

Oligonucleotide analogues with locked-amide linkages have therapeutic potential

Ysobel R. Baker¹, Cameron Thorpe¹, Jinfeng Chen¹, Laura M. Poller¹, Lina Cox¹, Pawan Kumar¹, Wooi F. Lim², Lillian Lie,¹ Graham McClorey², Sven Epple¹, Daniel Singleton³, Michael A. McDonough¹, Jack S. Hardwick¹, Kirsten E. Christensen¹, Matthew J. A. Wood², James P. Hall⁴, Afaf H. El-Sagheer^{1,5}, Tom Brown^{1*}.

1. Department of Chemistry, University of Oxford, Chemistry Research Laboratory, 12 Mansfield Road, Oxford, OX1 3TA, UK.

2. Department of Paediatrics, University of Oxford, LGC building, South Parks Road, Oxford, OX1 3QX, UK.

3. ATDBio Ltd, School of Chemistry, University of Southampton, Highfield, Southampton SO17 1BJ, UK.

4. Department of Pharmacy, Chemistry and Pharmacy Building, University of Reading, Whiteknights, Reading, RG6 6AD, UK.

5. Department of Science and Mathematics, Suez University, Faculty of Petroleum and Mining Engineering, Suez 43721, Egypt.

* Corresponding author, e-mail: tom.brown@chem.ox.ac.uk

Table of Contents

Experimental section	4
Small molecule synthesis.....	4
General.....	4
4-C-(Methanesulfonyloxymethyl)-5-O-methanesulfonyl-1,2-O-isopropylidene- α -D-ribofuranose 2	5
4-C-(Methanesulfonyloxymethyl)-5-O-methanesulfonyl-1,2-O-isopropylidene- α -D-erythro-pentofuranos-3-ulose 3	5
Ethyl 2-((3aR,6aR)-2,2-dimethyl-5,5-bis(((methylsulfonyl)oxy)methyl)dihydrofuro[2,3-d][1,3]dioxol-6(5H)-ylidene)acetate 4	6
Ethyl 2-((3aR,6S,6aR)-2,2-dimethyl-5,5-bis(((methylsulfonyl)oxy)methyl)tetrahydrofuro[2,3-d][1,3]dioxol-6-yl)acetate 5	7
(3R,4S)-4-(2-Ethoxy-2-oxoethyl)-5,5-bis(((methylsulfonyl)oxy)methyl)tetrahydrofuran-2,3-diyl diacetate 6	8
Thymine LNA acid precursor 7a	8
N ⁴ -Benzoylcytosine LNA acid precursor 7b	9
N ⁴ -Benzoyl methylcytosine LNA precursor 7c	10
N ⁶ -Benzoyladenine LNA acid precursor 7d	10
N ² -Isobutyrylguanine LNA acid precursor 7e	11
Thymine LNA acid 8a	12
N ⁴ -Benzoylcytosine LNA acid 8b	12
N ⁴ -Benzoyl methylcytosine LNA acid 8c	13
N ⁶ -Benzoyladenine LNA acid 8d	14
N ² -Isobutyrylguanine LNA acid 8e	14
5'-O-DMT thymine LNA acid 9a	15
5'-O-DMT N ⁴ -benzoylcytosine LNA acid 9b	16
5'-O-DMT N ⁴ -benzoyl methylcytosine LNA acid 9c	16
5'-O-DMT N ⁶ -benzoyladenine LNA acid 9d	17
5'-O-DMT N ² -isobutyrylguanine LNA acid 9e	18
N ₃ Thymine LNA S14 ¹	19
Amino thymine LNA S11 ¹	19
5'-N-MMT thymine LNA S12 ³	19
5'-N-MMT thymine LNA phosphoramidite 10 ³	20
Oligonucleotide synthesis	21
DNA synthesis and cleavage.....	21
RNA synthesis and cleavage.....	21
2'OMe phosphodiester oligonucleotide synthesis and cleavage	21
Phosphodiester oligonucleotide purification	21
Phosphorothioate oligonucleotide synthesis, cleavage and purification	22
Oligonucleotide analysis	22
LNA-amide modified oligonucleotide synthesis.....	24
Oligonucleotide segment synthesis	24
Amino monomer addition.....	24
Amide bond formation on resin (peptide coupling)	24
Cleavage of oligonucleotides from resin, deprotection and purification	24
Biophysical studies.....	24
UV melting experiments	24
Oligonucleotide X-Ray crystallography.....	25
Crystallisation	25
Data collection and processing	25
Structure solution, model building and refinement	25
Biological assays	26
Evaluation of stability in fetal bovine serum (FBS).....	26

Cell culture	26
Transfection with Lipofectamine 2000	26
Gymnosis experiments.....	26
Luciferase assay	26
WST-1 cell viability assay	26
Supplementary tables.....	28
Supplementary figures.....	32
Small molecule synthesis supplementary figures	32
UPLC and MS analysis of oligonucleotides with LNA-amide linkages	34
Representative UV melting curves	39
Nuclease resistance supplementary figure	44
XRD supplementary figures	44
Supplementary cell assay figures	49
UPLC-MS traces of LNA-amide modified oligonucleotides	51
Small molecule crystallography supplementary information	62
NMR spectra of compounds 2-9e	65
References.....	86

Experimental section

Small molecule synthesis

General

Unless otherwise stated, reactions were performed in oven-dried glassware under an inert argon using anhydrous solvents. Anhydrous solvents were collected from an mBraun SPS-800 bench top solvent purification system, having passed through anhydrous alumina columns. Solvents for phosphitylation reaction were degassed by bubbling with argon before used and pyridine and CH₂Cl₂ were further purified by distillation over KOH or CaH respectively. Anhydrous dichloroethane (Aldrich) was used as supplied without further purification. 3-O-Benzyl 4-C-(methanesulfonyloxymethyl)-5-O-methanesulfonyl-1,2-O-isopropylidene- α -D-ribofuranose was purchased from Carbosynth. All other chemicals were used as obtained from commercial sources without further purification.

Thin layer chromatography (TLC) was performed using Merck pre-coated 0.23 mm thick plates of Kieselgel 60 F254 and visualised using UV (λ = 254 nm) or by staining with KMnO₄, *p*-anisaldehyde, dinitrophenylhydrazine, iodine, or ninhydrin (depending on functionality). All retention factors (*R_f*) are given to 0.01 with the solvent system reported in parentheses. Column chromatography was carried out using Geduran Silica Gel 60 from Merck.

Melting points (mp) were measured using Gallenkamp melting point apparatus and are uncorrected.

¹H, ¹³C and ³¹P NMR spectra were recorded on a Bruker AVIIIHD 400, Bruker AVII 500 (with a ¹³C cryoprobe), or Bruker NEO 600 (with broadband helium cryoprobe) spectrometer operating at 400, 500 or 600 MHz respectively using an internal deuterium lock at ambient probe temperatures. ¹H NMR chemical shifts (δ) are quoted to the nearest 0.01 ppm and are referenced relative to residual solvent peak. Coupling constants (*J*) are given to the nearest 0.1 Hz. The following abbreviations are used to indicate the multiplicity of signals: s = singlet, d = doublet, t = triplet, q = quartet, m = multiplet, and br = broad. Data is reported as follows: chemical shift (multiplicity, coupling constant(s), integration). ¹³C NMR chemical shifts (δ) are quoted to the nearest 0.1 ppm and are reference relative to the deuterated solvent peak. NMR assignments are supported by DEPT, COSY, HMQC, and HMBC where necessary.

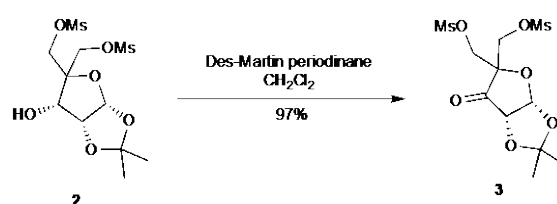
High resolution mass spectra (HRMS) were recorded on a Thermo Scientific Exactive Mass Spectrometer equipped with a Waters Equity autosampler and pump by the University of Oxford Chemistry Departmental Mass Spectrometry Service, and reported mass values are within \pm 5 ppm mass units unless otherwise stated.

Unless otherwise stated, yields refer to analytically pure compounds.

TLC (EtOAc:40-60 petroleum ether (PE), 7:3 v/v) R_f: 0.36;

¹³C NMR (101 MHz, CDCl₃): δ 114.1, 104.7, 84.3, 79.2, 72.7, 69.3, 68.6, 38.0, 37.7, 26.2, 26.0;

4-C-(Methanesulfonyloxymethyl)-5-O-methanesulfonyl-1,2-O-isopropylidene- α -D-erythro-pentofuranos-3-ulose **3**



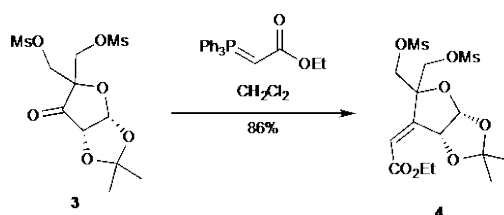
TLC (EtOAc:40-60 PE, 6:4 v/v) R_f : 0.24;

^1H NMR (400 MHz, CDCl_3): δ 6.16 (d, J = 4.1 Hz, 1H), 4.52 (d, J = 4.1 Hz, 1H), 4.46 (d, J = 11.0 Hz, 1H), 4.45 (d, J = 11.7 Hz, 1H), 4.33 (d, J = 11.7 Hz, 1H), 4.32 (d, J = 11.0 Hz, 1H), 3.11 (s, 3H), 3.03 (s, 3H), 1.56 (s, 3H), 1.39 (s, 3H);

^{13}C NMR (101 MHz, CDCl_3): δ 205.0, 115.6, 103.0, 84.3, 76.7, 69.5, 68.9, 38.2, 37.9, 27.2, 26.8;

HRMS (m/z): $[\text{M}+\text{Na}]^+$ calcd. for $\text{C}_{11}\text{H}_{18}\text{O}_{10}\text{NaS}_2^+$, 397.0234; found, 397.0231.

Ethyl 2-((3aR,6aR)-2,2-dimethyl-5,5-bis(((methylsulfonyl)oxy)methyl) dihydrofuro[2,3-d][1,3]dioxol-6(5H)-ylidene)acetate **4**



A solution of compound **3** (15.1 g, 40.4 mmol) and (carbethoxymethylene)triphenylphosphorane (16.9 g, 48.5 mmol, 1.2 eq) in CH_2Cl_2 (80 mL) was stirred at room temperature overnight. After removal of the solvent the resulting orange gum was triturated with EtOH, forming a white precipitate. The precipitate was collected by filtration, washed with cold EtOH, and dried under vacuum. The crude product was then purified by recrystallisation from hot EtOH to yield alkene **4** (15.4 g, 33.1 mmol) in 86% yield.

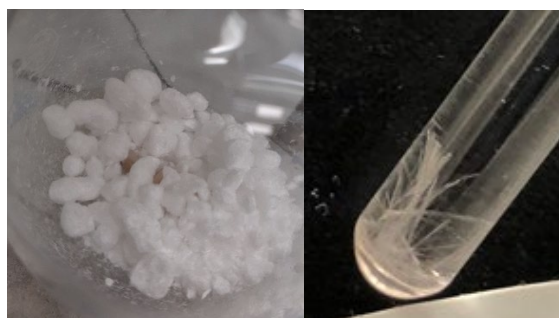
TLC (EtOAc:40-60 PE, 6:4 v/v) R_f : 0.64;

mp: 88-93 $^\circ\text{C}$ (crystallised from EtOH);

^1H NMR (400 MHz, CDCl_3): δ 6.07 (d, J = 1.3 Hz, 1H), 5.93 (d, J = 3.7 Hz, 1H), 5.79 (dd, J = 3.7, 1.3 Hz, 1H), 4.53 – 4.19 (m, 6H), 3.11 (s, 3H), 3.07 (s, 3H), 1.59 (s, 3H + H_2O), 1.41 (s, 3H), 1.32 (t, J = 7.1 Hz, 3H);

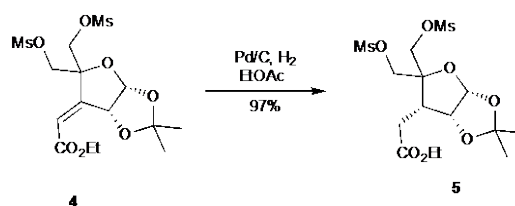
^{13}C NMR (101 MHz, CDCl_3): δ 164.0, 151.2, 121.4, 114.5, 105.6, 85.0, 78.7, 70.1, 69.5, 61.5, 38.2, 37.9, 27.2, 26.4, 14.2;

HRMS (m/z): $[\text{M}+\text{Na}]^+$ calcd. for $\text{C}_{15}\text{H}_{24}\text{O}_{11}\text{NaS}_2^+$, 467.0652; found, 467.0652.



Left) Crystalline product after work up; right) Crystals used for XRD studies

Ethyl 2-((3aR,6S,6aR)-2,2-dimethyl-5,5-bis(((methylsulfonyl)oxy)methyl)tetrahydrofuro[2,3-d][1,3]dioxol-6-yl)acetate **5**



A solution of **4** (13.0 g, 29.3 mmol) in EtOAc (300 mL) was placed under an atmosphere of argon before 5% palladium on activated carbon (1.3 g, 1.5 mmol, 5 mol%) was added. The flask was evacuated under vacuum and refilled with H₂ gas three times to ensure a hydrogen atmosphere and vigorously stirred overnight. The reaction was monitored by NMR. Once complete, the mixture was filtered through a pad of celite and the solvent removed under reduced pressure to yield **5** (12.7 g, 28.4 mmol) as a colourless solid in 97% yield which was used without further purification. The use of Pd/C and hydrogen gas along with flammable solvents poses a significant fire risk.

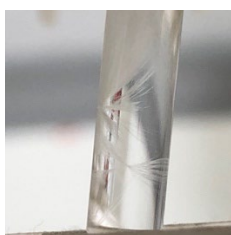
TLC (EtOAc:40-60 PE, 6:4 v/v) R_f: 0.64;

mp: 88-95 °C (crystallised from a mixture of MeOH and EtOH);

¹H NMR (400 MHz, CDCl₃): δ 5.85 (d, J = 3.9 Hz, 1H), 4.87 (dd, J = 5.2, 3.9 Hz, 1H), 4.59 (d, J = 10.8 Hz, 1H), 4.31 (d, J = 10.7 Hz, 1H), 4.30 (d, J = 10.8 Hz, 1H), 4.23 (d, J = 10.7 Hz, 1H), 4.18 (apparent dq, J = 7.1, 2.2 Hz, 2H), 3.12 (s, 3H), 3.07 (s, 3H), 2.91 – 2.65 (m, 2H), 2.57 (dd, J = 16.9, 5.5 Hz, 1H), 1.60 (s, 3H), 1.30 (s, 3H), 1.28 (t, J = 7.2 Hz, 3H);

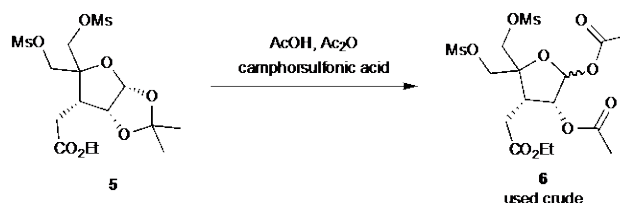
¹³C NMR (101 MHz, CDCl₃): δ 171.3, 112.9, 105.3, 84.1, 81.7, 70.1, 68.2, 61.3, 42.7, 38.1, 37.7, 28.6, 26.3, 25.5, 14.2;

HRMS (m/z): [M+Na]⁺ calcd. for C₁₅H₂₆O₁₁NaS₂⁺, 469.0809; found, 469.0811.



Crystals used for XRD studies

(3R,4S)-4-(2-Ethoxy-2-oxoethyl)-5,5-bis(((methylsulfonyl)oxy)methyl)tetrahydrofuran-2,3-diyl diacetate **6**



To a solution of compound **5** (4.9 g, 11.0 mmol) in acetic acid (50 mL) and acetic anhydride (38 mL) was added camphorsulfonic acid (CSA) (120 mg, 0.52 mmol) and the solution was stirred at 80 °C for 90 min. A second portion of CSA (120 mg, 0.52 mmol) was added and stirring continued at 80 °C for 90 min. This was repeated twice more, and the reaction left to stir overnight at 80 °C. The volatiles were removed under reduced pressure and the resulting brown gum was co-evaporated with toluene (3 x 50 mL), dissolved in EtOAc (150 mL), washed with a saturated aqueous solution of NaHCO₃ (5 x 100 mL), washed with brine (1 x 100 mL), dried over Na₂SO₄, and evaporated to dryness to yield crude compound **6** (5.3 g, assume quantitative) which was used without purification in the next step. We found the compound was not stable to column chromatography.

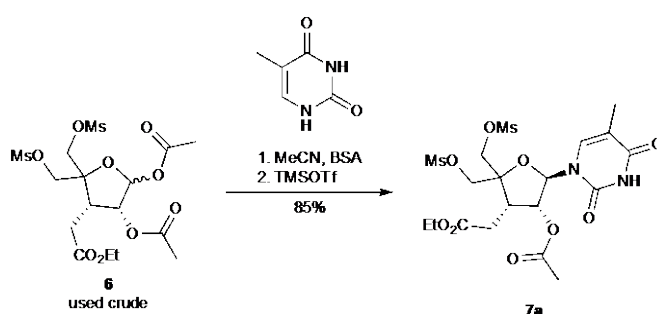
TLC (EtOAc:40-60 PE, 6:4 v/v) R_f: 0.38;

¹H NMR (400 MHz, CDCl₃): δ 6.10 (s, 1H), 5.32 (d, J = 5.0 Hz, 1H), 4.40 (d, J = 3.3 Hz, 2H), 4.28 (s, 2H), 4.20 – 4.11 (m, 2H), 3.08 (s, 3H), 3.07 (s, 3H), 3.03 (dd, J = 7.7, 4.9 Hz, 1H), 2.62 (t, J = 7.5 Hz, 2H), 2.14 (s, 3H), 2.11 (s, 3H), 1.26 (t, J = 7.2 Hz, 3H);

¹³C NMR (101 MHz, CDCl₃): δ 170.9, 169.5, 169.3, 97.8, 84.6, 77.8, 71.4, 66.9, 61.6, 40.4, 38.0, 37.6, 28.6, 21.1, 20.8, 14.2;

HRMS (m/z): [M+Na]⁺ calcd. for C₁₆H₂₆O₁₃NaS₂⁺, 513.0707; found, 513.0706.

Thymine LNA acid precursor **7a**



Crude compound **6** (2.5 g, 5.1 mmol) and thymine (0.8 g, 6.4 mmol, 1.25 eq) were co-evaporated with anhydrous MeCN (3 x 15 mL). The mixture was then dissolved in anhydrous MeCN (12.5 mL) and bis(trimethylsilyl)acetamide (BSA) (3.5 mL, 14.2 mmol, 2.8 eq) was added. The solution was heated to reflux for 1 h. The reaction was cooled to room temperature and TMSOTf (1.25 mL, 6.8 mmol, 1.4 eq) was added. The reaction was then heated to reflux overnight resulting in a dark red solution. The reaction was cooled to room temperature, diluted with CH₂Cl₂ (12.5 mL), and a half saturated aqueous solution of NaHCO₃ (25 mL) was added with stirring (bubbles are generated). The organic layer became a pale-yellow colour and was subsequently washed with saturated aqueous NaHCO₃ (25 mL) and brine (25 mL). The organic phase was dried over Na₂SO₄ and evaporated to dryness. The crude brown foam

was purified by column chromatography (0-7% MeOH in CH₂Cl₂) to give compound **7a** (2.42 g, 4.4 mmol) as a beige foam in 85% yield.

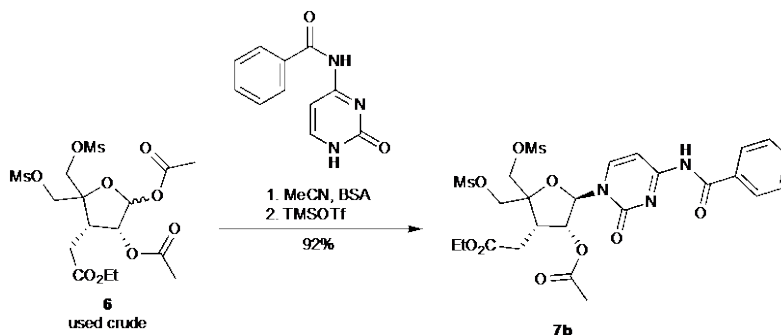
TLC (CH₂Cl₂:MeOH, 17:1 v/v) R_f: 0.55;

¹H NMR (400 MHz, CDCl₃): δ 9.29 (s, 1H), 7.03 (d, J = 1.2, 1H), 5.58 (dd, J = 7.6, 1.7, 1H), 5.49 (d, J = 1.7, 1H), 4.47 (s, 2H), 4.38 (d, J = 11.0, 1H), 4.32 (d, J = 11.0, 1H), 4.15 (q, J = 7.1, 2H), 3.55 (ddd, J = 9.6, 7.6, 6.2, 1H), 3.10 (s, 3H), 3.09 (s, 3H), 2.65 (dd, J = 16.8, 9.6, 1H), 2.57 (dd, J = 16.8, 6.2, 1H), 2.14 (s, 3H), 1.91 (d, J = 1.2, 3H), 1.25 (t, J = 7.1, 3H);

¹³C NMR (101 MHz, CDCl₃): δ 170.8, 170.3, 163.9, 150.3, 138.5, 111.6, 95.8, 85.5, 78.5, 70.1, 67.4, 61.5, 41.4, 37.9, 37.6, 29.1, 20.8, 14.3, 12.4;

HRMS (m/z): [M+Na]⁺ calcd. for C₁₉H₂₈N₂O₁₃NaS₂⁺, 579.0925; found 579.0924.

*N*⁴-Benzoylcytosine LNA acid precursor **7b**



Compound **6** (1.04 g, 2.1 mmol) and *N*⁴-benzoylcytosine (0.912 g, 4.0 mmol, 2.0 eq) were co-evaporated with anhydrous MeCN (3 x 15 mL). The mixture was then dissolved in anhydrous MeCN (12.5 mL) and BSA (1.0 mL, 4.1 mmol, 1.9 eq) was added. The suspension was heated to reflux for 1 h. The reaction was cooled to room temperature and TMSOTf (0.45 mL, 2.5 mmol, 1.2 eq) was added. The reaction was then heated to reflux overnight resulting in a dark red solution. The reaction was cooled to room temperature, diluted with CH₂Cl₂ (12.5 mL), and a half saturated aqueous solution of NaHCO₃ was added with stirring. The organic layer was subsequently washed with saturated aqueous NaHCO₃ (25 mL) and brine (25 mL). The organic phase was dried over Na₂SO₄ and evaporated to dryness. The crude brown foam was purified by column chromatography (50-100% EtOAc in 40-60 PE) to give **7b** (1.25 g, 1.9 mmol) as a pale-yellow foam in 92% yield.

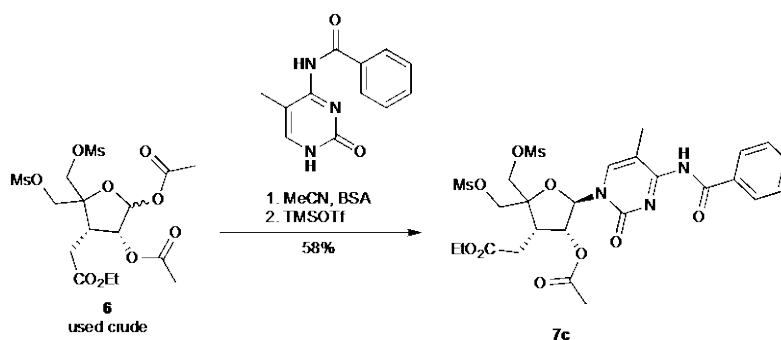
TLC (CH₂Cl₂:MeOH, 17:1 v/v) R_f: 0.53;

¹H NMR (400 MHz, CDCl₃): δ 8.97 (s, 1H), 7.93 (d, J = 7.7, 2H), 7.73 (d, J = 7.5, 1H), 7.65 – 7.50 (m, 4H), 5.67 (dd, J = 7.4, 1.5, 1H), 5.58 (d, J = 1.5, 1H), 4.62 – 4.49 (m, 2H), 4.45 – 4.36 (m, 2H), 4.16 (q, J = 7.1, 2H), 3.66 (apparent dt, J = 9.1, 7.0, 1H), 3.11 (s, 3H), 3.09 (s, 3H), 2.69 (dd, J = 16.8, 9.1, 1H), 2.59 (dd, J = 16.7, 6.8, 1H), 2.17 (s, 3H), 1.26 (t, J = 7.1, 3H);

¹³C NMR (151 MHz, CDCl₃): δ 170.7, 170.4, 166.3 (broad due to rotamers), 162.6, 153.3 (broad due to rotamers), 148.5, 133.8, 132.4, 129.3, 128.2, 97.8, 96.9 (broad due to rotamers), 86.7, 78.7, 70.1, 67.6, 61.5, 41.4, 38.0, 37.7, 29.3, 20.8, 14.3;

HRMS (m/z): [M+H]⁺ calcd. for C₂₅H₃₂O₁₃N₃S₂⁺, 646.1371; found, 646.1367.

*N*⁴-Benzoyl methylcytosine LNA precursor **7c**



A suspension of *N*⁴-benzoyl methylcytosine (808 mg, 3.5 mmol, 1.5 eq), compound **6** (1.13 g, 2.3 mmol) and BSA (1.5 mL, 6.1 mmol, 2.7 eq) in anhydrous MeCN (13.5 mL) was heated to reflux for 1 h. The solution was cooled to room temperature, TMSOTf (0.5 mL, 2.8 mmol, 1.2 eq) was added dropwise with stirring and the reaction was then heated to reflux overnight. After cooling to room temperature, the reaction was diluted with EtOAc (30 mL) and a saturated aqueous solution of NaHCO₃ (30 mL) was added slowly (generates bubbles). Stirring the biphasic mixture generated a precipitate, which was filtered removing the precipitate prior to workup. The organic layer was collected, washed with saturated aqueous NaHCO₃ (2 x 30 mL) followed by brine (30 mL), dried over MgSO₄, and evaporated to dryness to give an orange foam. This was purified by column chromatography (0-10% MeOH in CH₂Cl₂) to give **7c** (885 mg, 1.3 mmol) as a beige foam in 58% yield.

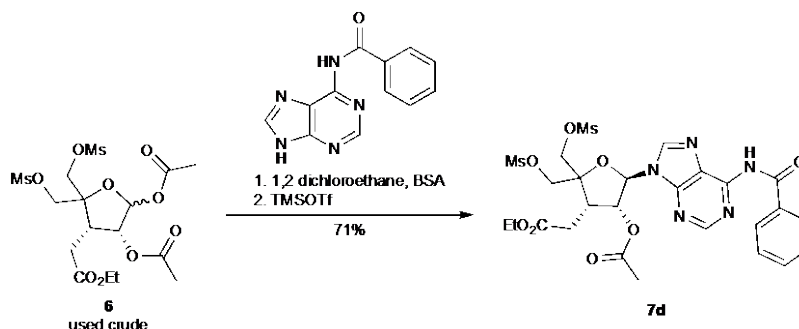
TLC (CH₂Cl₂:MeOH, 17:1 v/v) R_f: 0.5;

¹H NMR (400 MHz, CDCl₃): δ 13.24 (s, 1H), 8.34 – 8.29 (m, 2H), 7.54 (tt, J = 7.4, 1.4, 1H), 7.45 (t, J = 7.4, 2H), 7.21 (d, J = 1.2, 1H), 5.62 (dd, J = 7.5, 1.7, 1H), 5.54 (d, J = 1.7, 1H), 4.49 (d, J = 10.8, 2H), 4.46 (d, J = 10.8, 1H), 4.41 (d, J = 11.0, 1H), 4.33 (d, J = 11.0, 1H), 4.17 (q, J = 7.1, 2H), 3.58 (apparent dt, J = 9.2, 6.9, 1H), 3.11 (s, 3H), 3.09 (s, 3H), 2.67 (dd, J = 16.8, 9.2, 1H), 2.58 (dd, J = 16.8, 6.6, 1H), 2.17 (s, 3H), 2.12 (d, J = 1.2, 3H), 1.27 (t, J = 7.1, 3H);

¹³C NMR (151 MHz, CDCl₃): δ 180.0, 170.7, 170.2, 159.7, 147.8, 139.1, 137.1, 132.8, 130.2, 128.3, 112.7, 96.1, 85.7, 78.5, 69.8, 67.3, 61.5, 41.3, 38.0, 37.7, 29.1, 20.8, 14.3, 13.5;

HRMS (m/z): [M+H]⁺ calcd. for C₂₆H₃₄O₁₃N₃S₂⁺, 660.1528; found, 660.1522.

*N*⁶-Benzoyladenine LNA acid precursor **7d**



*N*⁶-Benzoyladenine (1.15 g, 4.8 mmol) and compound **6** (2.63 g, 5.3 mmol, 1.1 eq) were suspended in anhydrous 1,2-dichloroethane (22 mL) and BSA (3.13 mL, 12.8 mmol, 2.7 eq) was added. The solution

was heated to reflux for 1 h. The reaction was cooled to room temperature and TMSOTf (2.0 mL, 11 mmol, 2.3 eq) was added. The reaction was then heated to reflux overnight resulting in a dark red solution. The reaction was cooled to room temperature, diluted with CH₂Cl₂ (12.5 mL), and added to a saturated aqueous solution of NaHCO₃ (22 mL) slowly with stirring (bubbles are generated). The organic layer was subsequently washed with saturated aqueous NaHCO₃ (25 mL) and brine (25 mL), dried over Na₂SO₄, and evaporated to dryness. The crude brown foam was purified by silica column chromatography (0-100% EtOAc in 40-60 PE) to give compound **7d** (2.29 g, 3.4 mmol) as a beige foam in 71% yield.

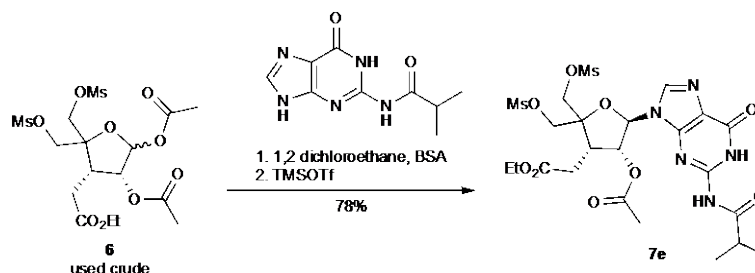
TLC (EtOAc) R_f: 0.35;

¹H NMR (400 MHz, CDCl₃): δ 9.17 (s, 1H), 8.80 (s, 1H), 8.12 (s, 1H), 8.04 – 7.93 (m, 2H), 7.64 – 7.55 (m, 1H), 7.51 (t, J = 7.51, 2H), 6.13 (d, J = 1.1, 1H), 5.88 (dd, J = 6.7, 1.1, 1H), 4.55 (d, J = 1.9, 2H), 4.48 (d, J = 10.9, 1H), 4.40 (d, J = 10.9, 1H), 4.16 (q, J = 7.1, 2H), 4.12 – 4.02 (m, 1H), 3.11 (s, 3H), 2.95 (s, 3H), 2.72 (apparent dd, J = 7.8, 4.9, 2H), 2.19 (s, 3H), 1.25 (t, J = 7.1, 3H);

¹³C NMR (101 MHz, CDCl₃): δ 170.7, 170.1, 164.8, 152.8, 151.1, 150.0, 142.6, 133.7, 133.0, 129.0, 128.0, 123.7, 90.8, 86.0, 79.0, 69.6, 67.0, 61.5, 41.6, 37.9, 37.6, 28.9, 20.8, 14.2;

HRMS (m/z): [M+H]⁺ calcd. for C₂₆H₃₂O₁₂N₅S₂⁺, 670.1483; found, 670.1482.

*N*²-Isobutyrylguanine LNA acid precursor **7e**



Compound **6** (2.6 g, 5.3 mmol) and *N*²-isobutyrylguanine (1.34 g, 6.1 mmol, 1.1 eq) were suspended in anhydrous 1,2 dichloroethane (22 mL) and BSA (3.1 mL, 12.5 mmol, 2.4 eq) was added. The suspension was heated to reflux for 1.5 h. The reaction was cooled to room temperature and TMSOTf (2.0 mL, 11 mmol, 2.1 eq) was added. The reaction was then heated to reflux for 2 h. The reaction was cooled to room temperature and added to a stirring solution of saturated aqueous NaHCO₃ (22 mL). The organic layer was subsequently washed with saturated aqueous NaHCO₃ (25 mL) and brine (25 mL). The organic phase was dried over Na₂SO₄ and evaporated to dryness. Purification by column chromatography (0-10% MeOH in EtOAc) gave **7e** (2.64, 4.1 mmol) as a pale-yellow foam in 78% yield.

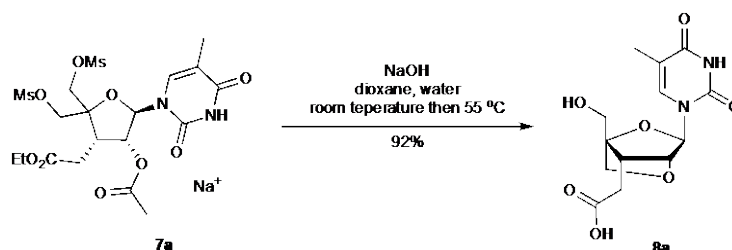
TLC (EtOAc:MeOH, 9:1 v/v) R_f: 0.45;

¹H NMR (400 MHz, CDCl₃): δ 12.16 (s, 1H), 9.44 (s, 1H), 7.75 (s, 1H), 5.96 (d, J = 1.1, 1H), 5.72 (dd, J = 6.5, 1.1, 1H), 4.72 (d, J = 10.5, 1H), 4.49 (d, J = 11.1, 1H), 4.42 (d, J = 10.5, 1H), 4.32 (d, J = 11.1, 1H), 4.25 (dt, J = 8.9, 6.6, 1H), 4.13 (apparent qd, J = 7.2, 1.1, 2H), 3.12 (s, 3H), 3.06 (s, 3H), 2.77 – 2.57 (m, 3H), 2.16 (s, 3H), 1.30 – 1.16 (m, 9H);

¹³C (101 MHz, CDCl₃): δ 179.4, 171.1, 170.0, 155.5, 148.1, 147.4, 139.2, 122.0, 91.0, 85.4, 78.5, 69.6, 67.6, 61.5, 41.4, 38.0, 37.7, 36.4, 28.6, 20.7, 19.0, 18.9, 14.2;

HRMS (m/z): [M+H]⁺ calcd. for C₂₃H₃₄O₁₃N₅S₂⁺, 652.1589; found, 652.1586.

Thymine LNA acid **8a**



Compound **7a** (1.0 g, 1.8 mmol) was dissolved in 1,4-dioxane (4.5 mL) and water (4.5 mL) and 2 M NaOH in water (9 mL, 18 mmol, 10 eq) was added. The reaction was stirred at room temperature for 2 h until the locking step and ester hydrolysis was complete (reaction progress monitored using LCMS). The reaction was then heated to 55 °C for 1 h. The reaction was evaporated to dryness and partitioned between CH₂Cl₂ (40 mL) and water (30 mL). The aqueous layer was washed with CH₂Cl₂ (3 x 10 mL). The aqueous phase was acidified using 1 M HCl and washed with CH₂Cl₂ (3 x 20 mL). The product was then extracted from the aqueous layer using 25% iPrOH in CH₂Cl₂ (4 x 10 mL, until no product remained in the aqueous layer as determined by TLC), dried over Na₂SO₄, and evaporated to dryness to give **8a** (516 mg, 1.7 mmol) as a white solid in 92% yield which was used without further purification.

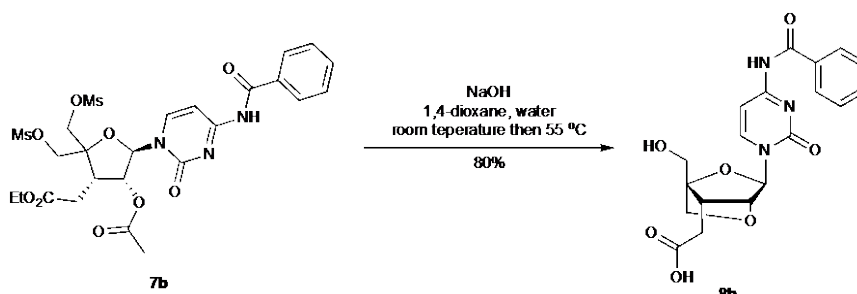
TLC (CH₂Cl₂:MeOH, 3:2 v/v + 2% Et₃N) R_f: 0.26;

¹H NMR (400 MHz, d₆-DMSO): δ 11.39 (s, 1H), 7.62 (d, J = 1.3, 1H), 5.44 (s, 1H), 4.35 (s, 1H), 3.81 (d, J = 13.0, 1H), 3.77 (d, J = 13.0, 1H), 3.73 (d, J = 8.5, 1H), 3.60 (d, J = 8.4, 1H), 3.31 (s, 1H), 2.41 (dd, J = 15.5, 2.7, 1H), 2.33 – 2.07 (m, 2H), 1.79 (d, J = 1.2, 3H);

¹³C NMR (101 MHz, d₆-DMSO): δ 173.4, 164.3, 150.5, 135.4, 108.8, 91.1, 86.8, 80.2, 71.5, 57.1, 39.7, 29.0, 12.9;

HRMS (m/z): [M-H]⁻ calcd. for C₁₃H₁₅O₇N₂⁻, 311.0885; found, 311.0882.

N⁴-Benzoylcytosine LNA acid **8b**



Compound **7b** (400 mg, 0.62 mmol) was dissolved in 1,4-dioxane (4 mL) and 1 M NaOH in water (2 mL, 2 mmol, 3.2 eq) was added. The reaction was stirred at room temperature for 2 h until the locking step and ester hydrolysis was complete (reaction progress monitored using LCMS). The reaction was then heated to 55 °C for 2 h. The reaction was evaporated to dryness and partitioned between CH₂Cl₂ (40 mL) and water (30 mL). The aqueous phase was washed with CH₂Cl₂ (3 x 10 mL), acidified using

1 M HCl and further washed with CH₂Cl₂ (3 x 20 mL). The product was then extracted from the aqueous layer using 25% iPrOH in CH₂Cl₂ (4 x 10 mL, until no product remains in the aqueous layer as determined by TLC), dried over Na₂SO₄, and evaporated to dryness to give **8b** (198 mg, 0.49 mmol) as a white solid in 80% yield which was used without further purification.

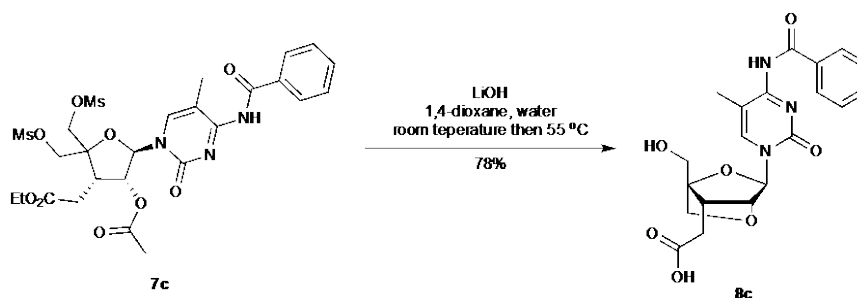
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.4;

¹H NMR (500 MHz, d₆-DMSO): δ 8.26 (d, J = 7.5, 1H), 8.00 (dd, J = 8.5, 1.3, 2H), 7.63 (tt, J = 7.5, 1.3, 1H), 7.55 – 7.48 (m, 2H), 7.41 (d, J = 7.5, 1H), 5.55 (s, 1H), 4.45 (s, 1H), 3.82 (d, J = 13.1, 1H), 3.77 (d, J = 13.1, 1H), 3.77 (d, J = 8.4, 1H), 3.65 (d, J = 8.4, 1H), 2.30 (s, 1H), 2.31 – 2.05 (m, 3H);

¹³C NMR (126 MHz, d₆-DMSO): δ 167.9, 167.4, 163.3, 154.0, 144.3, 133.2, 132.7, 128.5, 128.4, 95.9, 91.2, 87.4, 79.8, 71.1, 56.8, 40.1, 29.9;

HRMS (m/z): [M-H]⁻ calcd. for C₁₉H₁₈O₇N₃⁻, 400.1150; found, 400.1141.

*N*⁴-Benzoyl methylcytosine LNA acid **8c**



Compound **7c** (400 mg, 0.61 mmol) was dissolved in 1,4-dioxane (4 mL) and 1 M LiOH in water (2 mL, 2 mmol, 3.3 eq) was added. The reaction was stirred at room temperature for 2 h and then heated to 55 °C. After 1 h the reaction was complete as determined by LCMS. The reaction was evaporated to dryness and partitioned between CH₂Cl₂ (40 mL) and water (30 mL). The aqueous layer was washed with CH₂Cl₂ (3 x 40 mL), acidified with 1 M HCl, and washed once more with CH₂Cl₂ (40 mL). The product was then extracted from the aqueous layer using 15% iPrOH in CH₂Cl₂ (5 x 20 mL), until no product remained in the aqueous layer as determined by TLC, dried over Na₂SO₄, and evaporated to dryness to give **8c** (198 mg, 0.48 mmol) as a white solid in 78% yield which was used without further purification.

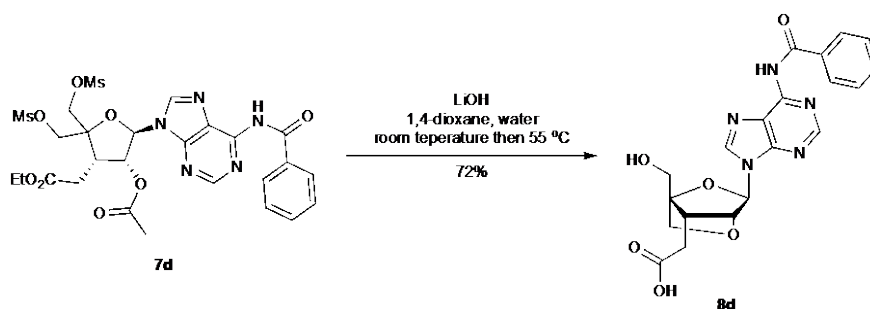
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.36;

¹H NMR (500 MHz, d₆-DMSO): δ 8.23 – 8.16 (m, 2H), 7.95 (s, 1H), 7.60 (t, J = 7.3, 1H), 7.51 (t, J = 7.6, 2H), 5.53 (s, 1H), 5.25 (br s, 1H), 4.46 (s, 1H), 3.85 (d, J = 13.1, 1H), 3.82 (d, J = 13.1, 1H), 3.77 (d, J = 8.5, 1H), 3.65 (d, J = 8.5, 1H), 2.42 (dd, J = 15.8, 3.2, 1H), 2.30 – 2.19 (m, 2H), 2.04 (s, 3H);

¹³C NMR (126 MHz, d₆-DMSO): δ 177.9, 172.9, 159.1, 147.2, 137.8, 136.5, 132.5, 129.3, 128.4, 109.1, 91.1, 87.0, 79.5, 71.1, 56.6, 39.0, 28.5, 13.4;

HRMS (m/z): [M+H]⁺ calcd. for C₂₀H₂₂O₇N₃⁺, 416.1452; found, 416.1452.

*N*⁶-Benzoyladenine LNA acid **8d**



Compound **7d** (500 mg, 0.75 mmol) was dissolved in 1,4-dioxane (4.8 mL) and 1 M LiOH in water (2.4 mL, 2.4 mmol, 3.2 eq). The reaction was stirred at room temperature for 2 h and then heated to 55 °C. After 2 h the product formation was analysed by LCMS. The reaction was not complete and a further 0.33 eq of 1 M LiOH (266 μ L) was added and the reaction stirred at 55 °C for 1 h. Once complete, the reaction was evaporated to dryness and partitioned between CH₂Cl₂ (20 mL) and water (20 mL). The aqueous layer was washed with CH₂Cl₂ (3 x 20 mL), acidified with 1 M HCl, and washed once more with CH₂Cl₂ (20 mL). The product was then extracted from the aqueous layer using 15% iPrOH in CH₂Cl₂ (5 x 20 mL), dried over Na₂SO₄, and evaporated to dryness to give **8d** (230 mg, 0.54 mmol) as a white solid in 72% yield which was used without further purification.

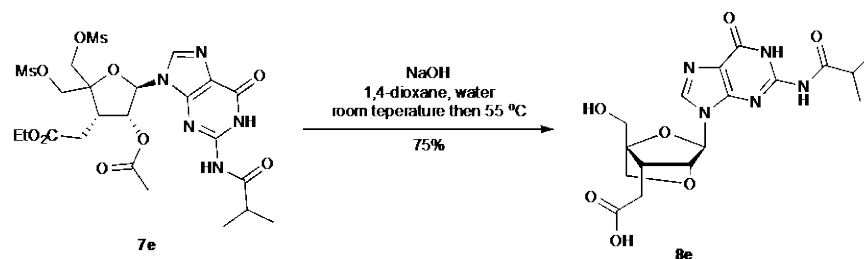
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.24;

¹H NMR (400 MHz, d₆-DMSO): δ 12.36 (s, 1H), 11.21 (s, 1H), 8.76 (s, 1H), 8.53 (s, 1H), 8.09 – 8.02 (m, 2H), 7.69 – 7.60 (m, 1H), 7.60 – 7.51 (m, 2H), 6.09 (s, 1H), 4.74 (s, 1H), 3.86 (m, 3H), 3.77 (d, *J* = 8.5, 1H), 3.32 (s, 1H), 2.57 (dd, *J* = 9.8, 4.1, 1H), 2.54 – 2.47 (m, 1H + solvent peak), 2.33 (dd, *J* = 17.1, 9.8, 1H);

¹³C NMR (101 MHz, d₆-DMSO): δ 173.4, 165.8, 152.3, 151.8, 150.8, 141.5, 133.8, 132.9, 129.0, 128.9, 126.2, 90.8, 86.0, 80.5, 72.0, 57.6, 41.3, 29.1;

HRMS (*m/z*): [M+H]⁺ calcd. for C₂₀H₂₀O₆N₅⁺, 426.1406; found, 426.1407.

