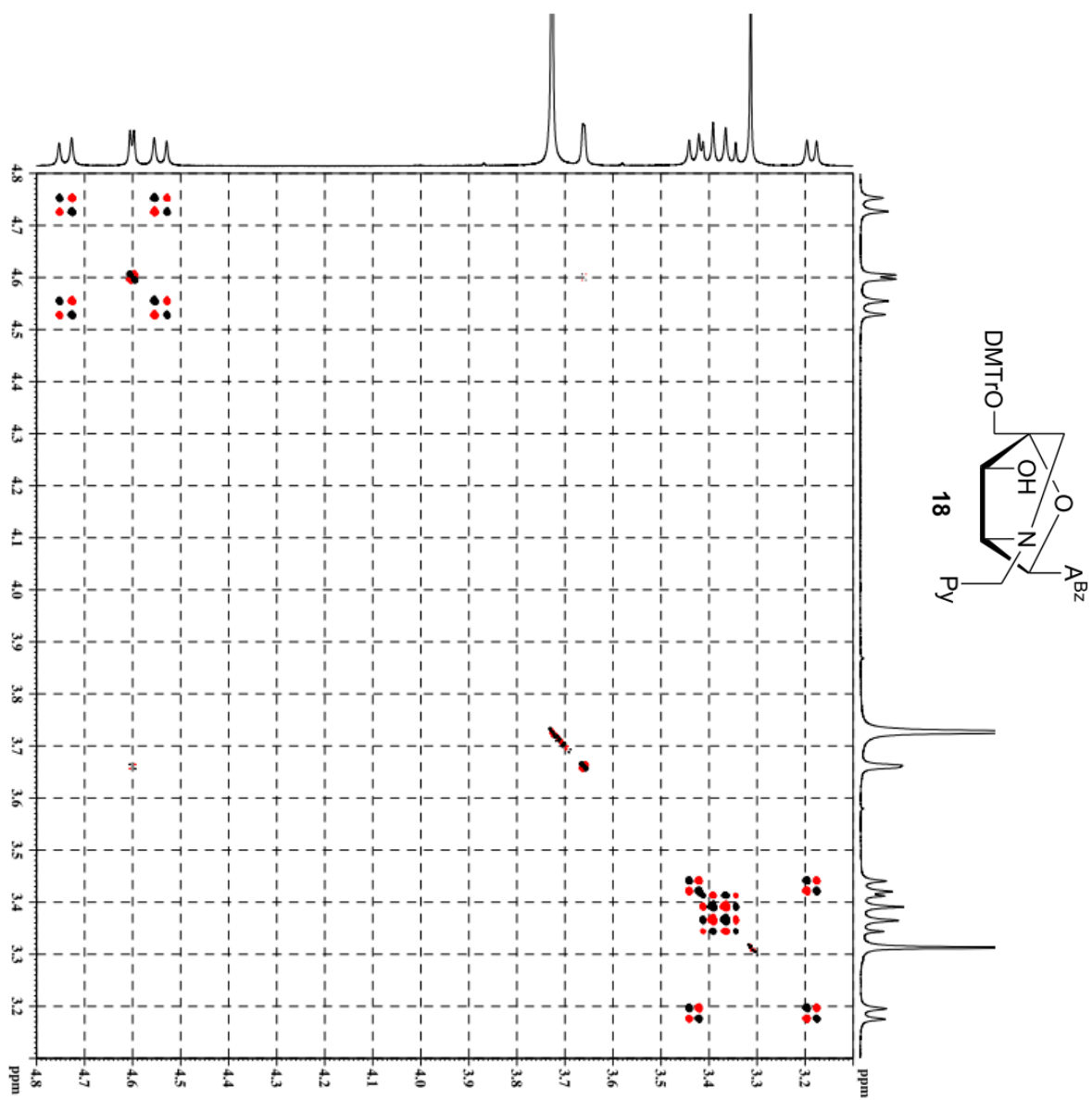




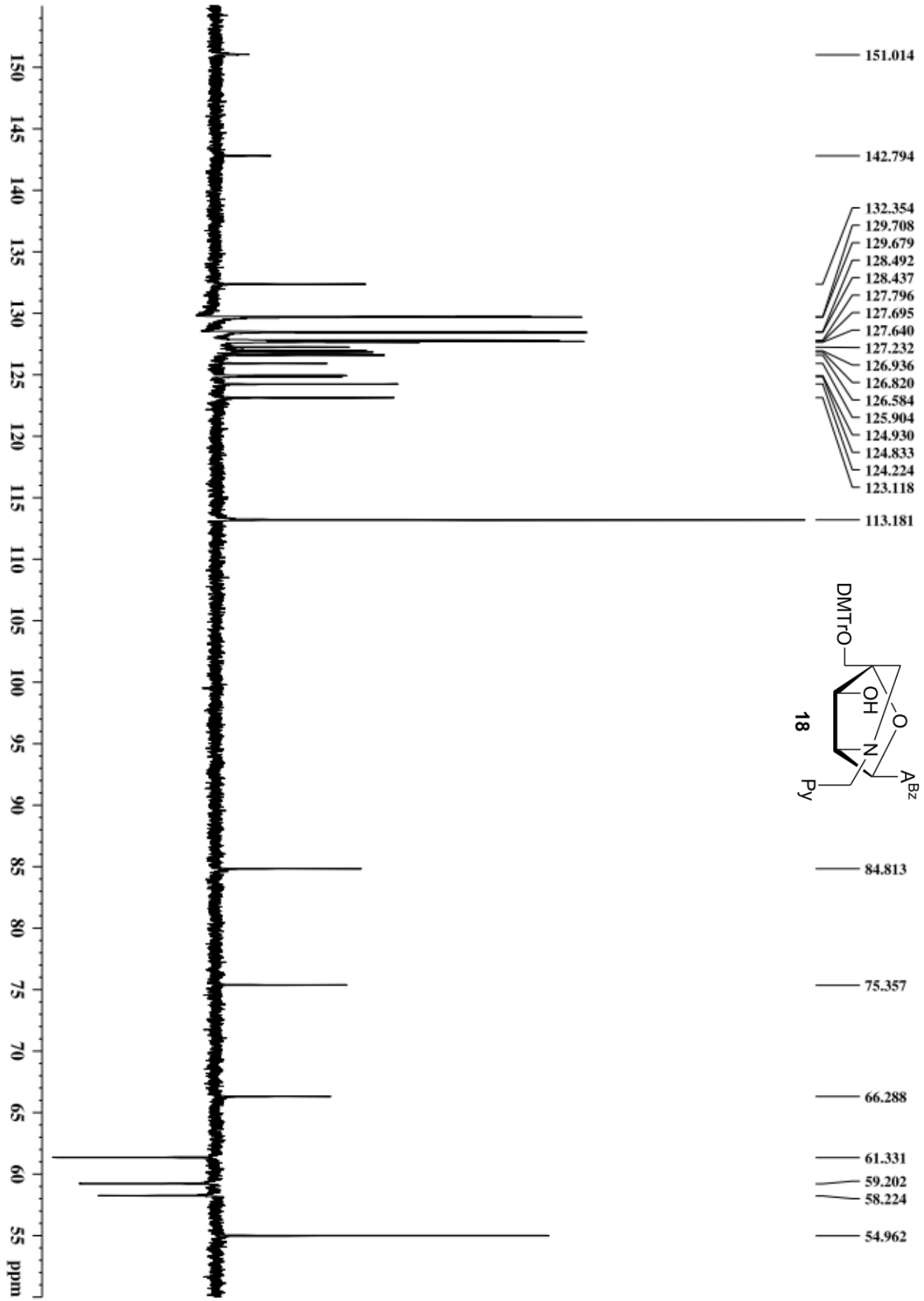


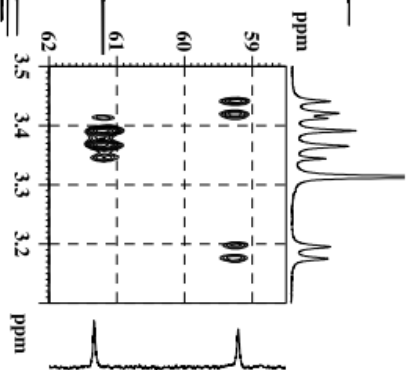