*N*²-Isobutyrylguanine LNA acid **8e**



To a solution of compound **7e** (105 mg, 0.17 mmol) in 1,4-dioxane (2 mL) was added 1 M NaOH in water (0.5 mL, 0.5 mmol, 3.0 eq). The reaction was stirred at room temperature for 3 h and then heated to 55 °C. After 1 h the reaction was complete as determined by LCMS. The reaction was evaporated to dryness and was partitioned between CH₂Cl₂ (20 mL) and water (20 mL). The aqueous layer was washed with CH₂Cl₂ (3 x 20 mL), acidified with 1 M HCl, and washed once more with CH₂Cl₂ (20 mL). NaCl was added to saturate the aqueous layer and the product was extracted from the

aqueous layer using 25% iPrOH in CH₂Cl₂ (5 x 20 mL), dried over Na₂SO₄, and evaporated to dryness to give **8e** (52 mg, 0.13 mmol) as a white solid in 75% yield which was used without further purification.

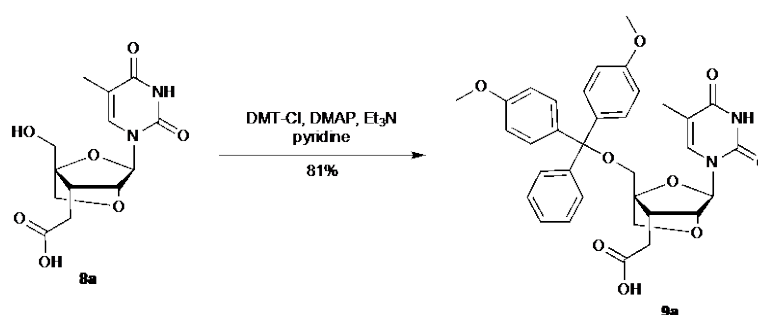
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.18;

¹H NMR (400 MHz, d₆-DMSO): δ 12.14 (s, 1H), 11.80 (s, 1H), 8.14 (s, 1H), 5.82 (s, 1H), 4.61 (s, 1H), 3.82 (apparent d, J = 9.8, 3H), 3.69 (d, J = 8.6, 1H), 2.78 (app h, J = 6.8, 1H), 2.55 – 2.46 (m, 2H and d₆-DMSO), 2.29 (dd, J = 17.8, 10.5, 1H), 1.11 (d, J = 6.8, 6H);

¹³C NMR (101 MHz, d₆-DMSO): δ 180.2, 172.9, 154.6, 148.4, 147.6, 136.1, 120.0, 90.3, 85.3, 80.1, 71.5, 57.1, 40.6, 34.7, 28.6, 18.9, 18.8;

HRMS (m/z): [M-H]⁻ calcd. for C₁₇H₂₀O₇N₅⁻, 406.1368; found, 406.1359.

5'-O-DMT thymine LNA acid **9a**



Compound **8a** (400 mg, 1.28 mmol) was dissolved in pyridine (18 mL) and Et₃N (0.25 mL, 1.8 mmol, 1.1 eq) and activated 3 Å molecular sieves were added. The solution was stirred at room temperature for 15 min before 4-dimethylaminopyridine (DMAP) (78 mg, 0.64 mmol, 0.5 eq) and 4,4'-dimethoxytrityl chloride (DMT-Cl) (1 g, 2.95 mmol, 2.3 eq) were added. The reaction was stirred at room temperature for 4 h before a second portion of DMT-Cl (0.8 g, 2.36 mmol, 1.8 eq) was added and the reaction was stirred at room temperature for 16 h. The molecular sieves were removed by filtration and the organic solvents were removed under vacuum. The resulting residue was purified by column chromatography (0-30% MeOH in EtOAc with a constant additive of 2% Et₃N). Following column chromatography, NMR showed significant amounts of Et₃N salts and the material was dissolved in EtOAc (25 mL) and was washed with H₂O (3 x 25 mL), dried over Na₂SO₄, and evaporated to dryness to yield **9a** (687 mg). Rather than risk degradation, the final product was not evaporated to complete dryness and was stored and used with 0.5 eq of Et₃N present (as determined by NMR), making the final yield 81%.

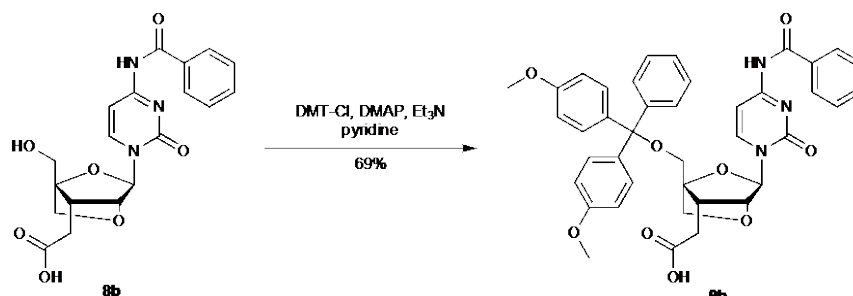
TLC (CH₂Cl₂:MeOH, 4:1 v/v, + 2% Et₃N) R_f: 0.18;

¹H NMR (400 MHz, DMSO-d₆): δ 11.43 (s, 1H), 7.61 (d, J = 1.1, 1H), 7.49 – 7.37 (m, 2H), 7.37 – 7.21 (m, 7H), 6.91 (dd, J = 9.0, 3.0, 4H), 5.48 (s, 1H), 4.42 (s, 1H), 3.74 (s, 6H), 3.64 (d, J = 8.6, 1H), 3.60 (d, J = 8.6, 1H), 3.50 (d, J = 11.4, 1H), 3.30 (d, J = 11.4, 1H under water peak), 2.50 – 2.45 (m, 8H, Et₃N counterion under solvent peak), 2.42 (dd, J = 9.4, 4.3, 1H), 2.17 (dd, J = 16.9, 9.4, 1H), 2.00 (dd, J = 16.9, 4.3, 1H), 1.59 (d, J = 1.1, 3H), 0.95 (t, J = 7.2, 4.5H, Et₃N);

¹³C NMR (151 MHz, d₆-DMSO): δ 172.6, 163.8, 158.2, 149.9, 144.6, 135.2, 135.0, 134.3, 129.7, 129.7, 128.0, 127.6, 126.9, 113.3, 113.3, 108.5, 89.2, 86.6, 85.8, 79.7, 71.3, 58.6, 55.0, 45.5 (Et₃N), 40.7, 28.6, 12.4, 10.7 (Et₃N);

HRMS (m/z): [M-H]⁻ calcd. for C₃₄H₃₃O₉N₂⁻, 613.2192; found, 613.2184.

5'-O-DMT *N*⁴-benzoylcytosine LNA acid **9b**



Compound **8b** (100 mg, 0.25 mmol) was dissolved in pyridine (4 mL) and Et₃N (0.05 mL, 0.36 mmol, 1.4 eq) and activated 3 Å molecular sieves were added. The solution was stirred at room temperature for 15 min before DMAP (16 mg, 0.13 mmol, 0.5 eq) and DMT-Cl (204 mg, 0.6 mmol, 2.5 eq) were added. The reaction was stirred at room temperature for 16 h before the molecular sieves were removed by filtration and the organic solvents removed under vacuum. The resulting residue was purified by column chromatography (0-30% MeOH in EtOAc with a constant additive of 2% pyridine) to give **9b** (122 mg) in 69% yield.

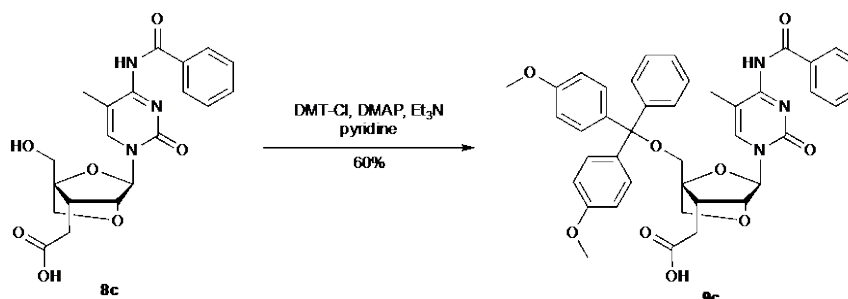
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.37;

¹H NMR (400 MHz, DMSO-d₆): δ 11.17 (s, 1H), 8.33 (d, J = 7.5, 1H), 8.01 (d, J = 7.4, 2H), 7.64 (t, J = 7.4, 1H), 7.52 (t, J = 7.6, 2H), 7.46 – 7.22 (m, 10H), 6.94 (d, J = 8.7, 4H), 5.62 (s, 1H), 4.53 (s, 1H), 3.77 (s, 6H), 3.67-3.63 (m, 2H), 3.51 (d, J = 11.1, 1H), 3.41 (d, J = 11.1, 1H), 2.39 (dd, J = 9.3, 4.0, 1H), 2.21 – 2.09 (m, 1H), 1.97 (dd, J = 16.6, 4.0, 1H);

¹³C NMR (151 MHz, d₆-DMSO): δ 173.2, 168.0, 163.4, 158.2, 154.0, 149.6 (pyridine), 144.4, 143.9, 135.1, 135.1, 133.2, 132.7, 129.7, 129.7, 128.5, 128.4, 128.0, 127.7, 126.9, 123.9, 113.3, 113.3, 95.8, 89.3, 87.6, 86.0, 79.3, 71.3, 58.4, 55.0, 40.1, 28.7.

HRMS (m/z): [M+H]⁺ calcd. for C₄₀H₃₈O₉N₃⁺, 704.2603; found, 704.2602.

5'-O-DMT *N*⁴-benzoyl methylcytosine LNA acid **9c**



Compound **8c** (100 mg, 0.24 mmol) was dissolved in pyridine (4 mL) and Et₃N (0.05 mL, 0.7 mmol, 1.5 eq) and activated 3 Å molecular sieves were added. The solution was stirred at room temperature

for 15 min before DMAP (16 mg, 0.36 mmol, 1.5 eq) and DMT-Cl (204 mg, 0.6 mmol, 2.5 eq) were added. The reaction was left to stir at room temperature for 16 h before the molecular sieves were removed by filtration and the organic solvents removed under vacuum. The resulting residue was purified by column chromatography (0-30% MeOH in EtOAc with a constant additive of 2% pyridine) to yield **9c** (114 mg). Rather than risk degradation, the final product was not evaporated to complete dryness and was stored and used with 1 eq of pyridine present (as determined by NMR), making the final yield 60%.

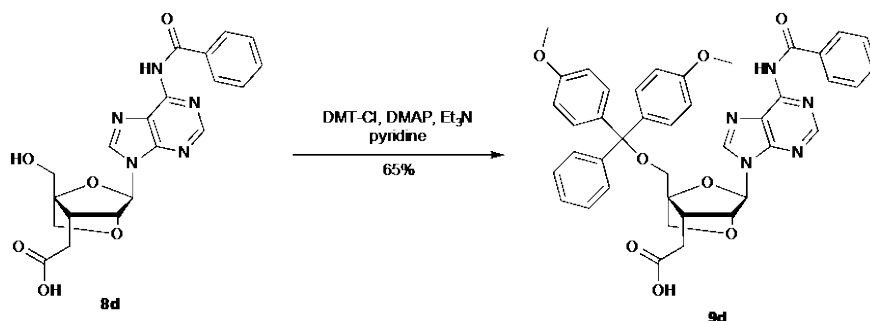
TLC (CH₂Cl₂:MeOH, 3:2 v/v, + 2% Et₃N) R_f: 0.37;

¹H NMR (500 MHz, DMSO-d₆): δ 8.65 – 8.45 (m, 2H, pyridine), 8.22 – 8.12 (m, 2H), 7.89 (s, 1H), 7.78 (tt, J = 7.6, 1.9, 1H, pyridine), 7.60 (t, J = 7.4, 1H), 7.50 (t, J = 7.7, 2H), 7.48 – 7.42 (m, 2H), 7.44 – 7.30 (m, 8H, pyridine), 7.29 – 7.24 (m, 1H), 6.93 (dd, J = 8.9, 4.0, 4H), 5.58 (s, 1H), 4.54 (s, 1H), 3.75 (s, 6H), 3.69 (d, J = 8.7, 1H), 3.66 (d, J = 8.7, 1H), 3.55 (d, J = 11.4, 1H), 3.36 (d, J = 11.4, 1H), 3.34 (br s, 1H), 2.47 (m, 1H under solvent peak), 2.25 (dd, J = 17.0, 8.9, 1H), 2.05 (dd, J = 17.0, 4.4, 1H), 1.87 – 1.75 (m, 3H);

¹³C NMR (126 MHz, d₆-DMSO): δ 177.6, 172.5, 159.2, 149.6 (pyridine), 147.1, 144.6, 137.1, 136.1 (pyridine), 135.2, 135.1, 132.6, 129.8, 129.3, 129.2, 128.4, 128.0, 127.6, 126.9, 123.9 (pyridine), 113.4, 113.3, 109.2, 89.6, 87.3, 85.9, 79.5, 71.3, 58.5, 55.1, 39.4, 28.4, 13.6;

HRMS (m/z): [M+H]⁺ calcd. for C₄₁H₄₀N₃O₉⁺, 718.2759, found, 718.2756.

5'-O-DMT N⁶-benzoyladenine LNA acid **9d**



Compound **8d** (62.5 mg, 0.15 mmol) was dissolved in pyridine (1.5 mL) and Et₃N (0.031 mL, 0.22 mmol, 1.5 eq) and activated 3 Å molecular sieves were added. The solution was stirred at room temperature for 15 min before DMAP (18 mg, 2 mmol, 1.3 eq) and DMT-Cl (100 mg, 0.29 mmol, 2 eq) were added. The reaction was stirred at room temperature for 2 h, and a second portion of DMT-Cl (100 mg, 0.29 mmol, 2.0 eq) was added. After 16 h the molecular sieves were removed by filtration and the organic solvents removed under vacuum. The resulting residue was purified by column chromatography (5-15% MeOH in EtOAc with a constant additive of 2% pyridine) to yield **9d** (76 mg). Rather than risk degradation, the final product was not evaporated to complete dryness and was stored and used with 0.72 eq of pyridine present (as determined by NMR), making the final yield 65%.

TLC (EtOAc:MeOH, 3:7 v/v, + 2% Et₃N) R_f: 0.50;

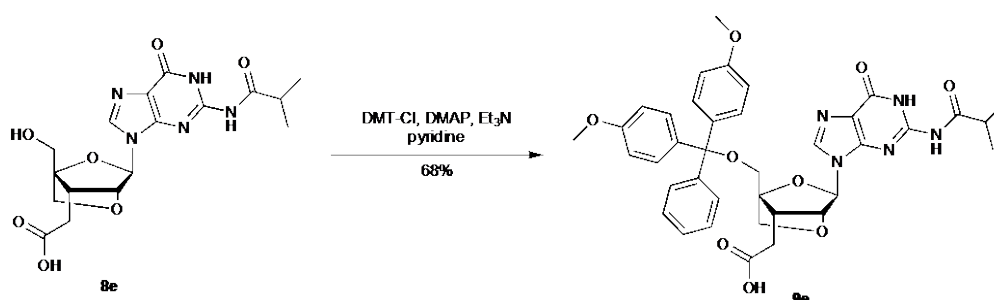
¹H NMR (500 MHz, DMSO-d₆): δ 12.63 (s, 1H), 11.27 (s, 1H), 8.78 (s, 1H), 8.60 – 8.55 (m, 1H, pyridine), 8.48 (s, 1H), 8.08 – 8.02 (m, 2H), 7.78 (tt, J = 7.6, 1.9, 0.5H, pyridine), 7.68 – 7.61 (m, 1H), 7.55 (t, J = 7.7, 2H), 7.43 – 7.22 (m, 10H, includes pyridine), 6.90 – 6.85 (m, 4H), 6.14 (s, 1H), 4.81 (s, 1H), 3.84 (d,

$J = 8.5, 1\text{H}$), 3.77 (d, $J = 8.5, 1\text{H}$), 3.73 (s, 6H), 3.47 (d, $J = 11.2, 1\text{H}$), 3.44 (d, $J = 11.2, 1\text{H}$), 2.73 (dd, $J = 9.7, 4.2, 1\text{H}$), 2.24-2.16 (m, 1H), 2.08 (dd, $J = 16.8, 4.2, 1\text{H}$);

^{13}C NMR (126 MHz, $\text{d}_6\text{-DMSO}$): δ 173.2, 165.7, 158.2, 151.8, 151.4, 150.4, 149.6 (pyridine), 144.6, 140.8, 133.3, 136.1 (pyridine), 135.2, 135.2, 133.4, 132.5, 129.8, 129.7, 128.5, 128.5, 127.9, 127.6, 126.9, 126.8, 125.6, 123.9 (pyridine), 113.3, 88.8, 85.7, 85.6, 80.0, 71.8, 59.5, 55.0, 41.6, 29.2;

HRMS (m/z): $[\text{M}+\text{H}]^+$ calcd. for $\text{C}_{41}\text{H}_{38}\text{O}_8\text{N}_5^+$, 728.2711; found, 728.2715.

5'-*O*-DMT N^2 -isobutrylguanine LNA acid **9e**



Compound **8e** (41 mg, 0.10 mmol) was dissolved in pyridine (1.7 mL) and Et_3N (0.023 mL, 0.17 mmol, 1.7 eq) and activated 3 Å molecular sieves were added. The solution was stirred at room temperature for 15 min before DMAP (6.7 mg, 0.05 mmol, 0.5 eq) and DMT-Cl (85 mg, 0.25 mmol, 2.5 eq) were added. The reaction was left to stir at room temperature for 16 h. The molecular sieves were removed by filtration and the organic solvents removed under vacuum. The resulting residue was purified by column chromatography (5-15% MeOH in EtOAc with a constant additive of 2% pyridine) to yield **9e** (52 mg). Rather than risk degradation, the final product was not evaporated to complete dryness and was stored and used with 0.65 eq of pyridine present (as determined by NMR), making the final yield 68%.

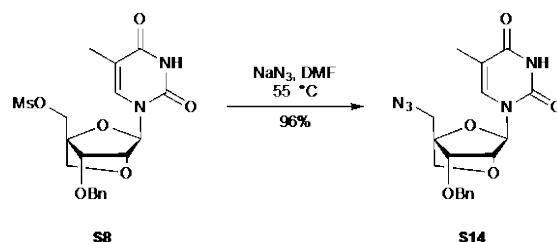
TLC (EtOAc:MeOH, 3:7 v/v, + 2% Et_3N) R_f : 0.53;

^1H NMR (500 MHz, DMSO-d_6): δ 8.97 – 8.40 (m, 1.2 H, pyridine), 8.11 (s, 1H), 7.91 – 7.56 (m, 0.6 H, pyridine), 7.39 – 7.34 (m, 3.4H, with 1.4H from pyridine), 7.30 (dd, $J = 8.6, 6.9, 2\text{H}$), 7.29 – 7.17 (m, 5H), 6.93 – 6.84 (m, 4H), 5.85 (s, 1H), 4.71 (s, 1H), 3.76 (d, $J = 8.4, 1\text{H}$), 3.73 (s, 6H), 3.71 (d, $J = 8.4, 1\text{H}$), 3.41 (d, $J = 11.1, 1\text{H}$), 3.31 (d, $J = 11.1, 1\text{H}$), 3.16 (s, 1H, MeOH), 2.79 (p, $J = 6.9, 1\text{H}$), 2.67 (dd, $J = 10.2, 3.9, 1\text{H}$), 2.10 – 1.94 (m, 2H), 1.11 (dd, $J = 6.9, 1.9, 6\text{H}$);

^{13}C NMR (126 MHz, $\text{d}_6\text{-DMSO}$): δ 180.2, 175.1 (broad), 158.2, 154.9, 148.4, 148.0, 144.7, 136.0, 135.2, 135.1, 129.7, 127.9, 127.6, 126.8, 120.4, 113.3, 113.3, 88.7, 85.6, 85.1, 80.1, 71.9, 59.5, 55.1, 42.5, 34.7, 30.4, 18.9, 18.9;

HRMS (m/z): $[\text{M}+\text{H}]^+$ calcd. for $\text{C}_{40}\text{H}_{34}\text{O}_9\text{N}_5^+$, 710.2821; found 710.2817.

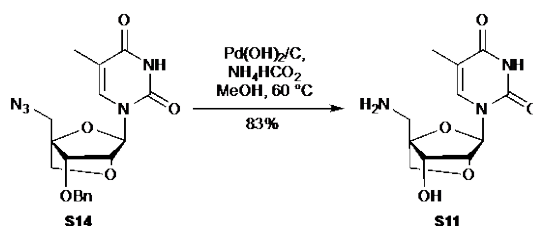
N₃ Thymine LNA **S14**¹



Compound **S14** was prepared based on a similar procedure outlined by Thorpe *et al.*¹ Compound **S8**² (3.5 g, 8.0 mmol) and NaN₃ (1.04 g, 16 mmol, 2 eq) were dissolved in DMF (40 mL) and the reaction was stirred at 50 °C for 5 h. Sodium azide is potentially explosive if handled in correctly. The solvent was removed under vacuum and the resulting residue was partitioned between EtOAc (40 mL) and water (40 mL). The organic layer was washed with water (2 x 40 mL), dried over Na₂SO₄, and evaporated to dryness to yield **S14** (2.96 g, 7.7 mmol) as a white solid in 96% yield which was used without purification. If required the compound can be purified by column chromatography (50-100% EtOAc in 40-60 PE).

Data consistent with literature¹.

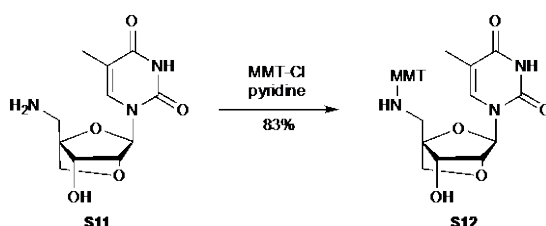
Amino thymine LNA **S11**¹



Compound **S11** (2.0 g, 5.2 mmol) and ammonium formate (4.0 g, 63 mmol, 12 eq) were dissolved in MeOH (100 mL) and 20 wt% palladium hydroxide on carbon (0.36 g, 0.52 mmol, 10 mol%) was added. The flask was flushed with argon and the reaction was stirred at 60 °C for 4 h. A large volume of gas is generated within the first hour of the reaction presenting a risk of over-pressurisation. The reaction was filtered through celite to remove the catalyst and the solvent was removed under vacuum. The resulting solid was purified by column chromatography (0-30% MeOH in EtOAc) to give **S11** (1.17 g, 4.3 mmol) as a white solid in 83% yield.

Data consistent with literature¹.

5'-N-MMT thymine LNA **S12**³



Amine **S11** (1.17 g, 4.3 mmol) was dissolved in anhydrous pyridine (50 mL) and 4-methoxytriphenylmethyl chloride (1.6 g, 5.2 mmol, 1.2 eq) was added in small portions. The reaction

was stirred at room temperature for 2 h before the solvents were removed under vacuum. The resulting residue was purified by column chromatography (0-30% EtOAc in 40-60 PE with a constant additive of 0.1% pyridine) to give **S12** (1.93 g, 3.6 mmol) as a pale-yellow foam in 83% yield.

TLC (EtOAc:hexane, 3:2 v/v, + 0.5% pyridine) R_f : 0.5;

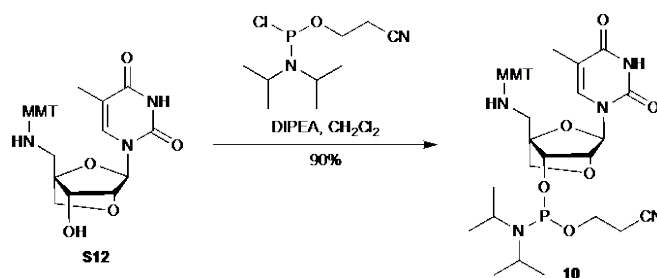
^1H NMR (400 MHz, CDCl_3): δ 9.32 (s, 1H), 7.65 (s, 1H), 7.48 – 7.45 (m, 4H), 7.38 – 7.37 (m, 2H), 7.29 – 7.24 (m, 4H), 7.17 (t, J = 7.3, 2H), 6.81 (d, J = 9.0, 2H), 5.61 (s, 1H), 4.46 (s, 1H), 4.26 (s, 1H), 4.00 (br s, 1H), 3.92 (d, J = 8.3, 1H), 3.78 (d, J = 8.2, 1H), 3.74 (s, 3H), 2.65 – 2.49 (m, 2H), 2.09 (t, J = 8.5, 1H), 1.92 (d, J = 1.2, 3H).

^{13}C NMR (101 MHz, CDCl_3): δ 164.1, 158.3, 150.0, 145.9, 145.8, 137.4, 134.7, 129.9, 128.5, 128.2, 126.8, 113.5, 110.5, 88.8, 87.2, 79.8, 72.7, 70.7, 70.4, 55.4, 40.2, 12.8;

HRMS (m/z): $[\text{M}+\text{Na}]^+$ calcd. for $\text{C}_{31}\text{H}_{31}\text{O}_6\text{N}_3\text{Na}^+$, 564.2105, found, 564.2103;

No spectroscopic data reported previously³.

5'-*N*-MMT thymine LNA phosphoramidite **10**³



Nucleoside **10** (1.1 g, 2.0 mmol) was dissolved in anhydrous degassed CH_2Cl_2 (10 mL). Degassed *N,N*-diisopropylethylamine (DIPEA) (883 μL , 5.1 mmol, 2.5 eq) and 2-cyanoethyl *N,N*-diisopropylchlorophosphoramidite (677 μL , 3.0 mmol, 1.5 eq) were added and the reaction was stirred under an argon atmosphere at room temperature for 2 h. The reaction mixture was diluted with CH_2Cl_2 (40 mL) and washed with a saturated aqueous solution of KCl (30 mL). The organic phase was dried over Na_2SO_4 and the solvents were removed under vacuum. The resulting pale-yellow oil was purified by column chromatography (40% EtOAc in hexane with a constant additive of 0.5% pyridine) to give the phosphoramidite **10** (1.3 g, 1.8 mmol) as a white foam in 90% yield.

TLC (EtOAc:hexane, 2:3 v/v, + 0.5% pyridine) R_f : 0.4;

^{31}P NMR (162 MHz, CDCl_3): δ 148.7, 148.3

HRMS (m/z): $[\text{M}-\text{H}]^-$ calcd. for $\text{C}_{40}\text{H}_{47}\text{O}_7\text{N}_5\text{P}^-$, 740.3219; found 740.3219.

Oligonucleotide synthesis

DNA synthesis and cleavage

DNA synthesis was performed on an Applied Biosystems 394 automated DNA/RNA synthesiser using a standard phosphoramidite cycle of detritylation, coupling, capping (unless stated elsewhere), and oxidation on a 1.0 μ mole scale. Trichloroacetic acid (TCA) (3% in CH_2Cl_2) was used for detritylation, 5-benzylthio-1*H*-tetrazole (BTT) (0.25 M in MeCN) was used as an activator, and oxidation was achieved using iodine (0.02 M in THF, pyridine and water). Pre-packed nucleoside SynBase™ CPG 1000/110 (Link Technologies) were used and β -cyanoethyl phosphoramidite monomers (dA(Bz), dG(iBu), dC(Bz) and dT, Sigma-Aldrich) were dissolved in anhydrous MeCN (0.1 M) immediately prior to use with coupling time of 50 s. LNA β -cyanoethyl phosphoramidite monomers (QIAGEN) were dissolved to a concentration of 0.1 M in either MeCN (LNA-T) or 25% THF/MeCN (LNA-mC(Bz)) immediately prior to use with a coupling time of 6 min. Stepwise coupling efficiencies were determined by automated trityl cation conductivity monitoring and were >98% in all cases. Cleavage and deprotection were achieved by exposure to concentrated aqueous ammonia solution for 60 min at room temperature followed by heating in a sealed tube for 5 h at 55 °C.

RNA synthesis and cleavage

RNA synthesis was performed on an Applied Biosystems 394 automated DNA/RNA synthesiser using a standard phosphoramidite cycle of detritylation, coupling, capping, and oxidation on a 1.0 μ mole scale. Coupling, capping and oxidation reagents were identical to those used for DNA synthesis except a solution of ethylthiotetrazole (ETT) (0.25 M in MeCN, Link Technologies) was used instead of BTT as the activator. Standard CPG resin (Link Technologies) was used and 2'-thiomorpholine-4-carbothioate (TC) protected monomers (A(Bz), C(Ac), G(iBu) and U, Sigma-Aldrich) were dissolved in anhydrous toluene/MeCN (1:1 v/v, 0.1 M) immediately prior to use. The coupling time for all monomers was 3 min. Stepwise coupling efficiencies were determined by automated trityl cation conductivity monitoring and in all cases were >97%. To deprotect and cleave the RNA, the solid support was exposed to dry ethylenediamine:toluene (1:1 v/v) for 6 h at room temperature, washed with toluene (3 x 1 mL), then MeCN (3 x 1 mL) and dried using argon. The cleaved RNA was eluted from the solid support with water.

2'OMe phosphodiester oligonucleotide synthesis and cleavage

2'OMe oligonucleotides were synthesised on an Applied Biosystems 394 automated DNA/RNA synthesiser using a standard phosphoramidite cycle of detritylation, coupling (unless otherwise stated), capping, and oxidation on a 1.0 μ mole scale. Detritylation, coupling, capping, oxidation and activation reagents are identical to those used for DNA synthesis. Pre-packed nucleoside SynBase™ CPG 1000/110 (Link Technologies) were used, and β -cyanoethyl phosphoramidite monomers (DMT-2'-O-Methyl-rA(Bz), DMT-2'-O-Methyl-rG(iBu), DMT-2'-O-Methyl-rC(Ac) and DMT-2'-O-Methyl-rU, Sigma-Aldrich) were dissolved in anhydrous MeCN (10% CH_2Cl_2 was added when 2'OMe U phosphoramidite was used) to a concentration of 0.1 M immediately prior to use with a coupling time of 6 min. LNA β -cyanoethyl phosphoramidite monomers (QIAGEN) were dissolved to a concentration of 0.1 M in either MeCN (LNA-T) or 25% THF/MeCN (LNA-mC(Bz)) immediately prior to use with a coupling time of 6 min. Stepwise coupling efficiencies were determined by automated trityl cation conductivity monitoring and were >98% in all cases. Cleavage and deprotection were achieved by exposure to concentrated aqueous ammonia solution for 60 min at room temperature followed by heating in a sealed tube for 5 h at 55 °C.

Phosphodiester oligonucleotide purification

Oligonucleotides were purified using a Gilson reverse-phase high performance liquid chromatography (RP-HPLC) system with ACE® C8 column (particle size: 10 μ m, pore size: 100 Å, column dimensions: 10 mm x 250 mm) with a gradient of buffer A (0.1 M TEAB, pH 7.5) to buffer B (0.1 M TEAB, pH 7.5

containing 50% v/v MeCN) and flow rate of 4 mL/min. The gradient of MeCN in triethylammonium bicarbonate (TEAB) was increased from 0% to 50% buffer B over 30 min. Elution was monitored by UV absorbance at 298 nm. After HPLC purification, oligonucleotides were freeze dried then dissolved in water without the need for desalting.

Phosphorothioate oligonucleotide synthesis, cleavage and purification

Oligonucleotides with a phosphorothioate rather than a phosphodiester backbone were synthesised as described above, except for a solution of 3-ethoxy-1,2,4-dithiazoline-5-one (EDITH, Link Technologies) in MeCN (0.05 M) was used as a sulfurising reagent in place of the oxidising solution. The sulfurisation time was extended to 3 min followed by sending fresh EDITH to the synthesis column and leaving it for another 3 min. Phosphorothioate modified oligonucleotides were isolated with the final 5'-DMT protecting group still in place (DMT-On). Following solid phase synthesis, the cyanoethyl groups were removed by a 15 min treatment with 20% diethylamine in MeCN. The resin was then washed with MeCN (5 x 1 mL) and dried by passing a stream of argon through the synthesis column. The oligonucleotides were cleaved from the solid support and deprotected by heating in a sealed glass vial at 55 °C for 5 h. The ammonia was removed under reduced pressure prior to oligonucleotide purification. The DMT-On oligonucleotides were purified by RP-HPLC and lyophilised. They were then dissolved in 0.5 mL of 80% acetic acid and incubated for 1 h at room temperature to remove the DMT group. The solution was neutralised with 0.5 mL of triethylammonium acetate buffer (2 M, pH 7) and the detritylated oligonucleotides were desalted using a NAP-10 column (Cytiva) then freeze dried.

Oligonucleotide analysis

All oligonucleotides were characterised by negative-mode ultra-performance liquid chromatography (UPLC) mass spectrometry using a Waters Xevo G2-XS QT of mass spectrometer with an Acquity UPLC system, equipped with an Acquity UPLC oligonucleotide BEH C18 column (particle size: 1.7 µm; pore size: 130 Å; column dimensions: 2.1 mm x 50 mm). Data were analysed using Waters MassLynx software or Waters UNIFI Scientific Information System software.

Synthesis of oligonucleotides containing single or multiple LNA-amides, phosphodiester/phosphorothioates and LNA/2'-OMe/deoxyribose sugars

B' = A^{bz}, G^{ibu}, C^{bz}, 5-MeC^{bz}, T

B = A, G, C, 5-MeC, T

R = H or OMe or LNA bridge

MMT = 4-monomethoxytrityl

DMT = 4,4'-dimethoxytrityl

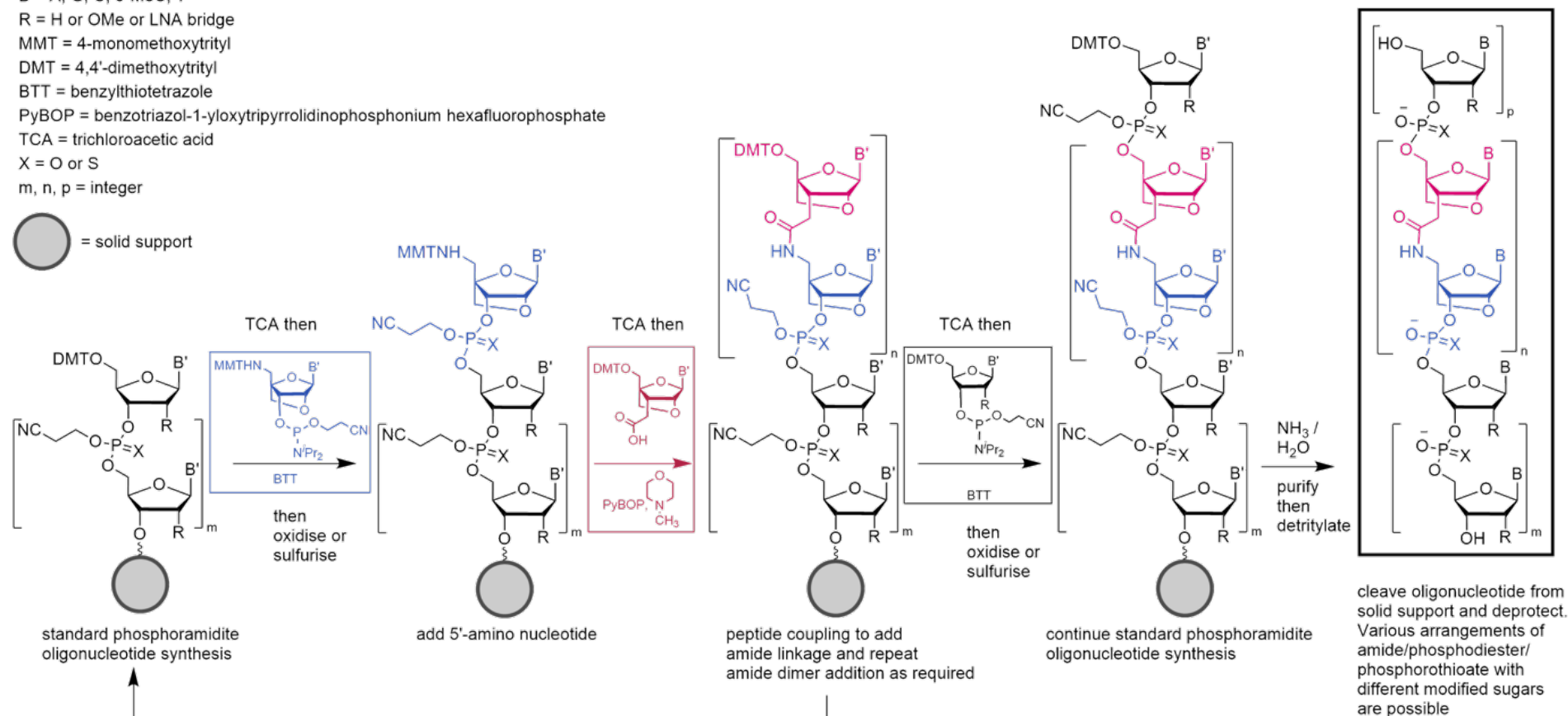
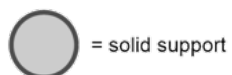
BTT = benzylthiotetrazole

PyBOP = benzotriazol-1-yloxytripyrrolidinophosphonium hexafluorophosphate

TCA = trichloroacetic acid

X = O or S

m, n, p = integer



Schematic overview of LNA amide modified oligonucleotide synthesis. Protocols for individual steps are outlined below.

LNA-amide modified oligonucleotide synthesis

Oligonucleotide segment synthesis

Oligonucleotide segments were synthesised as described, except that the capping step was omitted.

Amino monomer addition

The MMT-protected 5'-amino phosphoramidite monomer (either LNA **10**³ or commercially available deoxythymidyl **11**) was dissolved in anhydrous MeCN (0.1 M) immediately prior to use. The same conditions as above were used, but the coupling time was extended to 10 min. No capping step was used. The 5'-MMT protecting group was cleaved on the Applied Biosystems 394 automated synthesiser using TCA (3% in CH₂Cl₂) with an extended cleavage time of 2 min. The solid support was then washed with MeCN on the synthesiser for 3 min. To improve the coupling efficiency in the next step the solid support was washed with *N*-methylmorpholine in DMF (0.5% v/v, 1 mL) followed by DMF (3 x 1 mL).

Amide bond formation on resin (peptide coupling)

All amide couplings were performed manually in the synthesis column. A solution with 10 equivalents of acid monomer, 10 equivalents of PyBOP and 30 equivalents of *N*-methylmorpholine was first prepared in 400 µL of DMF. This was then taken up into a 1 mL syringe and loaded into the column before a second 1 mL syringe was attached to the other end of the synthesis column. The mixture was agitated every 10 min for 1 h. The columns were then washed with DMF (3 x 1 mL) followed by MeCN (5 x 1 mL) and dried by passing argon through the column. The column was then returned to the synthesiser to continue oligonucleotide synthesis.

Cleavage of oligonucleotides from resin, deprotection and purification

LNA-amide containing oligonucleotides were isolated with the final 5'-DMT protecting group still in place (DMT-On). Following solid phase synthesis, the cyanoethyl groups were removed by a 15 min treatment with 20% diethylamine in MeCN. The resin was then washed with MeCN (5 x 1 mL) and dried by passing a stream of argon through the synthesis column. The oligonucleotides were cleaved from the solid support and deprotected by heating in concentrated aqueous ammonia solution in a sealed glass vial at 55 °C for 5 h. The ammonia was removed under reduced pressure prior to oligonucleotide purification. The DMT-On oligonucleotides were purified by RP-HPLC. The elution of oligonucleotides was monitored by UV absorbance at 298 nm. The oligonucleotides were lyophilised and then dissolved in 0.5 mL of 80% acetic acid, and incubated for 1 h at room temperature to remove the DMT group. The solution was neutralised with 0.5 mL of triethylammonium acetate buffer (2 M, pH 7) and the detritylated oligonucleotides were desalted using a NAP-10 column (Cytiva), then freeze dried.

Biophysical studies

UV melting experiments

UV melting experiments were performed using a Cary 4000 scan UV-vis spectrophotometer. 3 nmol of each oligonucleotide was dissolved in 1 mL of 10 mM phosphate buffer containing 200 mM NaCl at pH 7.0. The samples were first denatured by heating to 85 °C (10 °C/min) and then annealed by slowly cooling to 20 °C (1 °C/min). Six successive cycles of heating and cooling were performed at a gradient of 1 °C/min whilst recording the change in UV absorbance at 260 nm. The built-in software was then used to calculate the melting temperature from the first derivative of the melting curve.

Oligonucleotide X-Ray crystallography

Crystallisation

DNA and RNA oligonucleotides were purified by HPLC, desalted by gel filtration (NAP-10) and then freeze dried. Oligonucleotide stock solutions (2 mM) were prepared in aqueous KCl (10 mM). DNA samples were combined with an equimolar ratio of complementary RNA to form their respective modified DNA:RNA hybrids to form 1 mM duplex (60 μ L). Single crystals of the DNA:RNA duplexes were obtained by the sitting drop vapour diffusion method. The Natrix HT sparse matrix screen (Hampton Research, HR2-131) was used to identify crystallisation hits for each modified duplex sample using high throughput (HT) methods. All HT screens were performed in CrystalMation Intelli-Plate 96-3 low-profile plates (Hampton Research, HR3-119). Reservoirs and drops were dispensed using an Art Robbins Phoenix automatic liquid handler. Reservoirs contained 80 μ L of Natrix HT solution and crystallisation drops (200 - 300 nL total volume) were placed in each of the three subwells; subwell 1, 200 nL oligo : 100 nL well solution; subwell 2, 100 nL oligo : 100 nL well solution; subwell 3, 100 nL oligo : 200 nL well solution (stock duplex concentration was 1 mM). Plates were sealed using optically clear Xtra-Clear Advanced Polyolefin StarSeal (StarLab) and incubated at 19 °C, crystals usually formed within one week (range 2-90 days, crystal size < 10 - 200 μ m). The unmodified DNA:RNA duplex was crystallised using adapted conditions from Kopka *et al.*⁴ Optimisation of these conditions were done in 24 well Cryschem sitting drop plates (Hampton Research, USA) using 4 μ L sitting drops consisting of 0.5 mM duplex, 12 mM Mg(OAc)₂, 0.6 mM spermidine.HCl, 0.075% (w/v) β -octylglucoside, 12 mM sodium cacodylate and 12% 2-methyl-2,4-pentanediol (MPD). This was equilibrated against a reservoir of H₂O:MPD (1:1 v/v, 400 μ L). To screen conditions, components of the drop were varied (6-16 mM Mg(OAc)₂, 0.2-1.2 mM spermidine.HCl, 0.075% (w/v) β -octylglucoside, 12 mM sodium cacodylate and 6-16% MPD. All other structures were obtained using hits from the NatrixHT screen (Hampton Research, USA). All samples were crystallised at 19 °C using the conditions outlined in Table S6.

Data collection and processing

Sample wells were opened and cryo protectant 20% glycerol in reservoir solution (2 μ L) was added. Crystals were harvested using cryoloops (0.01-0.05 mm) and immediately cryo-cooled by plunging into liquid N₂ (77 K), transferred into a cryo-vial and stored under liquid nitrogen at 77 K until data collection. Data collection was performed at Diamond Light Source (beamlines i03 or i04) or DESY in Hamburg (beamline P13). The high radiation damage resistance of the oligo duplex crystals permitted 100% beam transmission. Oscillation images (3600 images, 0.1 ° osc) were collected. The detector distance was set to obtain a maximum resolution of 0.5 Å greater than the expected diffraction limit to maximise spot separation (see Table S5) and reduce overlapping reflections and obtain maximal completeness. Data were auto processed using either fast_dp⁵, xia2_dials⁶ or xia2_3dii⁷. CC_{1/2} > 0.3 and completeness > 90%, crystal data quality was reviewed using Phenix.Xtriage. ON26^{xDNA}, ON29^{xDNA-Am-DNA}, and ON29^{xLNA-Am-DNA} duplexes all crystallised in the high symmetry space group *P* 6₁ and contained a single DNA:RNA hybrid in the asymmetric unit. In contrast, the ON30^{xLNA-Am-LNA} duplex was in the lower symmetry Space Group *P* 3₂21 with two DNA:RNA hybrids in each asymmetric unit.

Structure solution, model building and refinement

The structures were solved using the Molecular Replacement method and 1PJO PDB ID as the search model⁸,⁹ using PHASER 2.8.2¹⁰. Structure solutions resulted in TFZ score > 8.0 and LLG > 50 and correct solution was confirmed by visual inspection of electron density maps. The DNA:RNA models (some with modified backbone) were built and fit to the electron density using winCOOT¹¹. Model refinement was performed using REFMAC5¹² and PHENIX.REFINE¹³. Geometric restraints for the non-standard phosphoribosyl backbones were generated using JLIGAND⁸ or ACEDRG¹⁴. Model building continued until the observed electron density was satisfied and the R_{free} no longer decreased. Software packages and project management was handled using CCP4¹⁵ and Phenix¹³. Images were made using PYMOL graphic software (The PyMOL Molecular Graphics System, Version 2.3.2 Schrödinger, LLC).

Where necessary, data were reprocessed to achieve acceptable final statistics (i.e. $CC \frac{1}{2} > 0.3$). Reprocessing was performed using iMosflm, XDS or in-house using automated xia2 pipelines⁷. The data were then scaled and merged using Aimless¹⁶.

Biological assays

Evaluation of stability in fetal bovine serum (FBS)

Five nmol of each oligonucleotide was dissolved in Dulbecco's PBS (50 μ L) and FBS (50 μ L, Gibco, standard sterile-filtered) was added. The sample was mixed by pipetting and 20 μ L of this solution was immediately removed, mixed with formamide (20 μ L), snap frozen in liquid N₂, and stored at -80°C as a control (0 h). The remaining reaction mixtures were incubated at 37°C and aliquots (20 μ L) were taken at different time intervals, mixed with formamide (20 μ L), snap frozen in liquid N₂ and stored at -80°C . The samples were then analysed by denaturing 20% polyacrylamide gel.

Cell culture

HeLa pLuc/705 cells¹⁷ were cultured in Dulbecco's Modified Eagle Medium with GlutaMAX-I (Gibco) supplemented with 10% (v/v) FBS (Gibco) and 1 x Antibiotic-Antimycotic (Gibco) at 37°C in a humidified incubator with 5% CO₂.