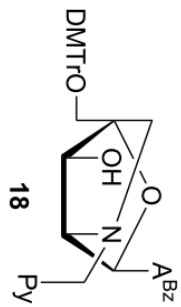
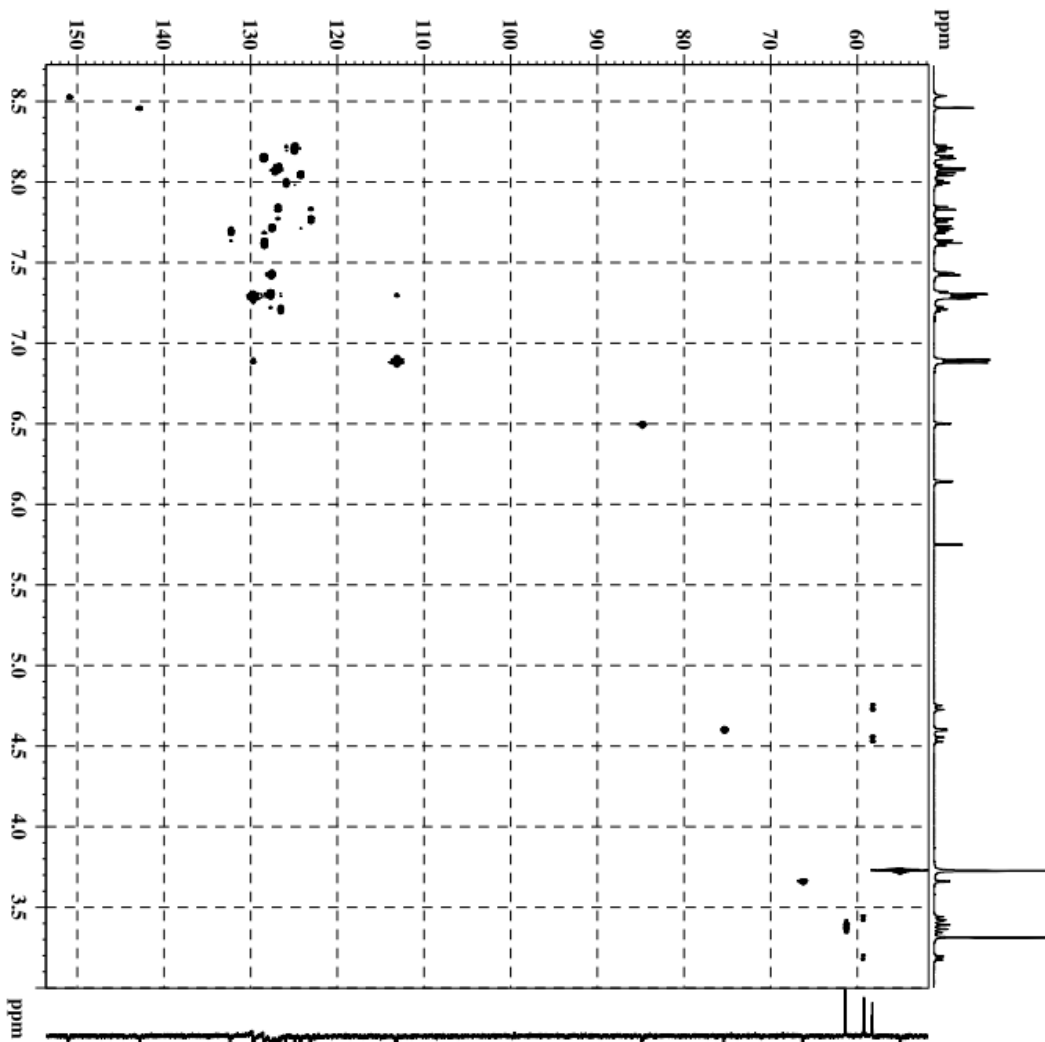


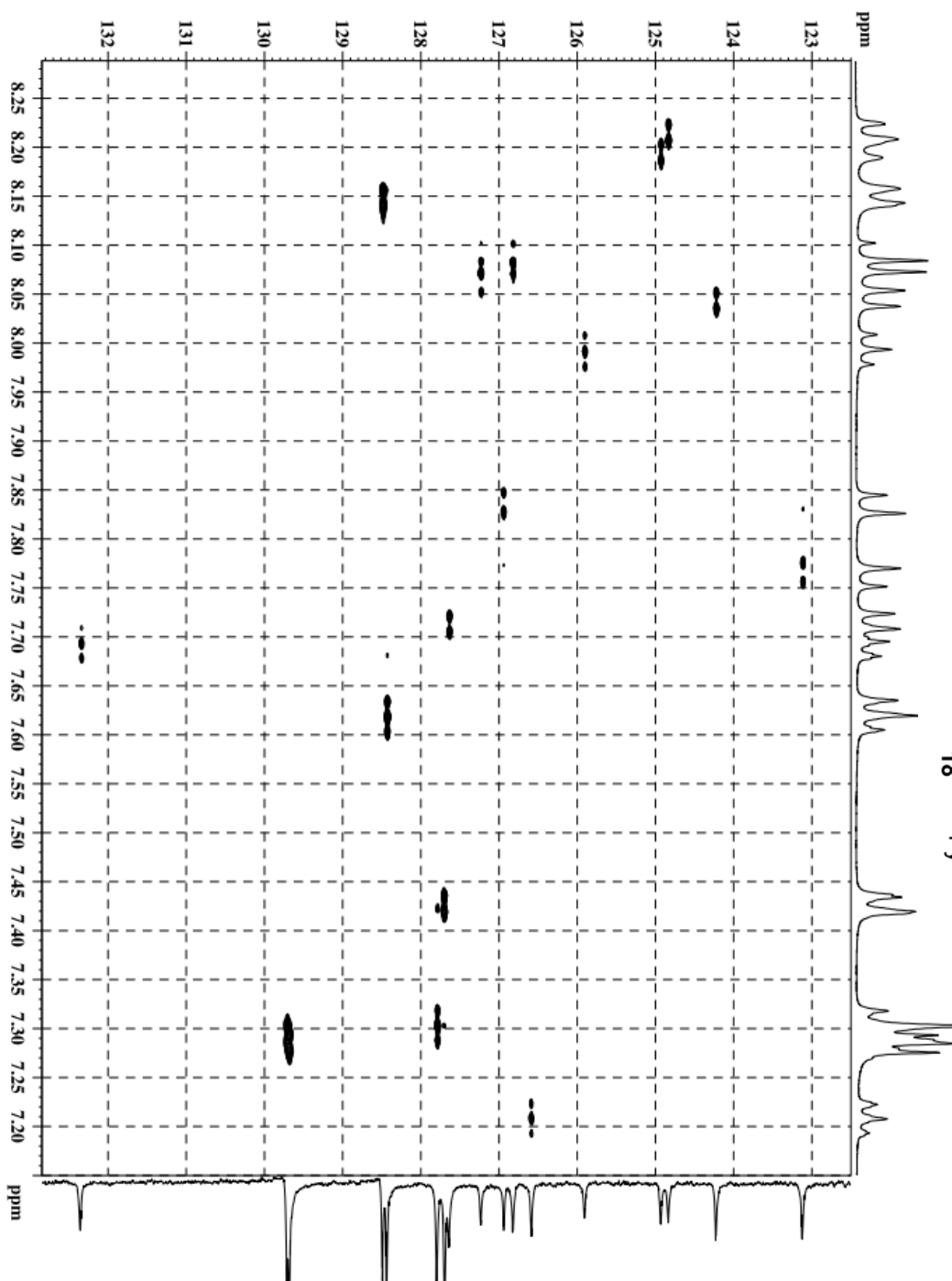
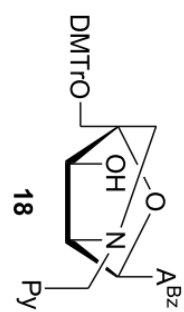


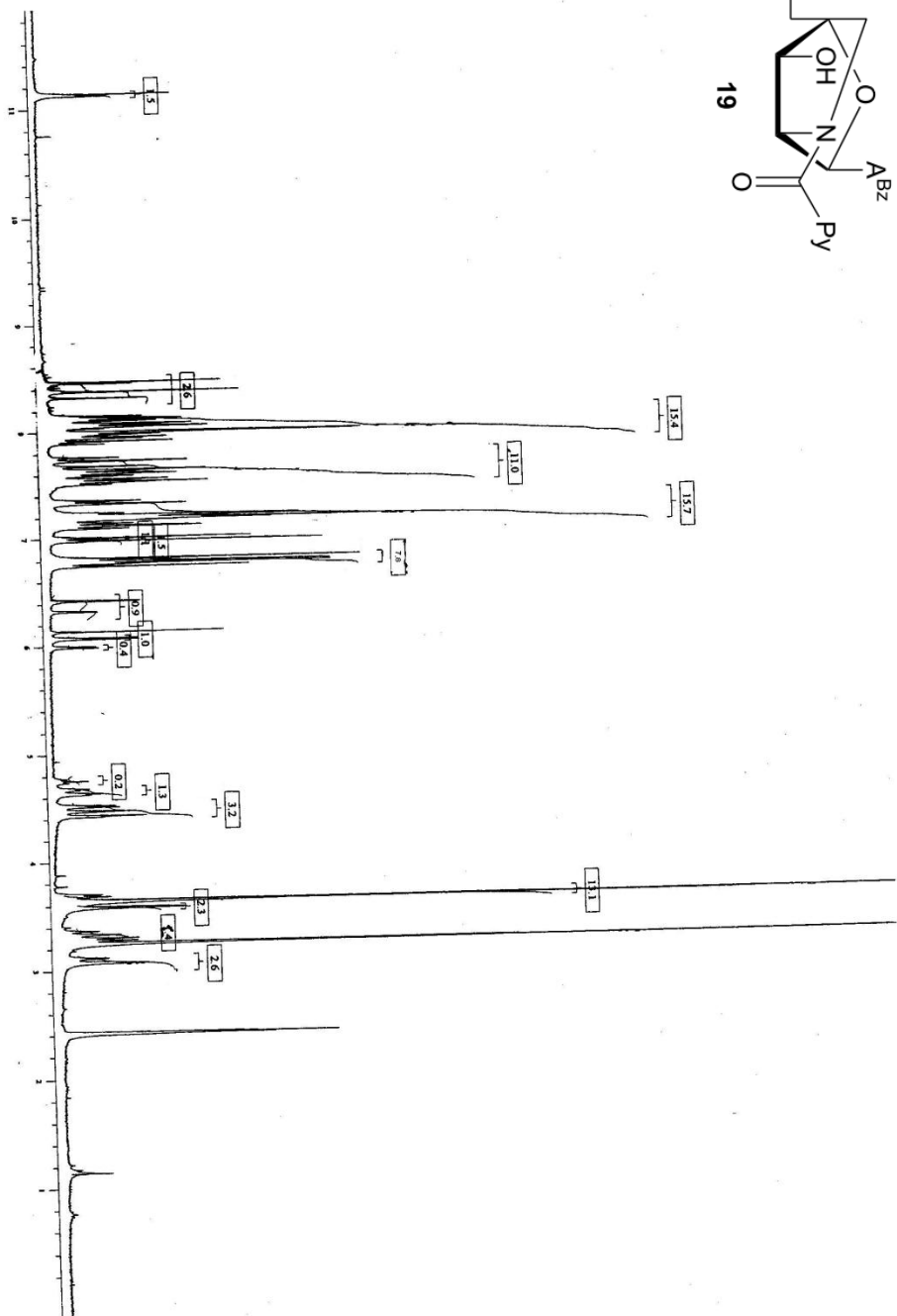
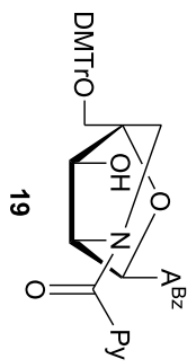