Transfection with Lipofectamine 2000

Cells were seeded at a density of 7000 cells/well in 100 μ L of culture media in 96 well plates 16 h before transfection to reach 70-80% cell confluency. Immediately prior to transfection, 5 μ L of Lipofectamine 2000 (Invitrogen) was diluted in 500 μ L OptiMEM (Gibco) and incubated at room temperature for 5 min before mixing with 4 pmol of lyophilised oligonucleotide dissolved in 500 μ L of OptiMEM. The resulting mixture was incubated at room temperature allowing complexation to occur. The complexes were then further diluted in OptiMEM to the concentrations required for the experiments. Culture media was removed from the cells and 100 μ L of the complexes added per well. The cells were then incubated at 37°C in a humidified incubator with 5% CO₂. After 4 h the media was replaced with 100 μ L of culture media and the cells were returned to the incubator for a further 20 h.

Gymnosis experiments

Cells were seeded at a density of 800 cells/well in 100 μ L in culture media in 96 well plates 16 h before the oligonucleotides were added. Lyophilised oligonucleotides were dissolved in OptiMEM immediately before addition to the cells. The media in each well was removed and replaced with 100 μ L of the oligonucleotide containing OptiMEM. The cells were then incubated for 96 h at 37°C in a humidified incubator with 5% CO₂.

Luciferase assay

The culture media was removed from the well and the cells were washed with 200 μ L of PBS. 100 μ L of GloLysisTM buffer (Promega) was added to each well. The plate was incubated at room temperature on the orbital shaker for 10 min to lyse the cells. 50 μ L of the cell lysate was added to 50 μ L of Bright-GloTM luciferase reagent (Promega) in a white 96 well plate and the luminescence was measured using a Clariostar plate reader. 25 μ L of the cell lysate was then used for protein quantification using a Pierce BCA protein assay kit in accordance with the manufacturer's guidelines, using GloLysis buffer as a blank standard. The luminescence values were divided by the total protein quantities and normalised to the values for untreated cells.

WST-1 cell viability assay

The cell viability was evaluated using the WST-1 cell proliferation reagent (Roche) in accordance with the manufacturer's guidelines. Briefly, cells were seeded, transfected using Lipofectamine 2000, and the media was changed to culture media after 4 h, as described above. The cells were then incubated for 20 h at 37°C in a humidified incubator with 5% CO₂ before WST-1 reagent (10 μ L) was added to each well. The cells were returned to the incubator for 4 h. The cells were shaken at 500 rpm for 1 min before 10 μ L of media was

removed from each well and added to a clear 96 well plate containing 90 μ L of water in each well and the absorbance at 440 nm was measured using a ClarioStar plate reader. This dilution step was necessary as the absorbance went above the accurate range of the instrument. Cells that were treated with OptiMEM instead of the oligonucleotide complexes were used as a 100% viability reference.

Supplementary tables

Table S1. List of oligonucleotides (ONs) used in this study with calculated and found mass spectrometry (MS) data. UPLC-MS traces for all ONs are given (Supplementary Fig. 3-7 and Fig. 26-36).

ON	Sequence (5' → 3')	Backbone	Expected	Found
<i>Single amide addition UV melting studies</i>				
ON1 ^{DNA-Am-DNA}	CGACGCT* <u>T</u> GCAGC	DNA	3896.7	3897.0
ON2 ^{LNA-Am-DNA}	CGACGCT* <u>T</u> GCAGC	DNA	3924.8	3925.0
ON3 ^{DNA-Am-LNA}	CGACGCT* <u>T</u> GCAGC	DNA	3924.8	3925.0
ON4 ^{LNA-Am-LNA}	CGACGCT* <u>T</u> GCAGC	DNA	3952.9	3953.0
ON5 ^{LNA-LNA}	CGACGCT <u>T</u> GCAGC	DNA	3995.5	3992.0
ON6 ^{DNA-DNA}	CGACGCTTGCAGC	DNA	3935.5	3936.0
<i>Single amide addition UV melting targets</i>				
ON7	GCTGCAAGCGTCG	DNA	3975.5	3976.0
ON8	GCUGCAAGCGUCG	RNA	4155.2	4156.5
ON9	GCUGCA <u>C</u> GCGUCG	RNA	4131.2	4132.0
ON10	GCUGC <u>C</u> AGCGUCG	RNA	4131.2	4132.0
ON11	GCUGCA <u>G</u> GCGUCG	RNA	4171.2	4171.5
ON12	GCUGC <u>G</u> AGCGUCG	RNA	4171.2	4172.4
<i>Multiple amide addition in different backbones</i>				
ON13 ^{DNA/1LAL/16PO}	CCTCTTAC <u>C</u> * <u>T</u> CAGTTACA	DNA, PO	5386.8	5387.5
ON14 ^{DNA/4LAL/13PO}	<u>C</u> * <u>T</u> <u>C</u> * <u>T</u> AC <u>C</u> * <u>T</u> CAG <u>T</u> * <u>T</u> ACA	DNA, PO	5438.7	5439.0
ON15 ^{DNA/17PO}	CCTCTTACCTCAGTTACA	DNA, PO	5369.6	5370.0
ON16 ^{2'OMe/4LAL/13PO}	<u>C</u> ^{Me} <u>C</u> * <u>T</u> <u>C</u> * <u>T</u> AC ^{Me} <u>C</u> * <u>T</u> CAG <u>T</u> * <u>T</u> ACA	2'OMe, PO	5766.9	5767.0
ON17 ^{2'OMe/17PO}	CCUCUUACCUCAGUUACA	2'OMe, PO	5824.7	5825.0
ON18 ^{2'OMe/4LAL/13PS}	<u>C</u> ^{Me} <u>C</u> * <u>T</u> <u>C</u> * <u>T</u> AC ^{Me} <u>C</u> * <u>T</u> CAG <u>T</u> * <u>T</u> ACA	2'OMe, PS	5976.2	5975.5
ON19 ^{2'OMe/8LNA/17PS}	<u>C</u> ^{Me} <u>C</u> <u>T</u> <u>T</u> AC ^{Me} <u>C</u> <u>T</u> CAG <u>T</u> <u>T</u> ACA	2'OMe, PS	6193	6195.7
ON20 ^{2'OMe/17PS}	CCUCUUACCUCAGUUACA	2'OMe, PS	6096.3	6097.6
<i>Multiple amide addition in different backbones UV melting targets</i>				
ON21	TGTAAGTGAAGTAAGAGG	DNA	5627.6	5628.5
ON22	UGUAACUGAGGUAAAGAGG	RNA	5858.9	5859.0
ON23	AGGTAAGAGG	DNA	3141.0	3141.5
ON24	AGGUAAGAGG	RNA	3286.8	3288.0
<i>Additional digestion oligonucleotide</i>				
ON25 ^{DNA/8LNA/17PO}	<u>C</u> ^{Me} <u>C</u> <u>T</u> <u>T</u> AC ^{Me} <u>C</u> <u>T</u> CAG <u>T</u> <u>T</u> ACA	DNA	5621.6	5622.8
<i>XRD oligonucleotides</i>				
ON26 ^{xDNA}	CTTTCTTTG	DNA	2974.9	2976.0
ON27 ^{xRNA}	CAAAGAAAAAG	RNA	3238.0	3240.0
ON28 ^{xDNA-Am-DNA}	CTT*TTCTTTG	DNA	2936.1	2937.0
ON29 ^{xLNA-Am-DNA}	CT <u>T</u> *TTCTTTG	DNA	2964.2	2964.5
ON30 ^{xLNA-Am-LNA}	CT <u>T</u> * <u>T</u> CTTTG	DNA	2992.3	2992.5
<i>Scrambled control splice-switching oligonucleotide</i>				
ON31 ^{2'OMe/17PS scrambled}	CCUCAUUCACUCGAUUA	2'OMe, PS	6096.3	6099.7
<i>Oligonucleotides in the supplementary information</i>				
ONS1	CGACGC <u>C</u> * <u>T</u> GCAGC	DNA	3937.8	3938.5
ONS2	CGACGC ^{Me} <u>C</u> * <u>T</u> GCAGC	DNA	3951.9	3953.0
ONS3	CGACGC <u>A</u> * <u>T</u> GCAGC	DNA	3961.9	3963.0
ONS4	CGACGC <u>G</u> * <u>T</u> GCAGC	DNA	3977.9	3978.5

Underlined red bases indicates a locked sugar; * is an amide bond in place of a phosphodiester, underlined blue bases indicates the position of the mismatch. Backbone denotes to the chemistry of inter-sugar linkages and the sugars not flanking an amide bond.

Table S2. Comparison of the melting temperatures of duplexes containing a single amide substitution of the phosphodiester backbone flanked by LNA on the 5', 3' or both sides within a DNA backbone hybridised to DNA or RNA.

ON	Sequence	DNA match	RNA match	RNA 5' C	RNA 3' C	RNA 5' G	RNA 3' G
		T_m (ΔT_m)	T_m (ΔT_m)	mismatch	mismatch	mismatch	mismatch
		ON7	ON8	T_m (ΔT_m) ON9	T_m (ΔT_m) ON10	T_m (ΔT_m) ON11	T_m (ΔT_m) ON12
ON1 ^{DNA-Am-DNA}	CGACGCT* <u>T</u> GCAGC	61.2 (-2.3)	61.0 (-0.4)	47.0 (-14.1)	50.2 (-10.8)	57.3 (-3.7)	56.6 (-3.4)
ON2 ^{LNA-Am-DNA}	CGACGC <u>T</u> *TGCAGC	63.1 (-0.3)	64.4 (+3.0)	50.2 (-14.2)	51.0 (-13.4)	58.5 (-5.9)	60.3 (-4.1)
ON3 ^{DNA-Am-LNA}	CGACGCT* <u>I</u> GCAGC	60.9 (-2.5)	63.9 (+2.5)	50.1 (-13.8)	52.5 (-11.4)	58.8 (-5.1)	56.9 (-7.0)
ON4 ^{LNA-Am-LNA}	CGACGC <u>I</u> * <u>I</u> GCAGC	63.4 (-0.1)	66.5 (+5.1)	53.3 (-13.2)	55.1 (-11.4)	59.8 (-6.7)	60.5 (-6.0)
ON5 ^{LNA-LNA}	CGACGC <u>I</u> <u>I</u> GCAGC	69.6 (+6.1)	74.1 (+12.7)	59.7 (-14.4)	59.9 (-14.2)	68.6 (-5.5)	67.3 (-2.3)
ON6 ^{DNAcontrol}	CGACGCTTGCAGC	63.5	61.4	46.2 (-15.2)	51.2 (-10.2)	57.4 (-4.0)	57.4 (-4.0)

T_m values were measured using 3.0 μ M concentrations of each oligonucleotide strand in 10 mM phosphate buffer (pH 7.0) containing 200 mM NaCl. I indicates a locked sugar and * is an amide bond in place of a phosphodiester. T_m values were calculated as the maximum of the first-derivative of the melting curve (A_{260} vs T) and reported as the average of at least two independent experiments. ΔT_m for matched sequences = modified – ON6^{DNAcontrol}; ΔT_m for mismatched = Match - RNA mismatch. Target ON sequences, where X denotes the mismatch. ON7 = GCTGCAAGCGTCG; ON8 = GCUGCAAGCGUCG; ON9 = GCUGCAGCGUCG; ON10 = GCUGCCAGCGUCG; RNA ON11 = GCUGCAGGCGUCG. ON12 = GCUGCGAGCGUCG. Representative melting curves are given (Supplementary Fig. S8-13).

Table S3. Comparison of the relative melting temperatures of duplexes containing 0, 1 or 4 amide linkages flanked by LNA on both sides hybridised to DNA or RNA.

ON	Sequence (5' → 3')	backbone	DNA T_m (ΔT_m)	RNA T_m (ΔT_m)
a				
ON13 ^{DNA/1LAL/16PO}	CCTCTTAC <u>C</u> TICAGTTACA	DNA, PO	60.9 (+1.8)	65.8 (+2.2)
ON14 ^{DNA/4LAL/13PO}	<u>C</u> * <u>C</u> * <u>T</u> * <u>T</u> * <u>I</u> ACC <u>C</u> * <u>T</u> CAG <u>I</u> * <u>T</u> ACA	DNA, PO	64.2 (+5.1)	76.6 (+13.0)
ON15 ^{DNA/17PO}	CCTCTTACCTCAGTTACA	DNA, PO	59.1	63.6
b				
ON14 ^{DNA/4LAL/13PO}	<u>C</u> * <u>C</u> * <u>T</u> * <u>T</u> * <u>I</u> ACC <u>C</u> * <u>T</u> <i>cag</i> <u>I</u> * <i>t</i> aca	DNA, PO	46.5 (+7.0)	64.3 (+17.5)
ON15 ^{DNA/17PO}	CCTCTTACCT <i>cagttaca</i>	DNA, PO	39.5	46.8
c				
ON16 ^{2'OMe/4LAL/13PO}	<u>C</u> ^{Me} * <u>C</u> * <u>T</u> * <u>T</u> * <u>I</u> AC <u>C</u> ^{Me} * <u>T</u> <i>cag</i> <u>I</u> * <i>t</i> aca	2'OMe, PO	53.2 (+19.1)	72.3 (+9.3)
ON17 ^{2'OMe/17PO}	CCUCUUACCU <i>caguuaca</i>	2'OMe, PO	34.1	63.0
d				
ON18 ^{2'OMe/4LAL/13PS}	<u>C</u> ^{Me} * <u>C</u> * <u>T</u> * <u>T</u> * <u>I</u> AC <u>C</u> ^{Me} * <u>T</u> <i>cag</i> <u>I</u> * <i>t</i> aca	2'OMe, PS	48.1 (+25.4)	67.4 (+10.3)
ON19 ^{2'OMe/8LNA/17PS}	<u>C</u> ^{Me} <u>CT</u> <u>CT</u> <u>TT</u> AC <u>C</u> ^{Me} <u>CT</u> <i>cag</i> <u>tt</u> <i>t</i> aca	2'OMe, PS	59.0 (+36.3)	>80
ON20 ^{2'OMe/17PS}	CCUCUUACCU <i>caguuaca</i>	2'OMe, PS	22.7	57.1

Experimental conditions as in Table S2. **a** = comparison of DNA ONs against full length targets, **b** = comparison of DNA ONs against 10-mer targets, **c** = comparison of 2'OMe/PO ONs, **d** = comparison of 2'OMe/PS ONs. Backbone: PO = phosphodiester, PS = phosphorothioate, DNA = deoxyribose sugars, 2'OMe = 2'OMe RNA sugars. X indicate a locked sugar and * indicates an amide bond in place of a phosphodiester, LAL indicates the number of LNA-flanked amide bonds. DNA target (ON21) = TGTAAGTGGTAAGAGG; RNA target (ON22) = UGUUACUGAGGUAAGAGG. Truncated DNA target (ON23) = AGGTAAGAGG. Truncated RNA target (ON24) = AGGUAAGAGG. ΔT_m = modified – control. Bases in lower case italic remain single stranded on duplex formation and do not contribute to T_m . Representative melting curves are given (Supplementary Fig. 14-17).

Table S4. Sequences of oligonucleotides used in crystallographic studies.

ON	Sequence (5' → 3')	backbone
ON26 ^{xDNA}	CTTTTCTTTG	DNA
ON27 ^{xRNA}	CAAAGAAAAG	RNA
ON28 ^{xDNA-Am-DNA}	CTT*TTCTTTG	DNA
ON29 ^{xLNA-Am-DNA}	CT <u>I</u> *TTCTTTG	DNA
ON30 ^{xLNA-Am-LNA}	CT <u>I</u> * <u>I</u> TTCTTTG	DNA

I indicates a locked sugar and * indicates an amide bond in place of a phosphodiester.

Table S5. Summary of data processing for XRD structures of DNA:RNA hybrids containing amide and LNA modifications. Data was validated using pdb validation. Each dataset was collected from a single crystal, values shown in parenthesis are for the highest resolution shell.

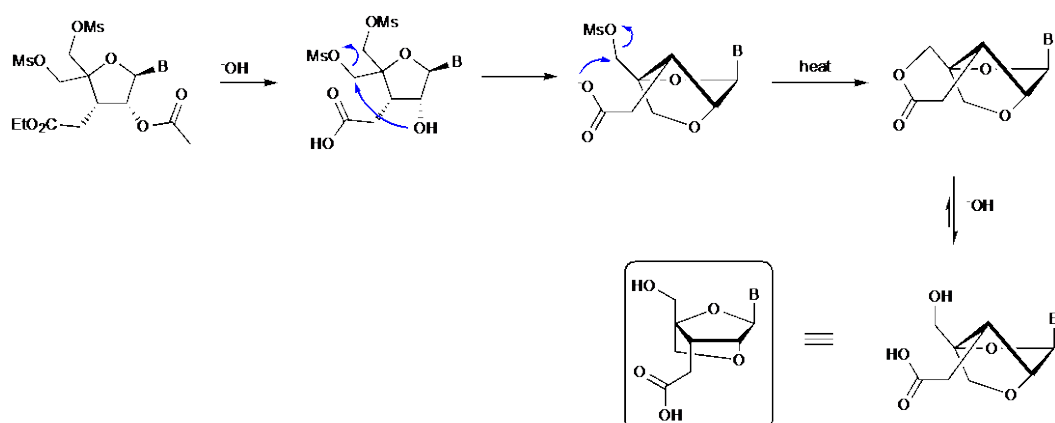
Data collection	ON26 ^{xDNA} :ON27 ^{xRNA}	ON28 ^{xDNA-Am-DNA} : ON27 ^{xRNA}	ON29 ^{xLNA-Am-DNA} : ON27 ^{xRNA}	ON30 ^{xLNA-Am-LNA} : ON27 ^{xRNA}
PDB ID	7NRP	7OOS	7OZZ	7OOO
Space group	<i>P</i> 6 ₁	<i>P</i> 6 ₁	<i>P</i> 6 ₁	<i>P</i> 3 ₂ 21
Cell dimensions				
<i>a</i> , <i>b</i> , <i>c</i> / Å	53.34, 53.34, 45.88	55.14, 55.14, 45.96	54.12, 54.12, 48.84	49.15, 49.15, 90.96
α , β , γ / °	90.00 90.00 120.00	90.00 90.00 120.00	90.00 90.00 120.00	90.00 90.00 120.00
Detector distance / cm	19.8	48.5	48.5	17.0
Exposure time per image / s	0.090	0.038	0.056	0.040
Resolution (Å)	27.17-2.67 (2.80-2.67)	47.75-2.60 (2.70-2.60)	27.06-2.70 (2.77-2.70)	31.08-2.56 (2.63-2.56)
No. unique reflections	2243	2517	2283	4398
<i>R</i> _{meas}	0.081 (1.776)	0.121 (1.124)	0.055 (1.816)	0.078 (3.673)
<i>I</i> / σ (<i>I</i>)	25.2 (1.7)	8.9 (2.2)	23.0 (1.1)	19.8 (0.8)
<i>CC</i> _{1/2}	0.996 (0.646)	0.943 (0.645)	0.999 (0.421)	0.999 (0.329)
Completeness /%	98.8 (97.0)	99.9 (100.0)	99.9 (92.6)	99.4 (94.2)
Multiplicity	19.3 (16.0)	7.5 (7.1)	9.7 (9.0)	18.7 (18.5)
Refinement				
Resolution / Å	27.17-2.67 (2.76-2.67)	47.75-2.60 (2.69-2.60)	27.06-2.70 (2.79-2.70)	31.08-2.56 (2.65-2.56)
No. reflections	2226	2502	2267	4349
<i>R</i> _{work} / <i>R</i> _{free}	0.170, 0.191	0.218, 0.234	0.200, 0.237	0.237, 0.261
No. atoms / ASU	422	419	416	837
DNA	197	196	198	434
RNA	217	217	217	400
Mg ²⁺	-	-	-	2
As	1	-	-	-
Sr ²⁺	-	2	-	-
K ⁺	-	-	1	-
Ligand atoms	7	4	-	1
Wilson <i>B</i> factor (Å ²)	75.0	68.0	102.1	95.1
r.m.s. deviations				
Bond lengths / Å	0.009	0.005	0.007	0.008
Bond angles / °	1.20	0.53	0.76	0.94
r.m.s.d Unmod / Å	-	0.45	0.42	2.51

Table S6. DNA:RNA duplex crystallisation conditions.

Structure	Conditions	
	Drop solution	Well solution
Unmodified ON26 ^{xDNA} :ON27 ^{xRNA}	0.5 mM duplex 12 mM Mg(OAc) ₂ 0.6 mM spermidine.HCl 0.075% β-octylglucoside 12 mM sodium cacodylate pH 5.8 12% MPD	MPD:H ₂ O, 1:1
Amide ON28 ^{xDNA-Am-DNA} :ON27 ^{xRNA}	0.5 mM duplex 20 mM LiCl 40 mM SrCl ₂ ·6H ₂ O 20 mM sodium cacodylate trihydrate pH 7.0 15% (v/v) MPD 6.0 mM spermine tetrahydrochloride	double the concentration of the drop solution without the oligonucleotide duplex
LNA-amide ON29 ^{xLNA-Am-DNA} :ON27 ^{xRNA}	0.5 mM duplex 40 mM NaCl 6.0 mM KCl 20 mM sodium cacodylate trihydrate pH 7.0 17.5% MPD 6.0 mM spermine tetrahydrochloride	double the concentration of the drop solution without the oligonucleotide duplex
LNA-Am-LNA ON30 ^{xLNA-Am-LNA} :ON27 ^{xRNA}	0.5 mM duplex 40 mM NaCl 6.0 mM KCl 20 mM sodium cacodylate trihydrate pH 6.0 15% (v/v) MPD 6.0 mM spermine tetrahydrochloride	double the concentration of the drop solution without the oligonucleotide duplex

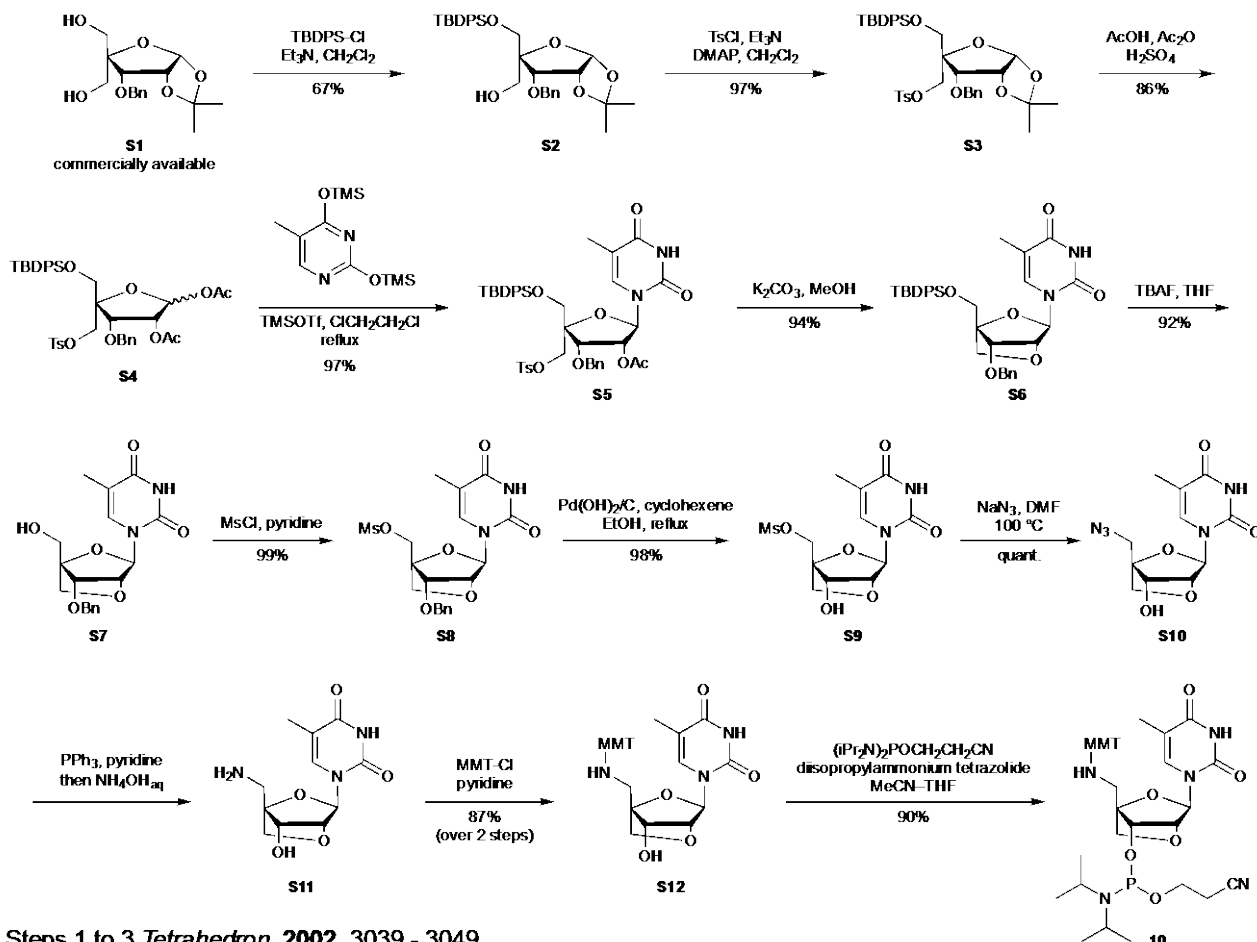
Supplementary figures

Small molecule synthesis supplementary figures

**Figure S1.** Proposed neighbouring group participation accounting for the facile displacement of the 5'-mesyl by a hydroxide. Here the carboxylate displaces the 5'-mesyl forming a lactone which is subsequently opened by hydrolysis.

Obika route

36% yield in 12 steps from commercially available material

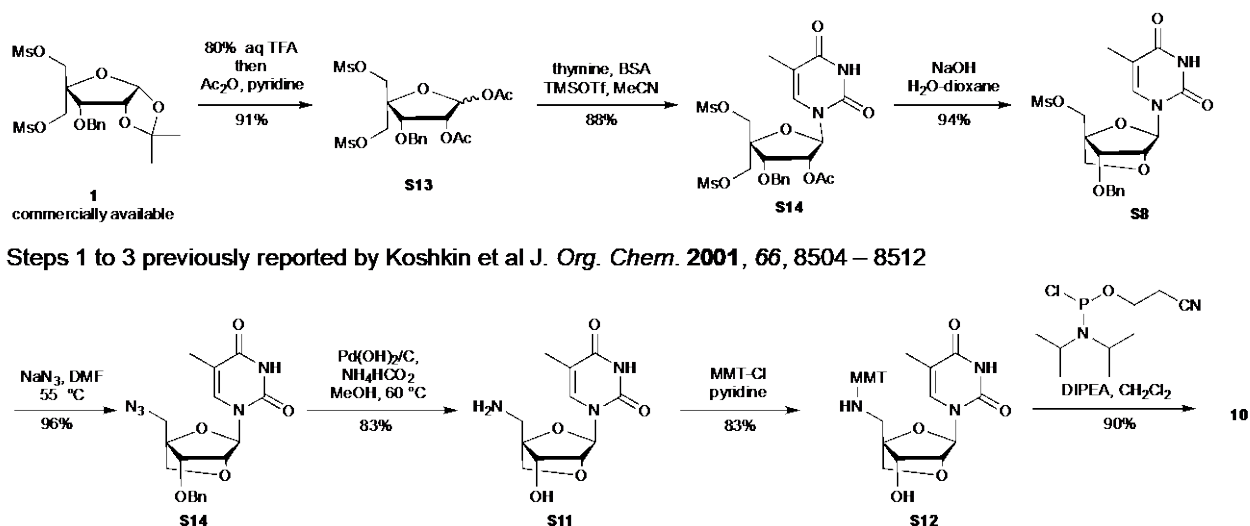


Steps 1 to 3 *Tetrahedron*, **2002**, 3039 - 3049

Steps 4 to 12 *Chem Commun.*, **2003**, 2202 - 2203

Our improved route via Koshkin route to intermediate **S8**

45% overall yield in 7 steps from commercially available starting material



Steps 1 to 3 previously reported by Koshkin et al *J. Org. Chem.* **2001**, *66*, 8504 – 8512

Figure S2. Synthesis route used for 5'-amino LNA phosphoramidite **10** via the synthesis for **S8** reported by Koskin *et al.*² and how it compares with the route previously reported by Obika *et al.*³ We have previously reported the synthesis of **S14** and **S11**¹, but have now reduced the equivalents of NaN₃ from 7 to 2 during the S_N2 step and have identified conditions to reduce the azide and cleave the benzyl in a single step, improving the scalability of the synthesis.

UPLC and MS analysis of oligonucleotides with LNA-amide linkages

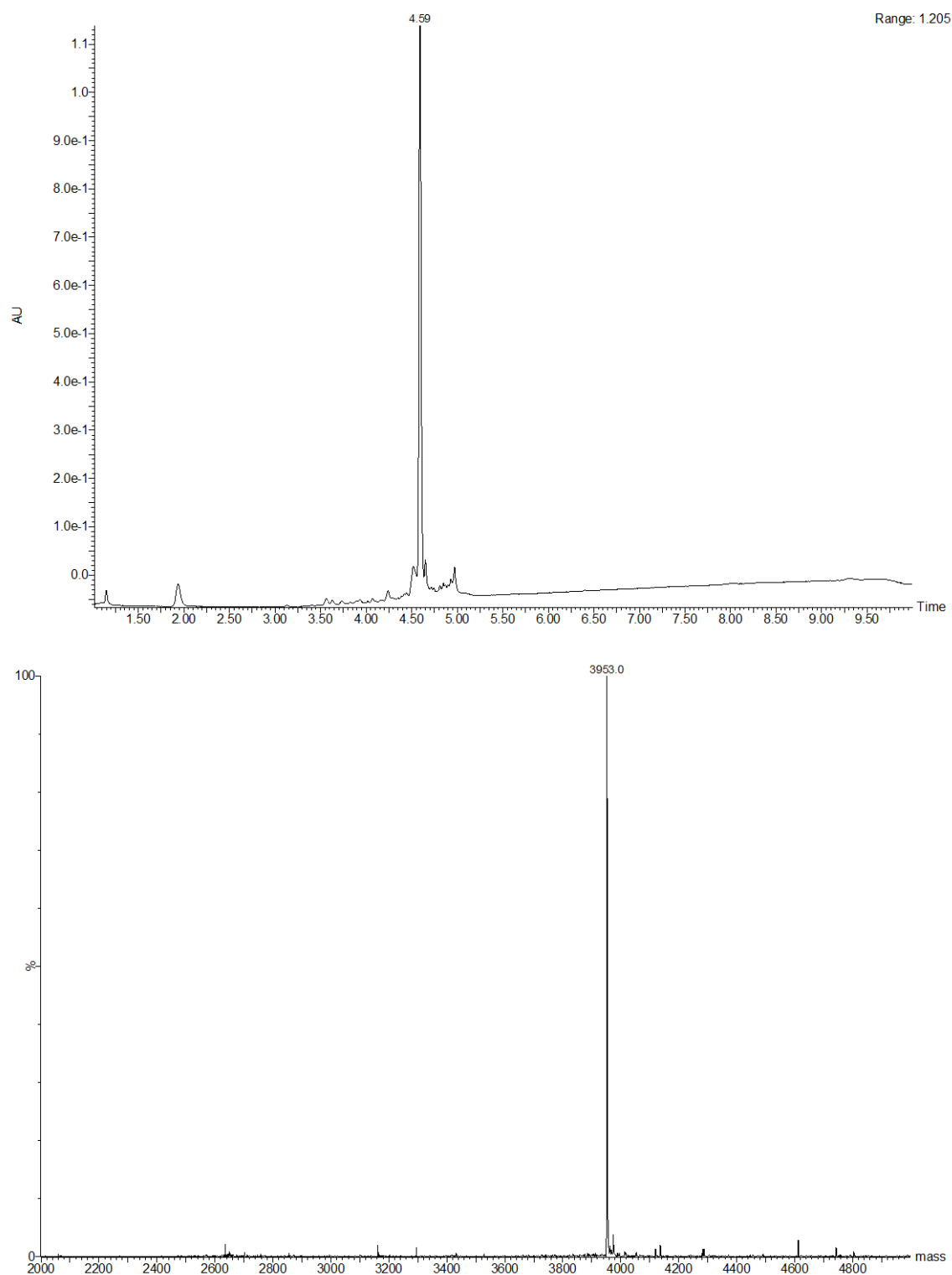


Figure S3. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES^-) of $\text{ON4}^{\text{LNA-Am-LNA}}$ without purification. Required 3952.9 Da, found 3953.0 Da. CGACGCT***T**GCAGC. This demonstrates that compound **9a** is compatible with solid phase oligonucleotide synthesis.

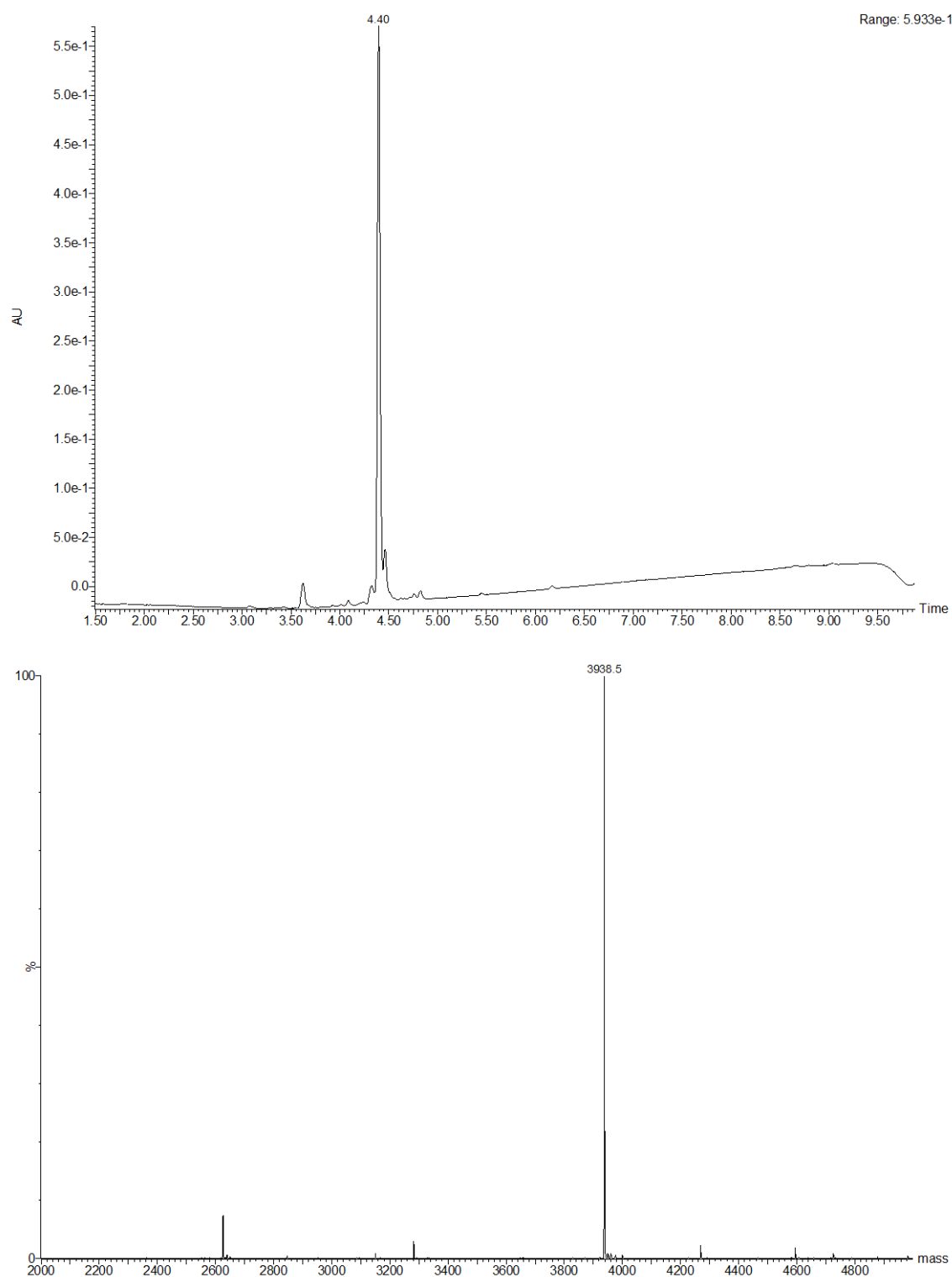


Figure S4. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ONS1 without purification. Required 3937.8 Da, found 3938.5 Da. CGACGCC*IGCAGC. This demonstrates that compound **9b** is compatible with solid phase oligonucleotide synthesis.

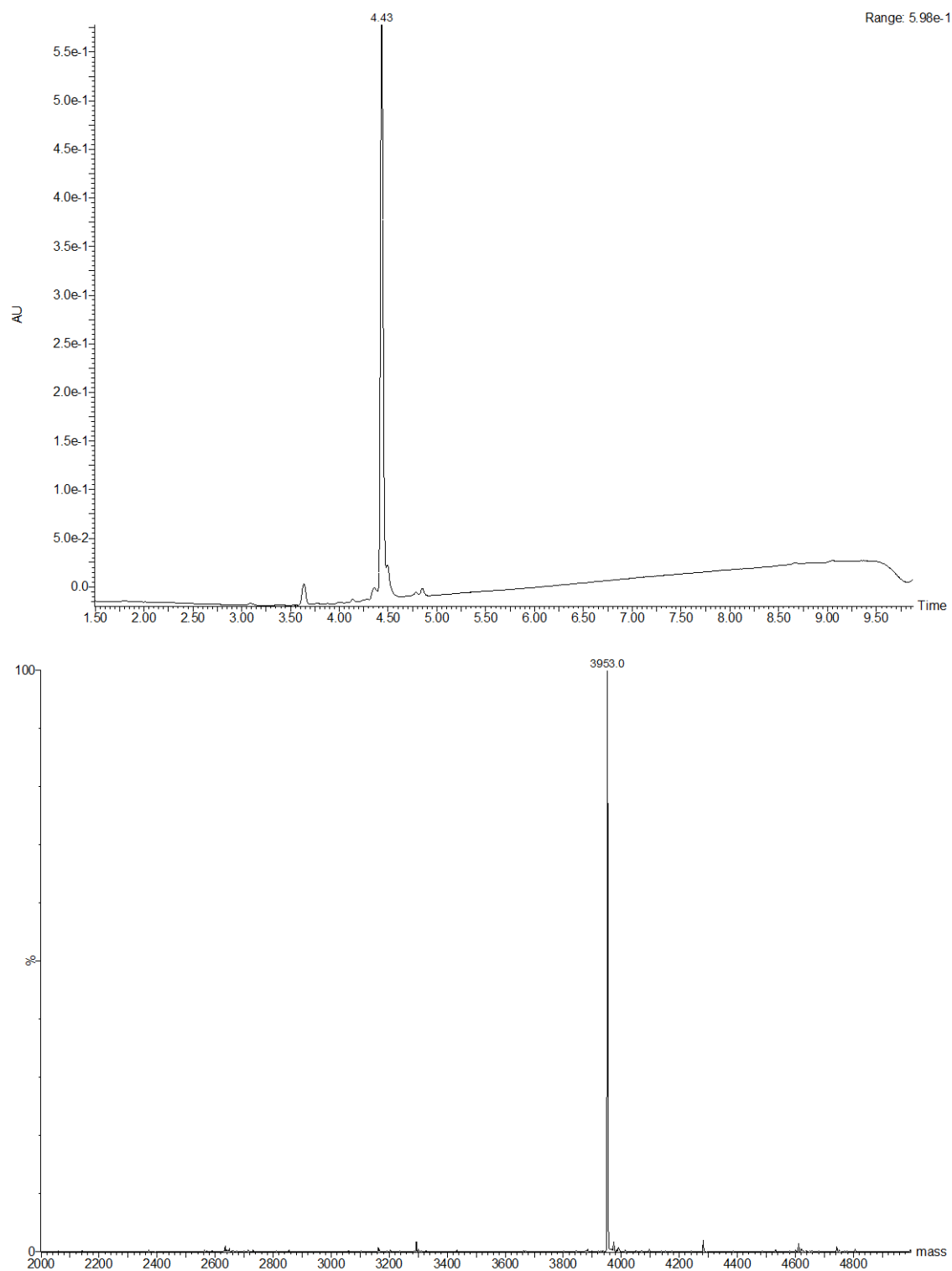


Figure S5. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ONS2 without purification. Required 3951.9 Da, found 3953.0 Da. CGACGC^{Me}C*^TGCAGC. This demonstrates that compound **9c** is compatible with solid phase oligonucleotide synthesis.

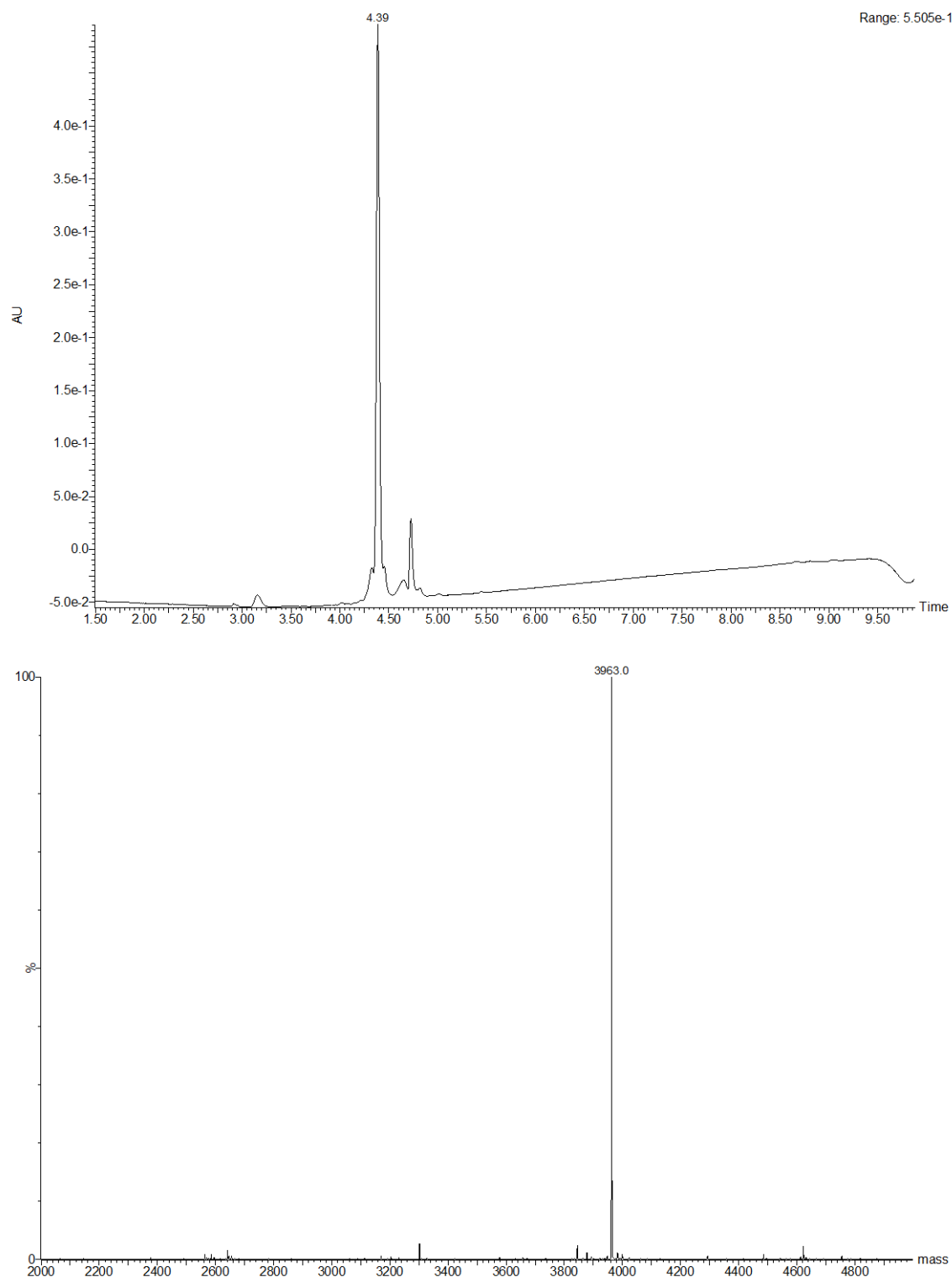


Figure S6. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ONS3 without purification. Required 3961.9 Da, found 3963.0 Da. CGACGC**A*****I**GCAGC. This demonstrates that compound **9d** is compatible with solid phase oligonucleotide synthesis.