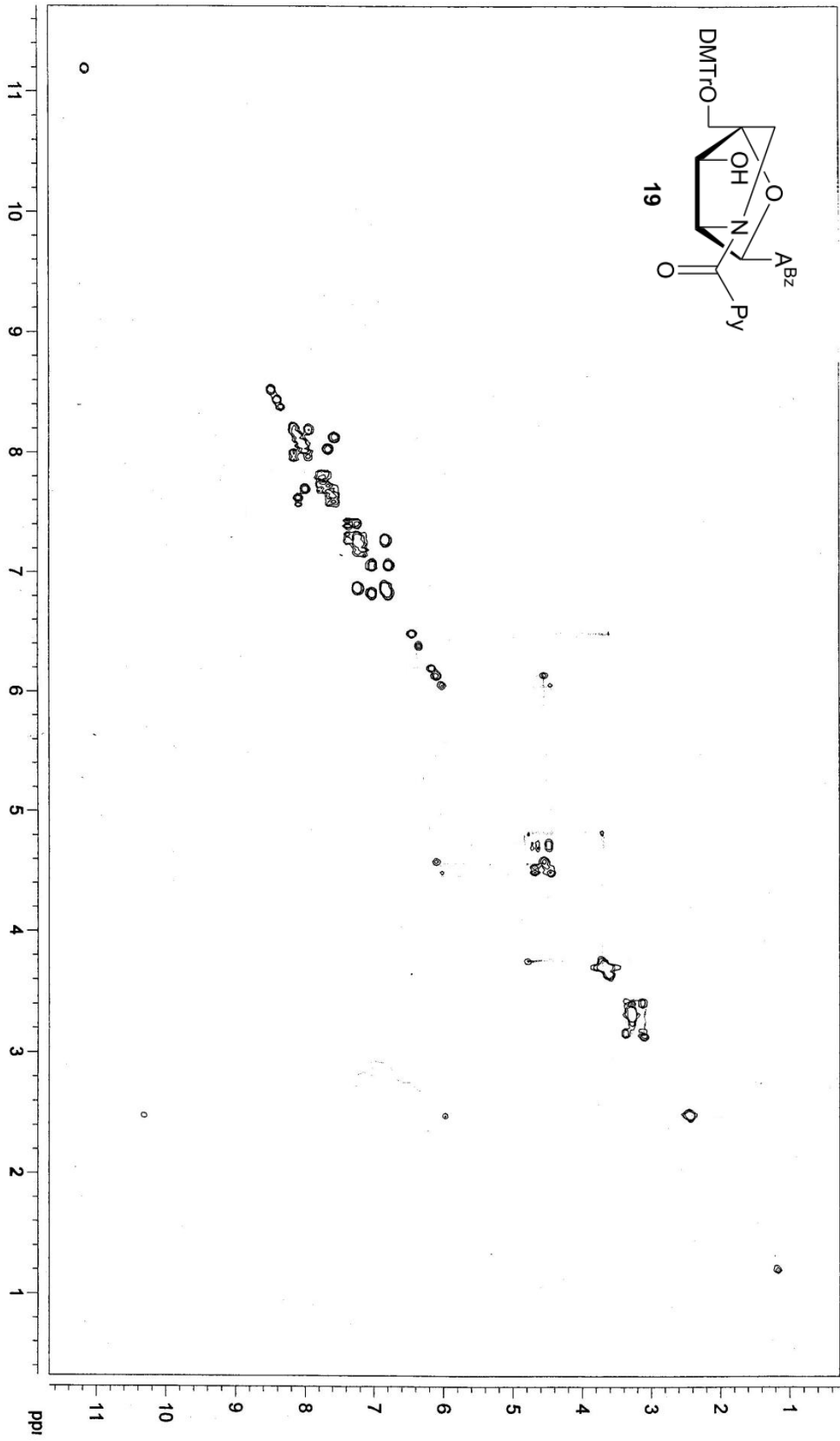


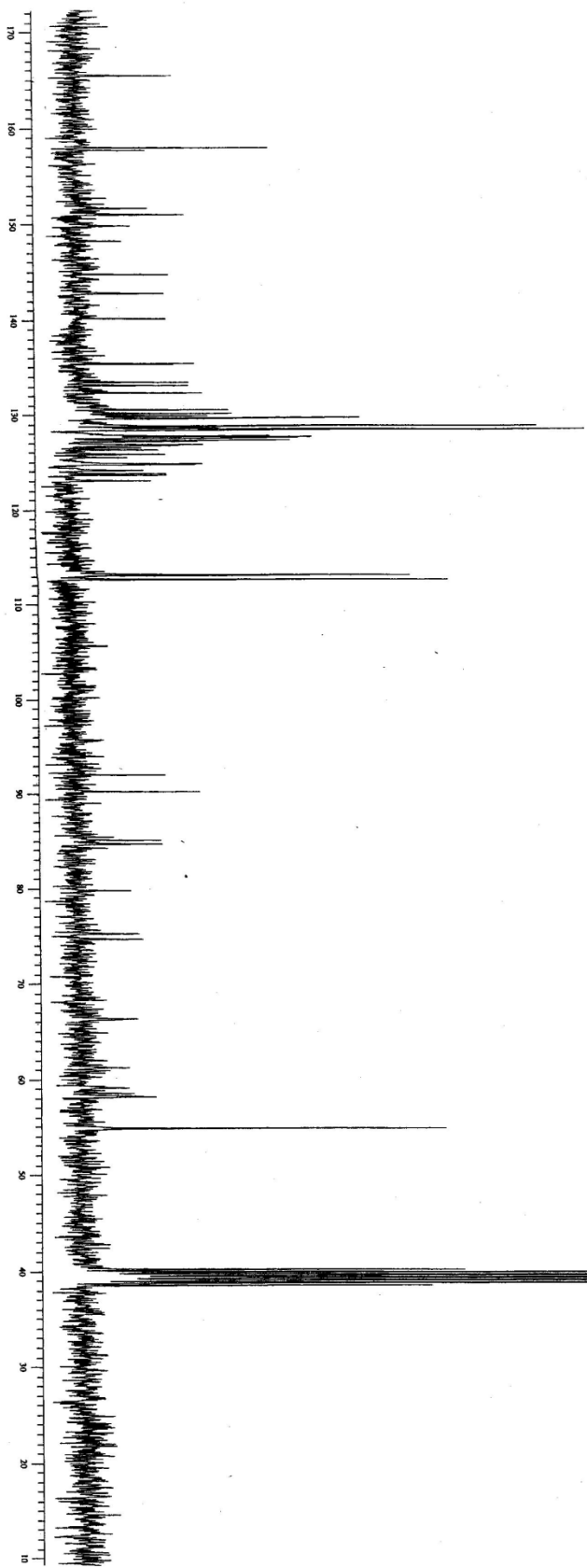
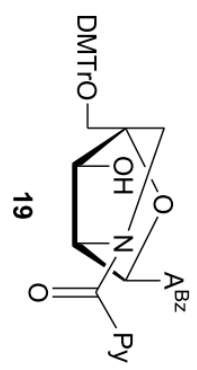