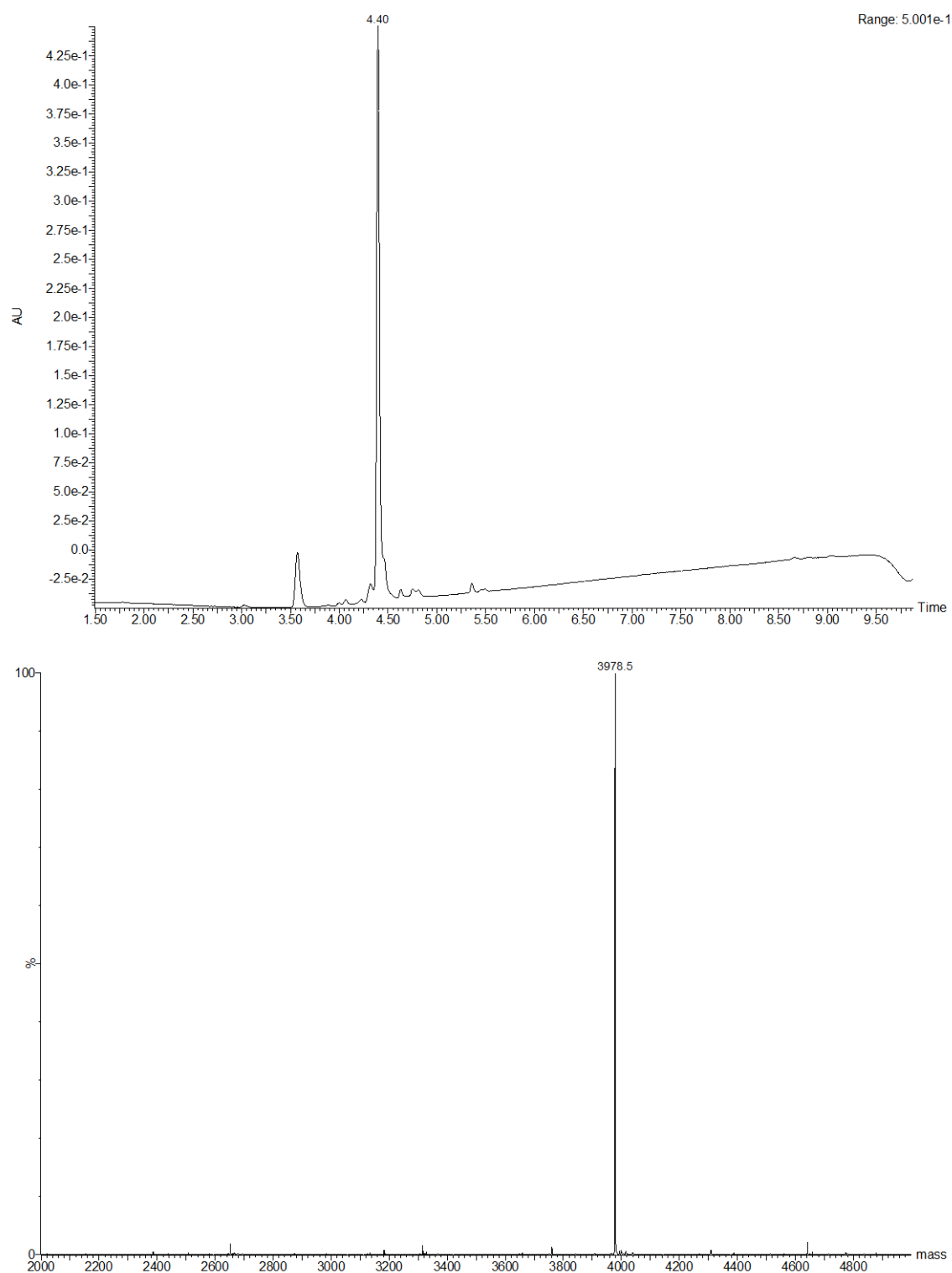


Figure S7. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ONS4 without purification. Required 3977.9 Da, found 3978.5 Da. CGACGCG***I**GCAGC. This demonstrates that compound **9e** is compatible with solid phase oligonucleotide synthesis.

Representative UV melting curves

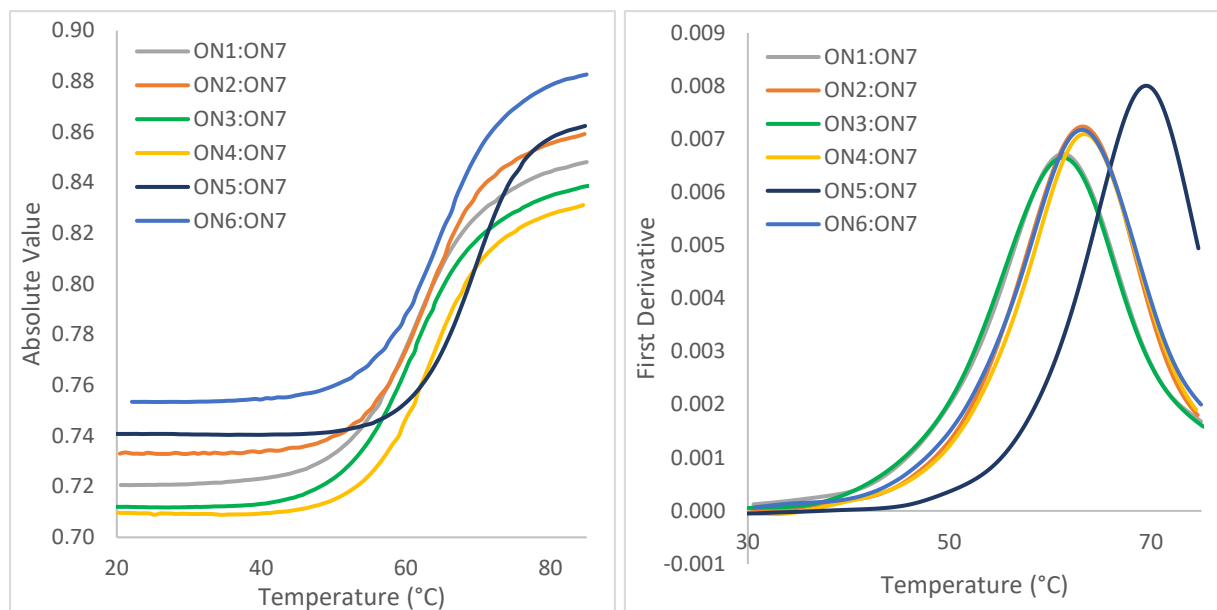


Figure S8. UV melting studies for modified ONs against complementary DNA (ON7) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μM of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

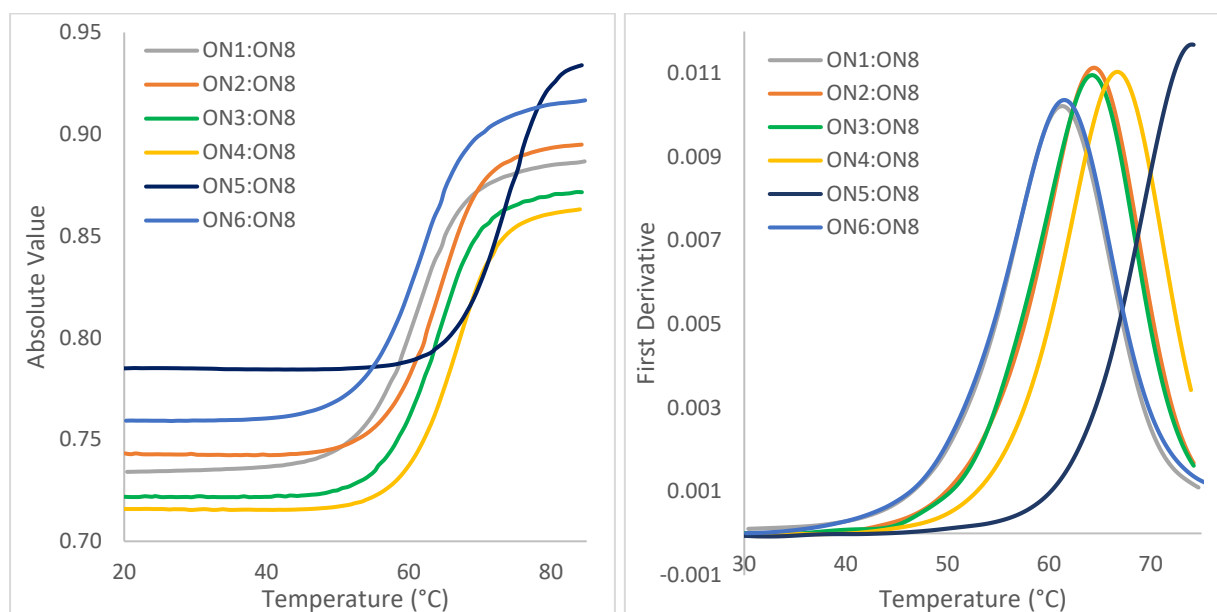


Figure S9. UV melting studies for modified ONs against complementary RNA (ON8) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μM of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

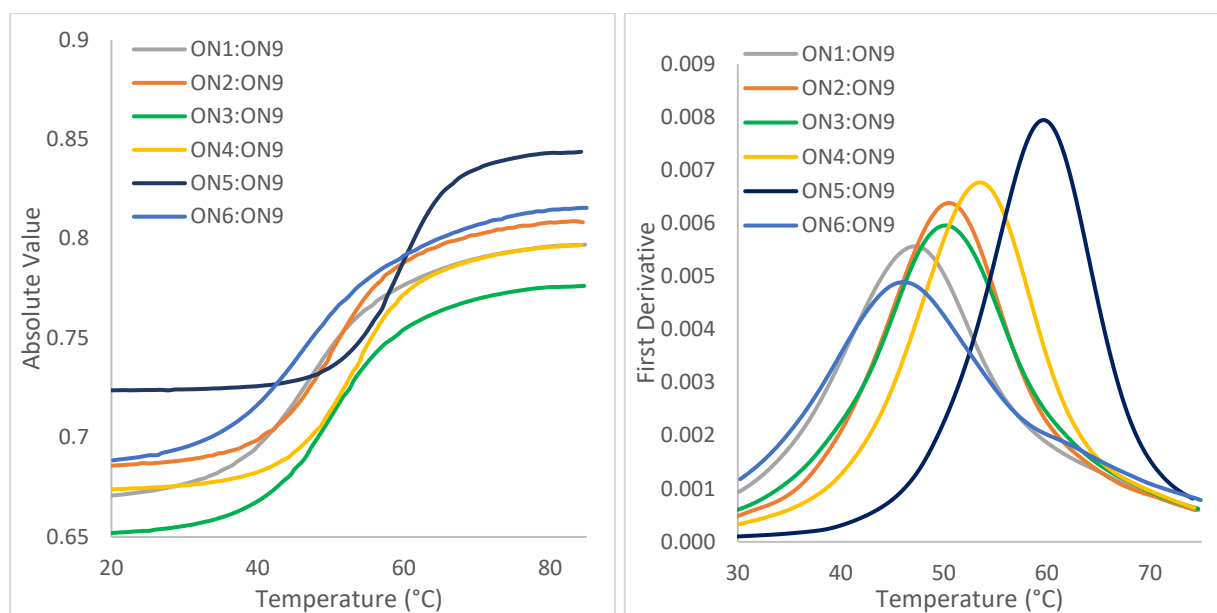


Figure S10. UV melting studies for modified ONs against RNA with a C mismatch 5' of the amide (ON9) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

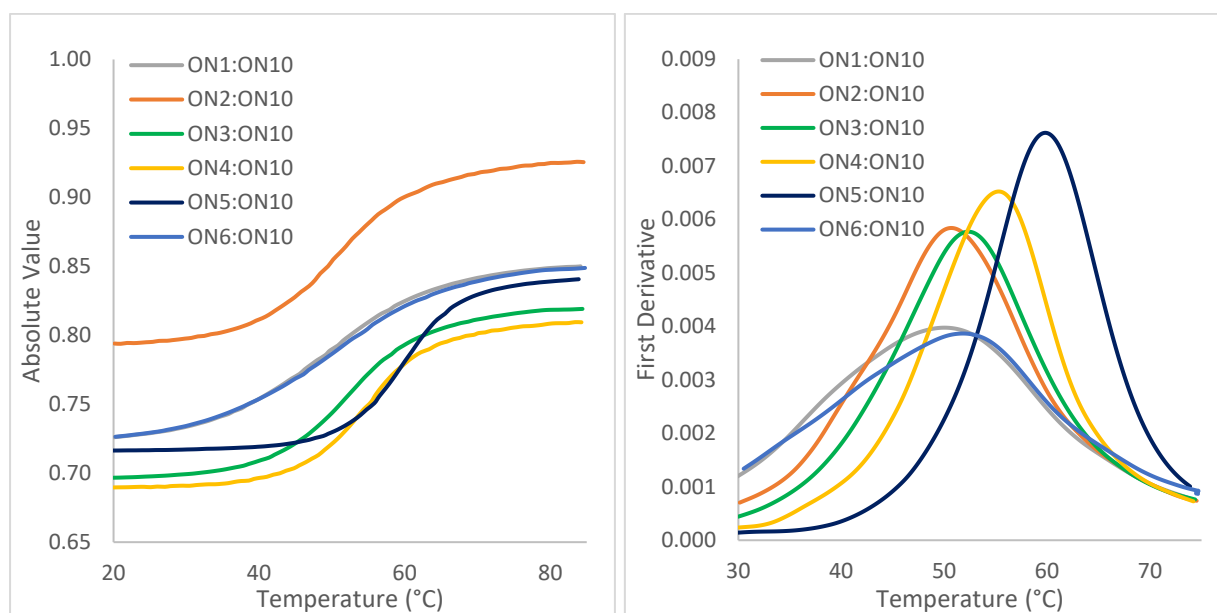


Figure S11. UV melting studies for modified ONs against RNA with a C mismatch 3' of the amide (ON10) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

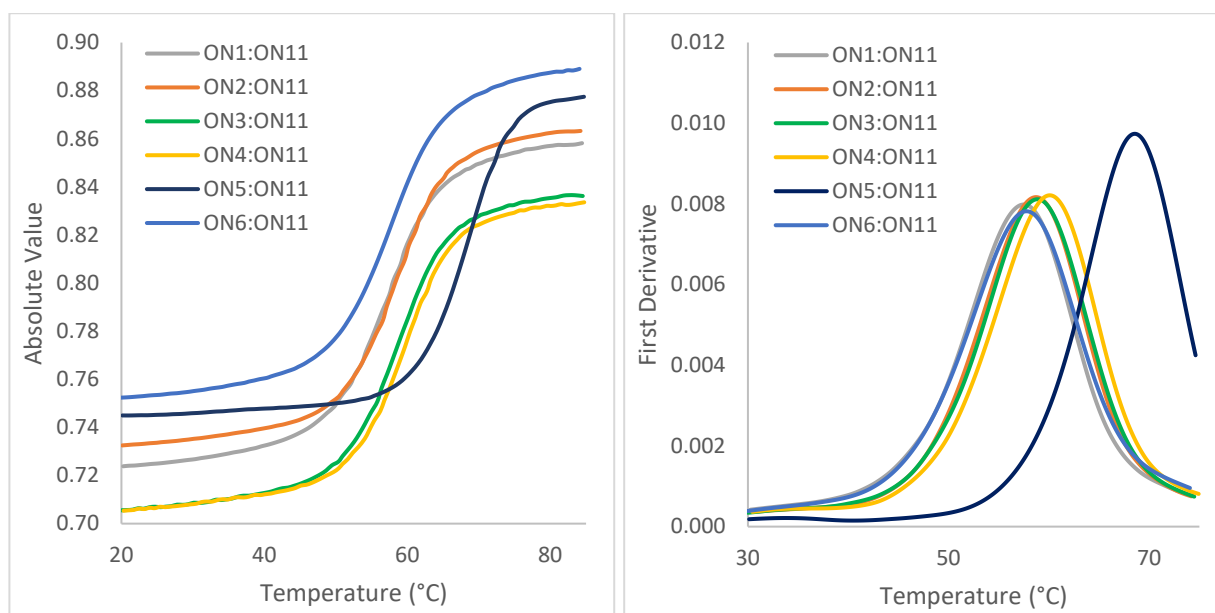


Figure S12. UV melting studies for modified ONs against RNA with a G mismatch 5' of the amide (ON11) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

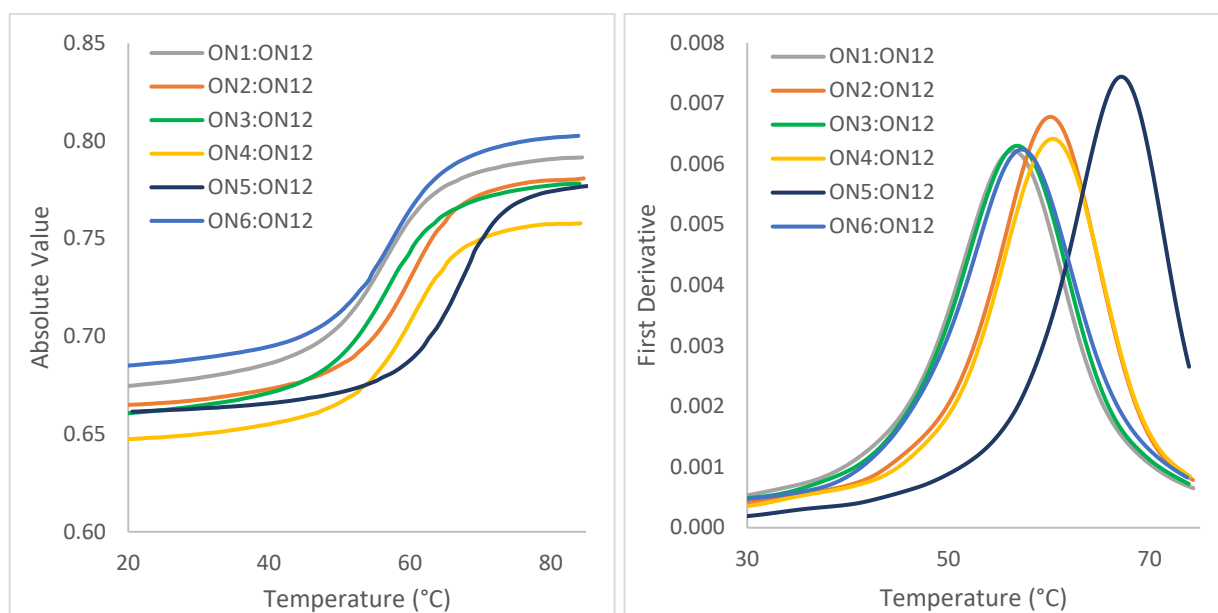


Figure S13. UV melting studies for modified ONs against RNA with a G mismatch 3' of the amide (ON12) (Supplementary Table 2). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

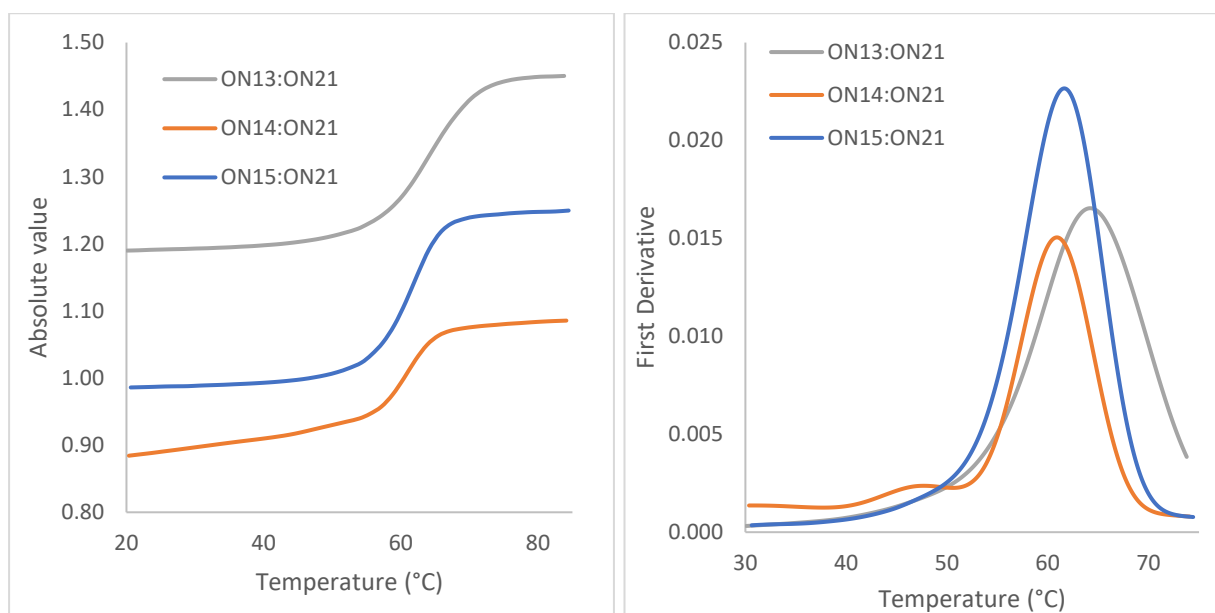


Figure S14. UV melting studies comparing 0, 1 and 4 additions of LNA-amide against a complementary DNA target (ON21) (Supplementary Table 3). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

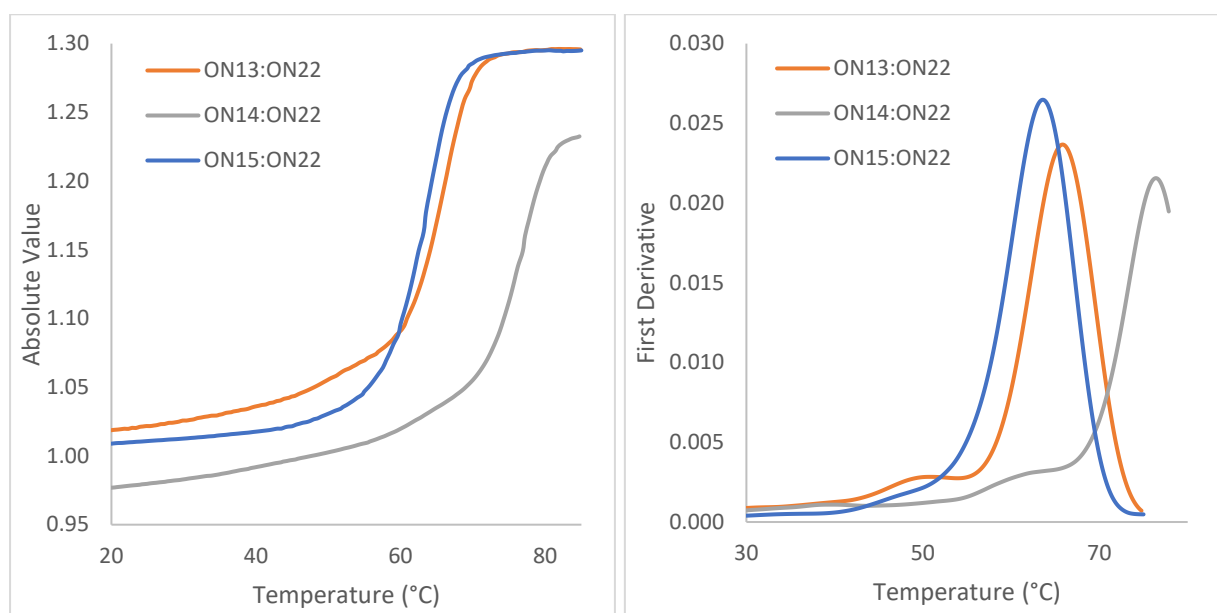


Figure S15. UV melting studies comparing 0, 1 and 4 additions of LNA-amide against a complementary RNA target (ON22) (Supplementary Table 3). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves.

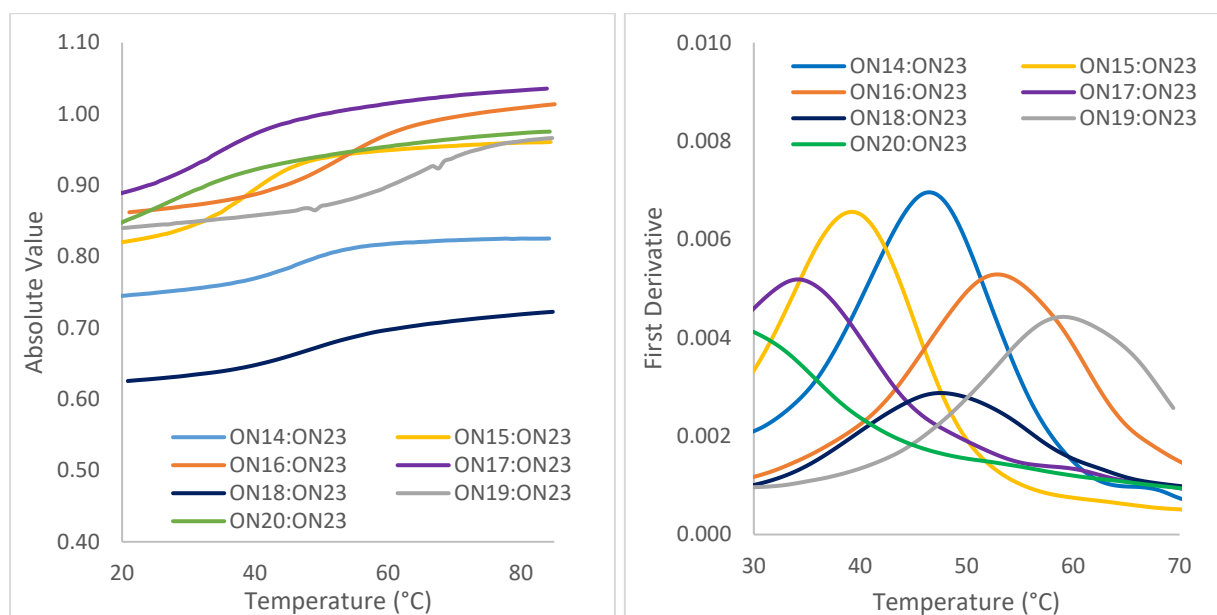


Figure S16. UV melting studies for modified ONs against truncated DNA target ON23 (Supplementary Table 3). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves. The complementary DNA target was truncated so that the melting temperatures were in the range of the instrument. The truncated DNA strand covers the critical modified region of the modified ONs.

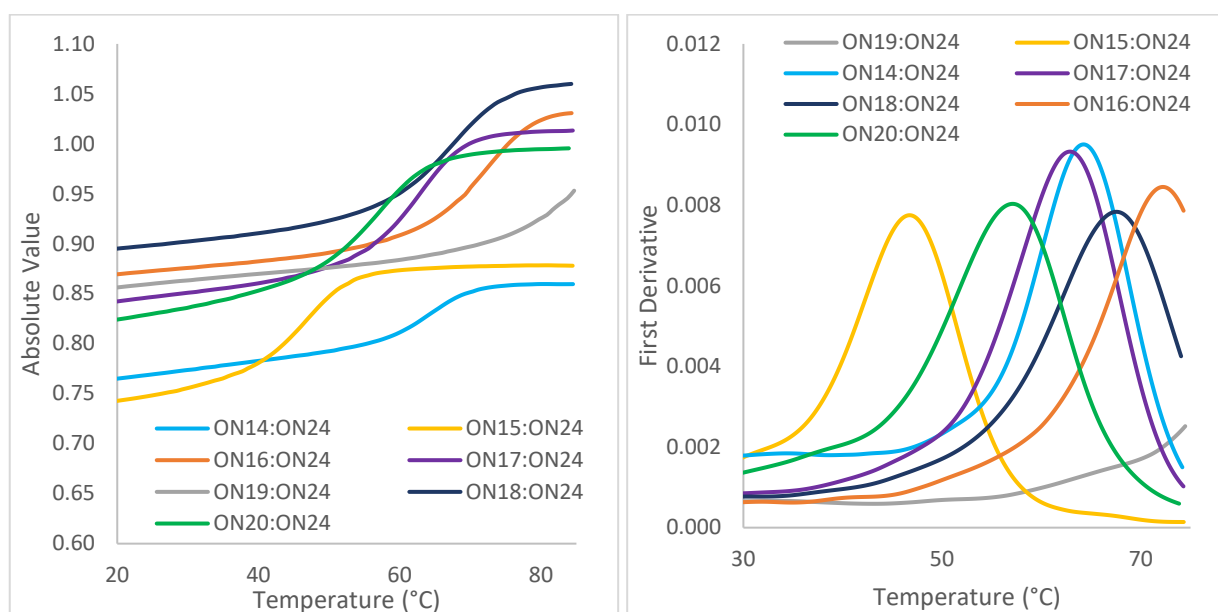


Figure S17. UV melting studies for modified ONs against truncated RNA target ON24 (Supplementary Table 3). Left) Representative UV melting curves measured using 3 μ M of each ON in pH 7.0 phosphate buffer containing 200 mM NaCl; Right) 1st derivative of melting curves. The complementary RNA target was truncated so that the melting temperatures were in the range of the instrument. The truncated RNA strand covers the critical modified region of the modified ONs.

Nuclease resistance supplementary figure

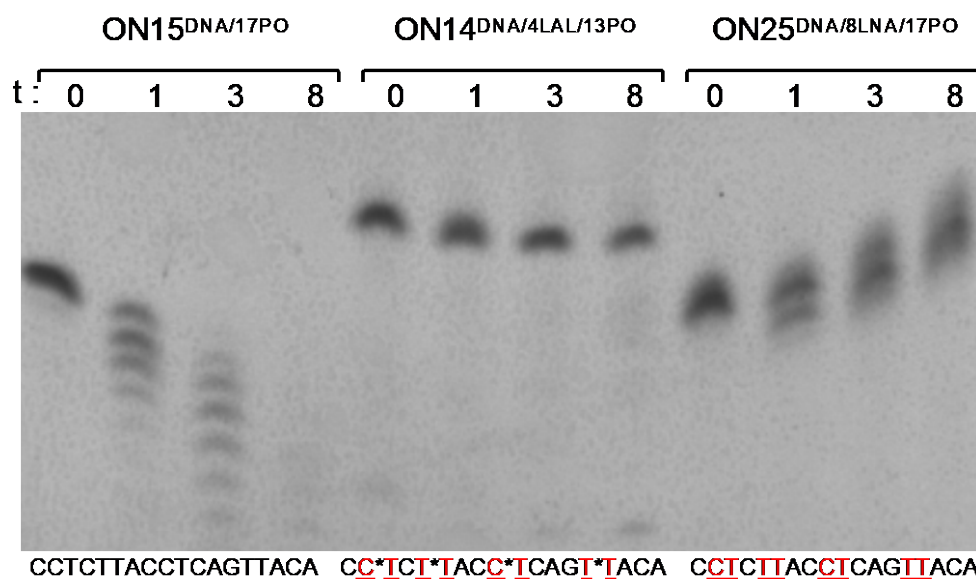


Figure S18. Denaturing polyacrylamide gel electrophoresis (PAGE) analysis of modified ONs after incubation in FBS:PBS (1:1). t = incubation time in hours. Underlined red bases indicate a locked sugar and * is an amide bond in place of a phosphodiester.

XRD supplementary figures

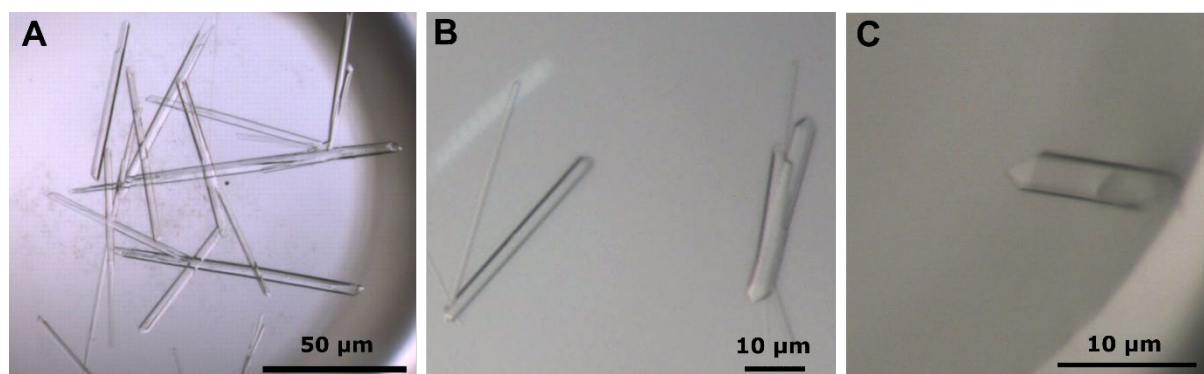
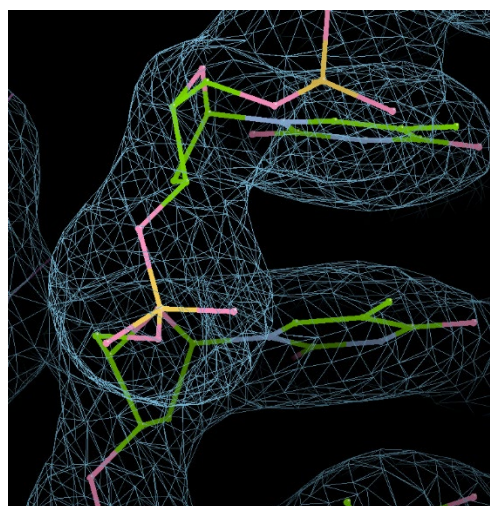
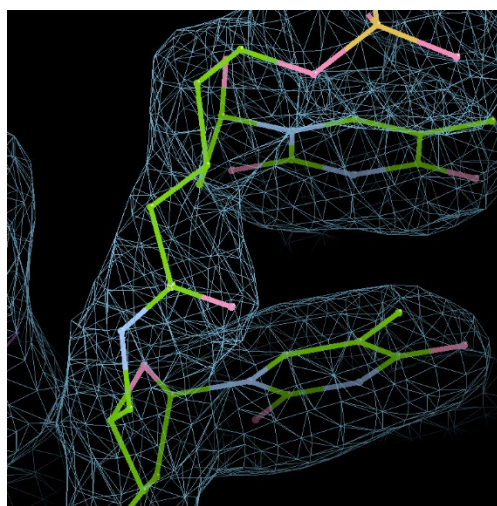


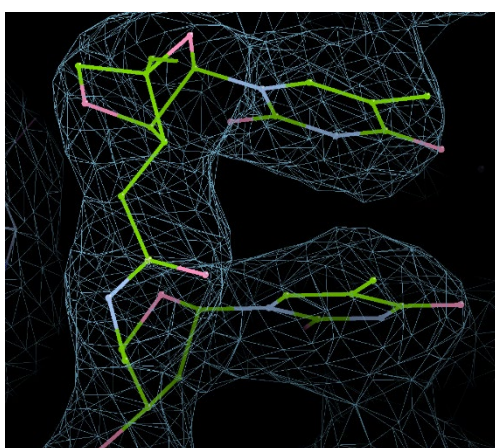
Figure S19. Example of crystals obtained from vapor diffusion. A) ON26^{xDNA}:ON27^{xRNA}, B) ON29^{xLNA-Am-DNA}:ON27^{xRNA}, C) ON30^{xLNA-Am-LNA}:ON27^{xRNA}



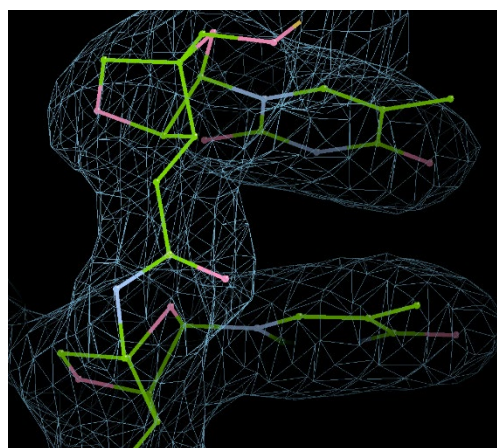
ON26^xDNA



ON28^xDNA-Am-DNA



ON29^xLNA-Am-DNA



ON30^xLNA-Am-LNA

Figure S20. $2F_o - F_c$ electron density map (blue), at the 1σ contour level, centred on the unmodified phosphate (top left) or amide linkage for the four nucleic acid crystal structures reported in this manuscript. Atoms are coloured according to type with carbon in green, nitrogen in light blue and oxygen in red.

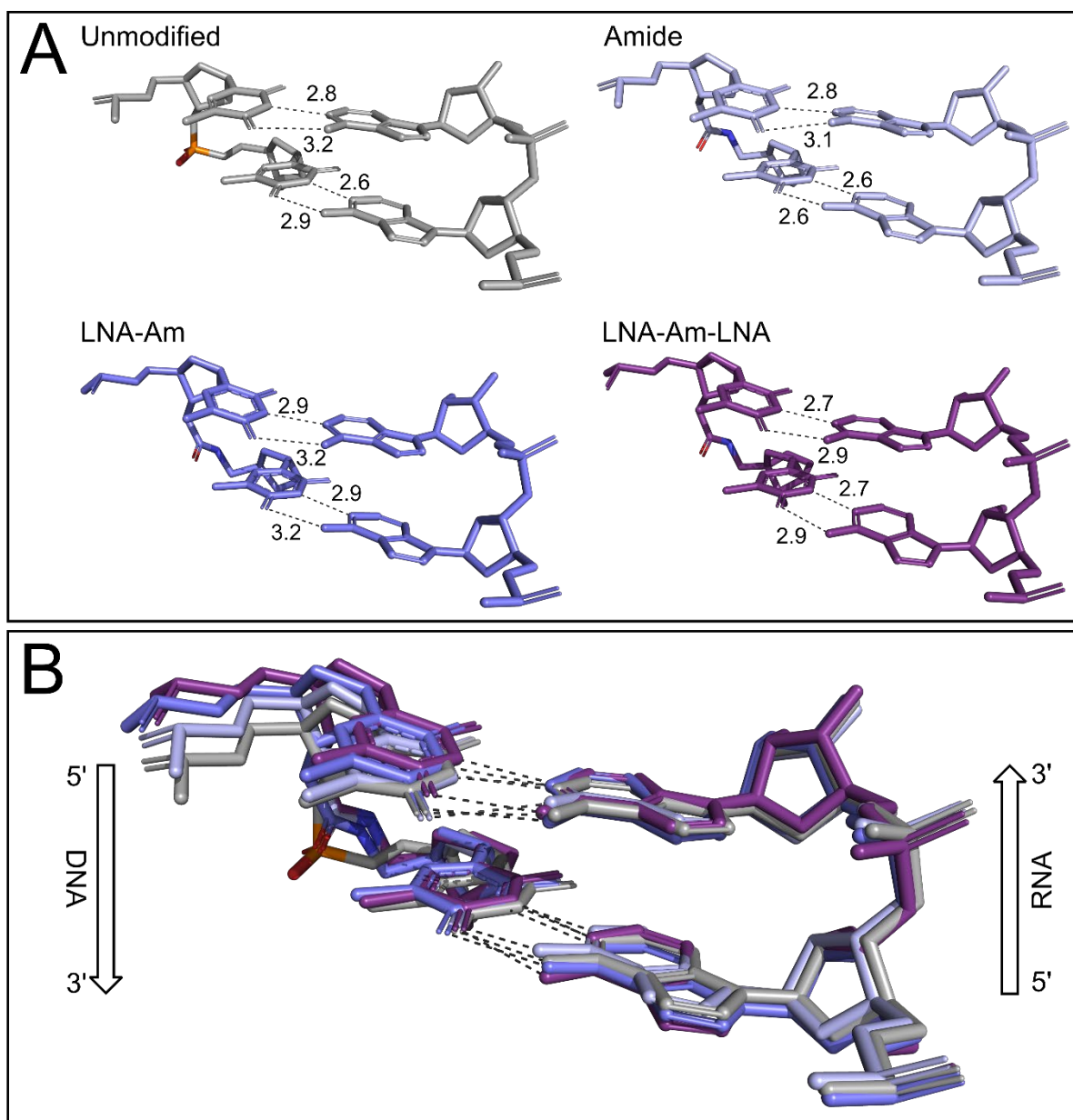


Figure S21. A) Hydrogen-bonding interactions of the 7 A-T, 8 A-T base pair steps surrounding the site of modification. Unmodified (ON26^{xDNA}) = grey, amide (ON28^{xDNA-Am-DNA}) = light blue, LNA-Am (ON29^{xLNA-Am-DNA}) = dark blue and LNA-Am-LNA (ON30^{xLNA-Am-LNA}) = purple. Modifications are contained within the DNA strand (left side) and hydrogen bond distances between Watson-Crick base pairs are shown. B) Overlay of above structures showing base pair step structural similarity.

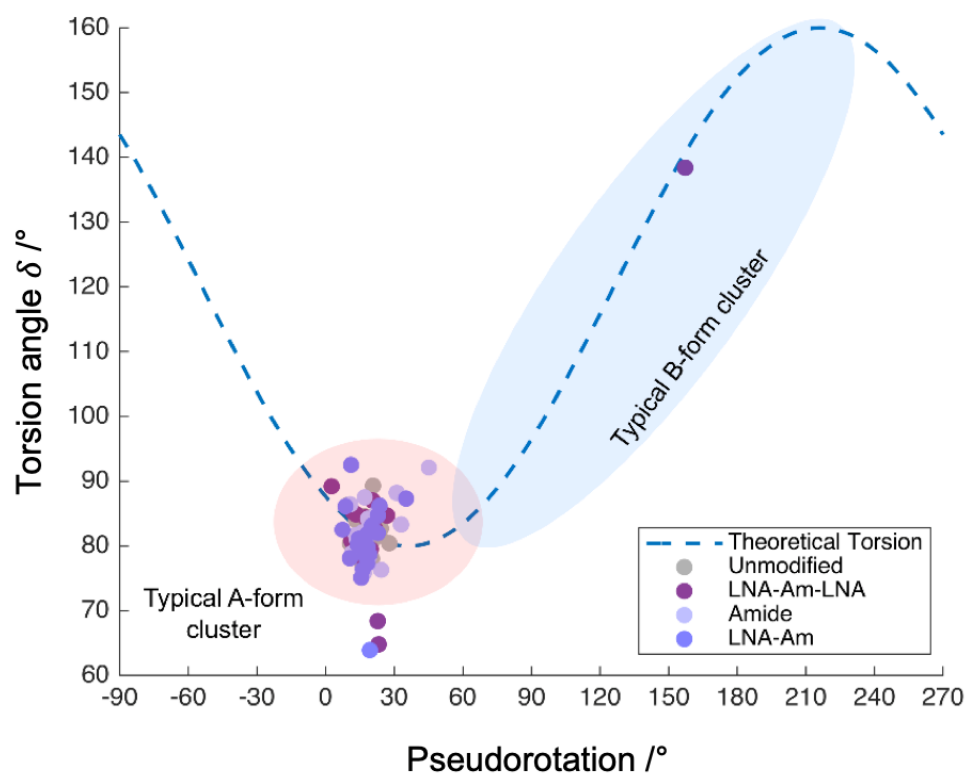


Figure S22. Pseudorotation vs torsion angles of angle δ used to define sugar pucker conformations. Torsion data points were calculated using w3DNA 2.0 software and each point represents a single sugar conformation within a corresponding duplex. Each duplex has 20 data points and the clustering of these points can be interpreted to determine duplex form. The theoretical torsion angle is represented by equation ($\delta = 40 \cos(P + 144) + 120$). In general, A-form duplexes have consistent pseudorotations 0-60° known as 3'-*endo* conformation. B-form duplexes have a larger distribution of pseudorotations 0-240°. Legend) Unmodified = ON26^{xDNA}:ON27^{xRNA}; LNA-Am-LNA = ON30^{xLNA-Am-LNA}:ON27^{xRNA}; Amide = ON28^{xDNA-Am-DNA}:ON27^{xRNA}; LNA-Am = ON29^{xLNA-Am-DNA}:ON27^{xRNA}.

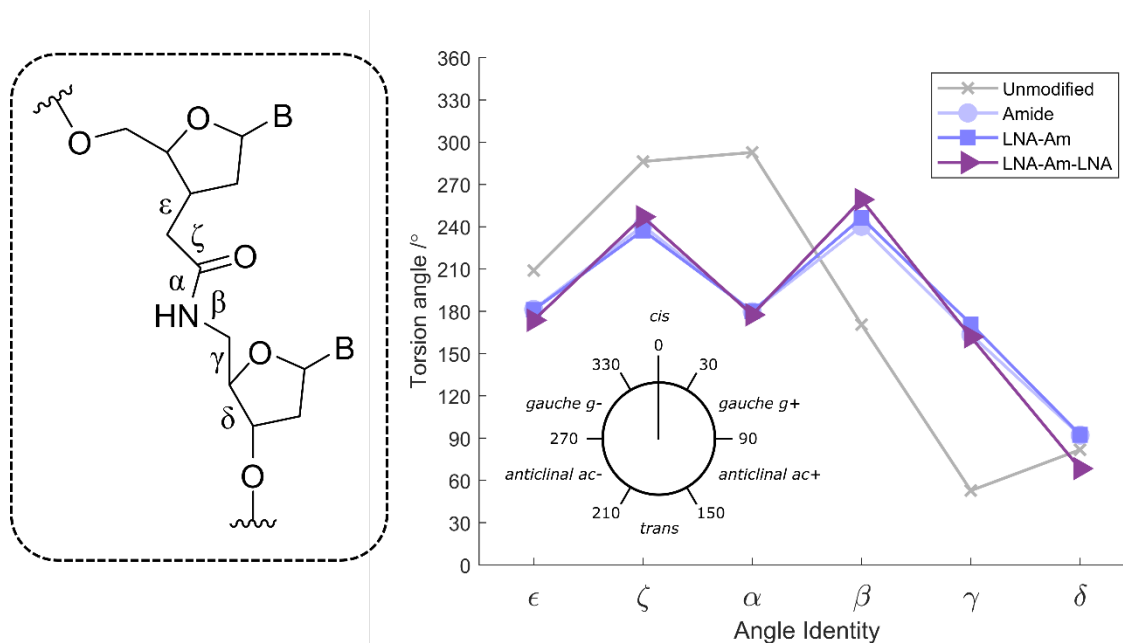


Figure S23. Torsion angle comparison between amide modified backbones. Specific torsions are given by their respective symbol ($\epsilon \rightarrow \delta$, right). Modified backbones are located at the 7A-T base pair step. Also included is the 7A-T phosphodiester step from the unmodified duplex. In general, all amide backbones, regardless of LNA modification have similar torsion angles. Legend) Unmodified = ON26^{xDNA}:ON27^{xRNA}; LNA-Am-LNA = ON30^{xLNA-Am-LNA}:ON27^{xRNA}; Amide = ON28^{xDNA-Am-DNA}:ON27^{xRNA}; LNA-Am = ON29^{xLNA-Am-DNA}:ON27^{xRNA}.

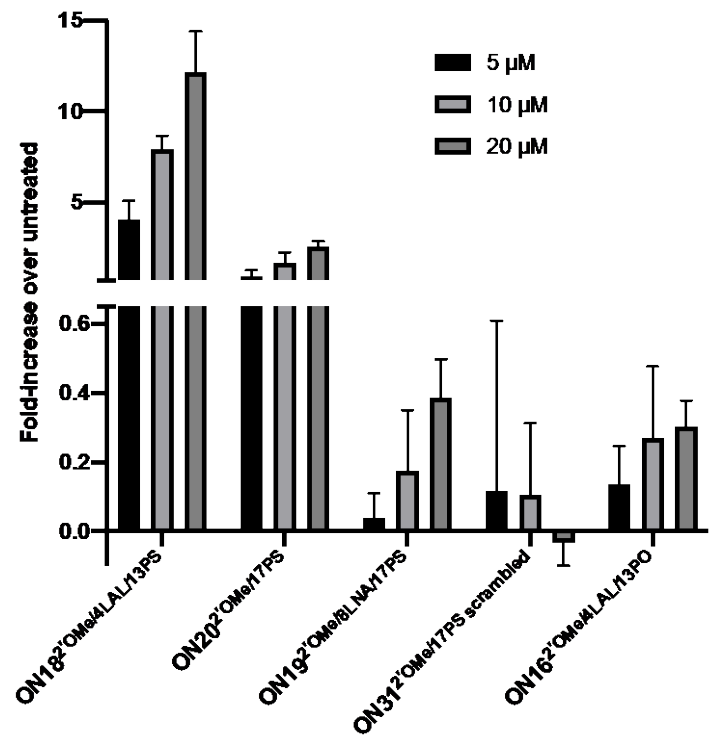


Figure S24. LNA-flanked amides increase the gymnotic delivery and activity of ONs that contain PS linkages. Luciferase activity was measured and normalised to both protein quantity and untreated cells.

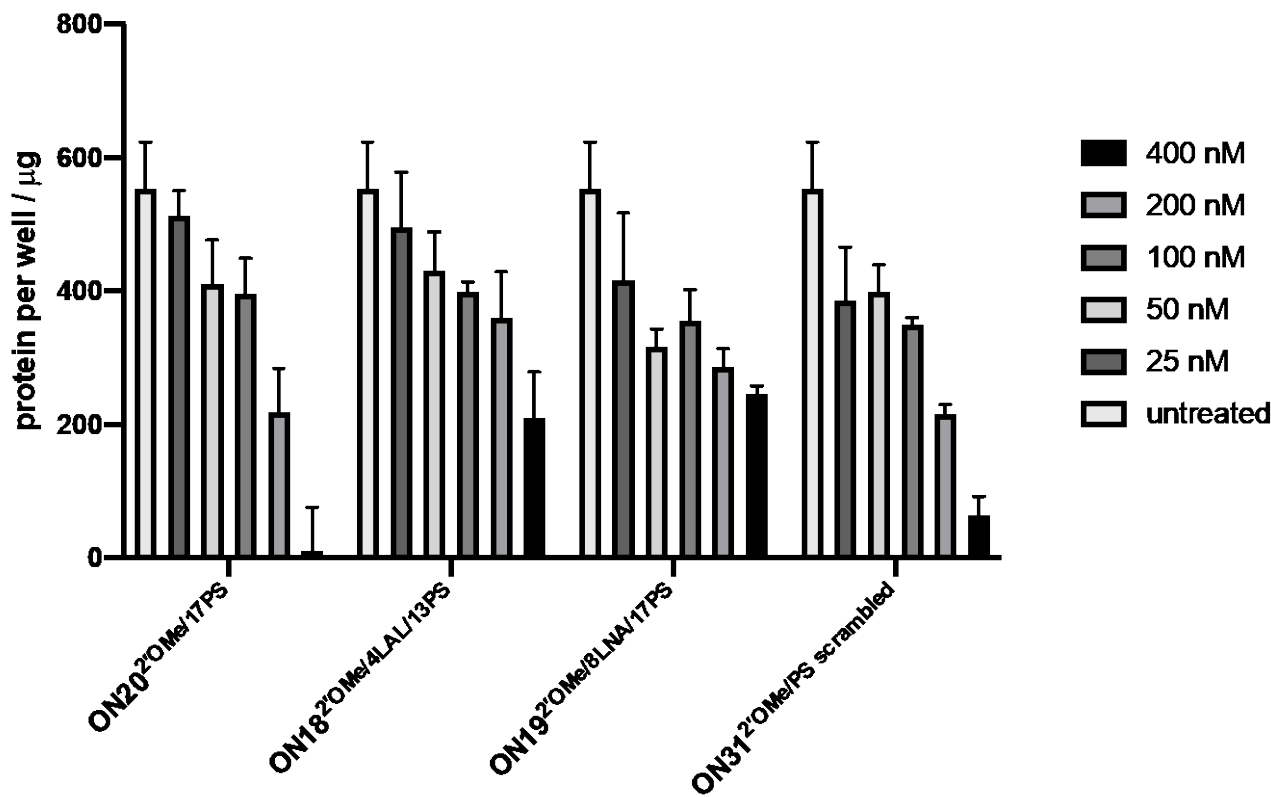


Figure S25. Amount of protein per well 24 h after pLuc705 HeLa cells were transfected with ONs using lipofectamine 2000 (LF2000) at the concentrations indicated. A significant drop in protein was observed at higher concentrations indicating toxicity. Higher protein was observed for the amide modified ON, suggesting that LNA-flanked amides reduce toxicity of ONs transfected with LF2000.

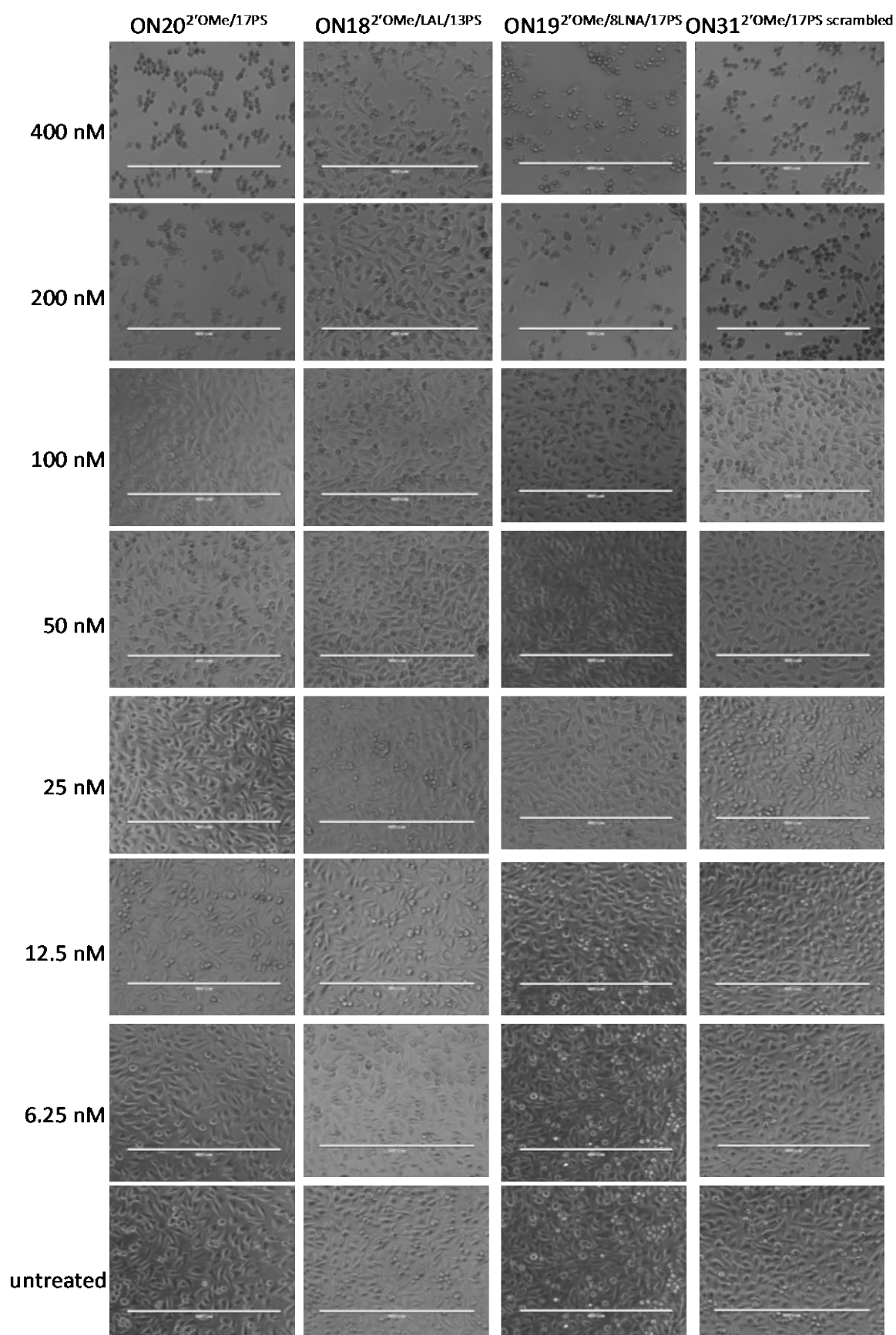


Figure S26. Microscope images 24 h after transfection with LF2000 at the concentrations indicated. The cell morphology suggests that addition of an amide reduces the toxicity of Th-ONs transfected with LF2000 at higher concentrations. Scale bars represent 400 μ m.

UPLC-MS traces of LNA-amide modified oligonucleotides

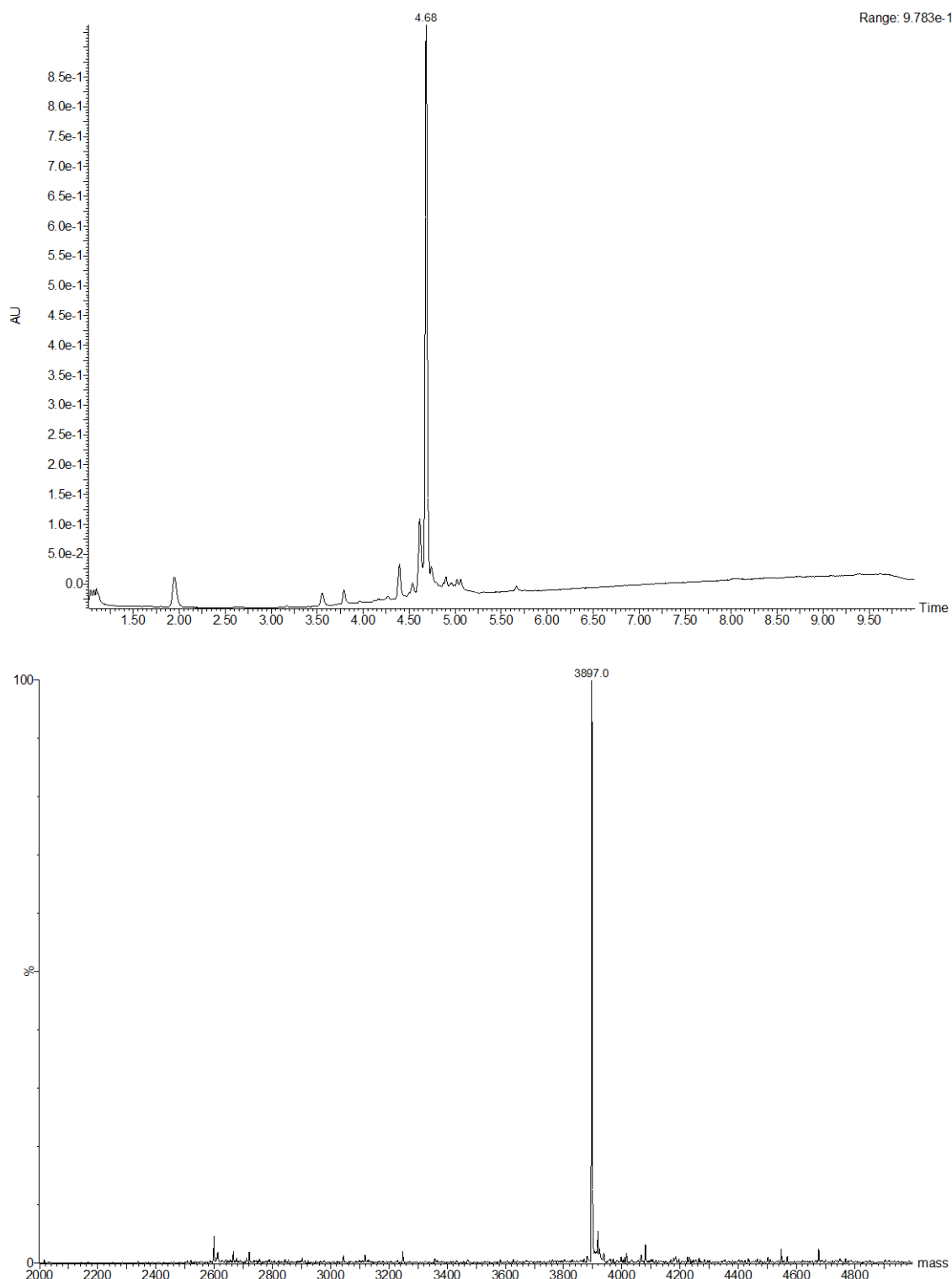


Figure S27. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES^-) of $\text{ON1}^{\text{DNA-Am-DNA}}$ without purification. Required 3896.7 Da, found 3897.0 Da. CGACGCT*TCGAGC (DNA, phosphodiester backbone).

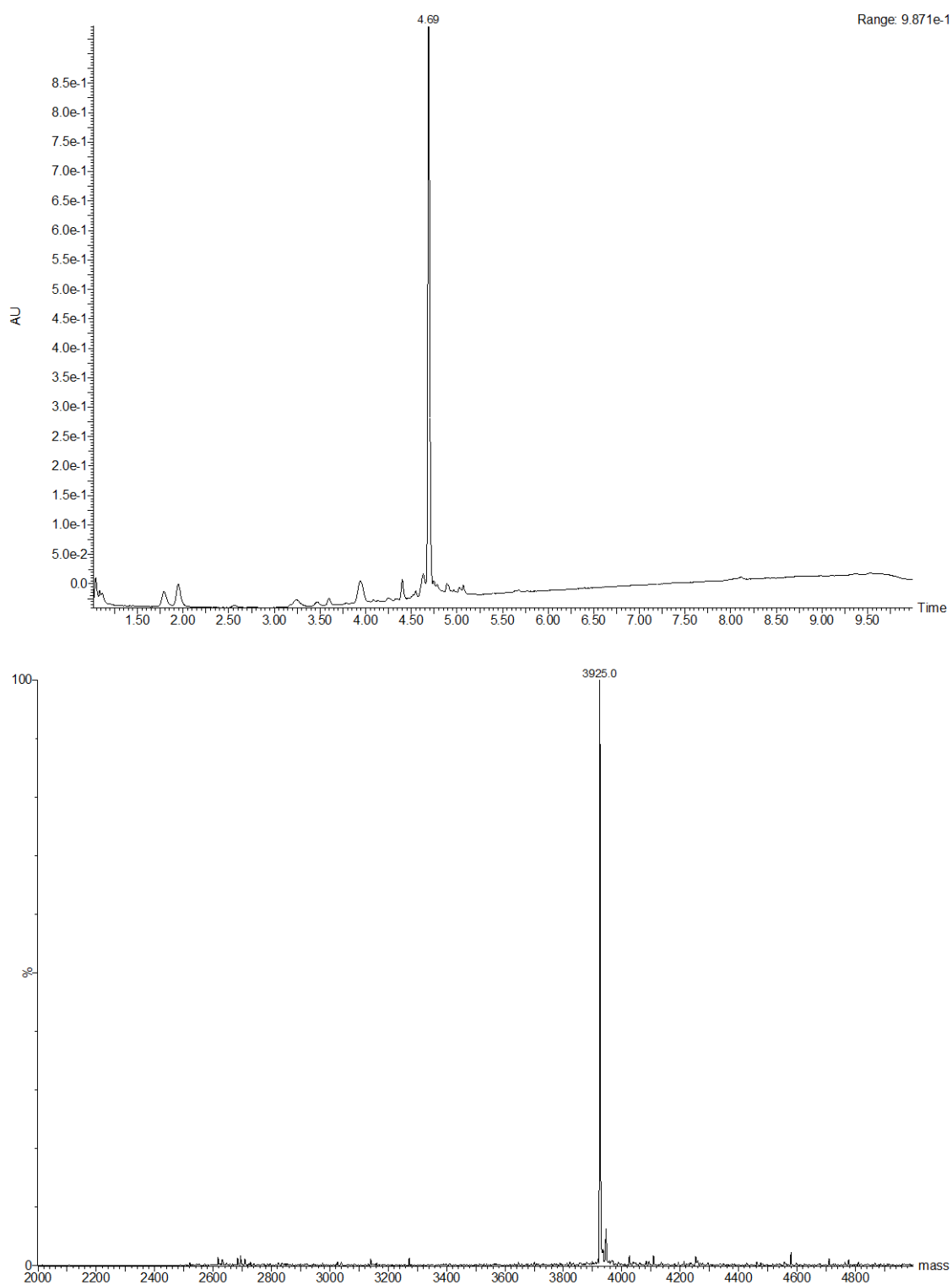


Figure S28. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON2^{LNA-Am-DNA} without purification. Required 3924.8 Da, found 3925.0 Da. CGACGCT*TGCAGC (DNA, phosphodiester backbone).

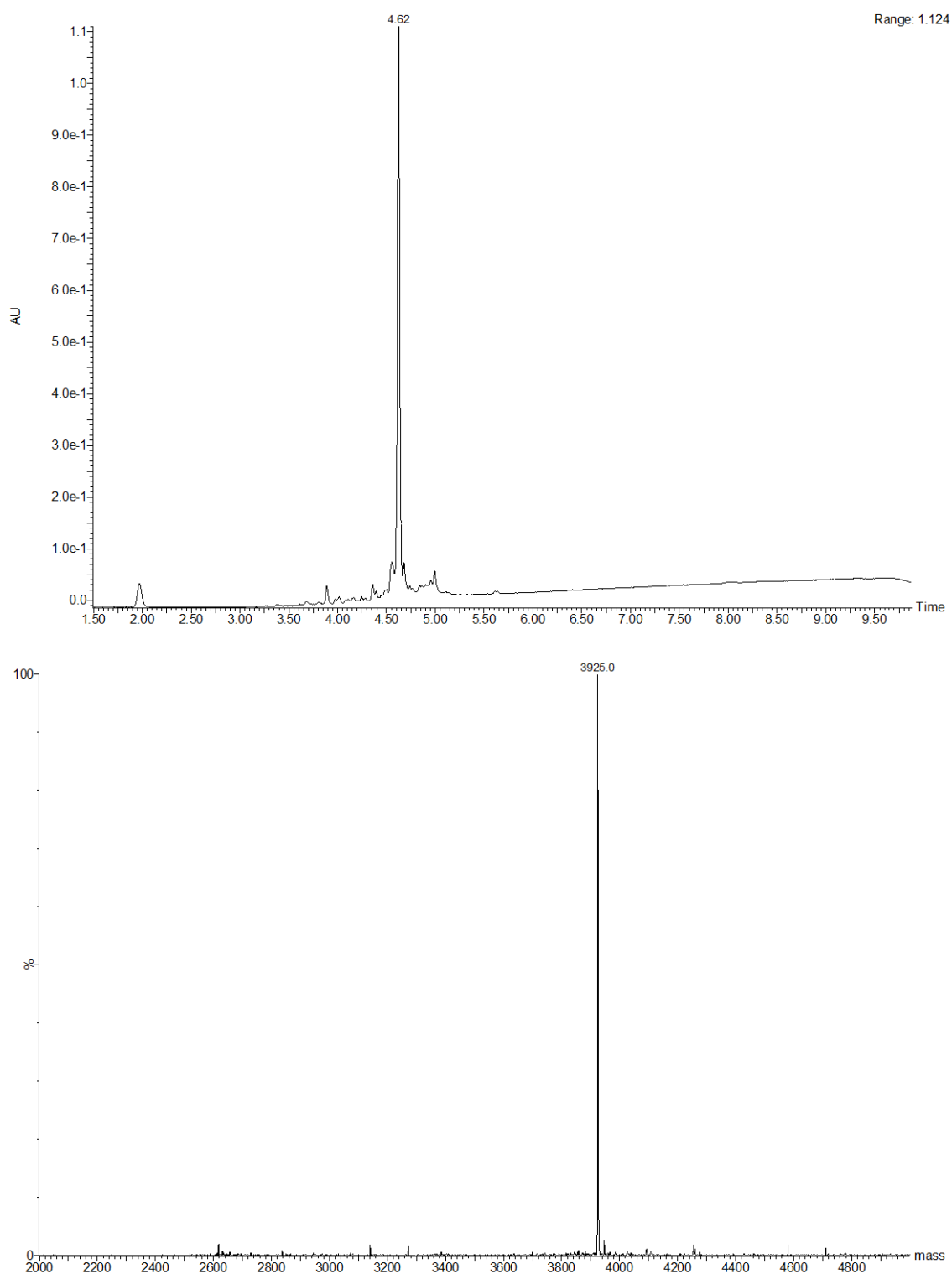


Figure S29. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON3^{DNA-Am-LNA} without purification. Required 3924.8 Da, found 3925.0 Da. CGACGCT***T**GCAGC (DNA, phosphodiester backbone).

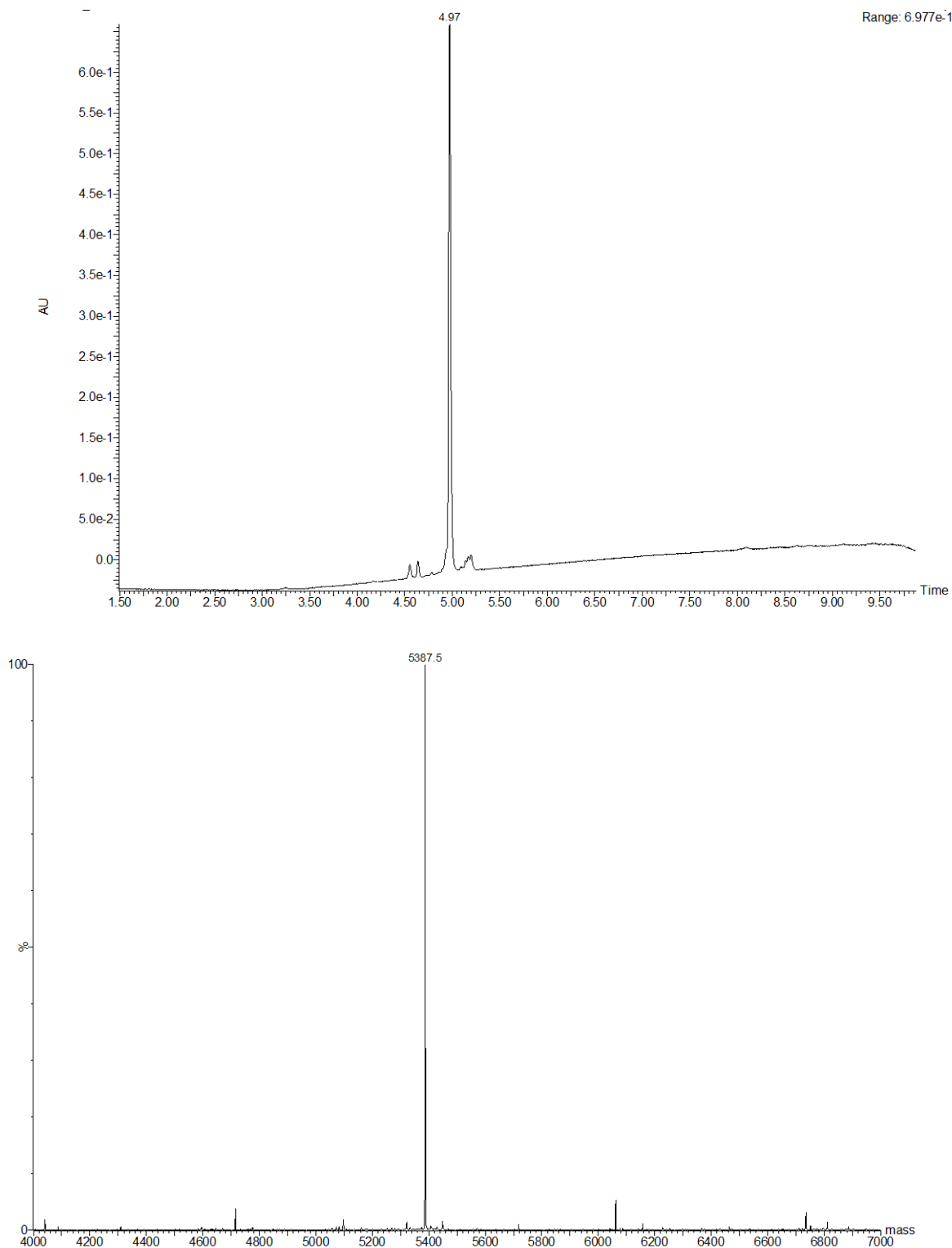


Figure S30. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON13^{DNA/1LAL/16PO} without purification. Required 5386.8 Da, found 5387.5 Da. CCTCTAC^C*^ICAGTTACA (DNA, phosphodiester backbone).

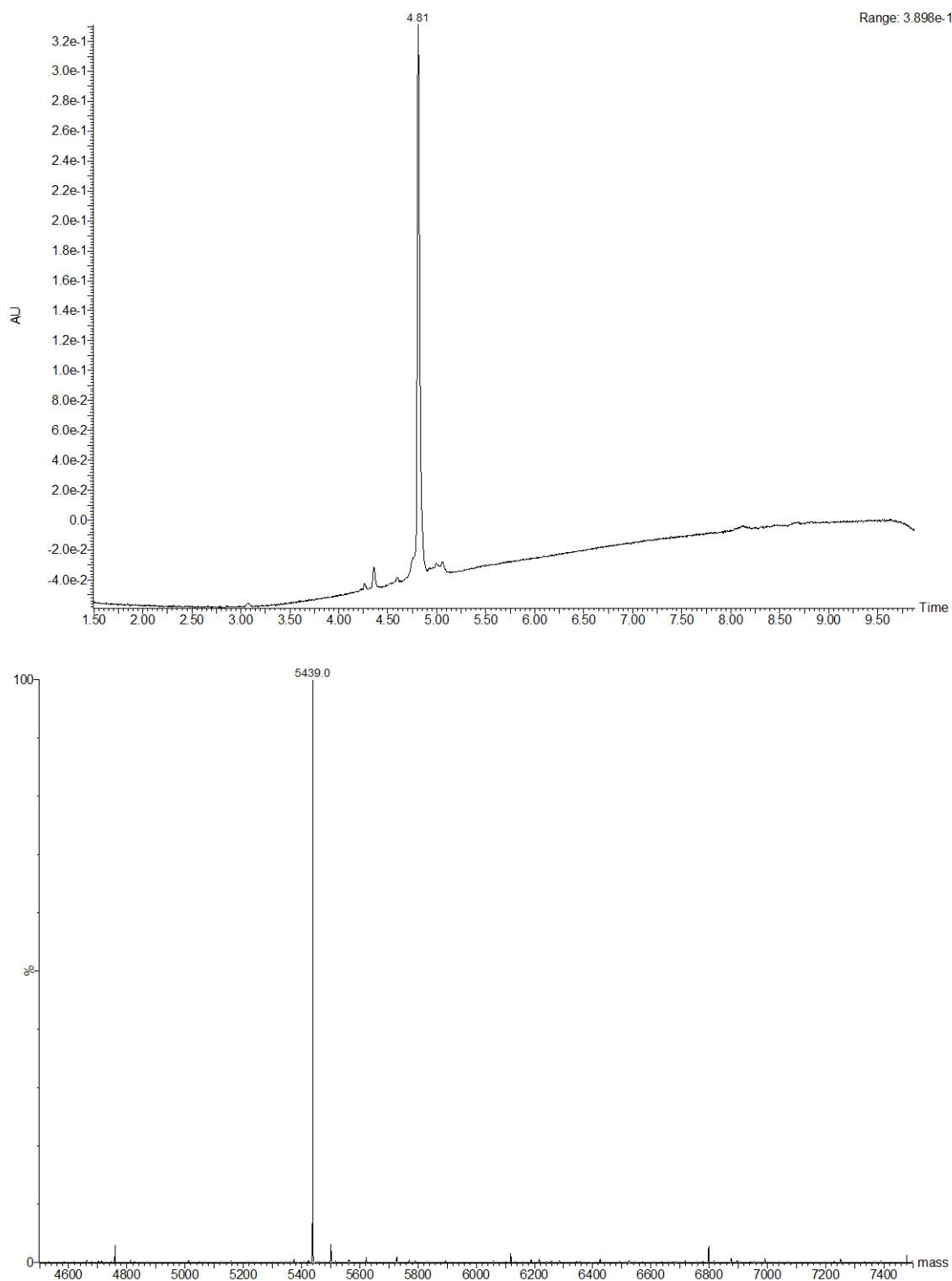


Figure S31. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ESI⁺) of ON14^{DNA/4LA/13PO} without purification. Required 5438.7 Da, found 5439.0 Da. **C*****I****C****T*****I****A****C****C*****I****C****A****G****T*****I****A****C**A (DNA, phosphodiester backbone).

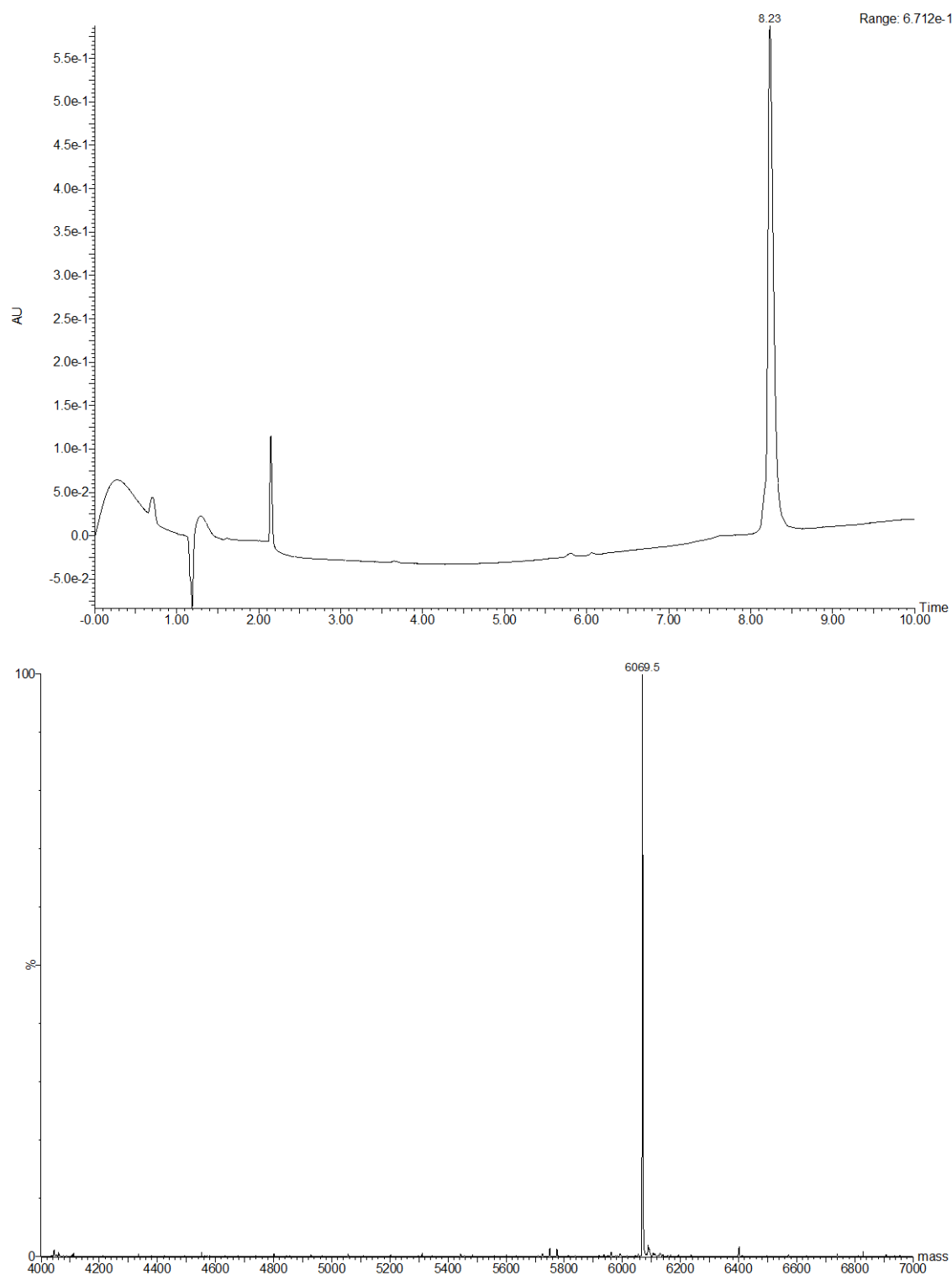


Figure S32. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES^-) of 5'-DMT protected ON16^{2'OMe/4LAL/13PO} after HPLC purification. Purification with DMT on yielded a higher purity oligonucleotide. Required 6069.3 Da, found 6069.5 Da. DMT-C^{Me}C*ICI*IAC^{Me}C*ICAGI*IACA (2'OMe, phosphodiester backbone).

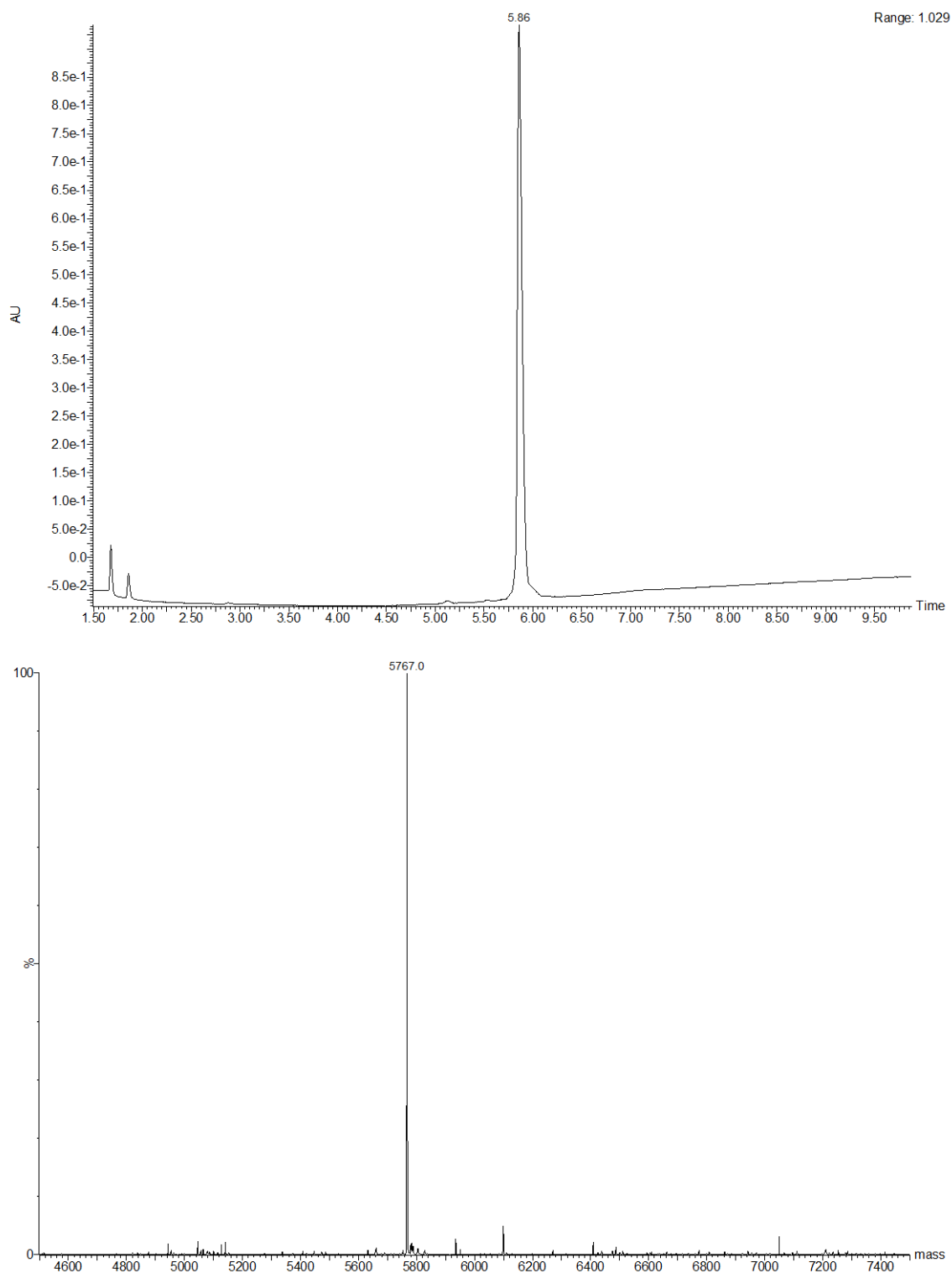


Figure S33. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON16^{2'OMe/4LAL/13PO} after HPLC purification. Required 5766.9 Da found, 5767.0 Da. C^{Me}C*ICT*IAC^{Me}C*ICAGT*IACA (2'OMe, phosphodiester backbone).

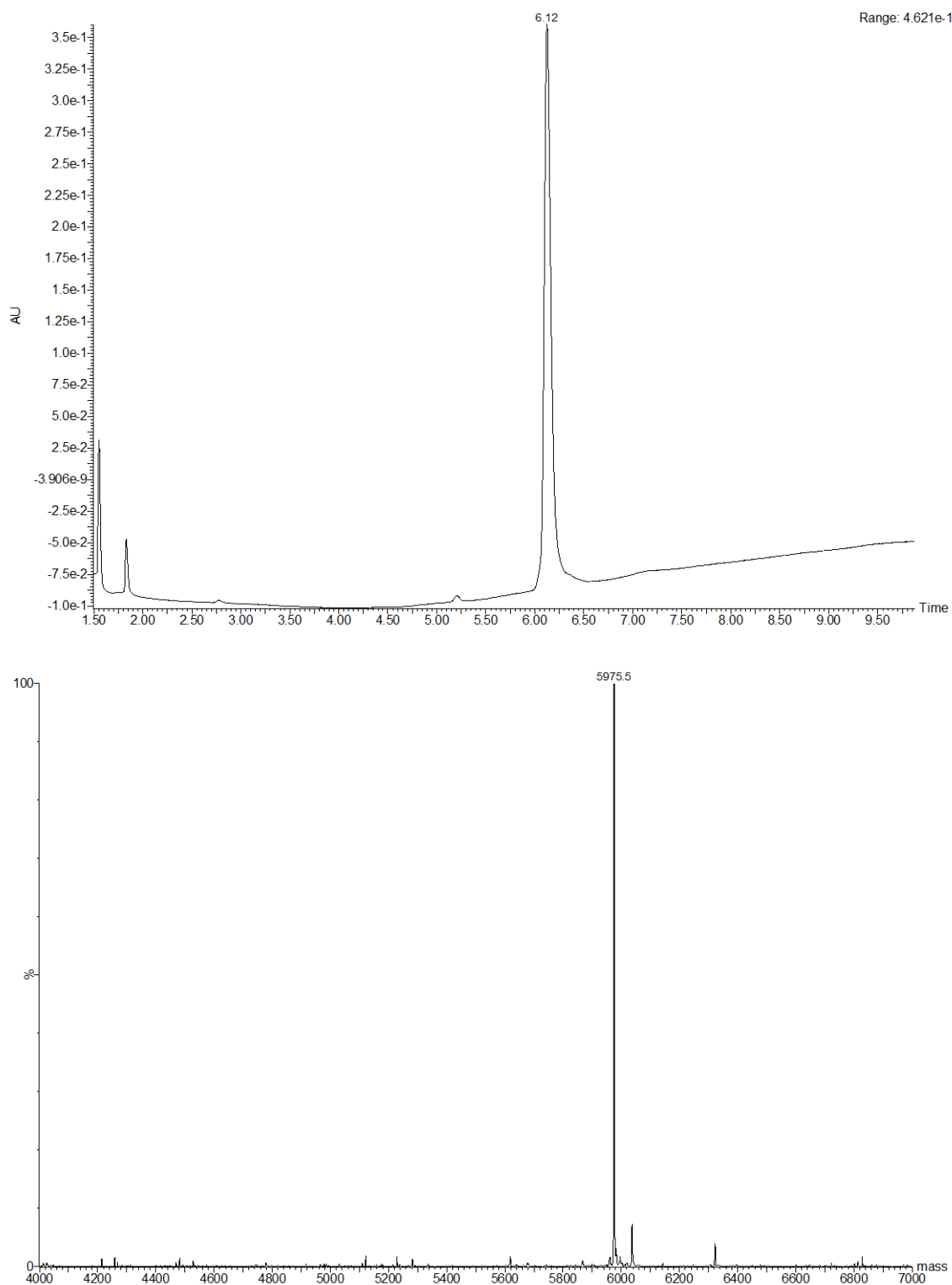


Figure S34. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON18^{2'OMe/4LAL/13PS} after HPLC purification. Required 5976.2 Da, found 5975.5 Da. C^{Me}C*ICI*TAC^{Me}C*ICAGI*IACA (2'OMe, phosphorothioate backbone).

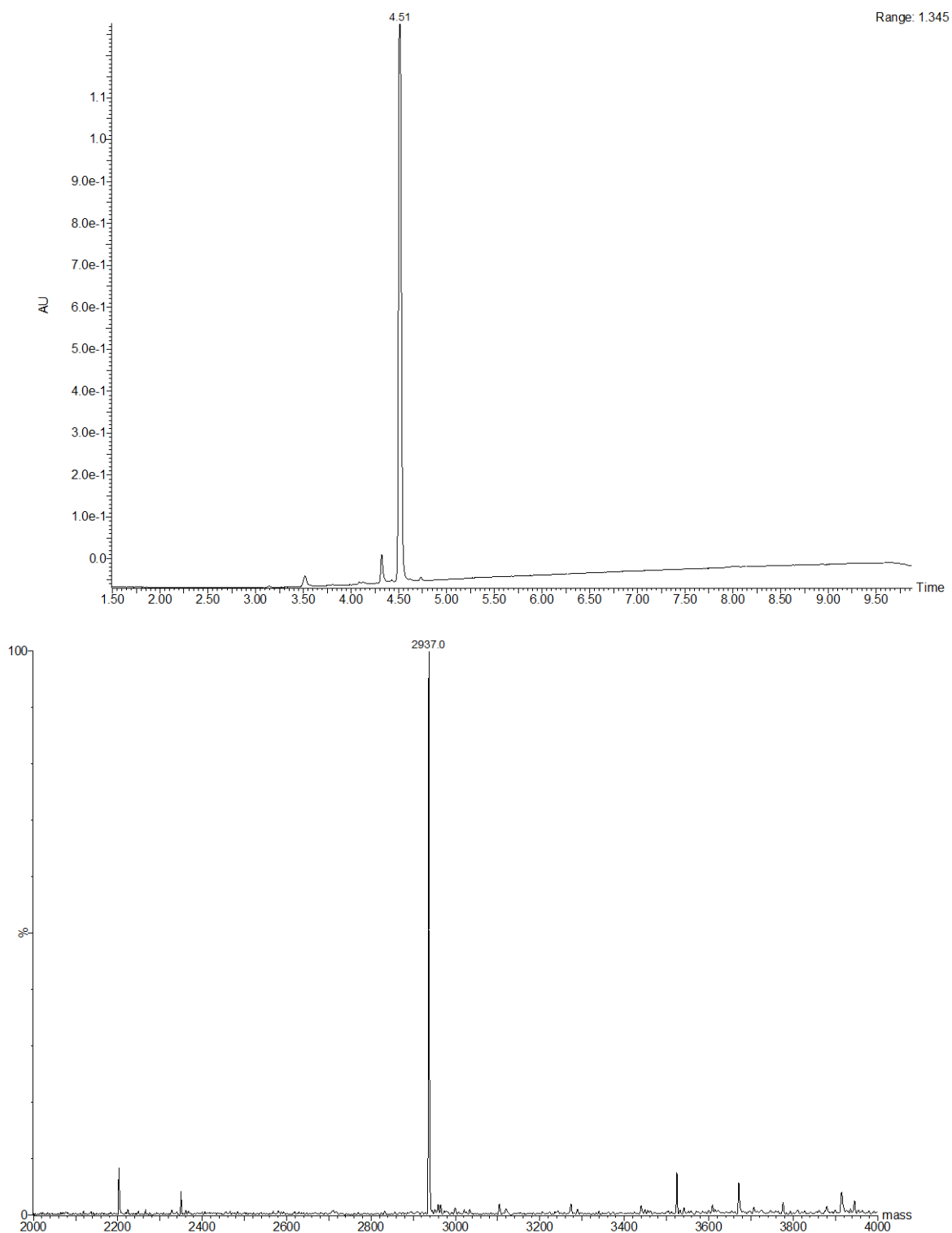


Figure S35. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON28^xDNA-Am-DNA following HPLC purification. Required 2936.1 Da, found 2937.0 Da. CTT*TTCTTTG (DNA, phosphodiester backbone).