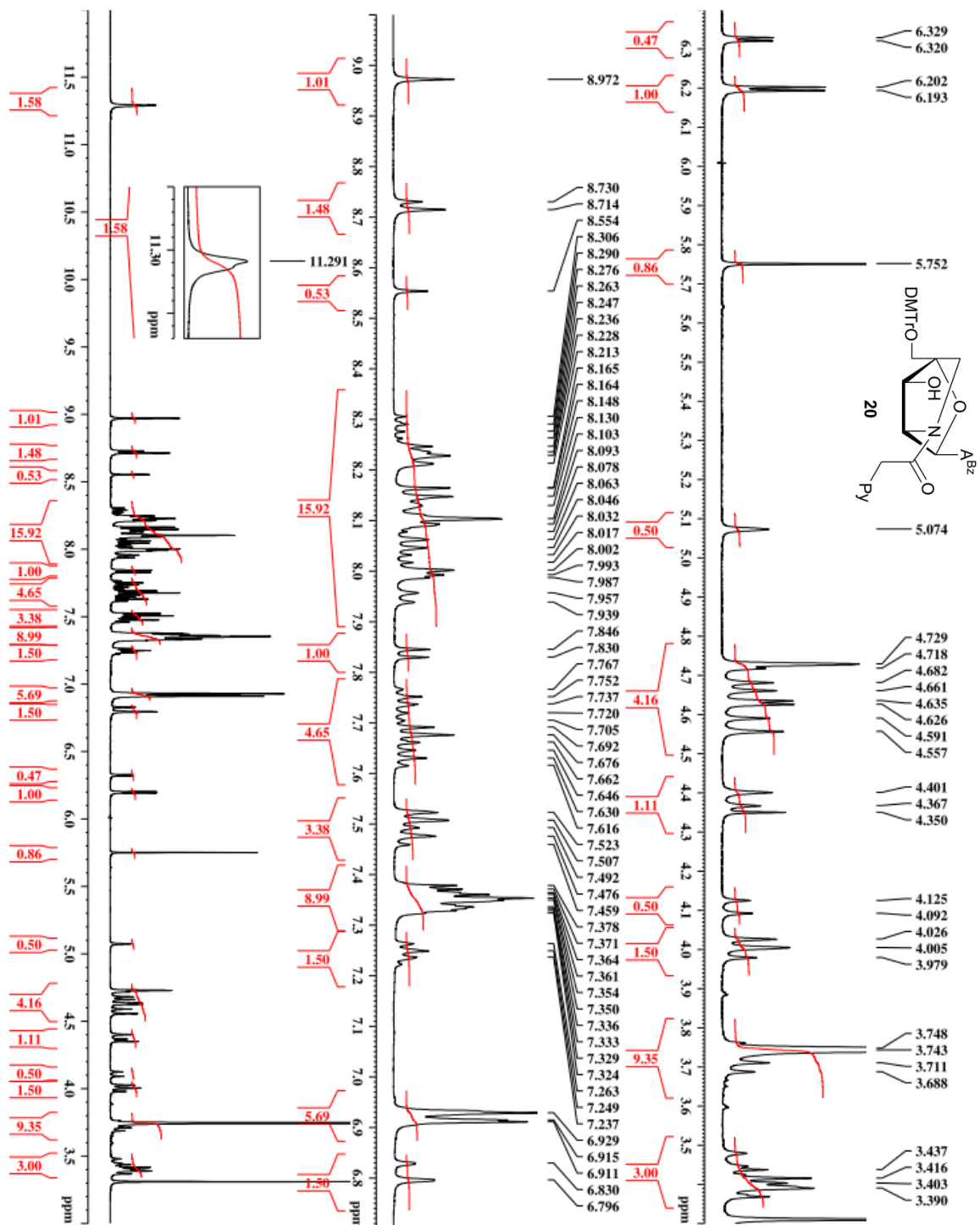


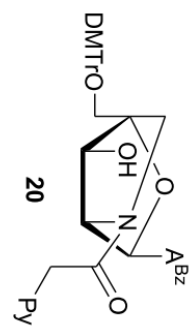
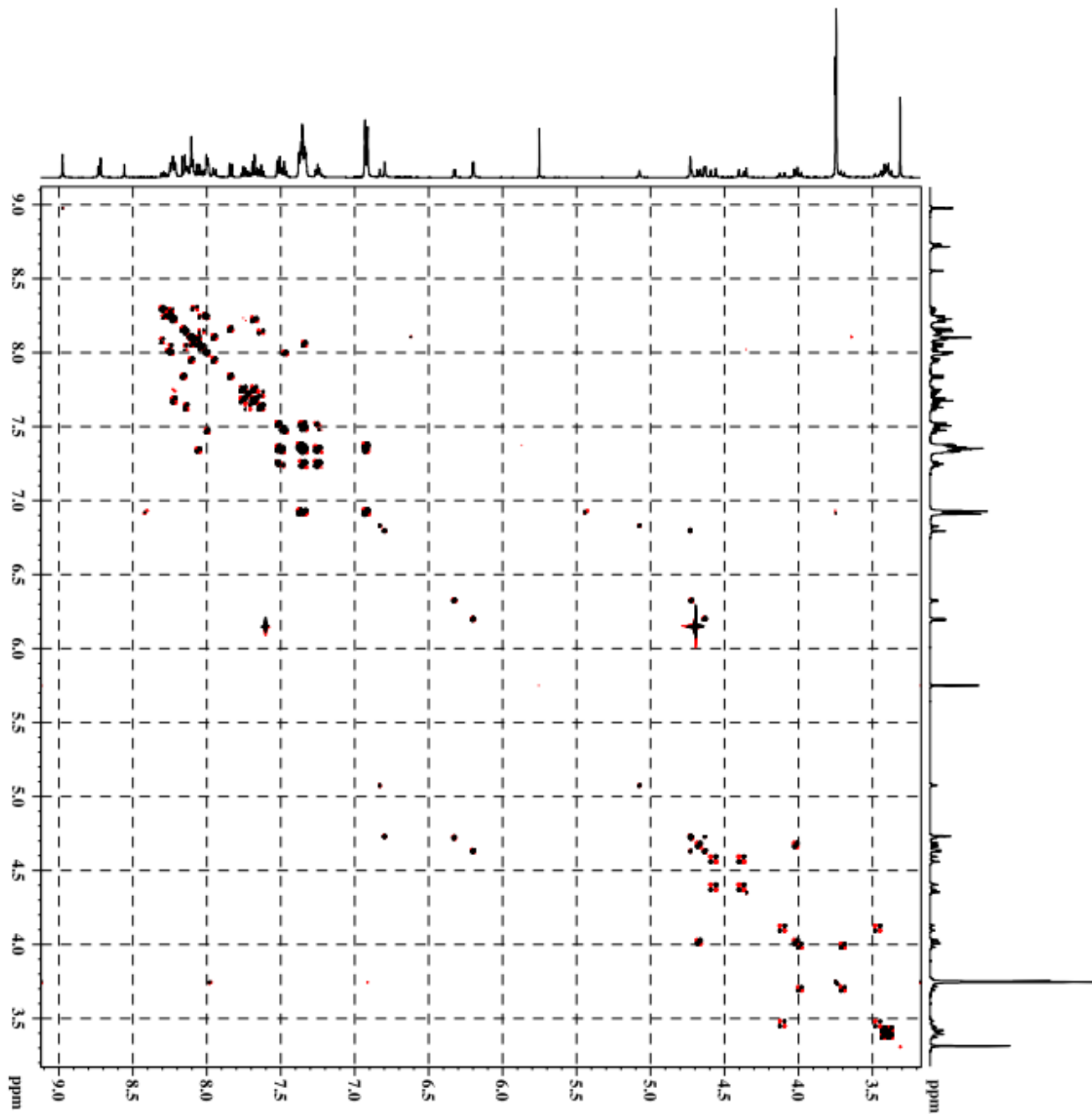