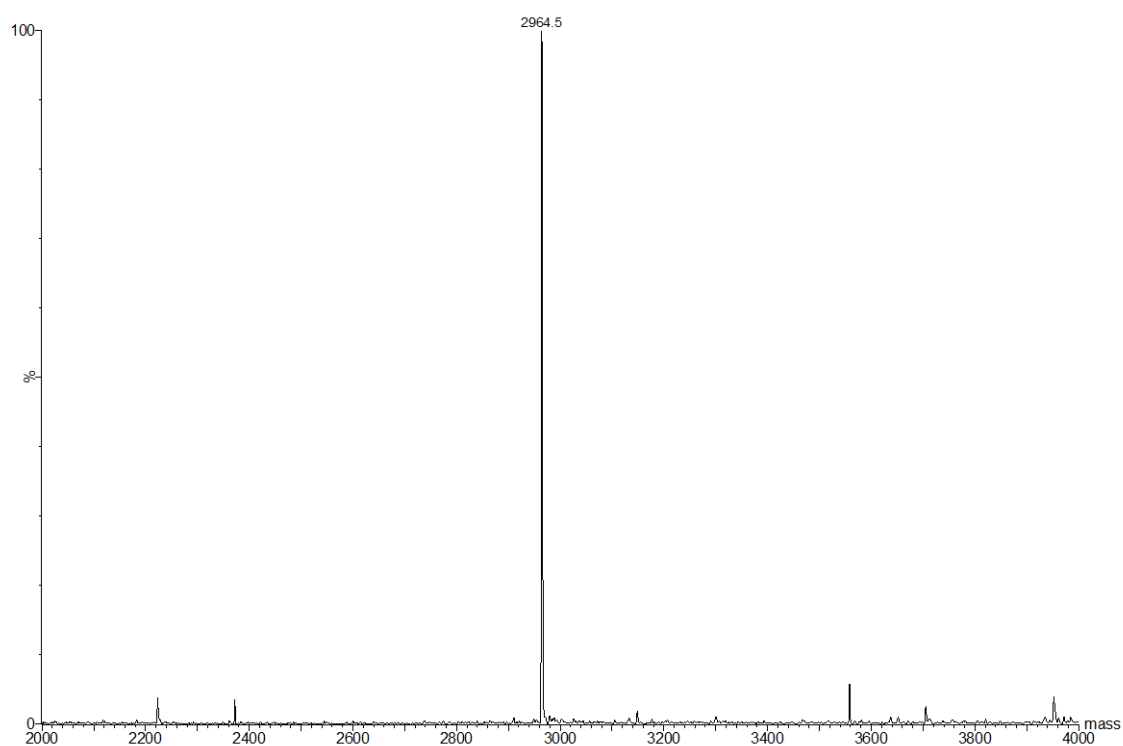
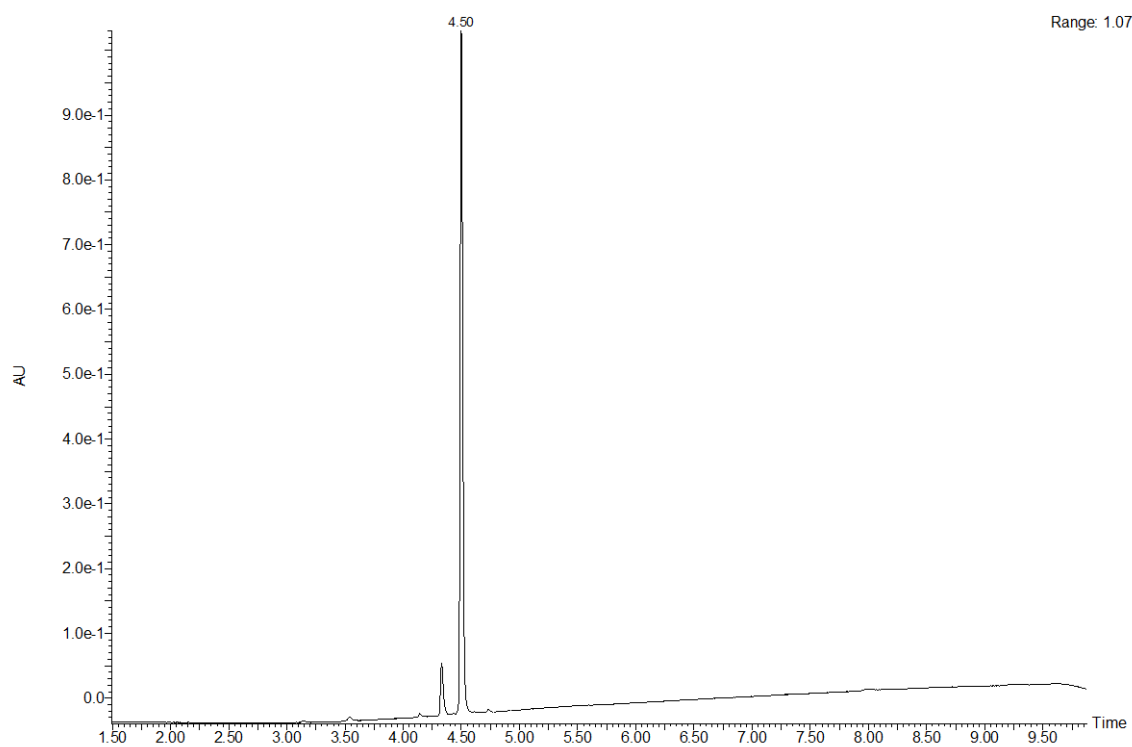


Figure S36. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON29^xLNA-Am-DNA after HPLC purification. Required 2964.2 Da, found 2964.5 Da. CTI*TTCTTTG (DNA, phosphodiester backbone).

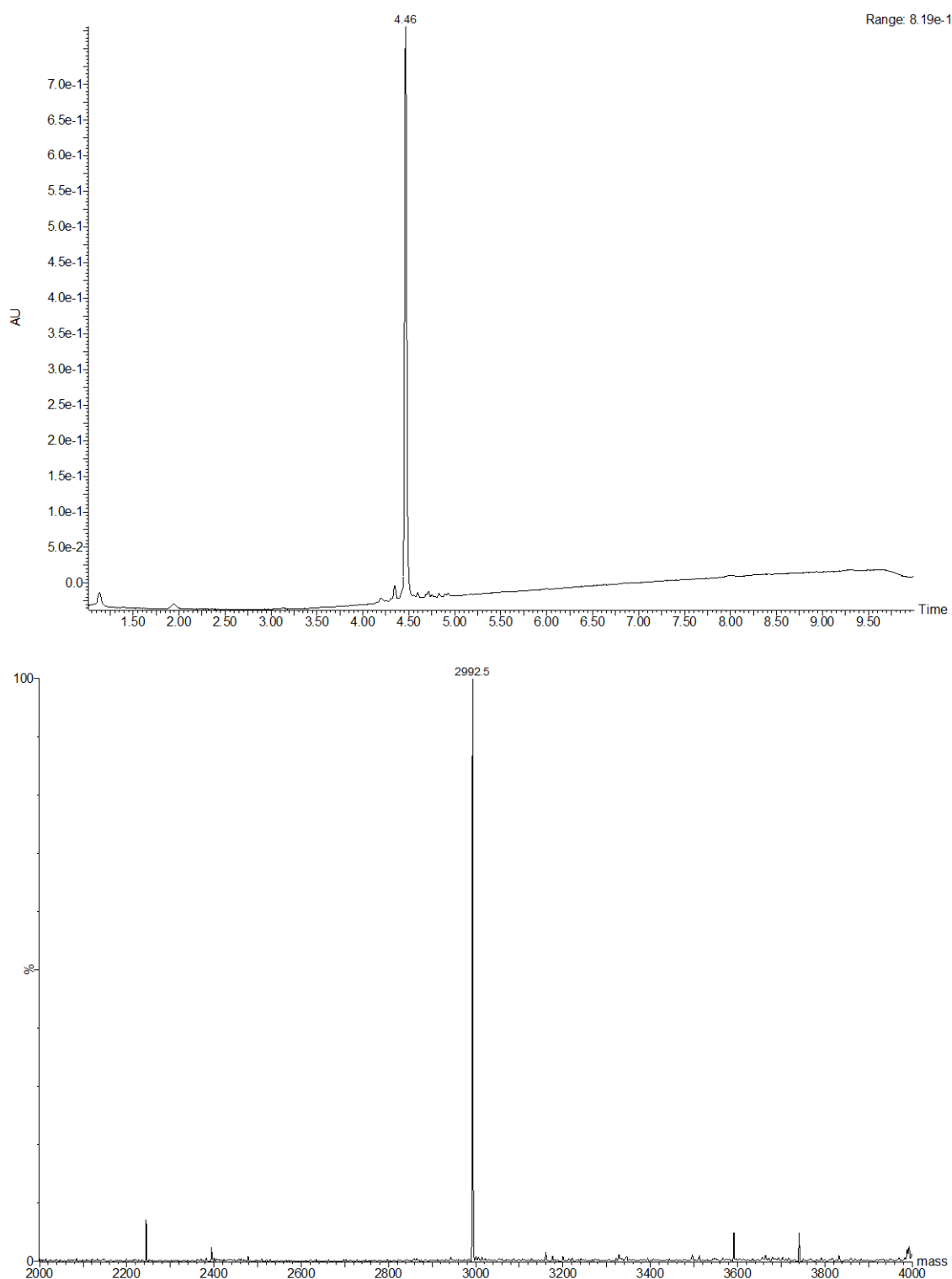
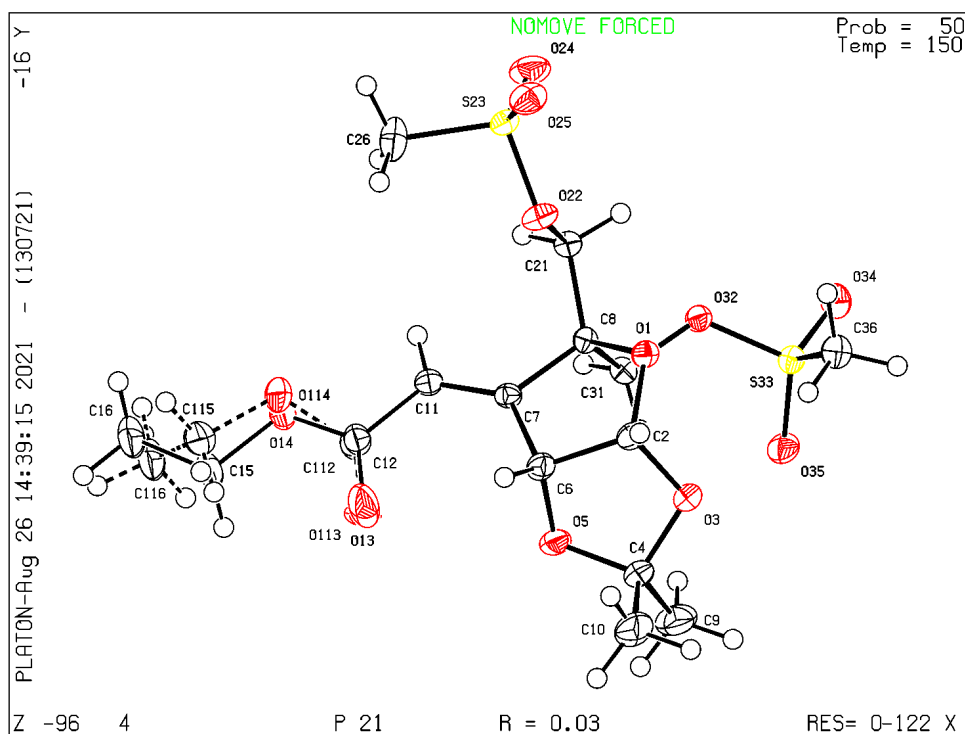


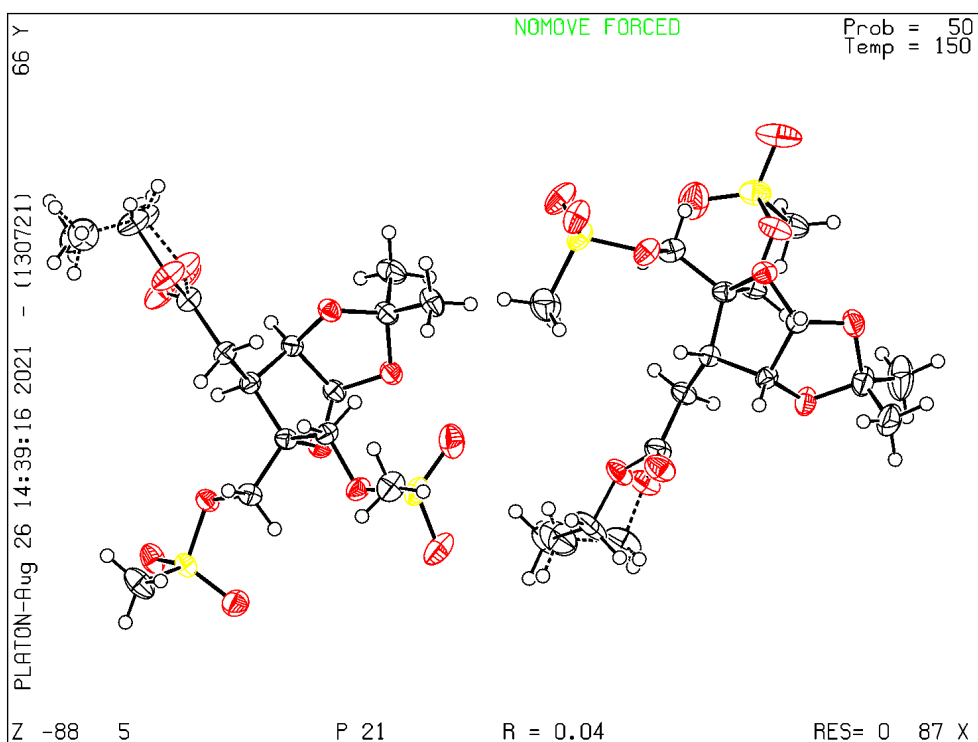
Figure S37. Reverse-phase UPLC (UV absorbance at 260 nm) and mass spectrum (ES⁻) of ON30^{xLNA}-Am-LNA without purification. Required 2992.3 Da, found 2992.5 Da. CTI*ITCTTTG (DNA, phosphodiester backbone).

Small molecule crystallography supplementary information

Single crystal X-ray diffraction data were collected using a (Rigaku) Oxford Diffraction SuperNova diffractometer and CrysAlisPro. Structures were solved using 'Superflip'¹⁸ before refinement with CRYSTALS^{19, 20} as per the CIF provided in the Supplementary Information. Crystallographic data have been deposited with the Cambridge Crystallographic Data Centre (CCDC 2105684-5) and can be obtained via www.ccdc.cam.ac.uk/data_request/cif.



Ellipsoid plot of compound 4



Ellipsoid plot of compound 5

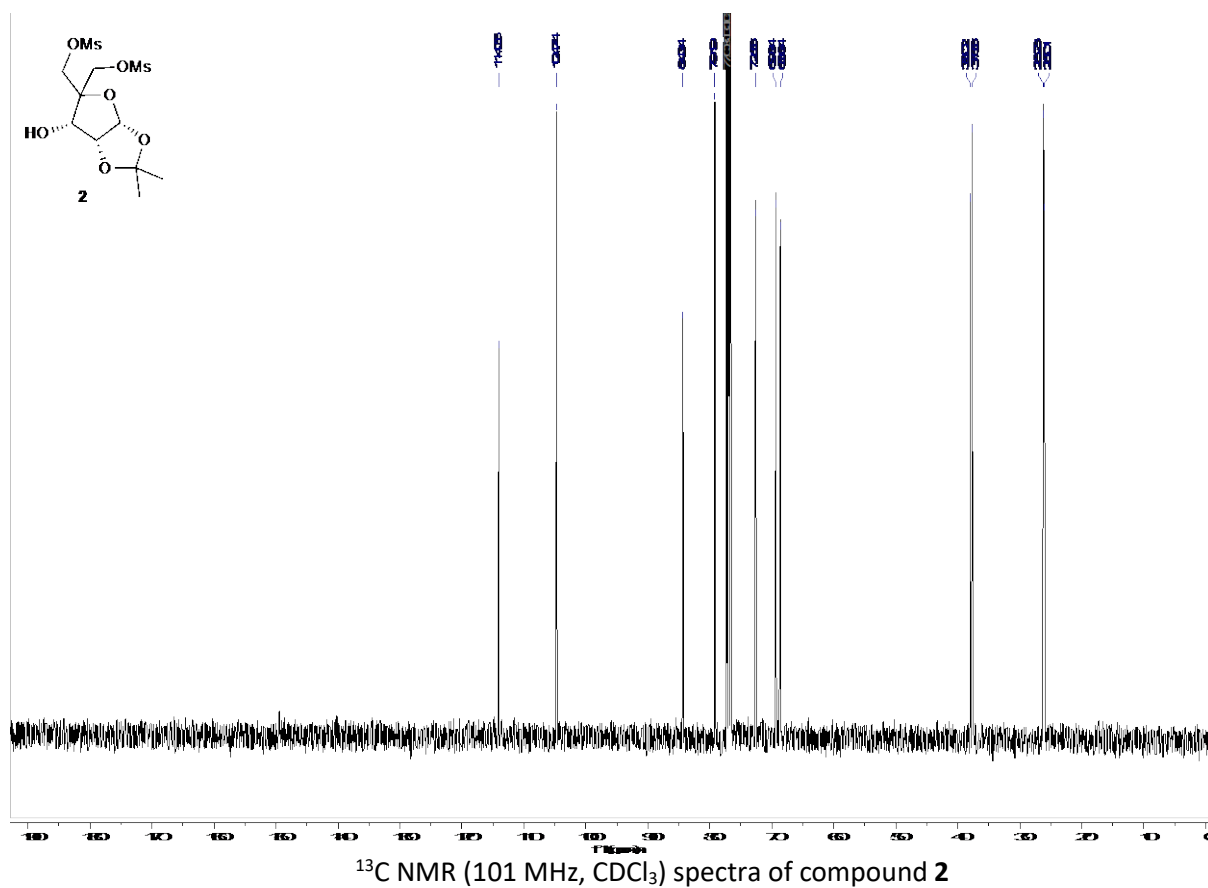
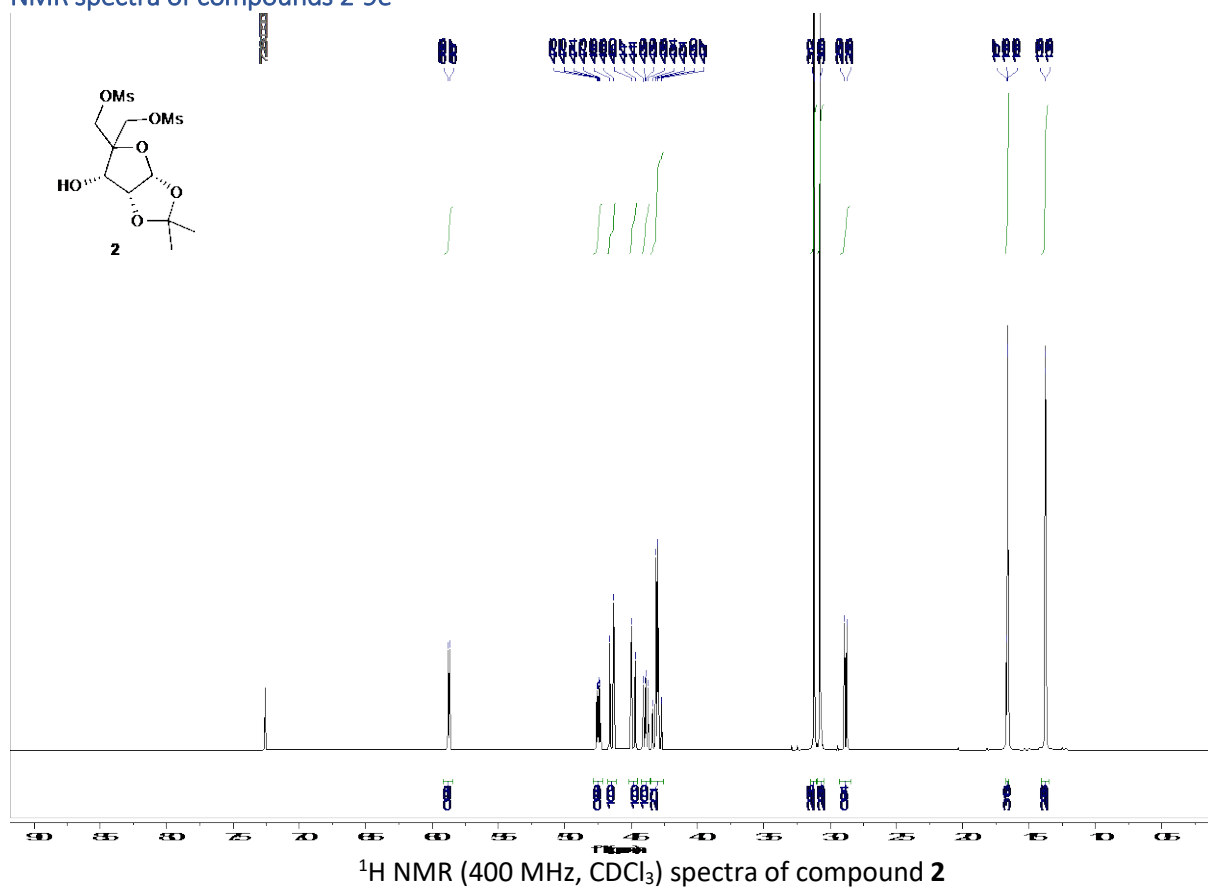
Crystal data and structure refinement for **4**.

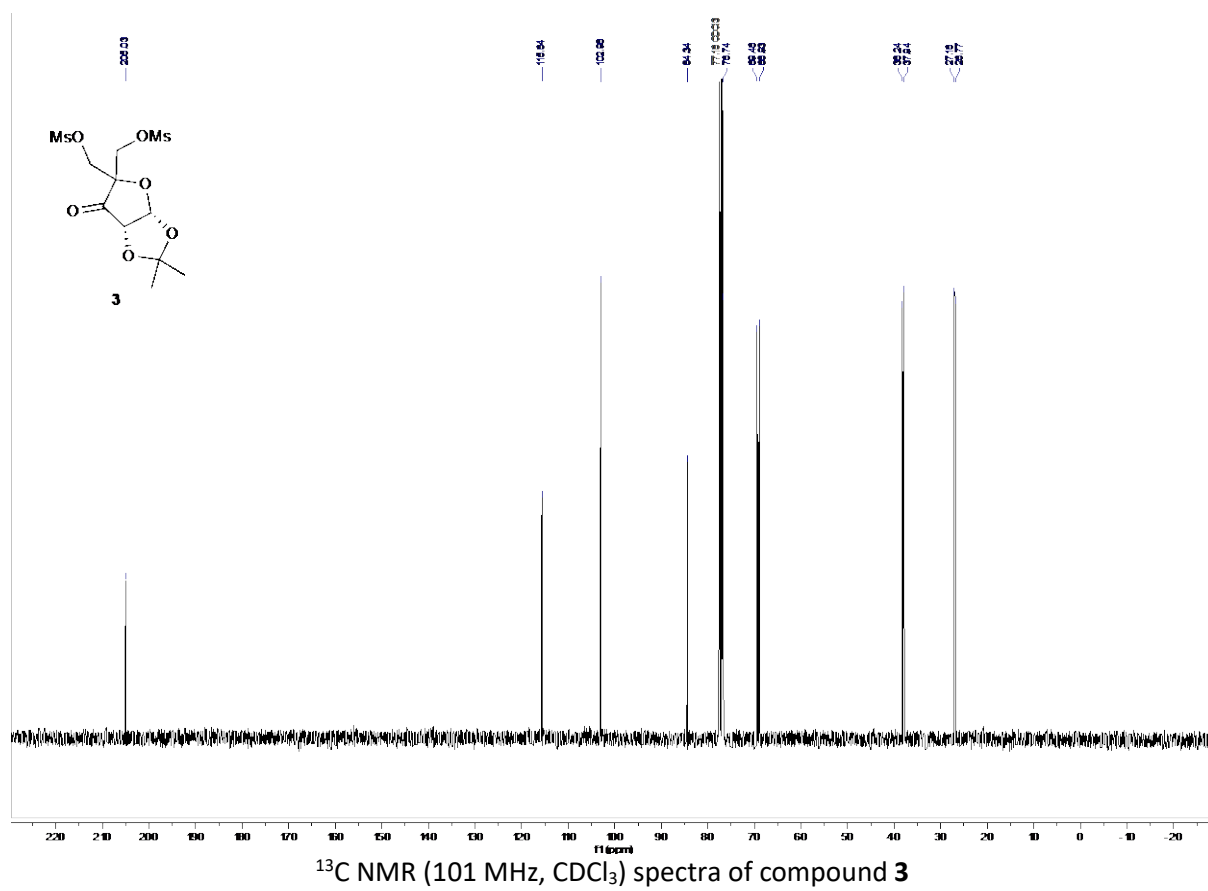
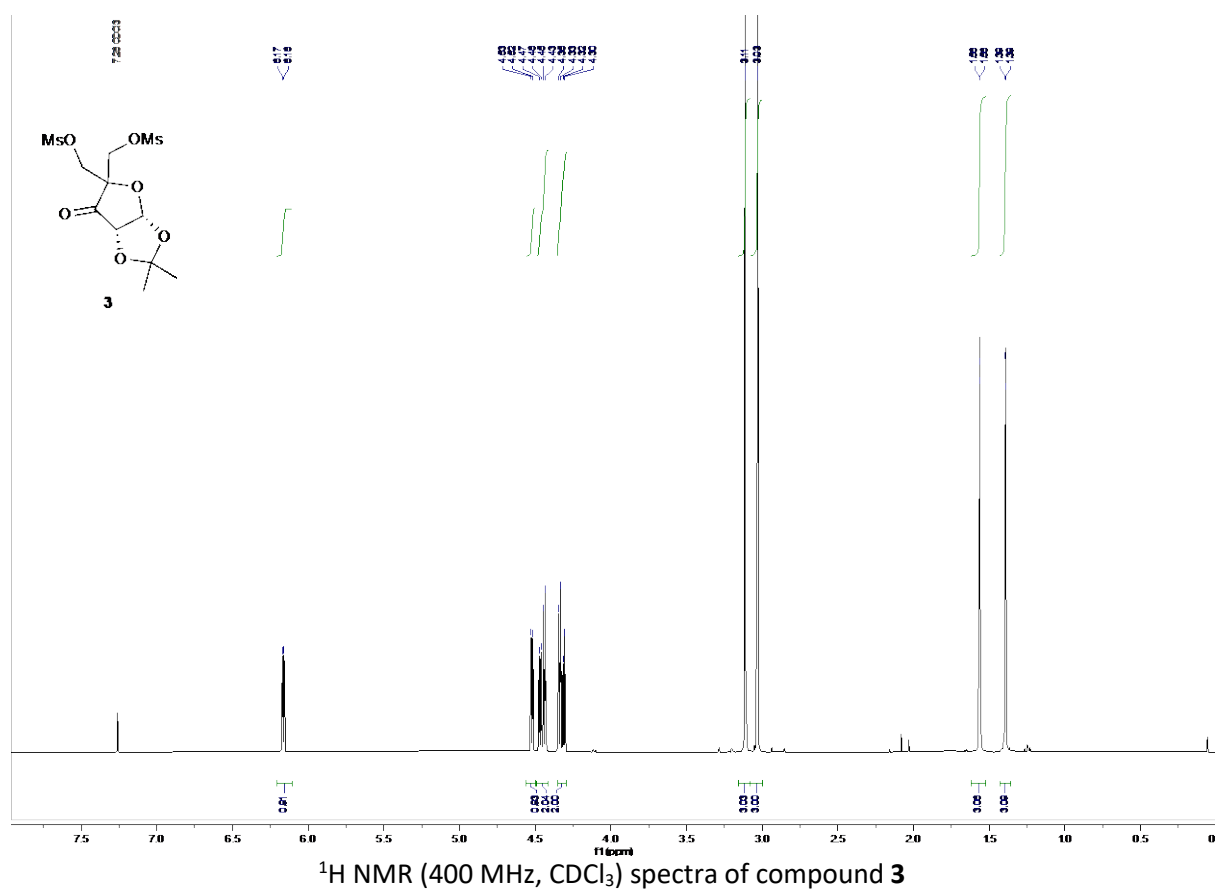
Empirical formula	C ₁₅ H ₂₄ O ₁₁ S ₂	
Formula weight	444.48	
Temperature	150 K	
Wavelength	1.54184 Å	
Crystal system	Monoclinic	
Space group	P 2 ₁	
Unit cell dimensions	a = 12.0289(2) Å	α = 90°.
	b = 5.42400(10) Å	β = 97.7502(15)°.
	c = 15.2984(2) Å	γ = 90°.
Volume	989.02(3) Å ³	
Z	2	
Density (calculated)	1.492 Mg/m ³	
Absorption coefficient	2.962 mm ⁻¹	
F(000)	468.000	
Crystal size	0.28 x 0.09 x 0.06 mm ³	
Theta range for data collection	3.708 to 76.217°.	
Index ranges	-14 ≤ h ≤ 15, -6 ≤ k ≤ 6, -17 ≤ l ≤ 19	
Reflections collected	11945	
Independent reflections	4099 [R(int) = 0.029]	
Completeness to theta = 74.692°	99.8 %	
Absorption correction	Semi-empirical from equivalents	
Max. and min. transmission	0.84 and 0.68	
Refinement method	Full-matrix least-squares on F ²	
Data / restraints / parameters	4098 / 29 / 289	
Goodness-of-fit on F ²	1.0094	
Final R indices [I > 2σ(I)]	R1 = 0.0261, wR2 = 0.0655	
R indices (all data)	R1 = 0.0264, wR2 = 0.0661	
Absolute structure parameter	-0.001(6)	
Extinction coefficient	19(2)	
Largest diff. peak and hole	0.11 and -0.09 e.Å ⁻³	

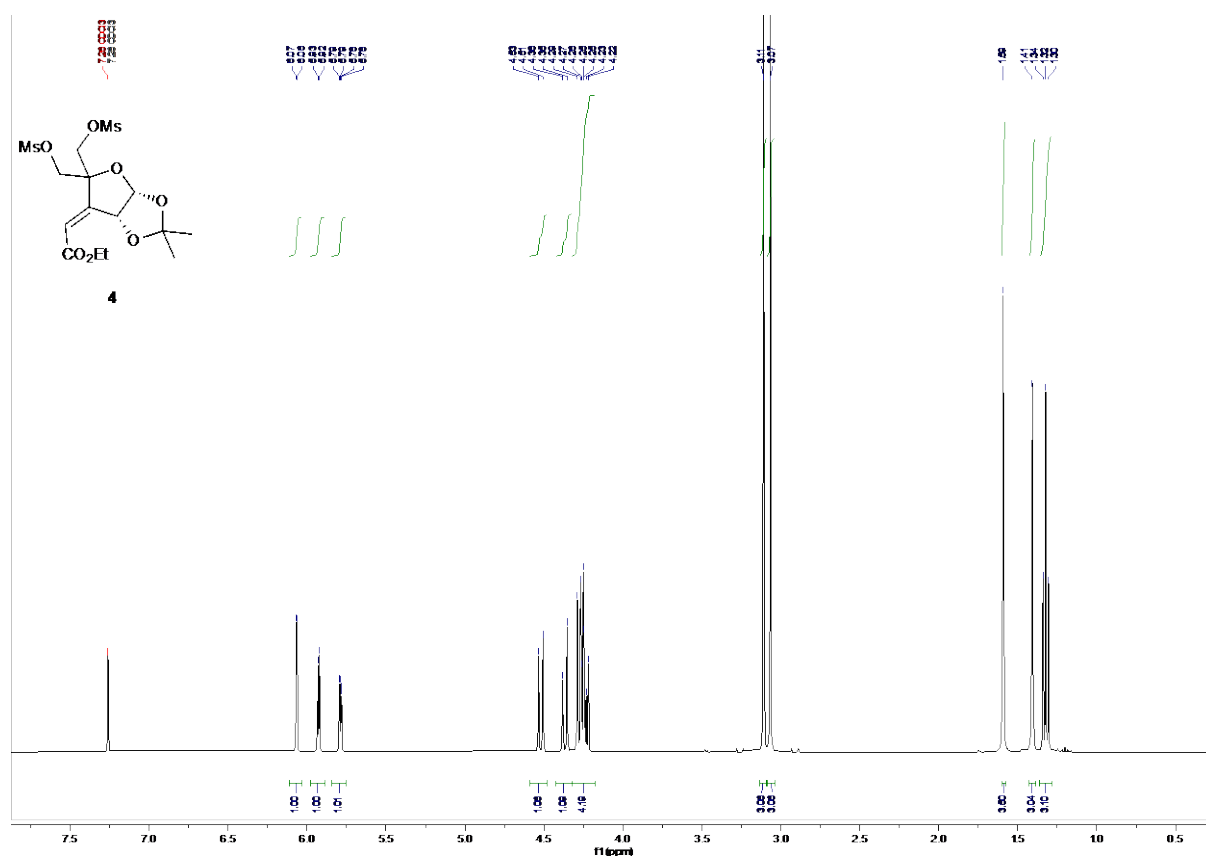
Crystal data and structure refinement for 5.

Empirical formula	C15 H26 O11 S2	
Formula weight	446.50	
Temperature	150 K	
Wavelength	1.54184 Å	
Crystal system	Monoclinic	
Space group	P 2 ₁	
Unit cell dimensions	a = 5.61600(10) Å	α = 90°.
	b = 18.1625(4) Å	β = 93.200(2)°.
	c = 19.9906(5) Å	γ = 90°.
Volume	2035.87(8) Å ³	
Z	4	
Density (calculated)	1.457 Mg/m ³	
Absorption coefficient	2.878 mm ⁻¹	
F(000)	944.000	
Crystal size	0.18 x 0.07 x 0.02 mm ³	
Theta range for data collection	3.290 to 76.463°.	
Index ranges	-6 ≤ h ≤ 6, -22 ≤ k ≤ 22, -24 ≤ l ≤ 25	
Reflections collected	24089	
Independent reflections	8349 [R(int) = 0.051]	
Completeness to theta = 74.169°	99.6 %	
Absorption correction	Semi-empirical from equivalents	
Max. and min. transmission	0.94 and 0.83	
Refinement method	Full-matrix least-squares on F ²	
Data / restraints / parameters	8348 / 143 / 553	
Goodness-of-fit on F ²	0.9988	
Final R indices [I > 2σ(I)]	R1 = 0.0399, wR2 = 0.0927	
R indices (all data)	R1 = 0.0457, wR2 = 0.0978	
Absolute structure parameter	-0.010(9)	
Largest diff. peak and hole	0.47 and -0.25 e.Å ⁻³	

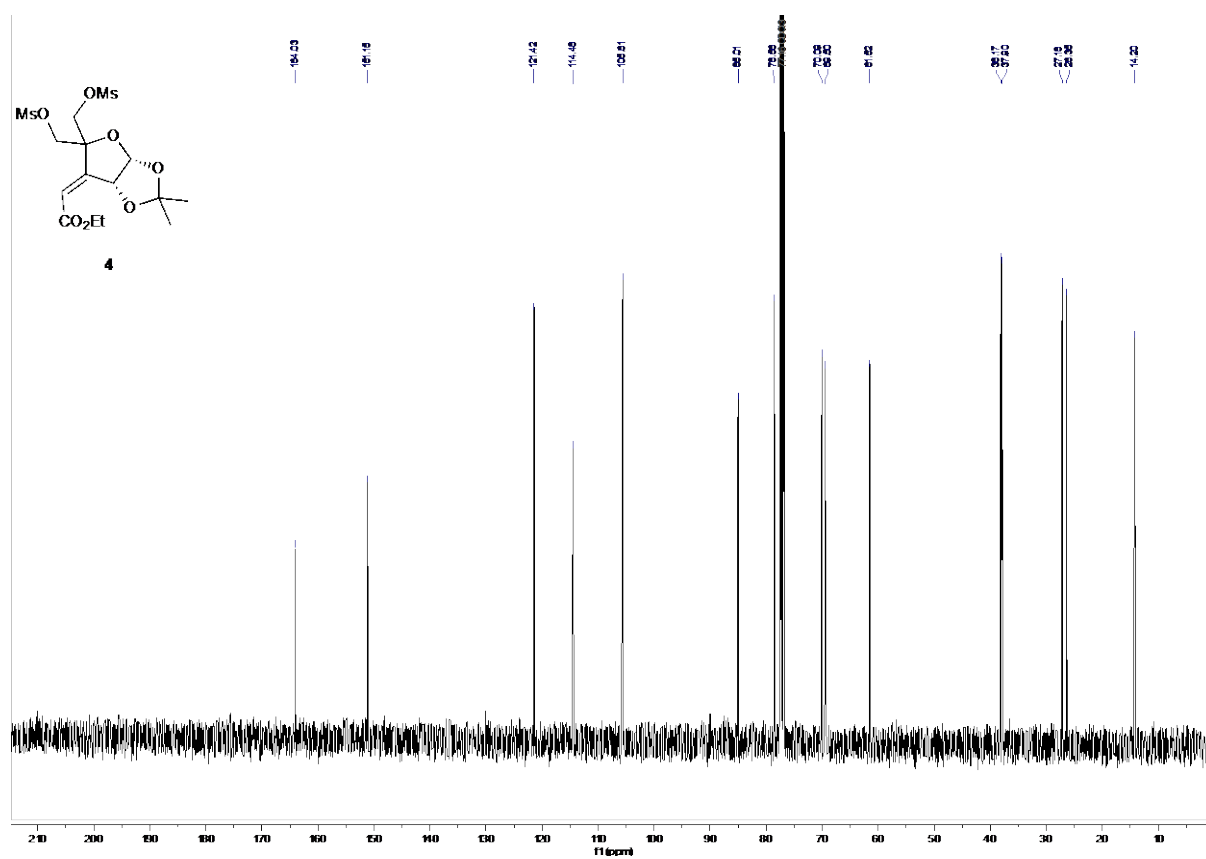
NMR spectra of compounds 2-9e



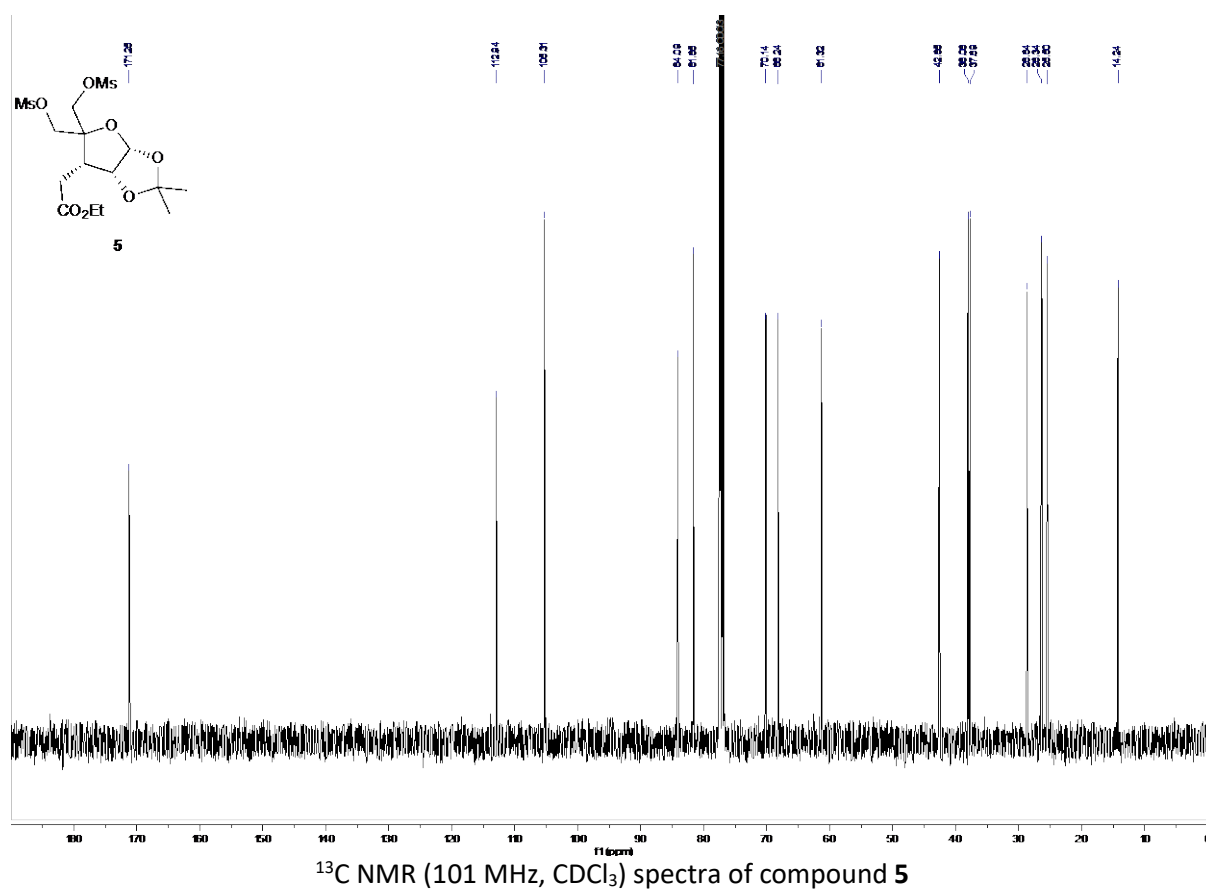
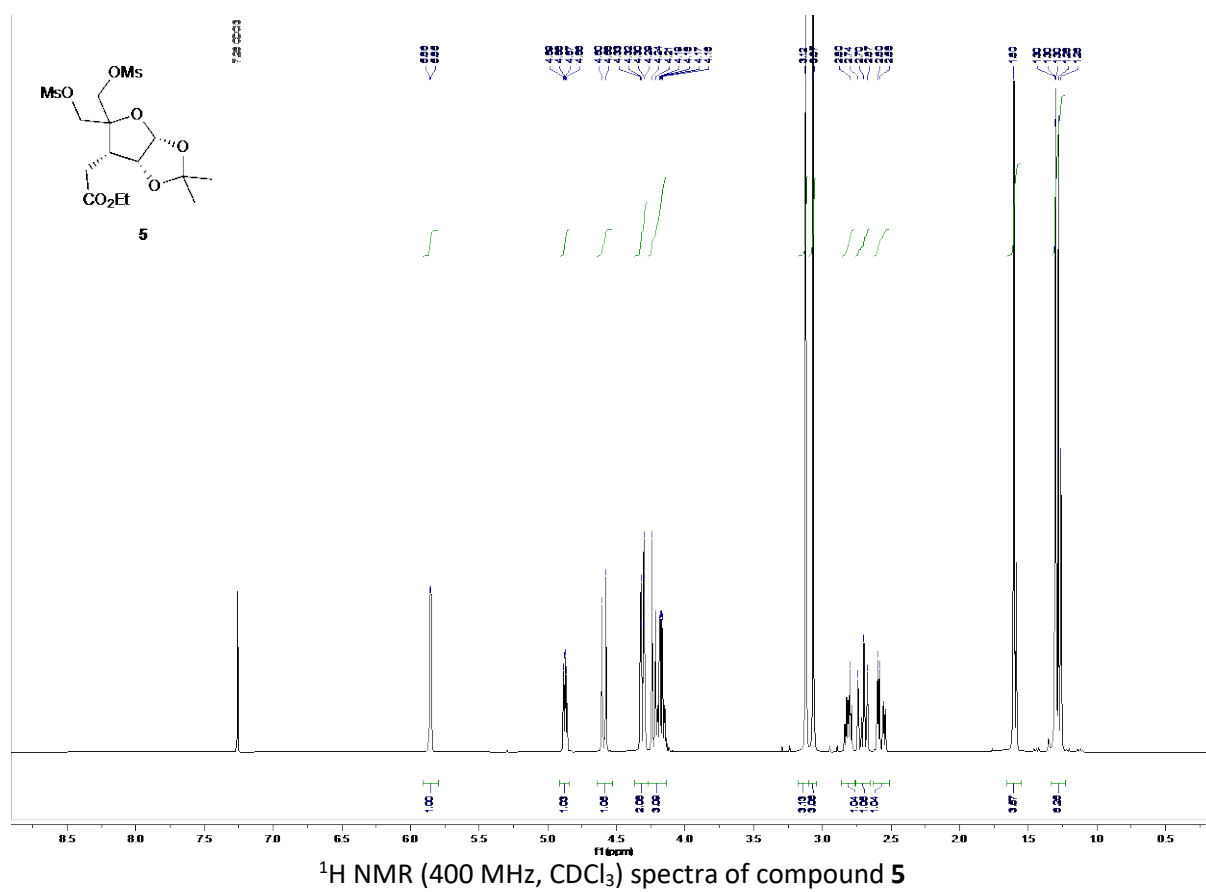