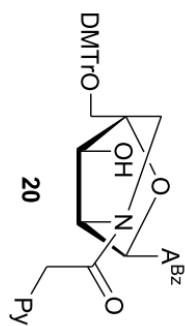
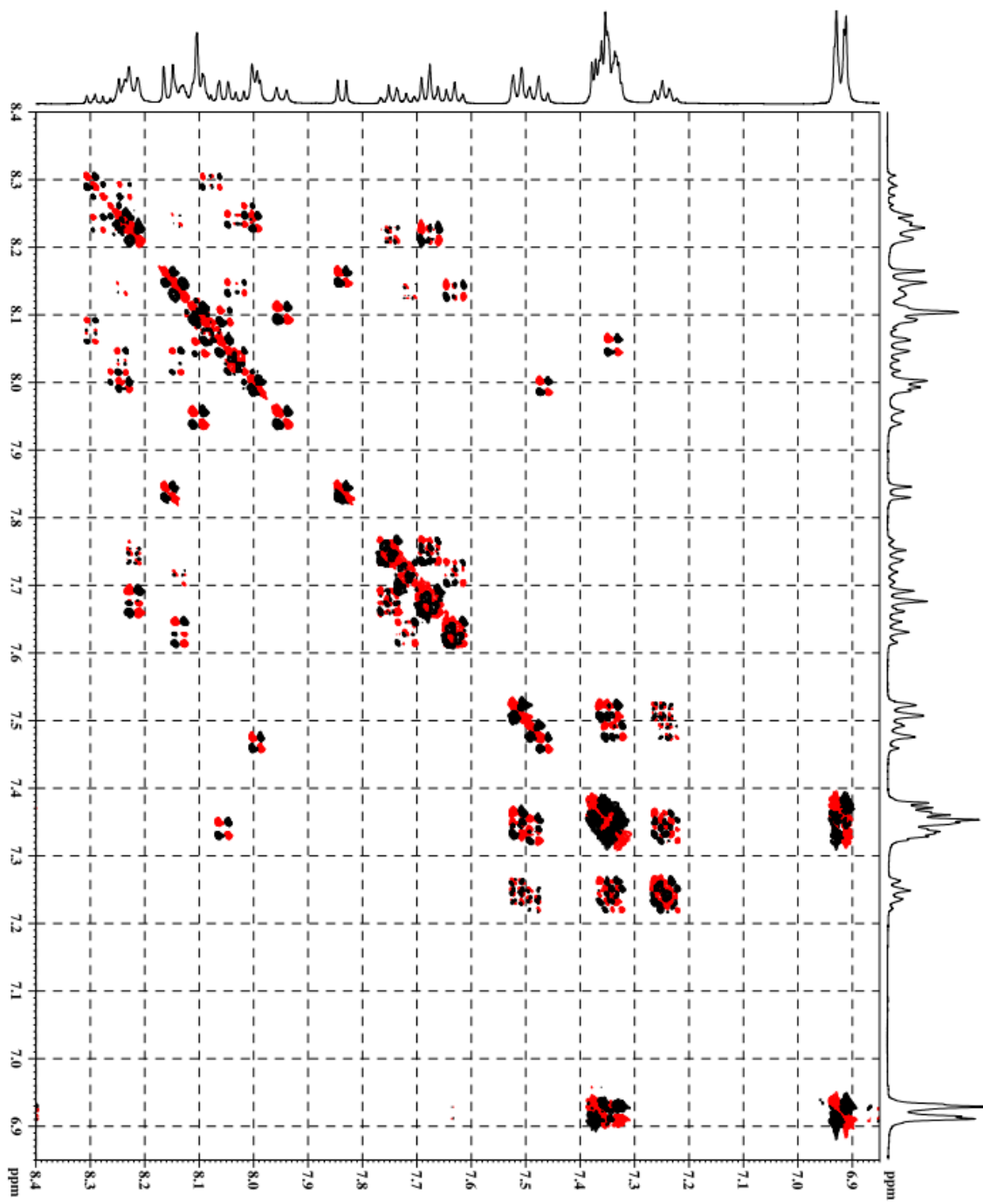
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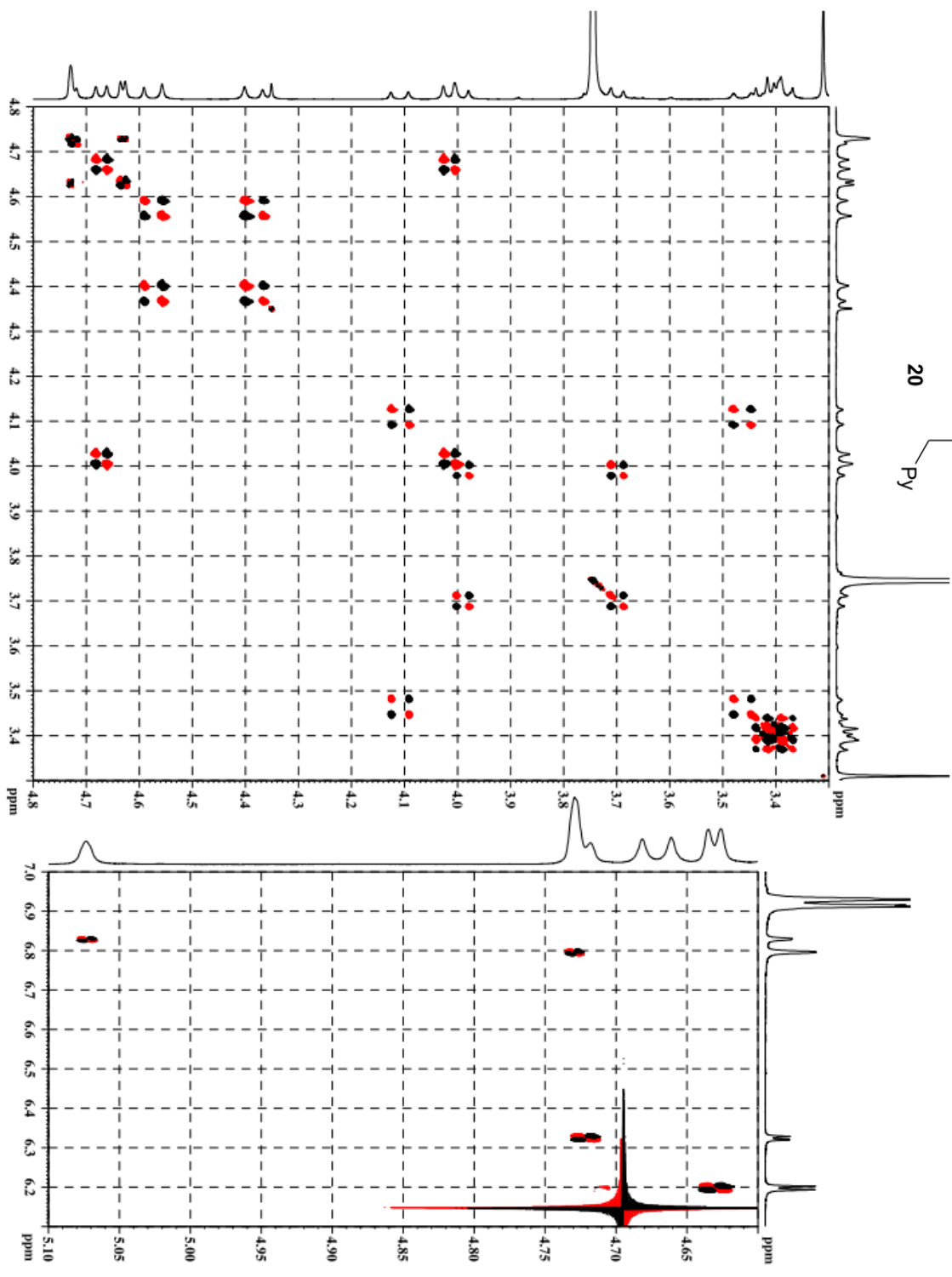
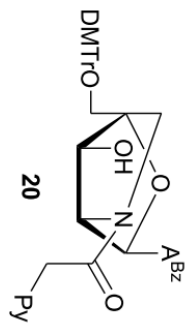


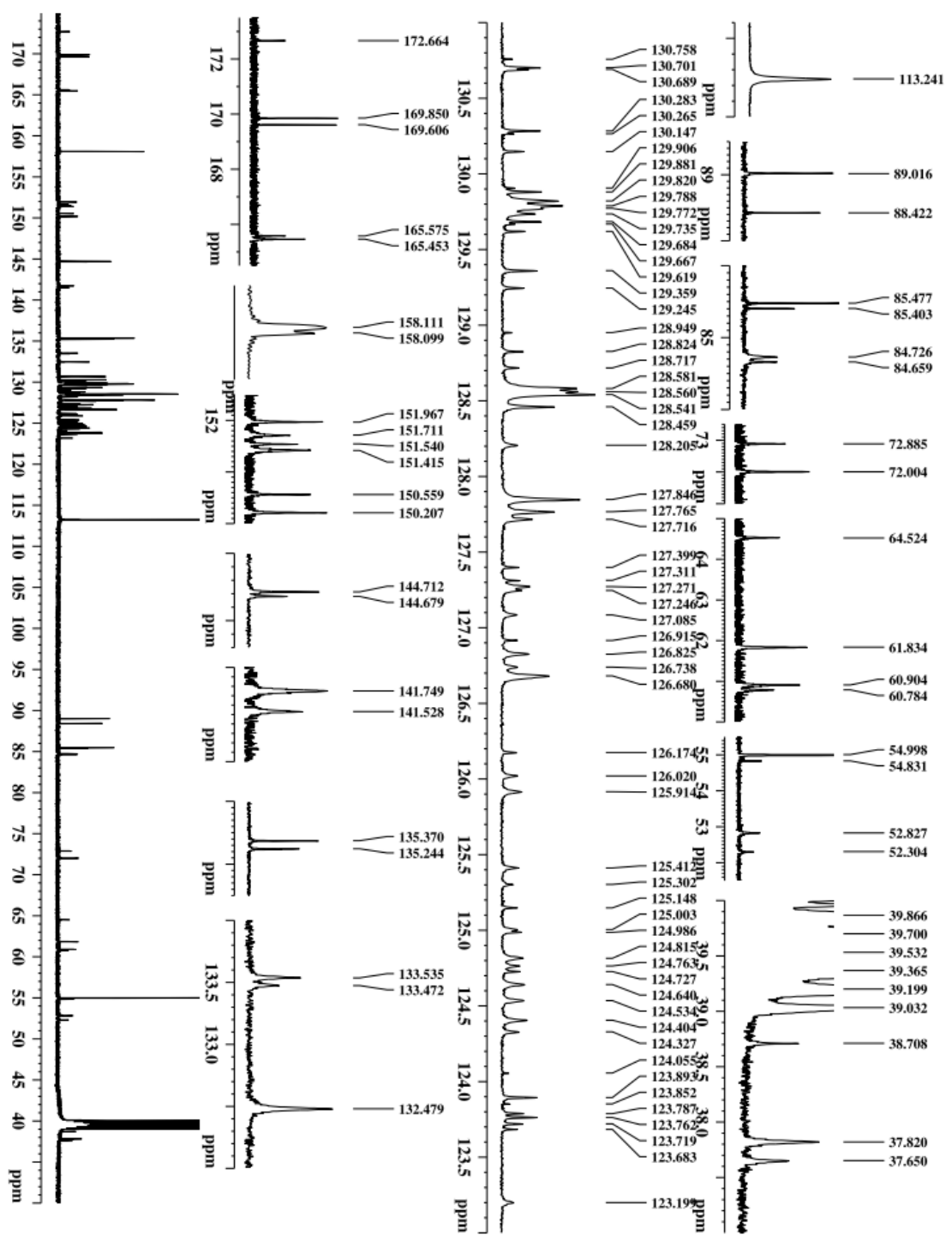
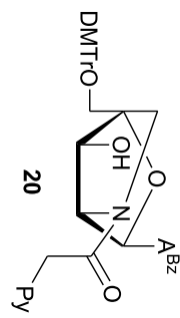


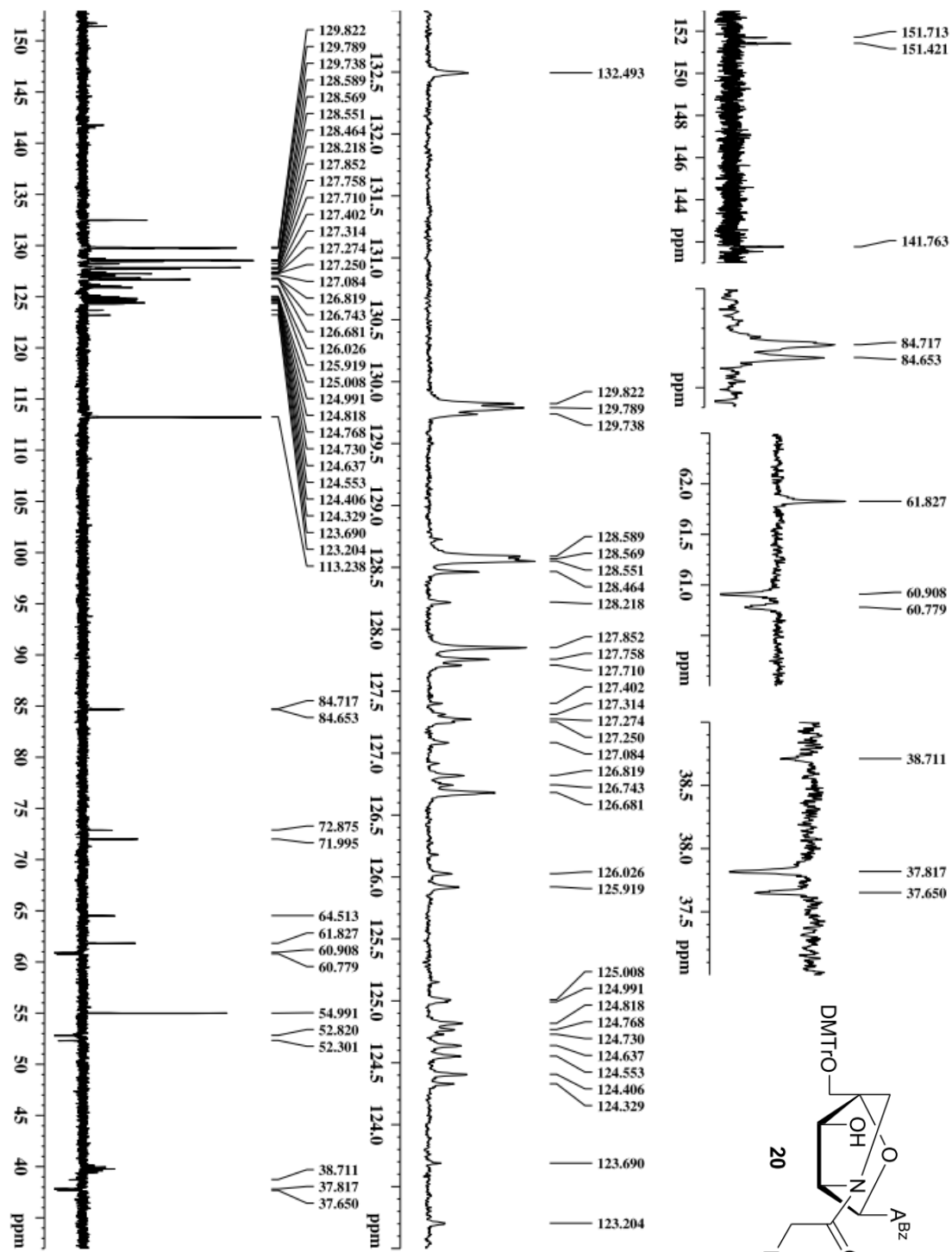


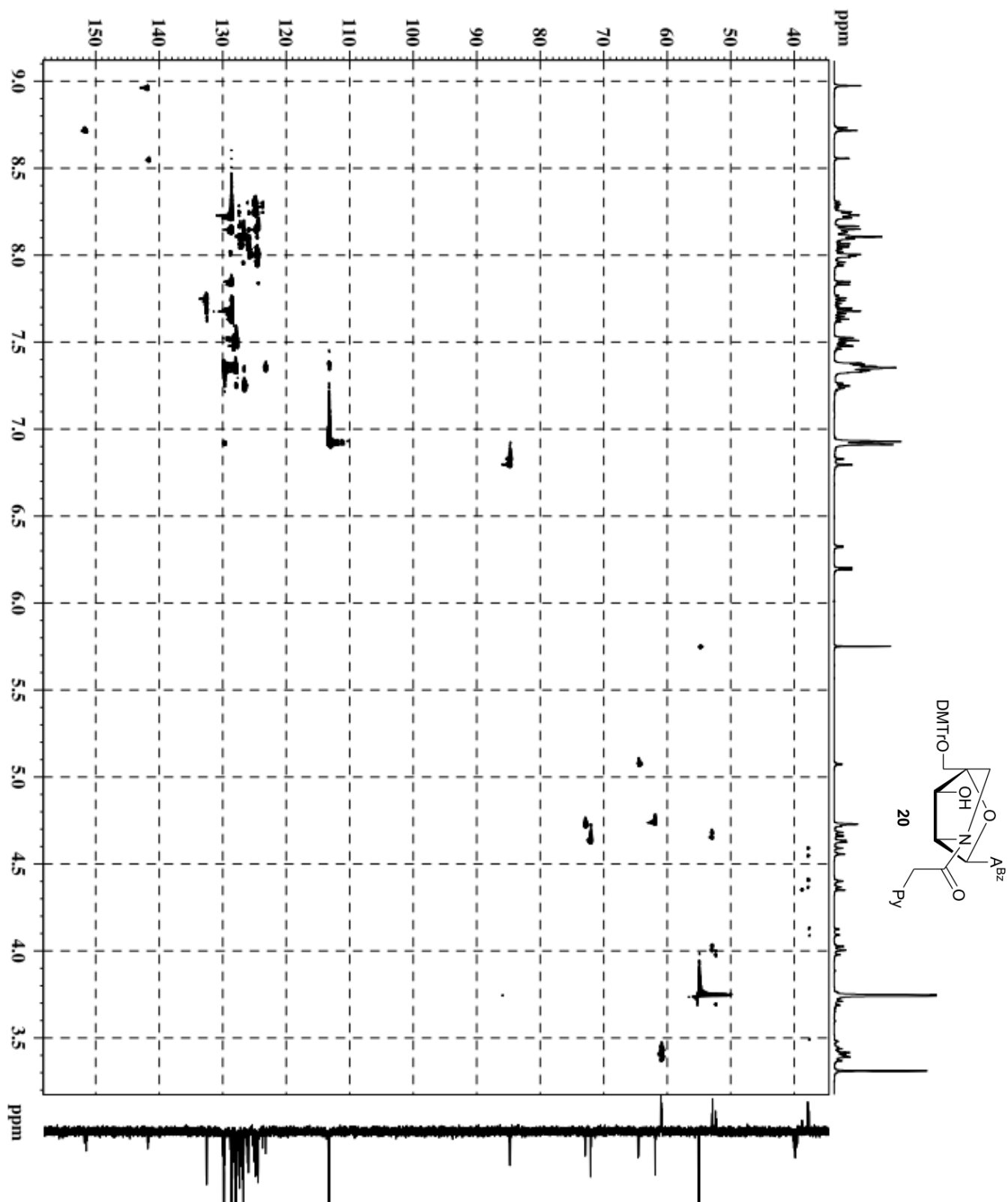


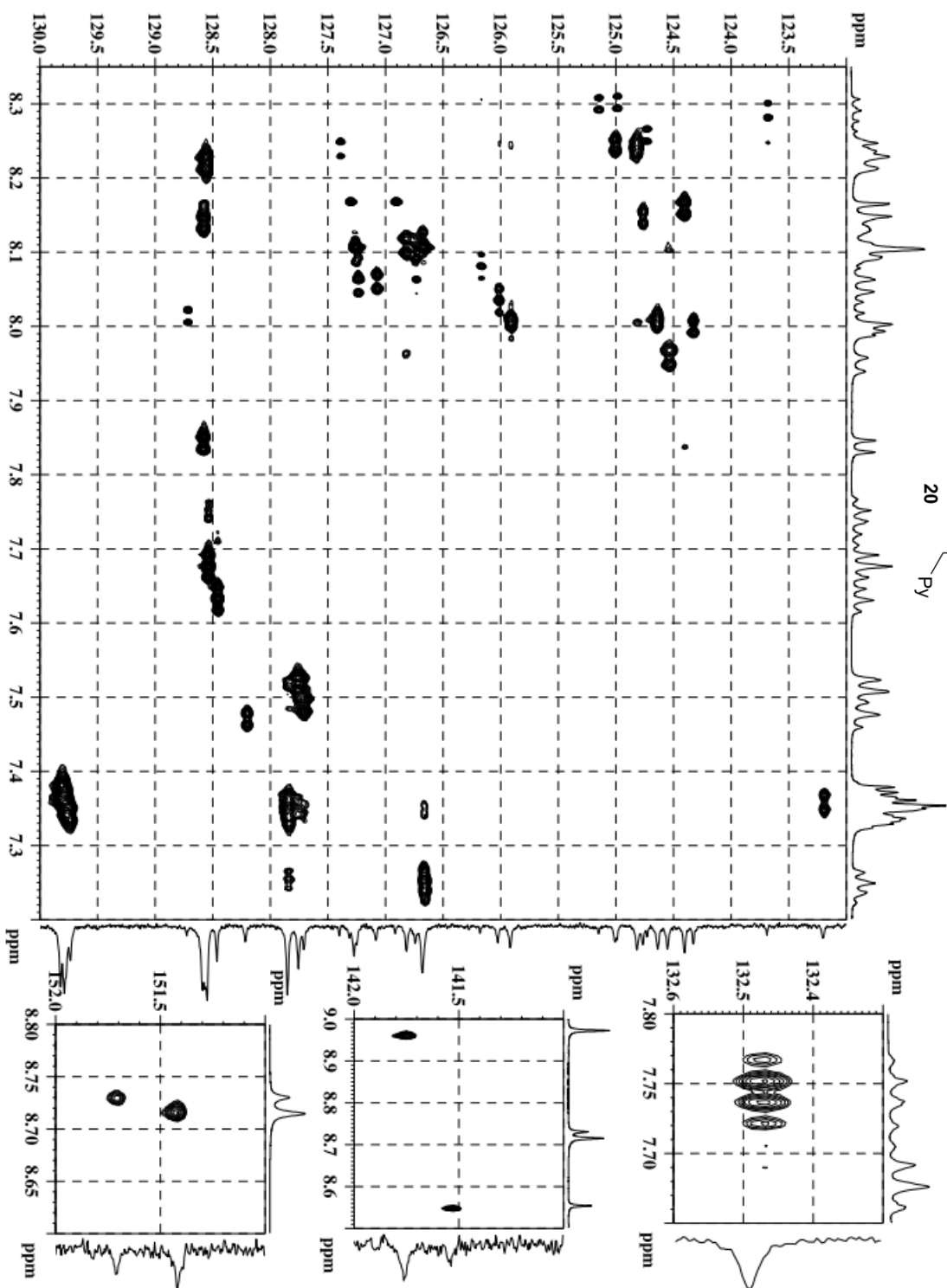
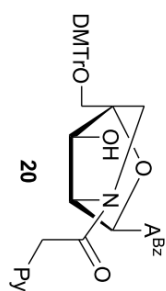


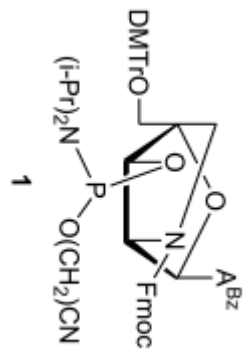