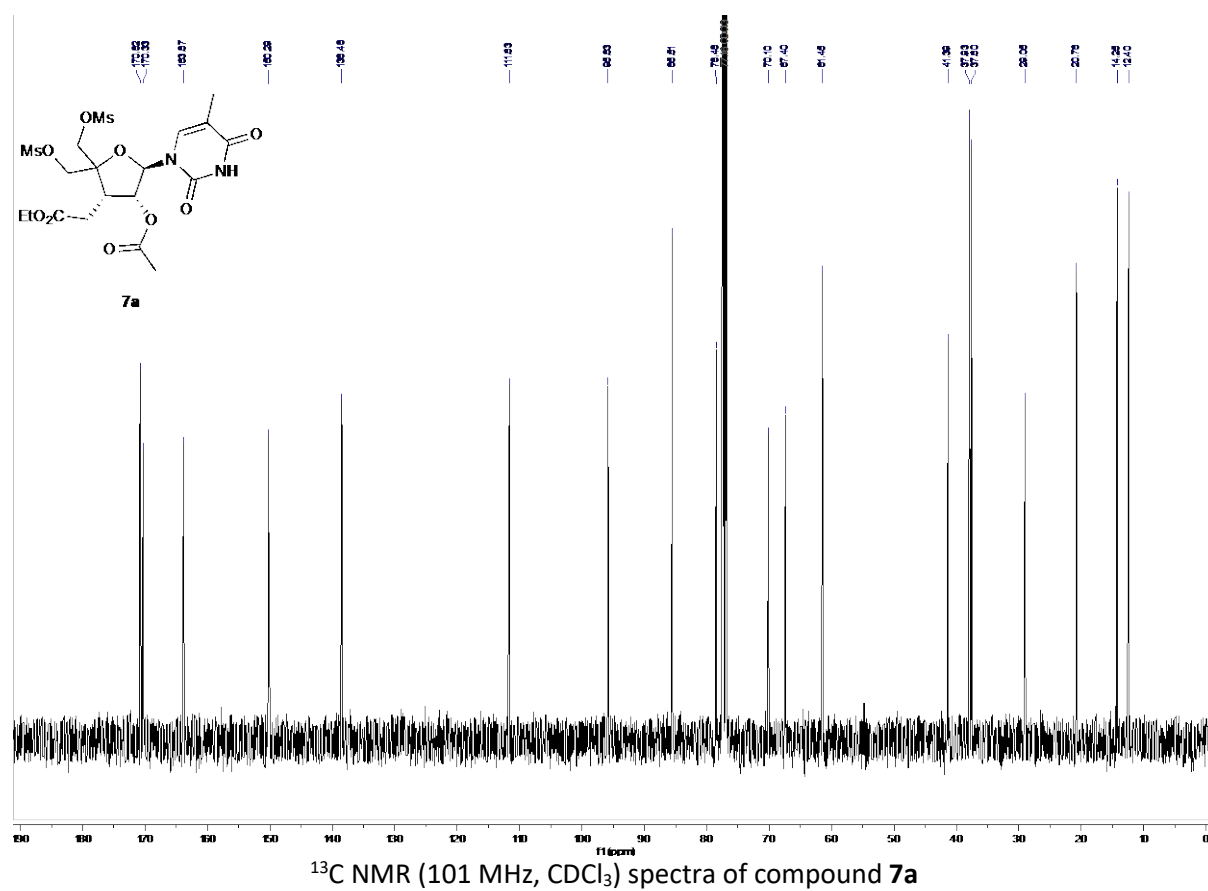
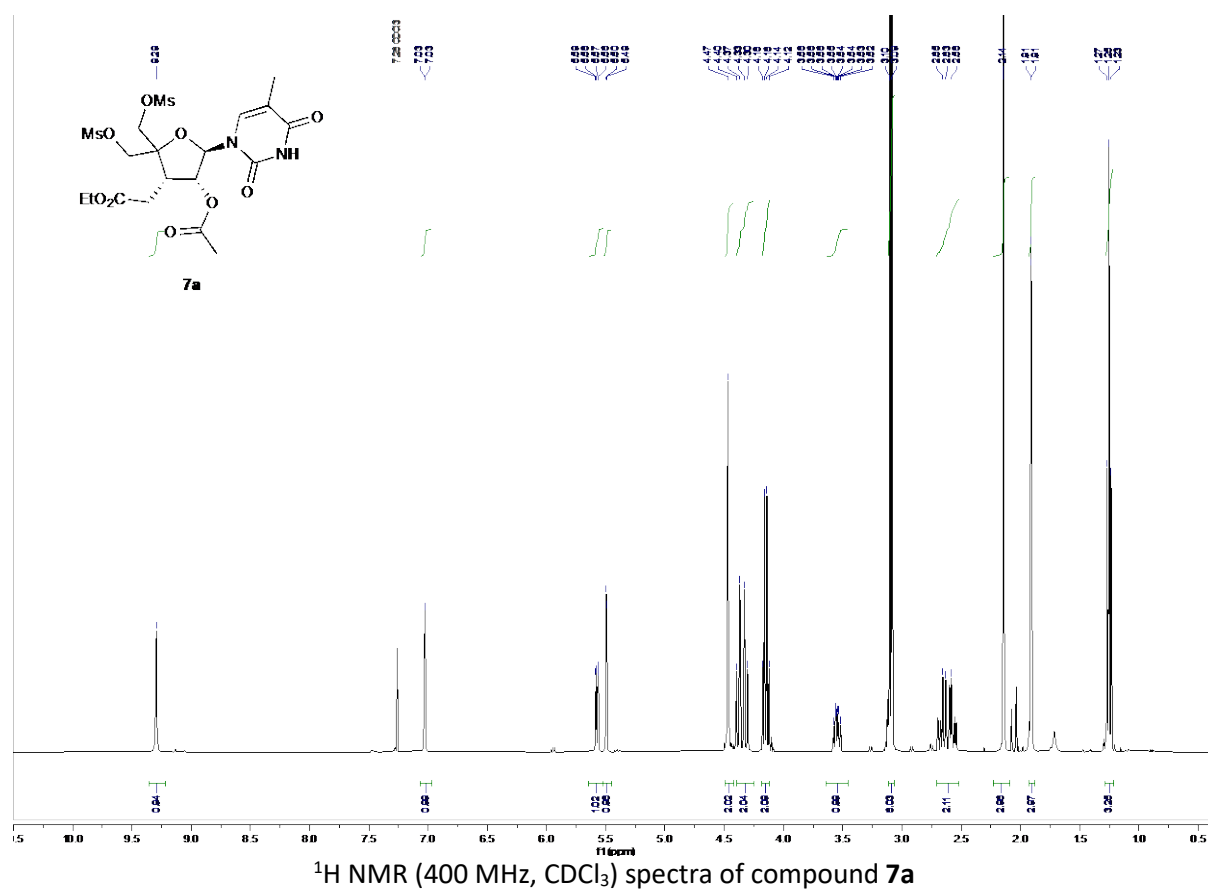


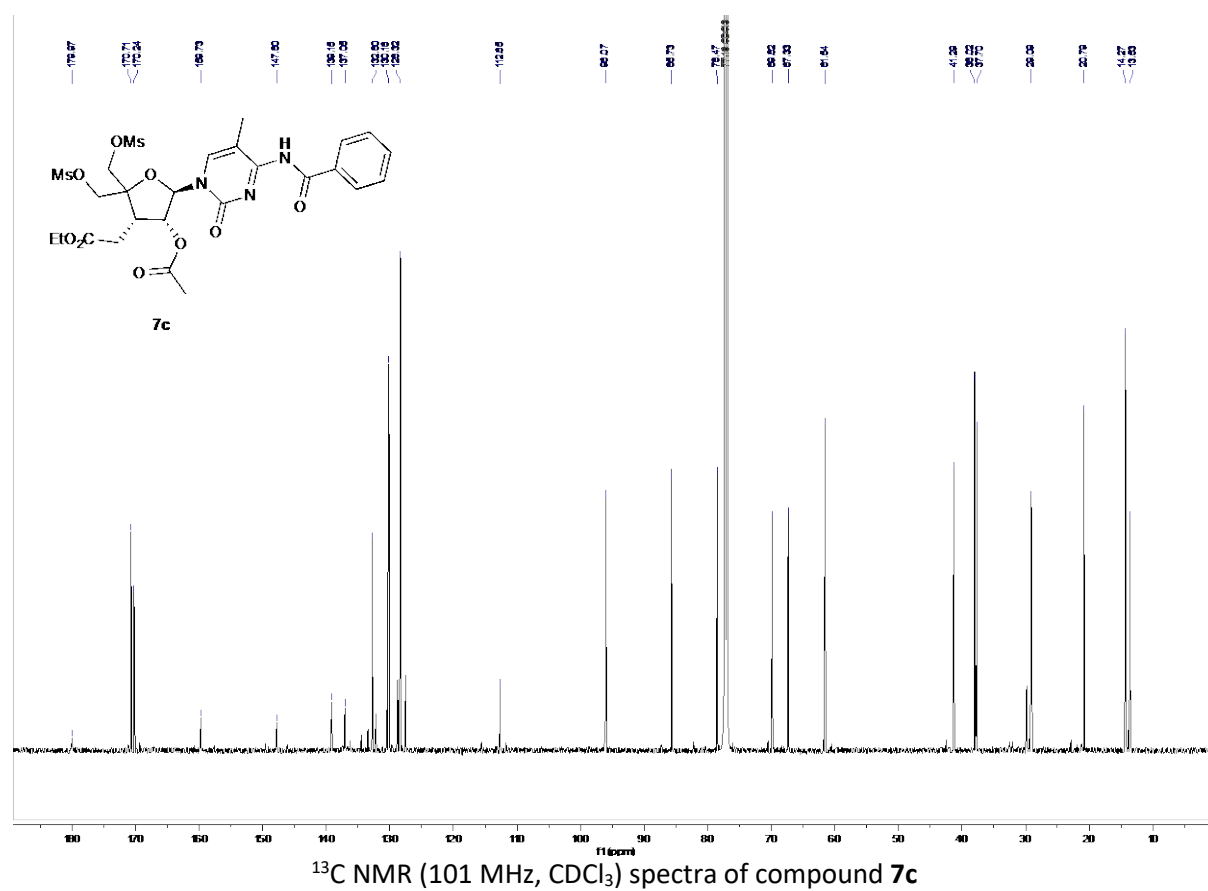
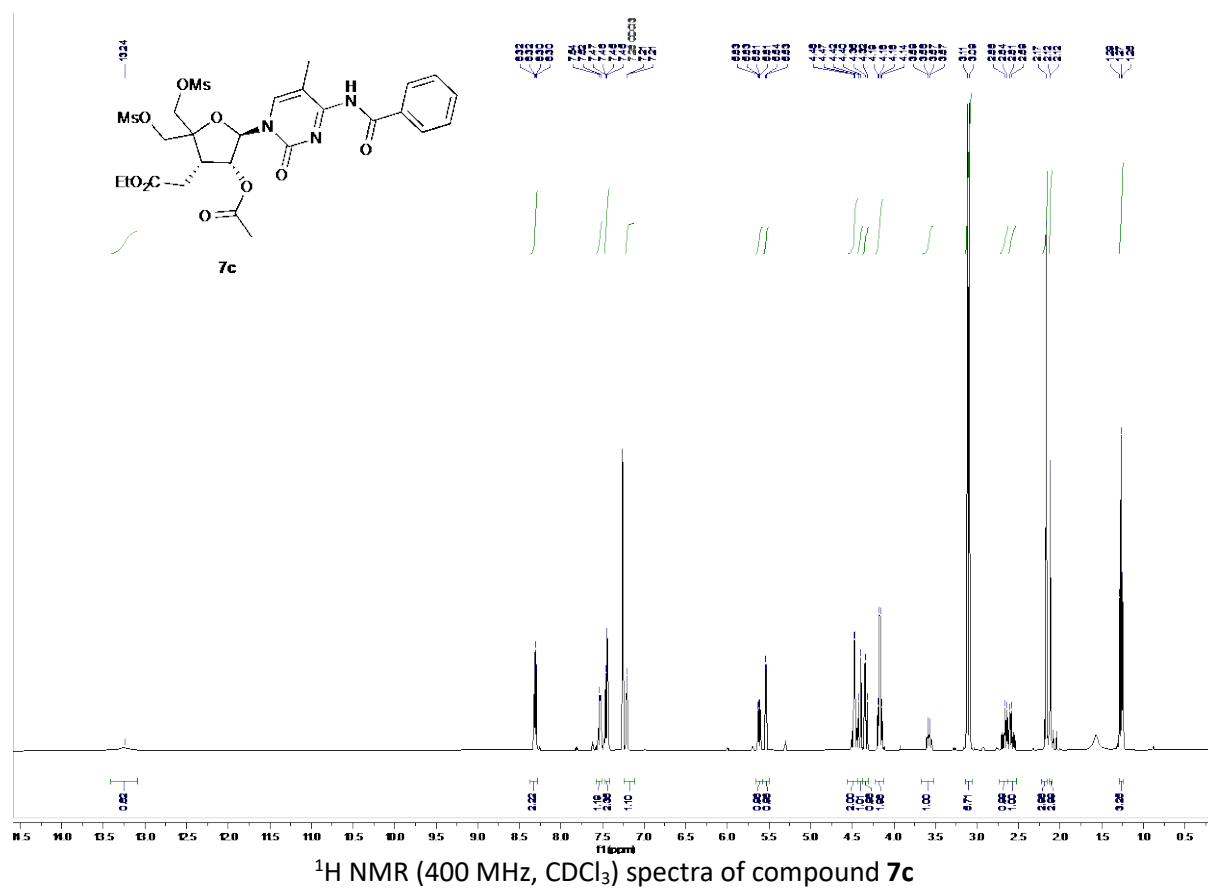
¹H NMR (400 MHz, CDCl₃) spectra of compound **4**

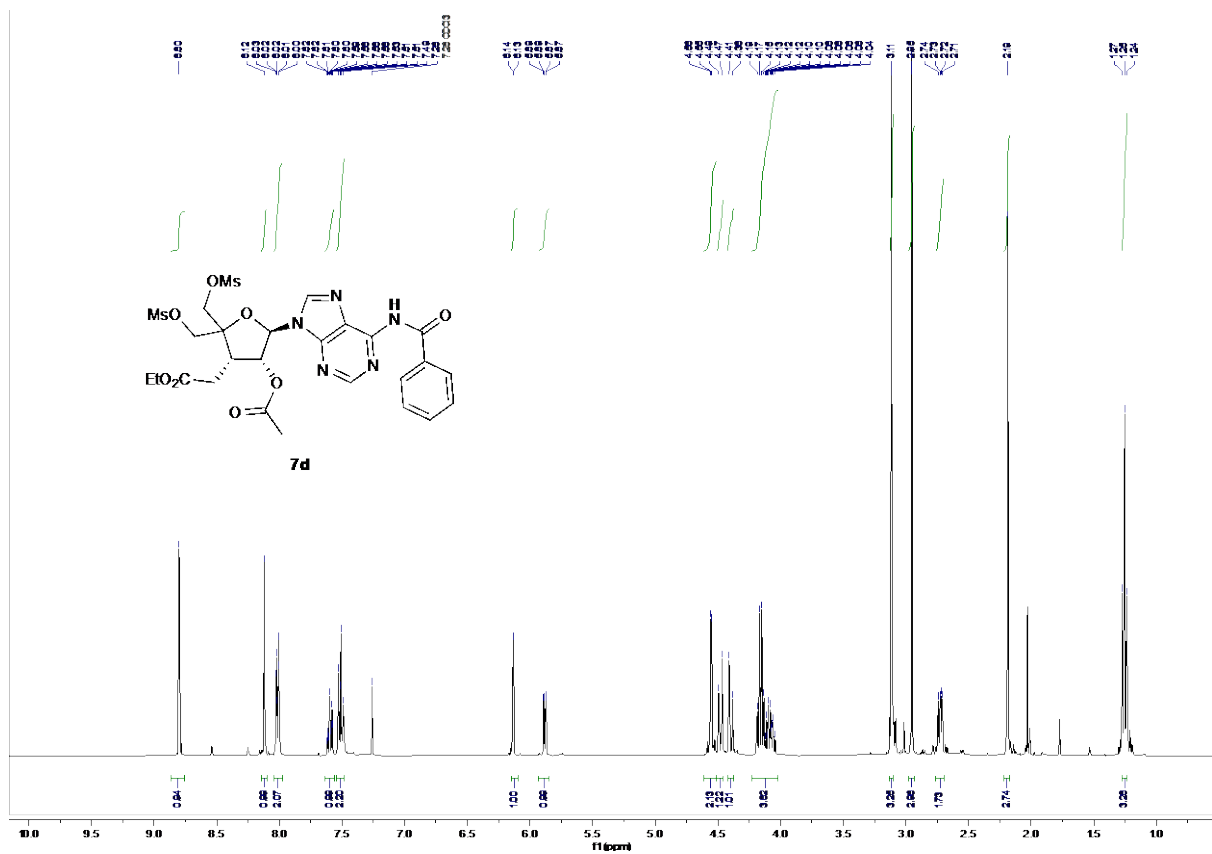


¹³C NMR (101 MHz, CDCl₃) spectra of compound **4**

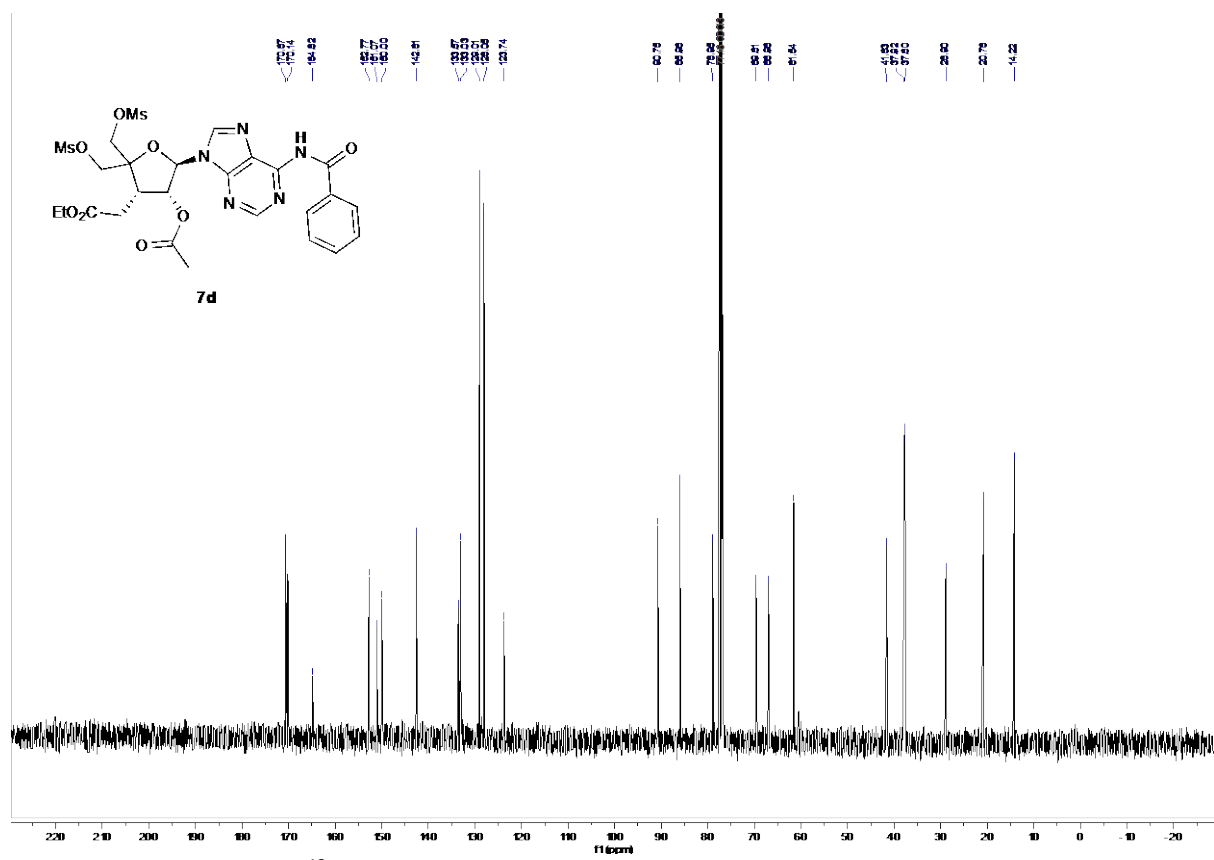




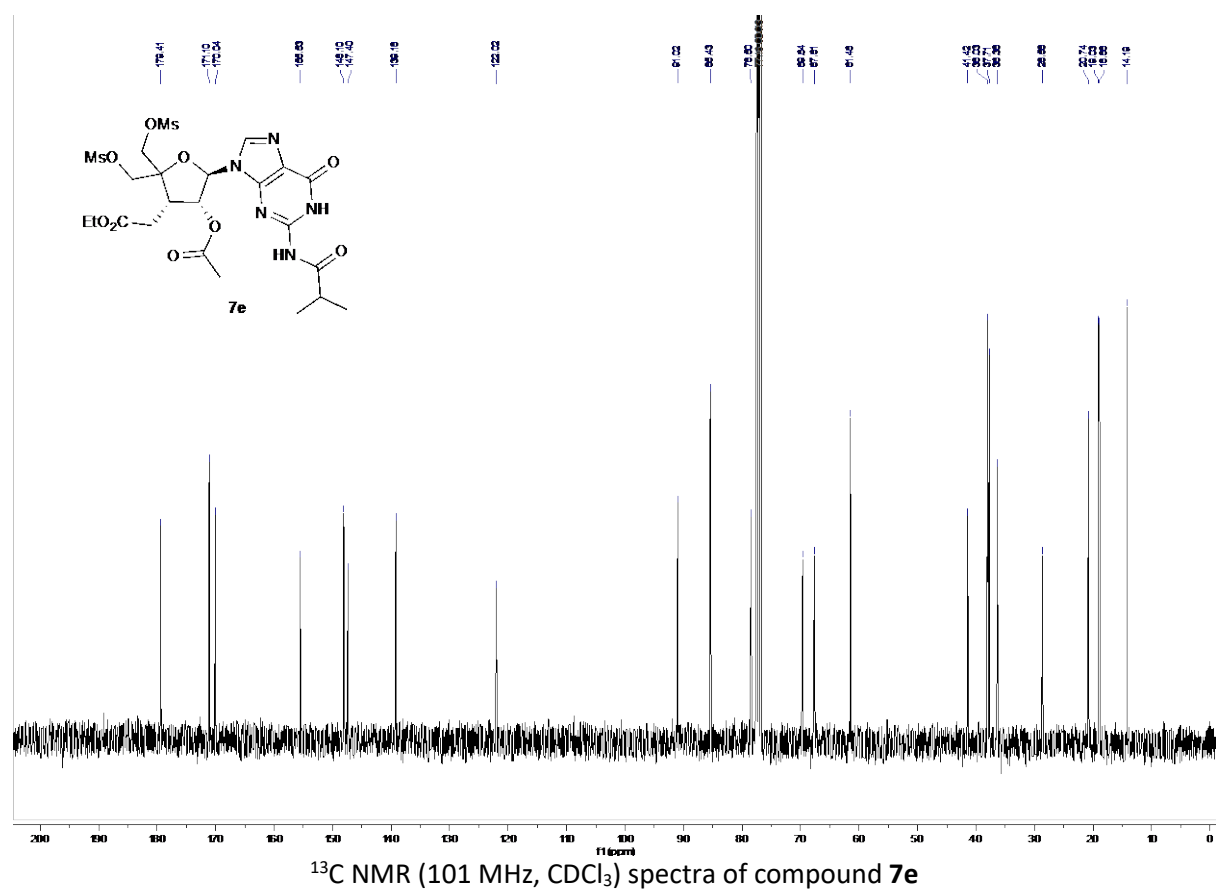
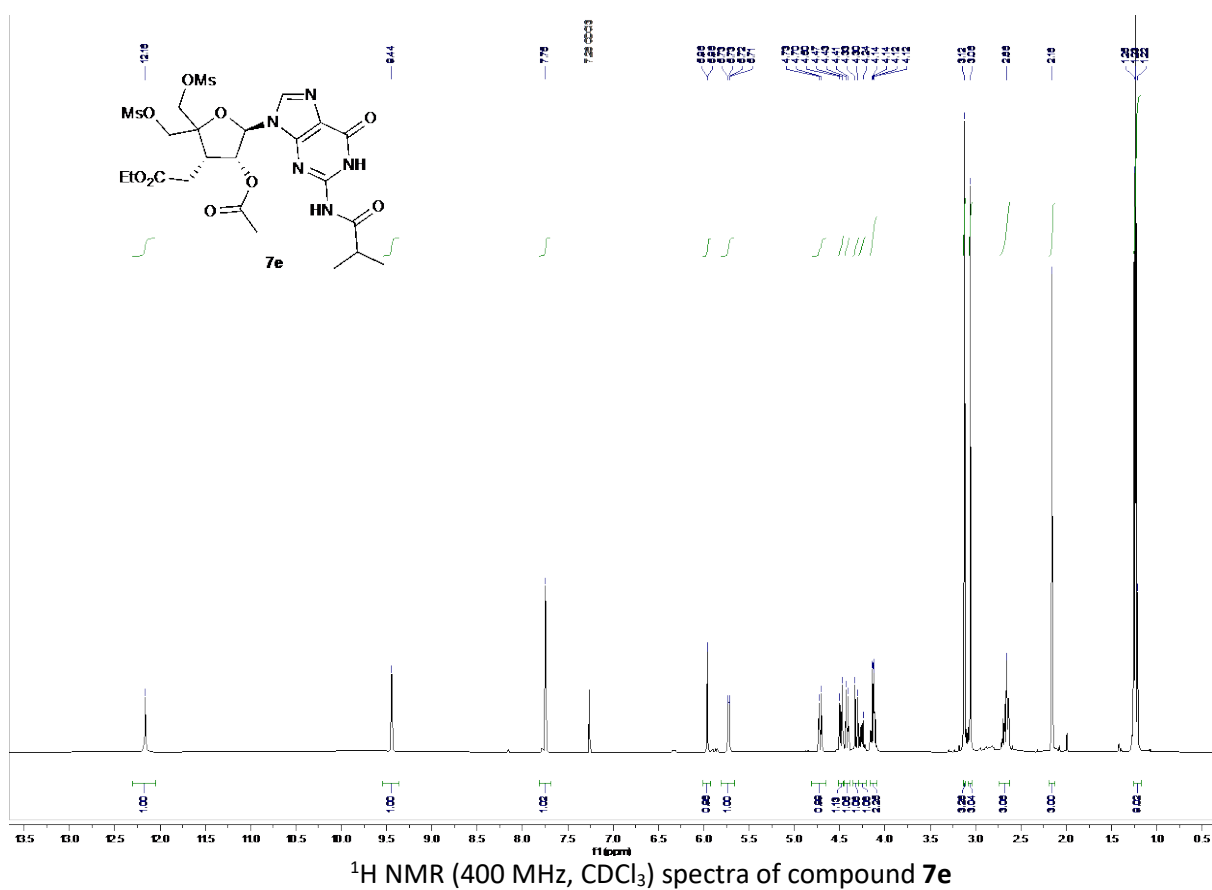


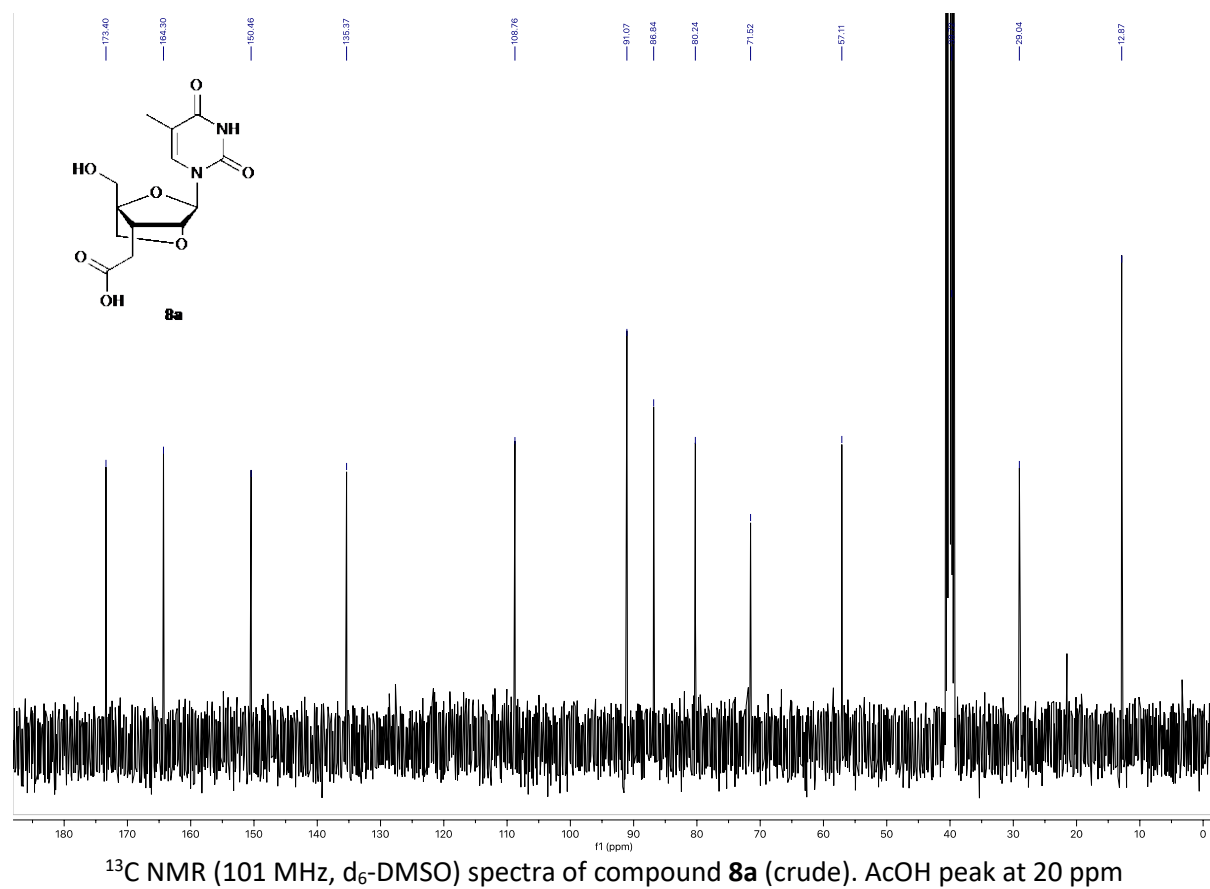
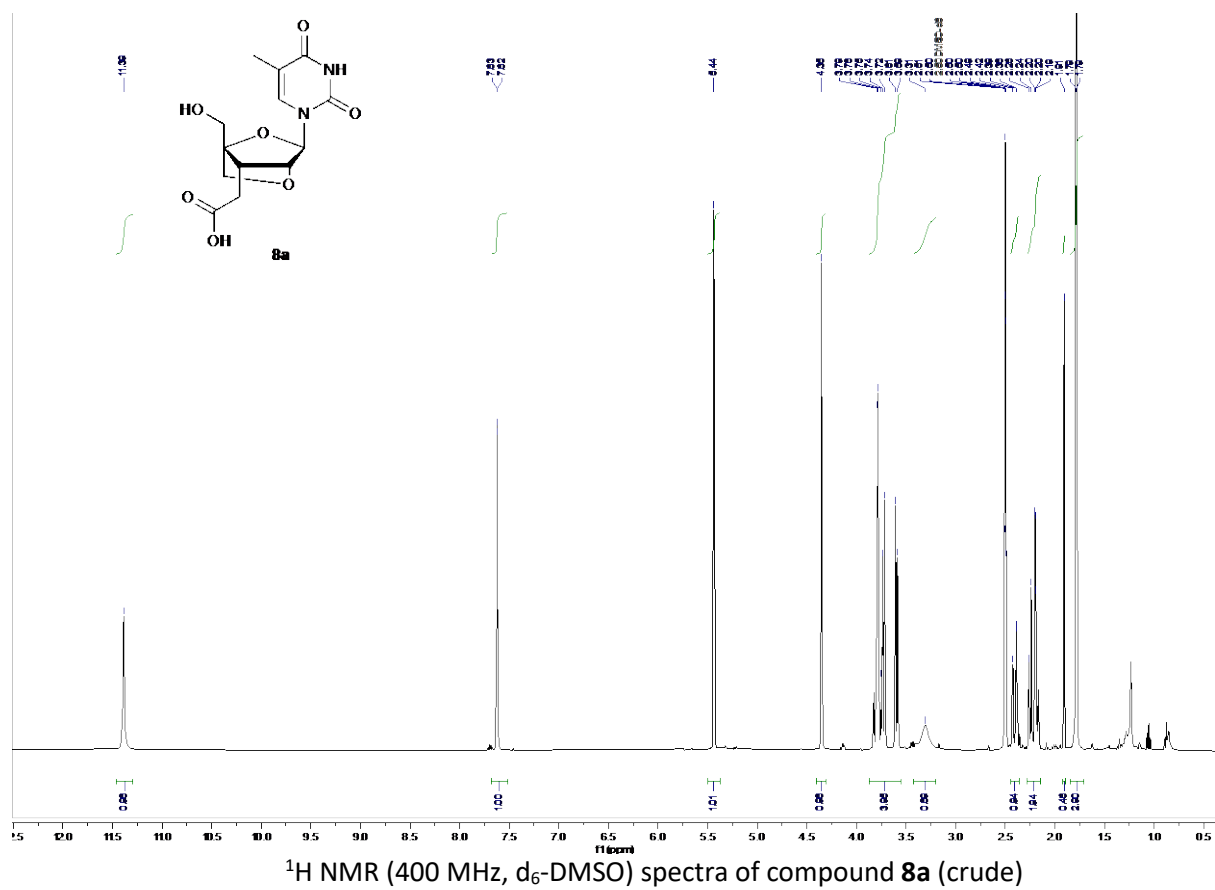


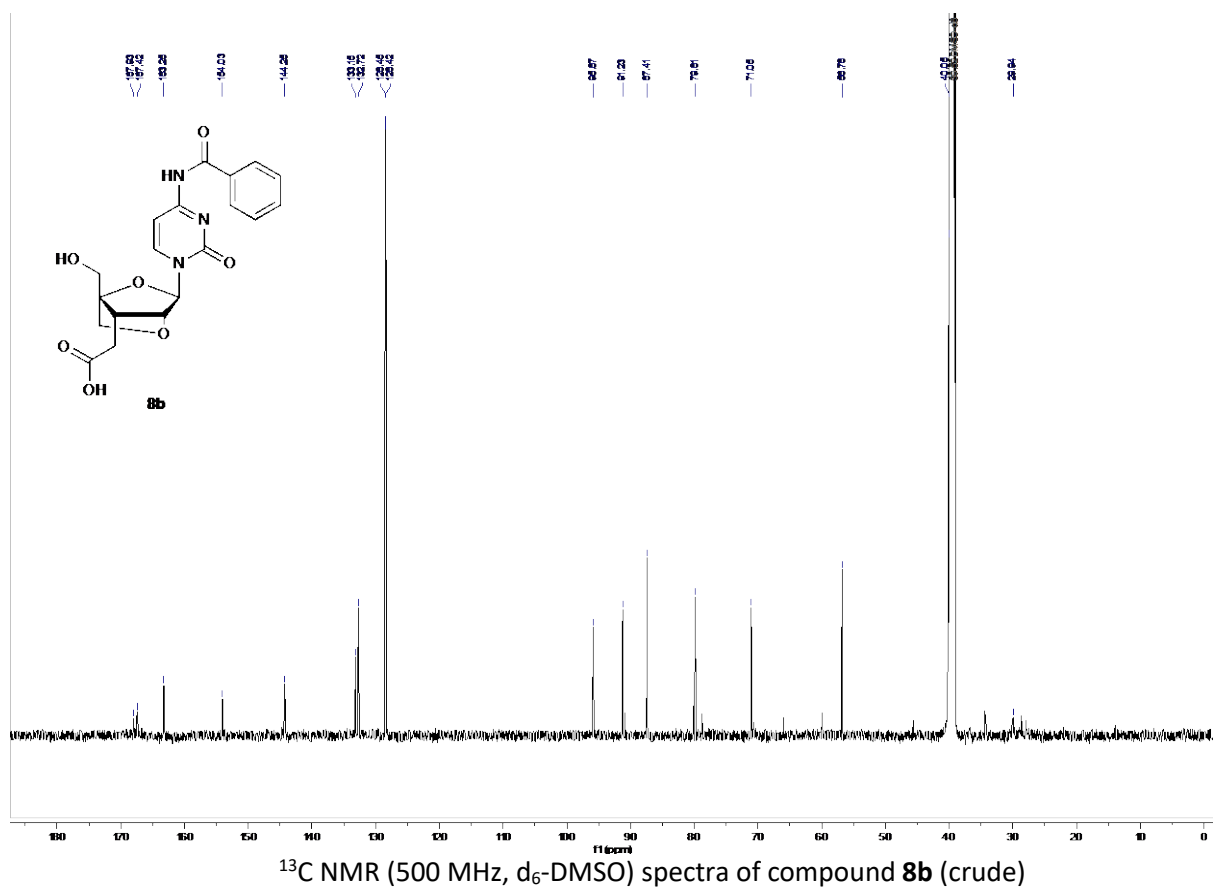
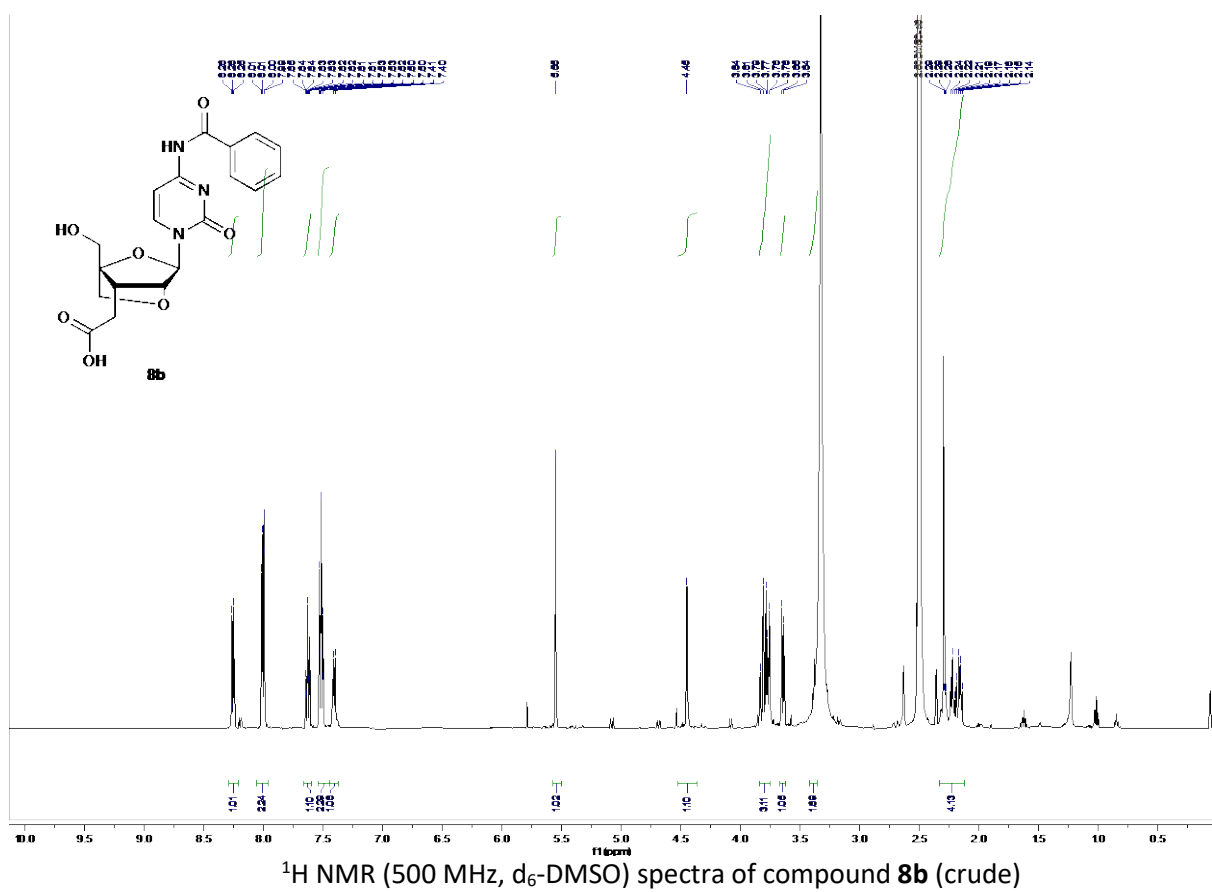
¹H NMR (400 MHz, CDCl₃) spectra of compound **7d**

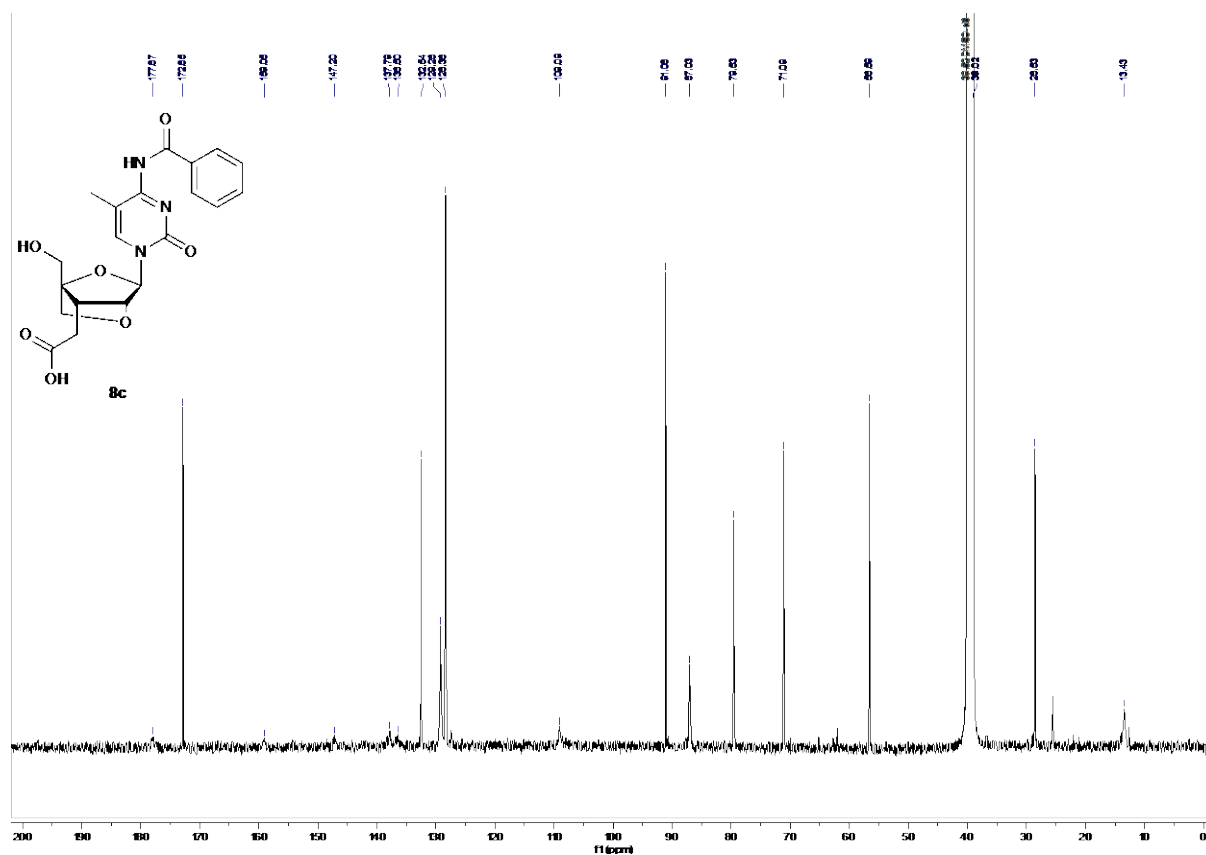
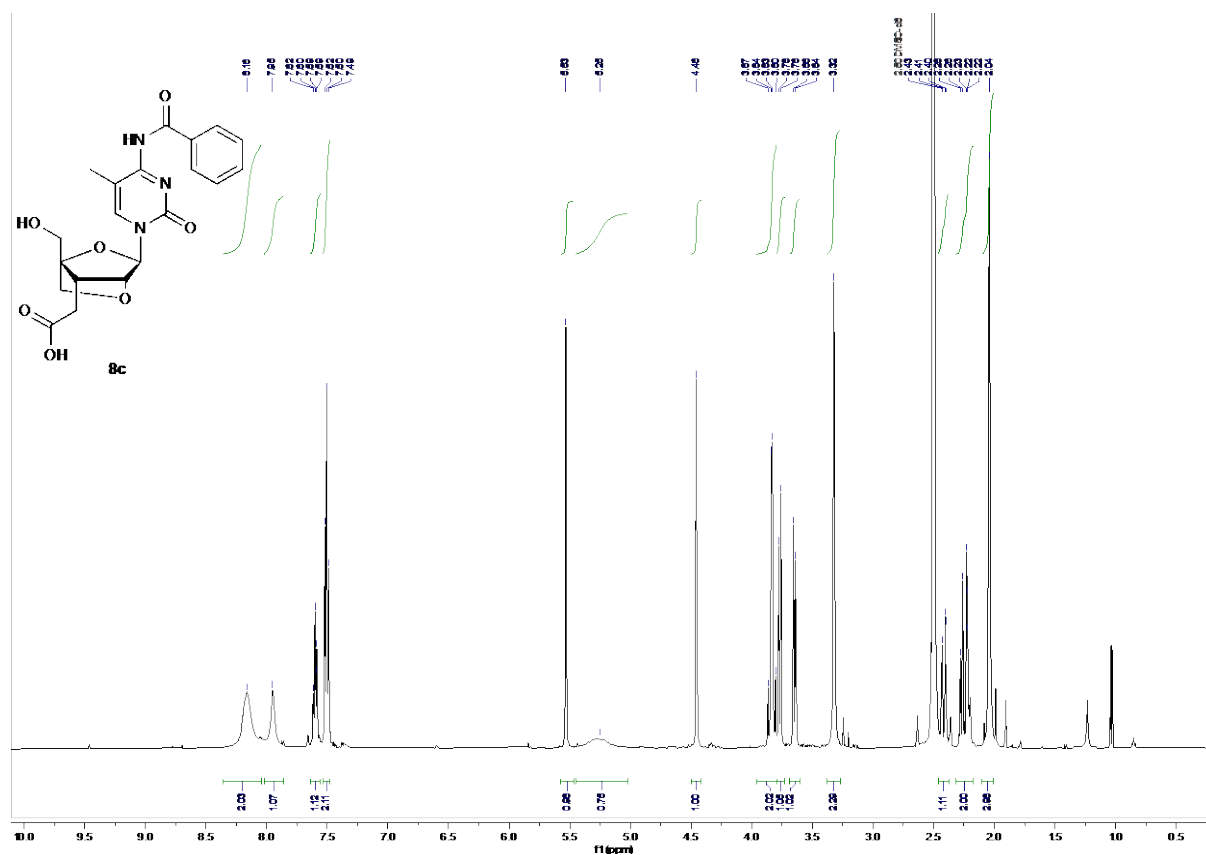