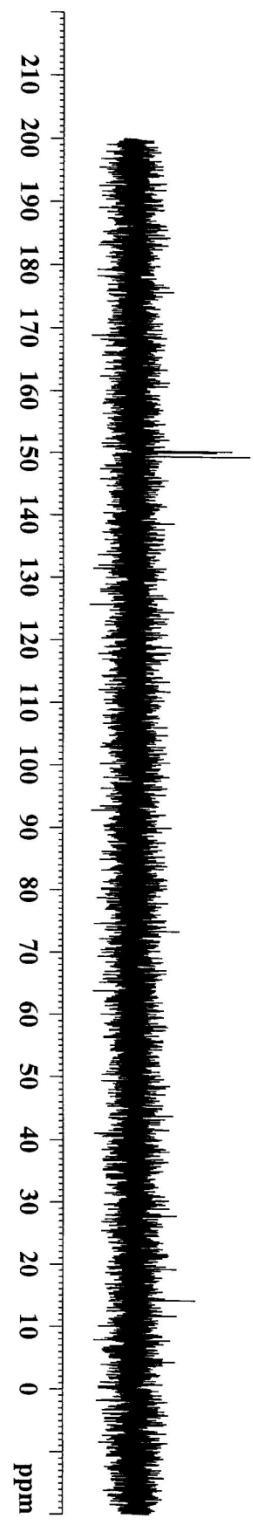
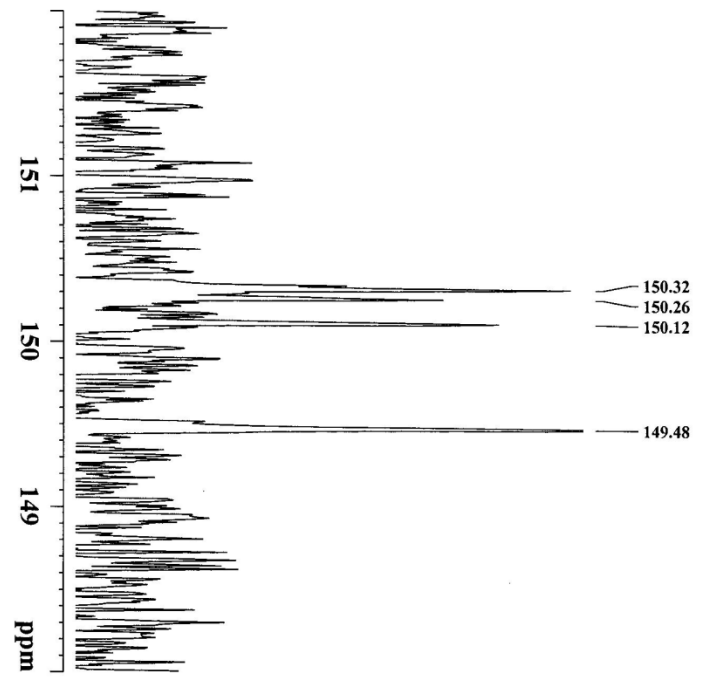


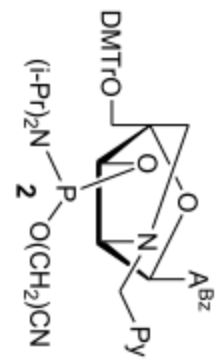






150.32
 150.26
 150.12
 149.48





150.565
148.378