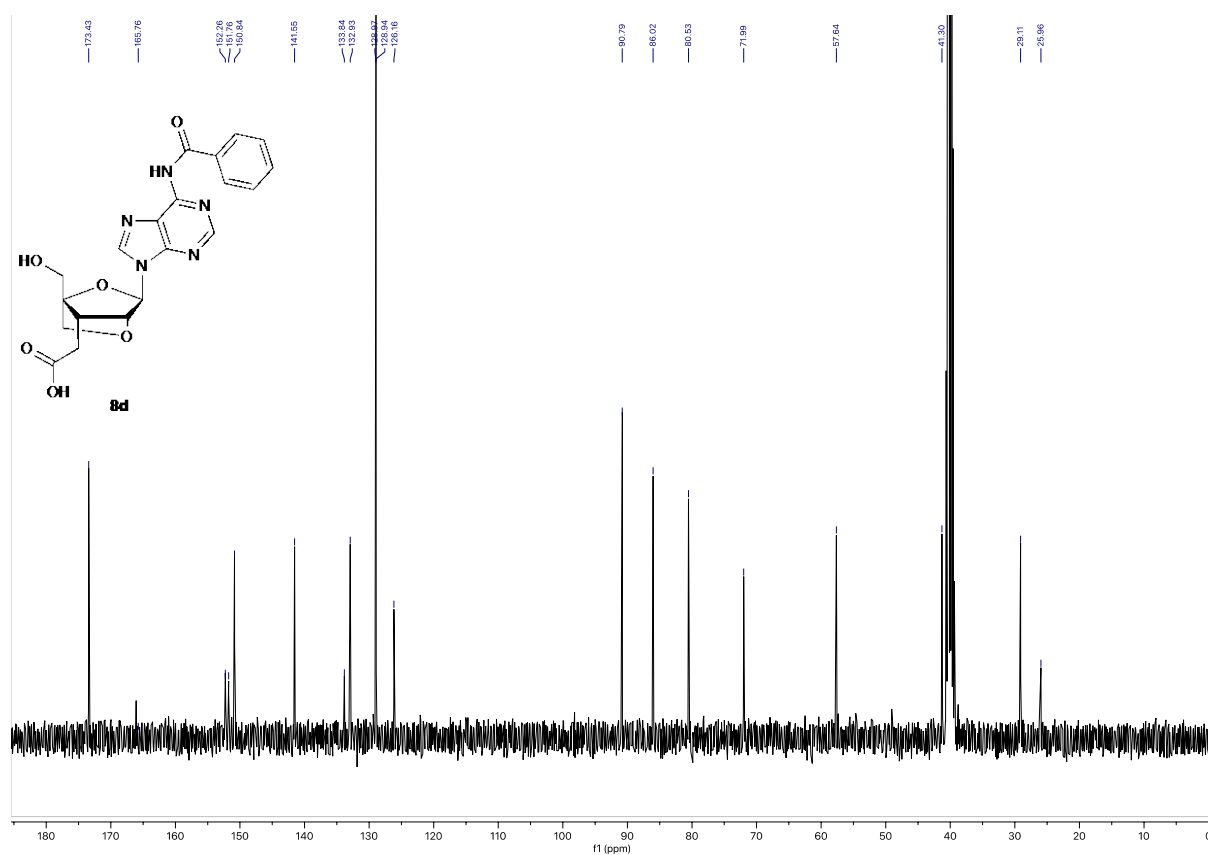
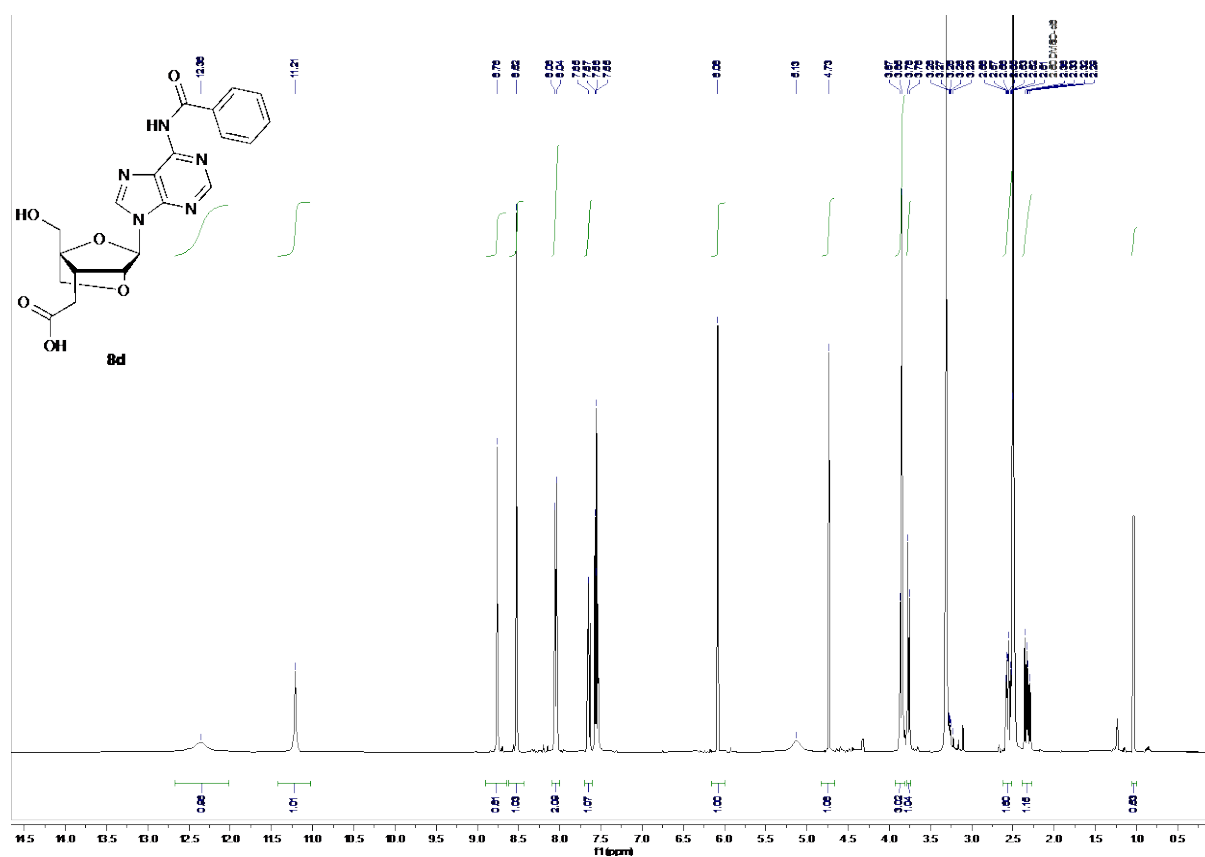
¹³C NMR (101 MHz, CDCl₃) spectra of compound **7d**

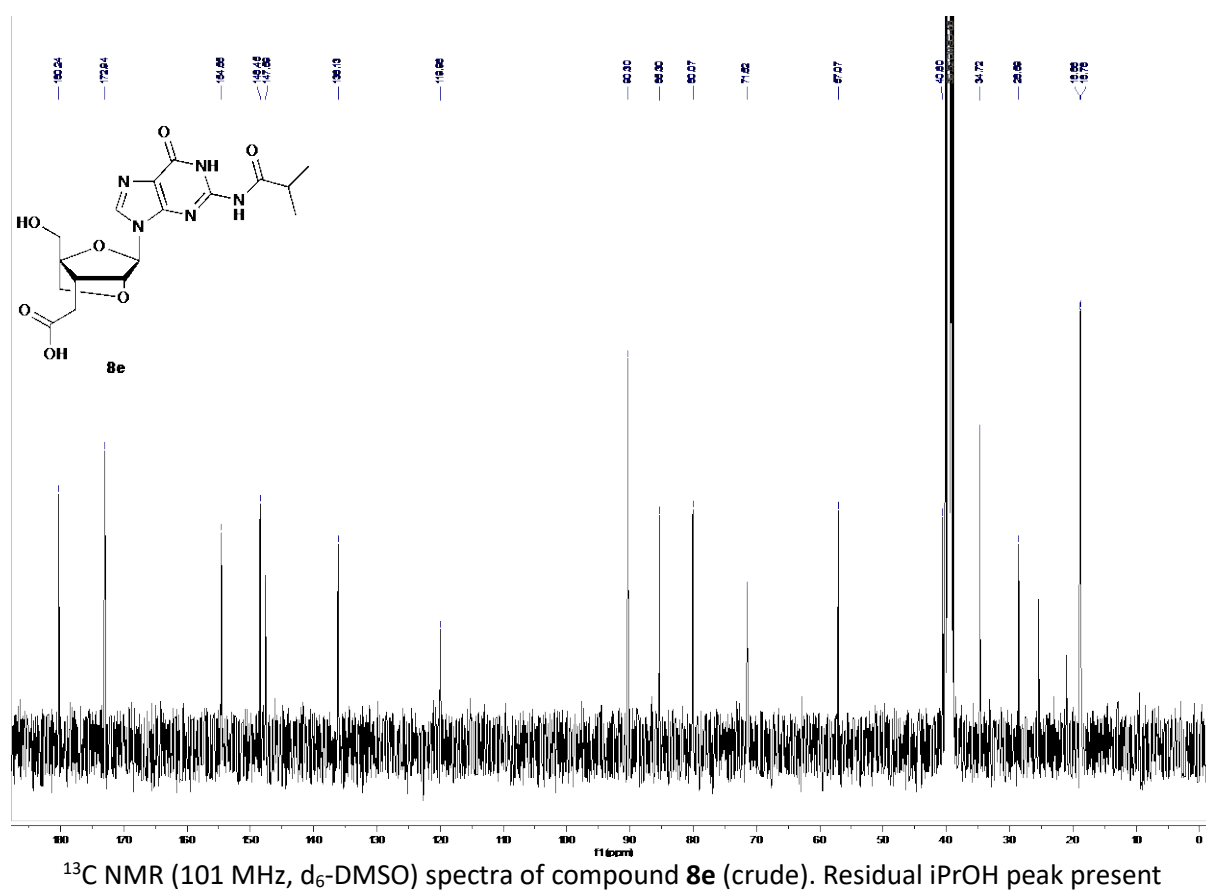
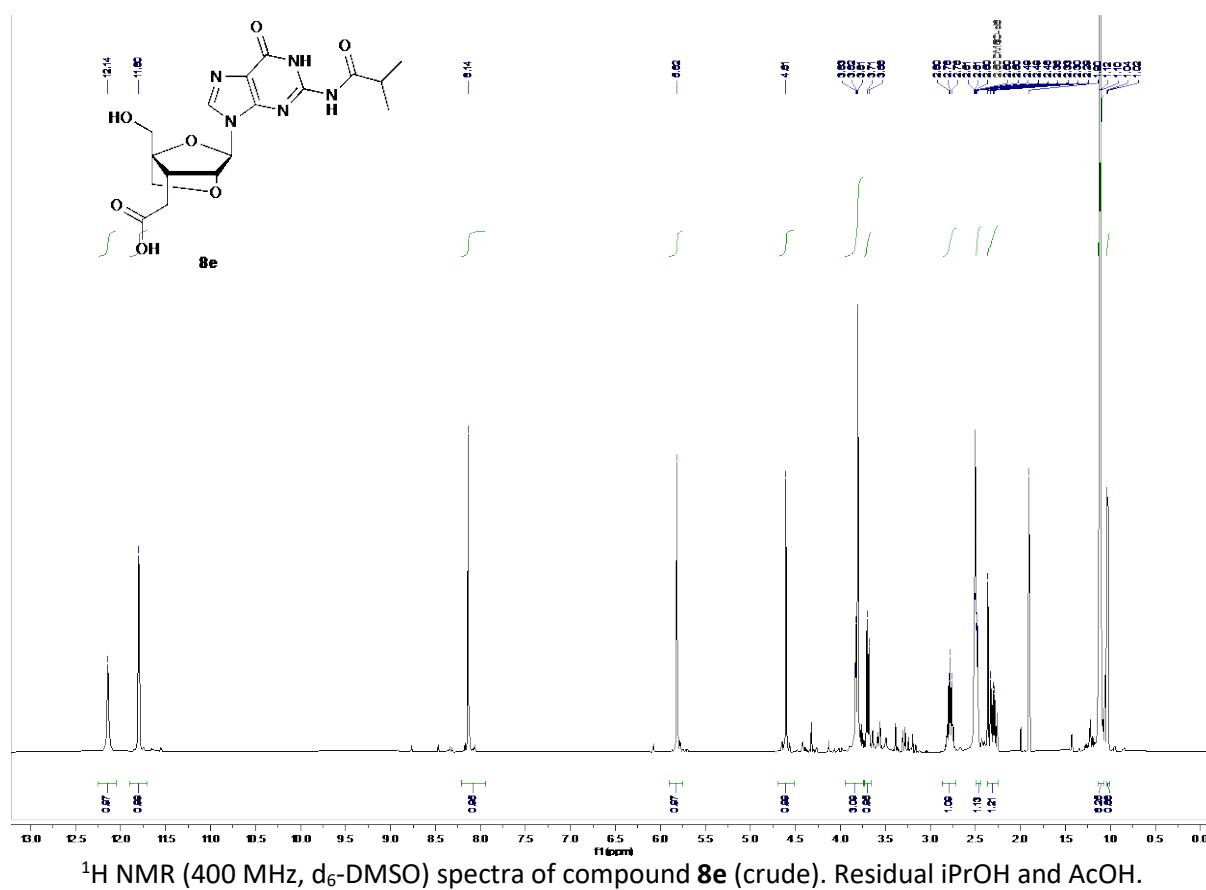


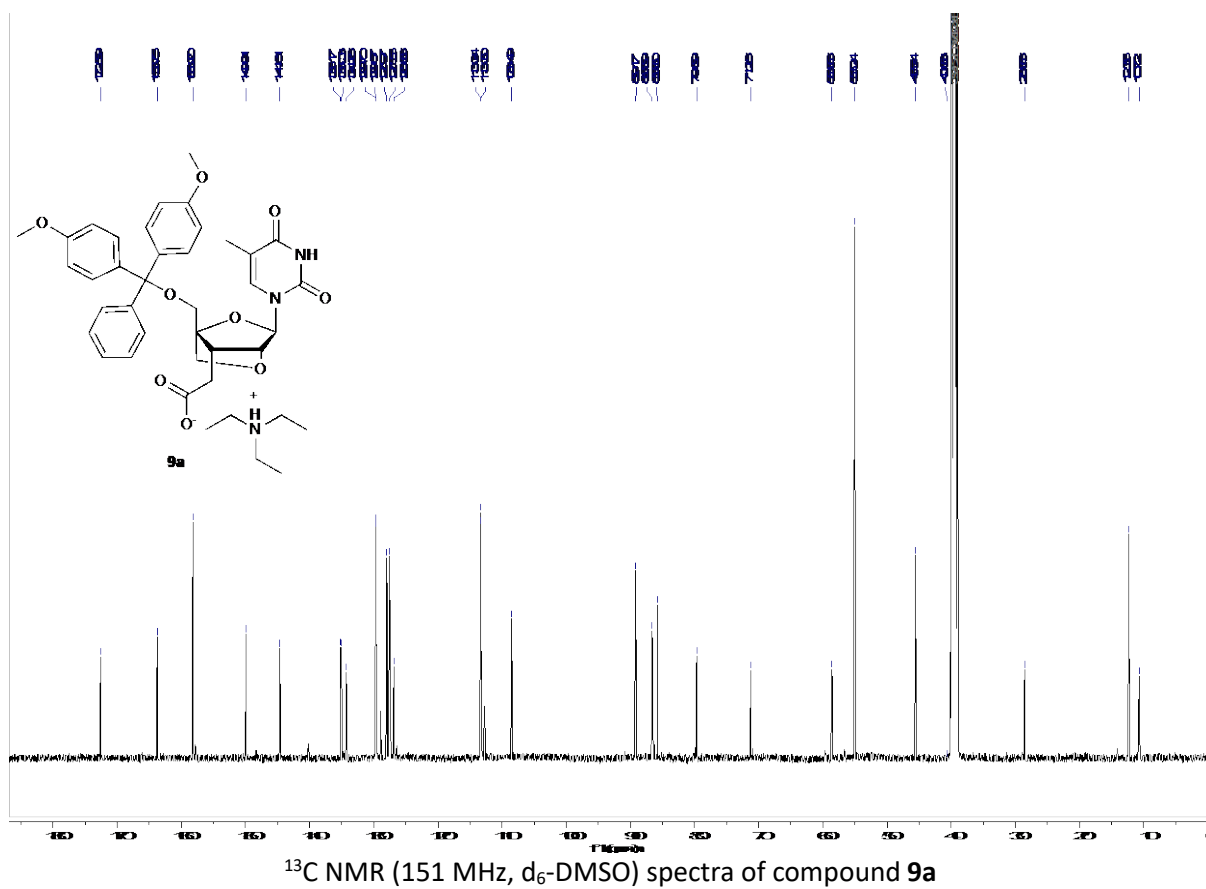
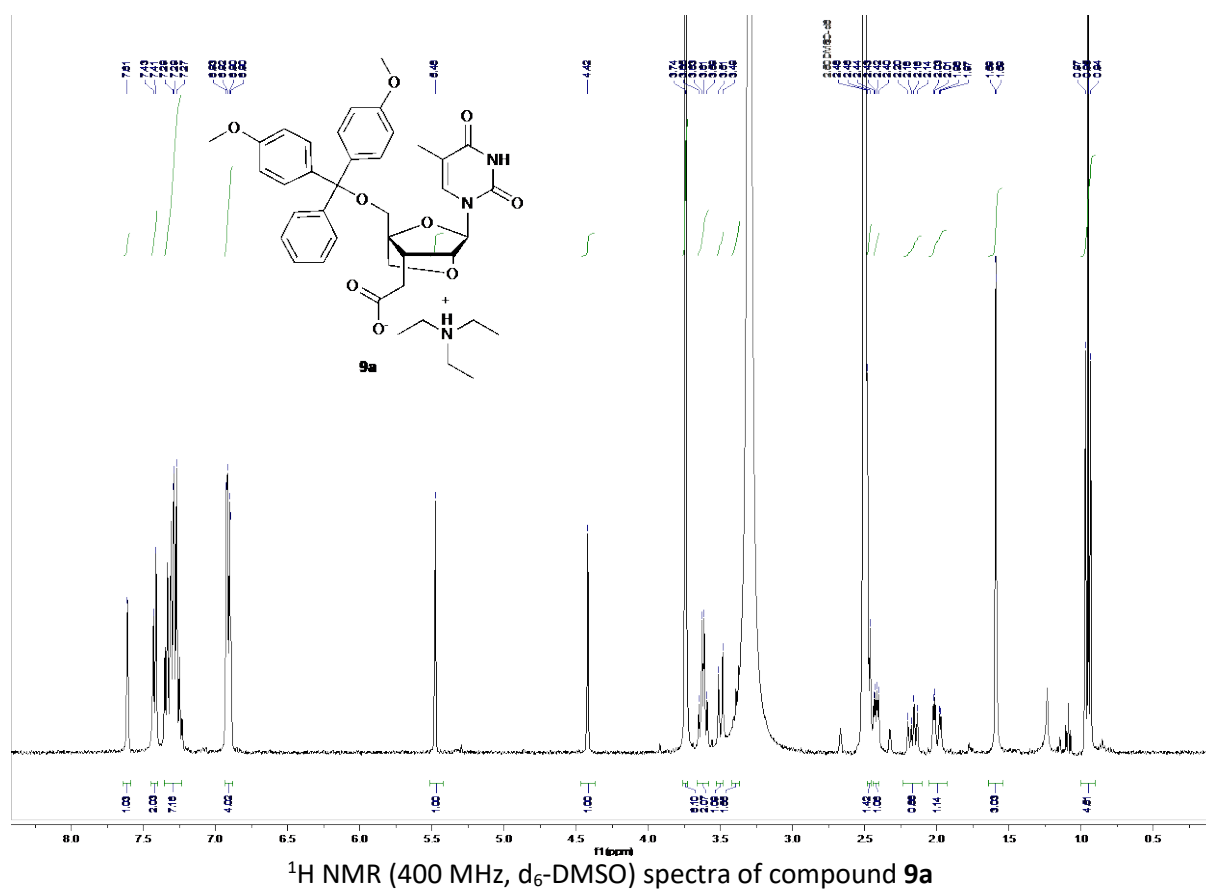


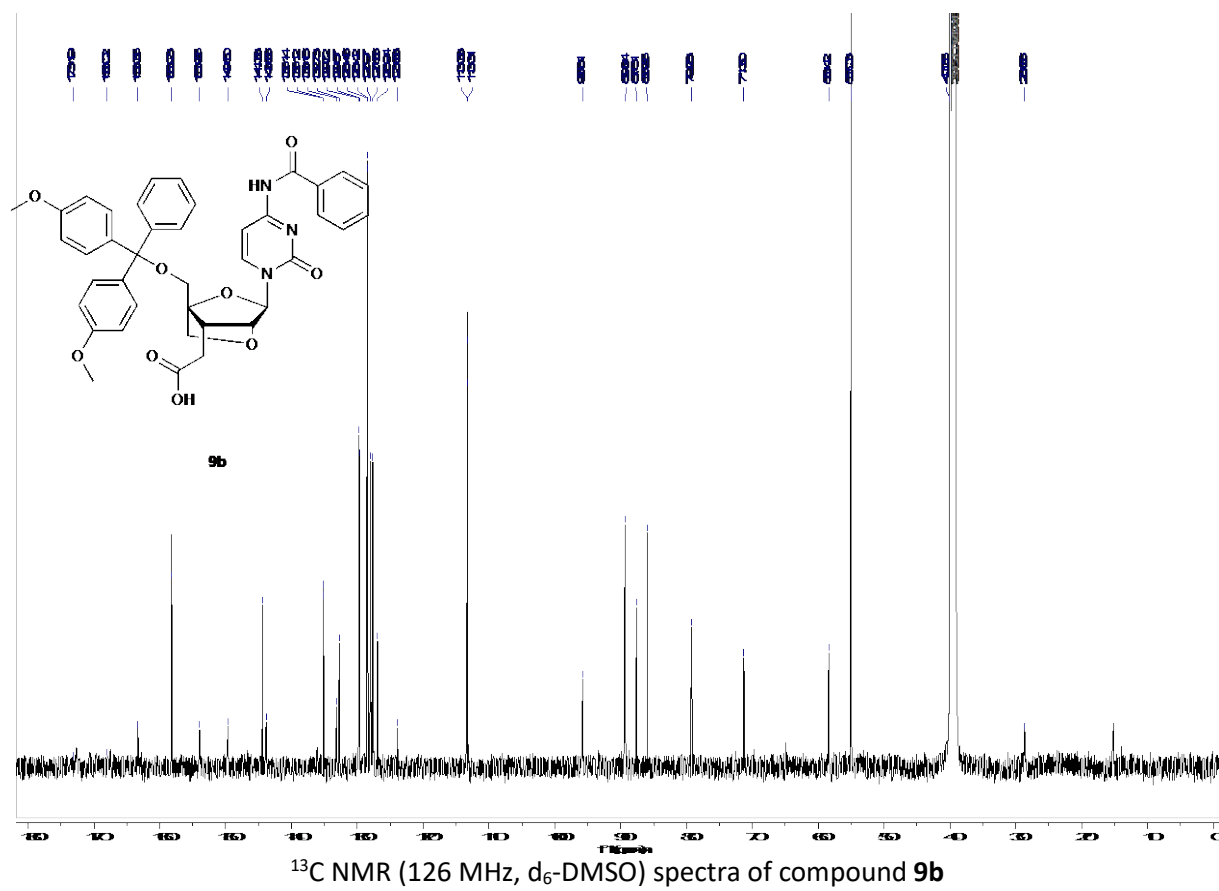
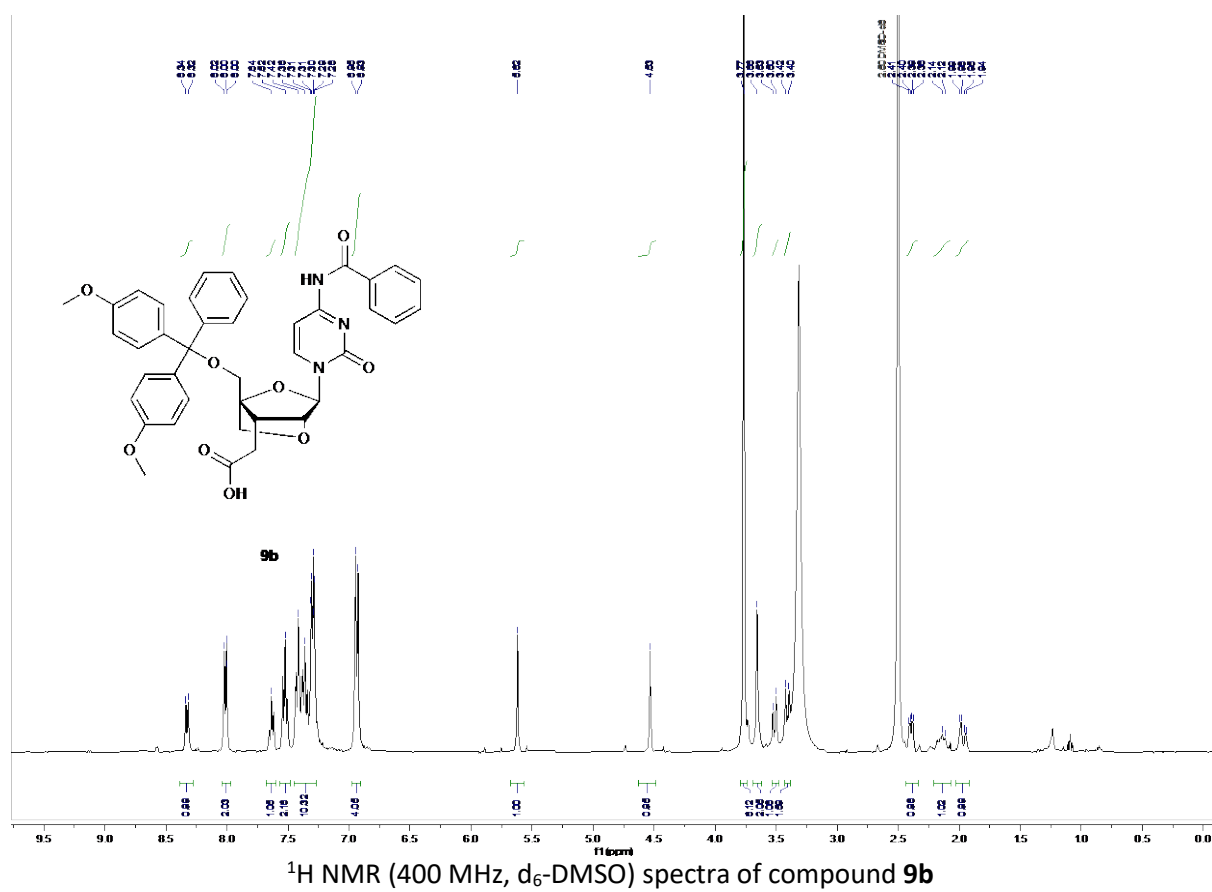


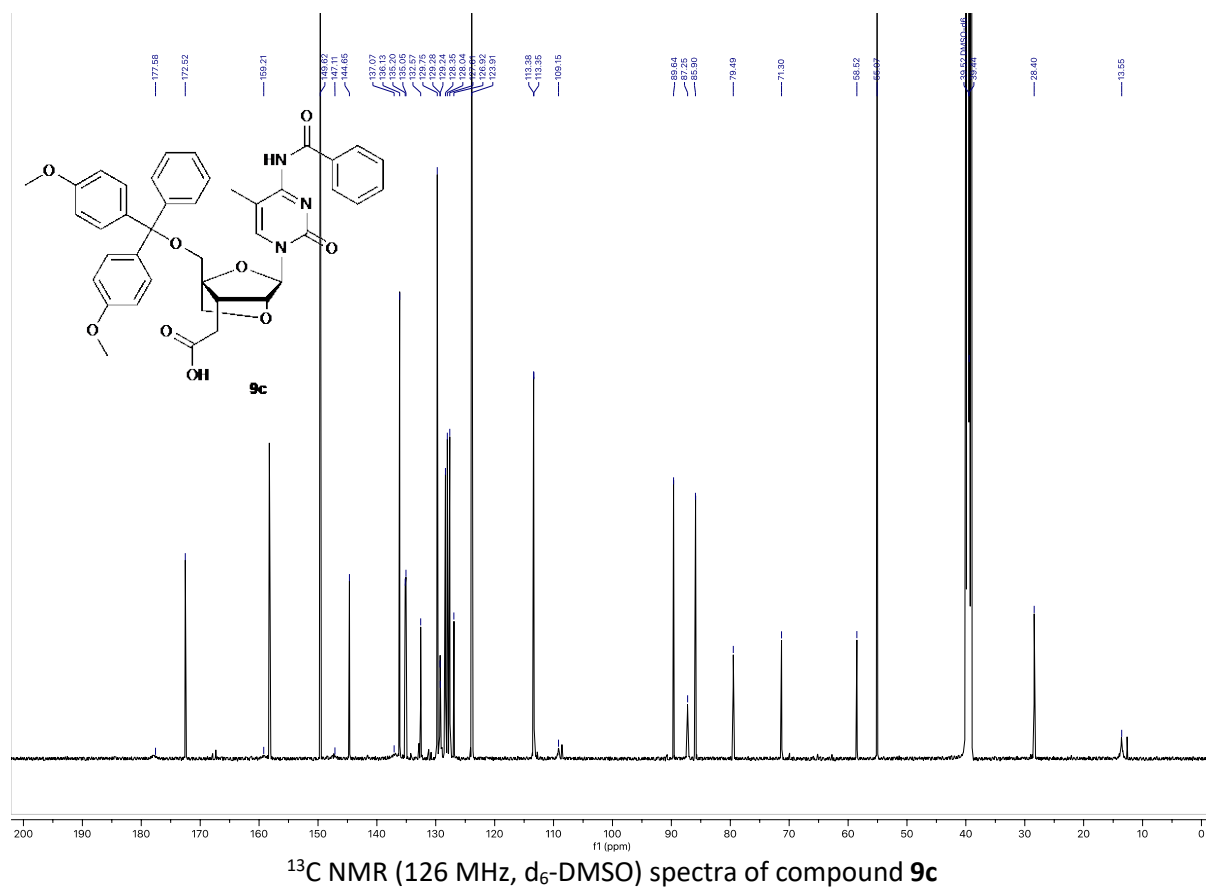
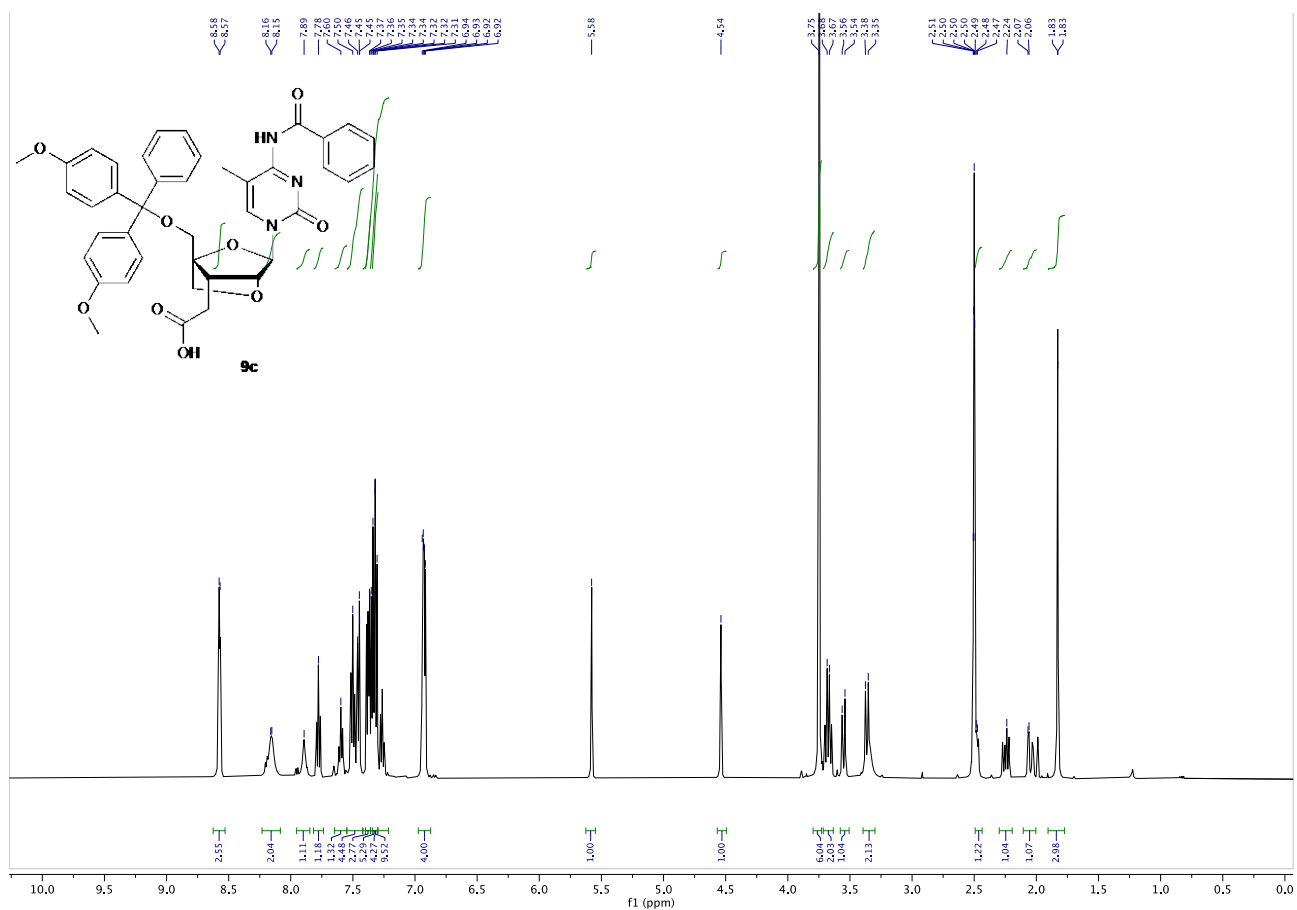


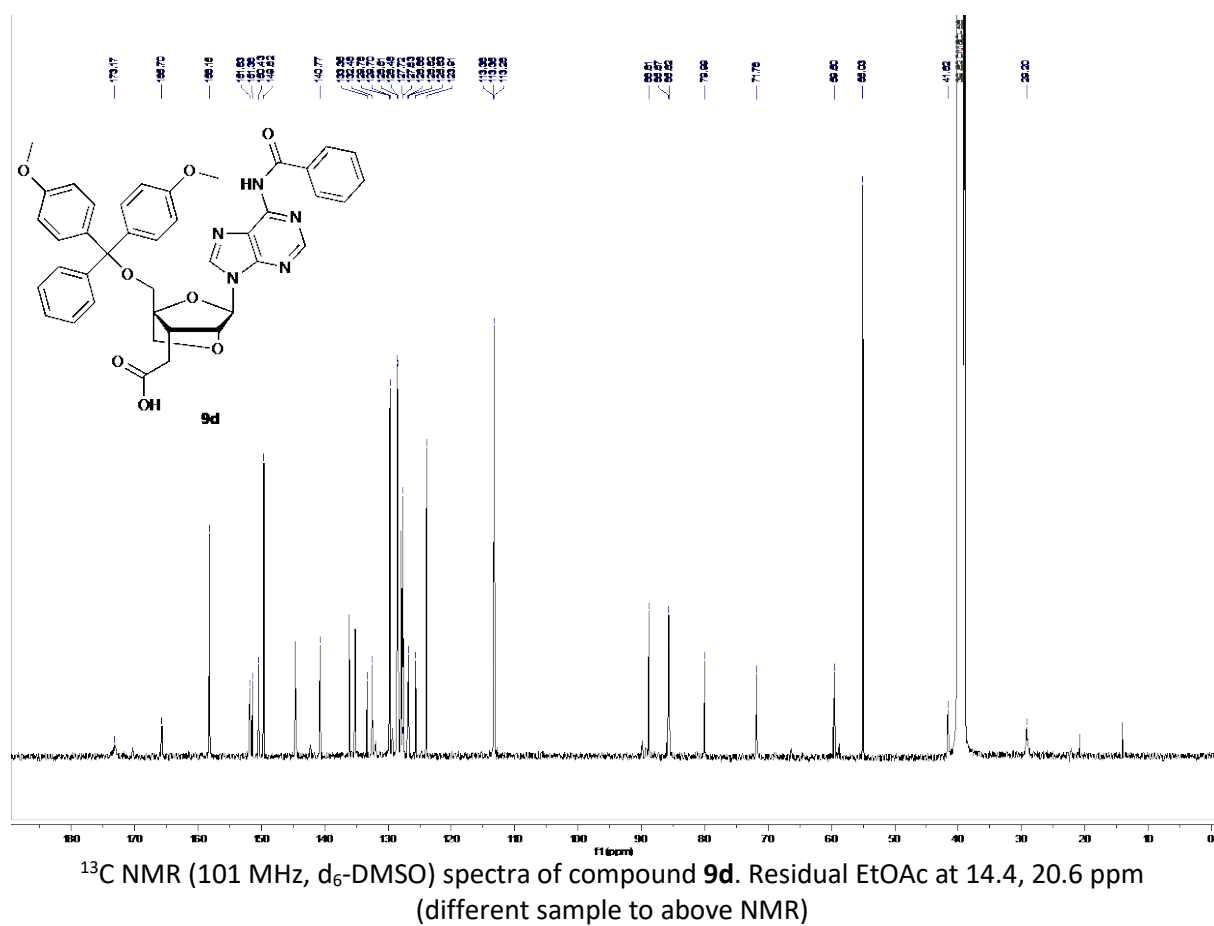
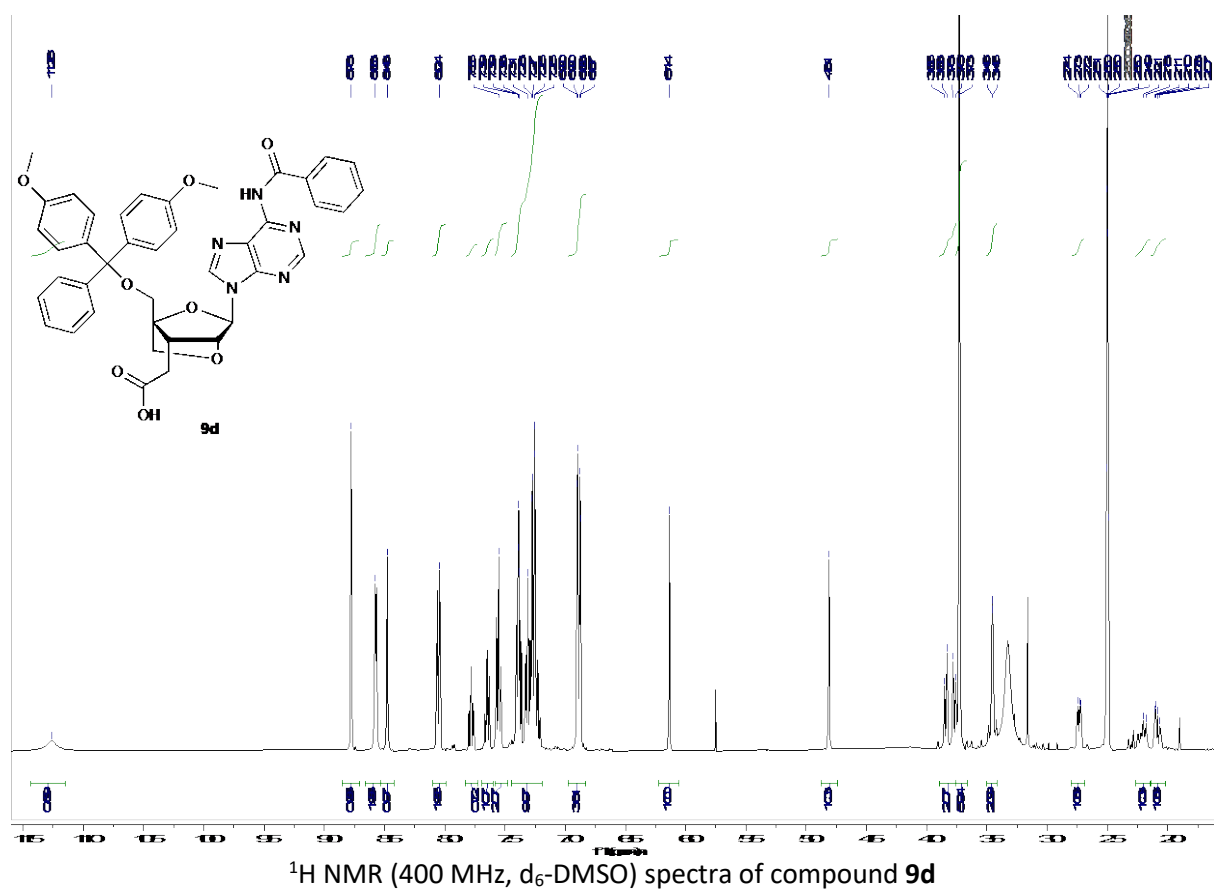


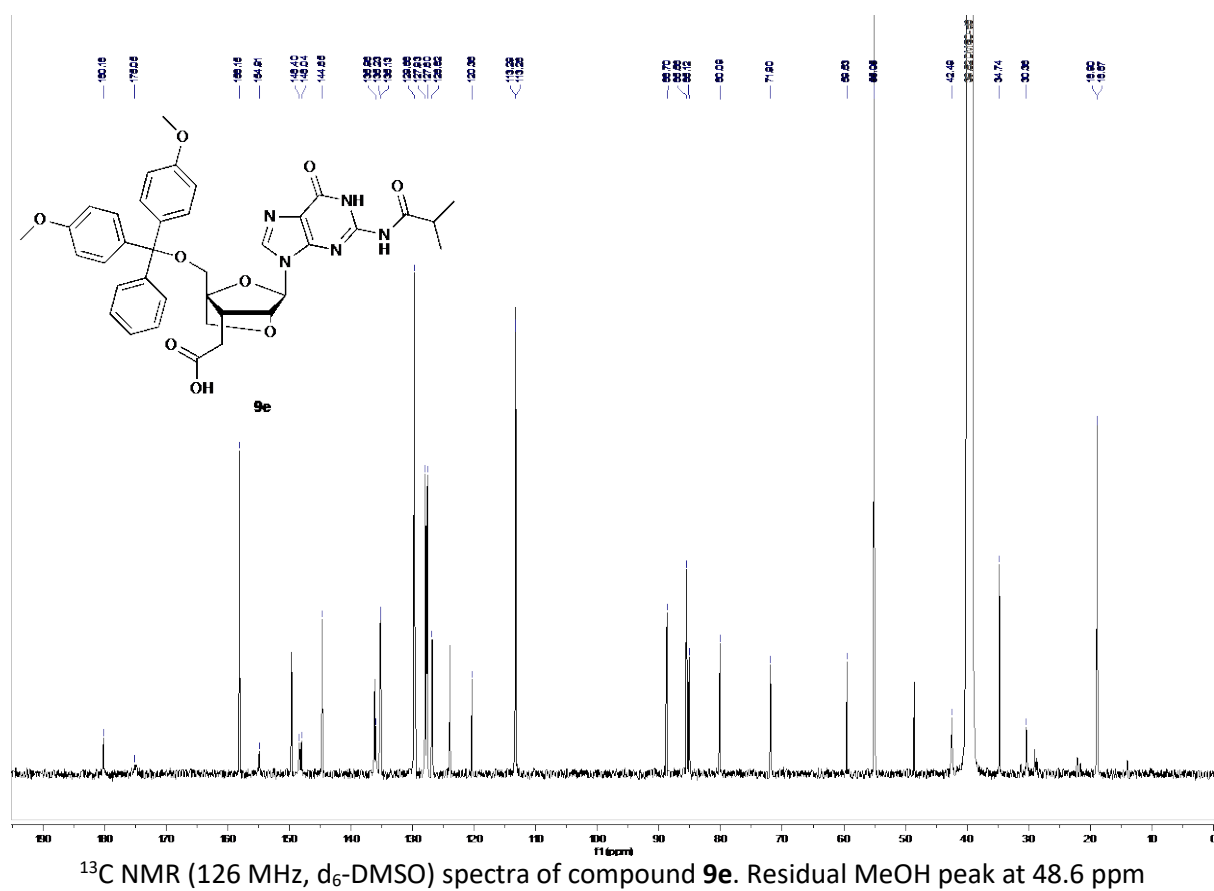
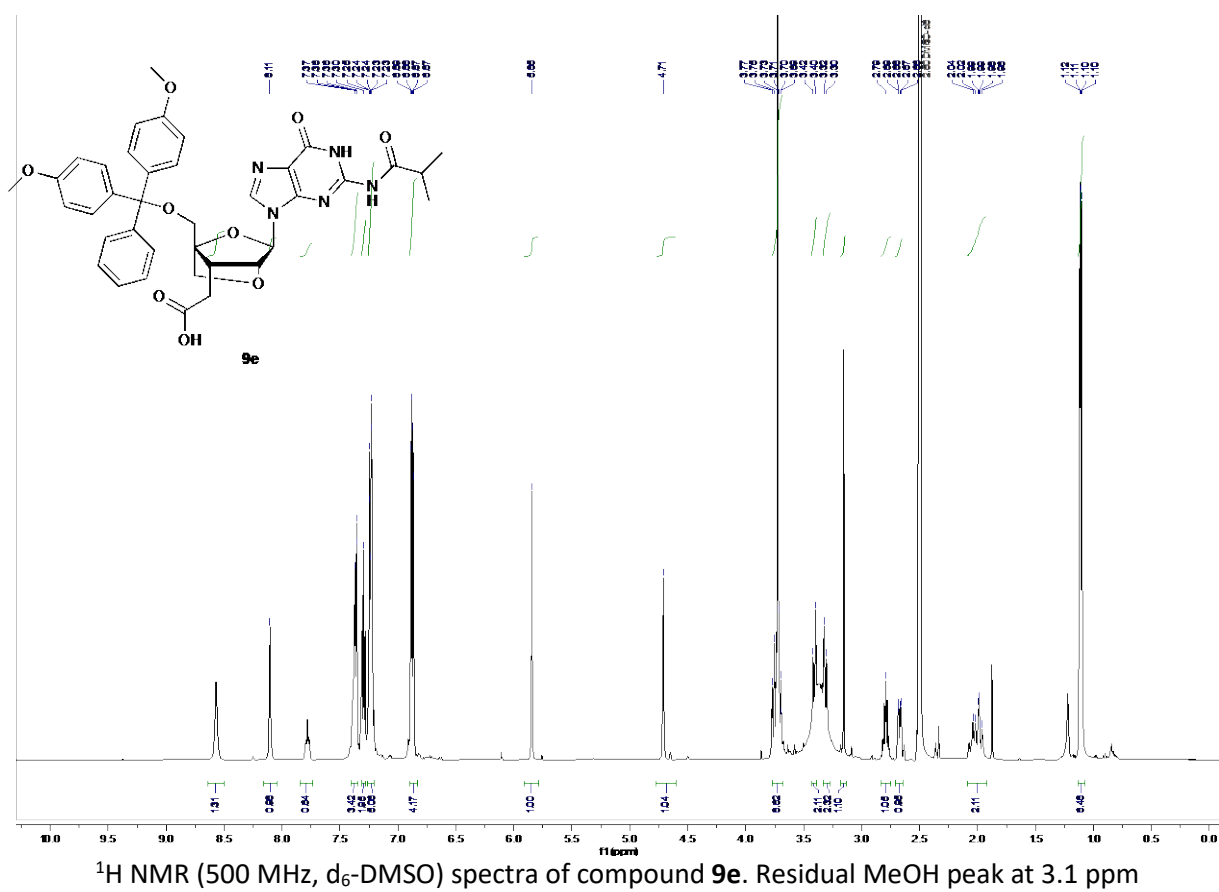


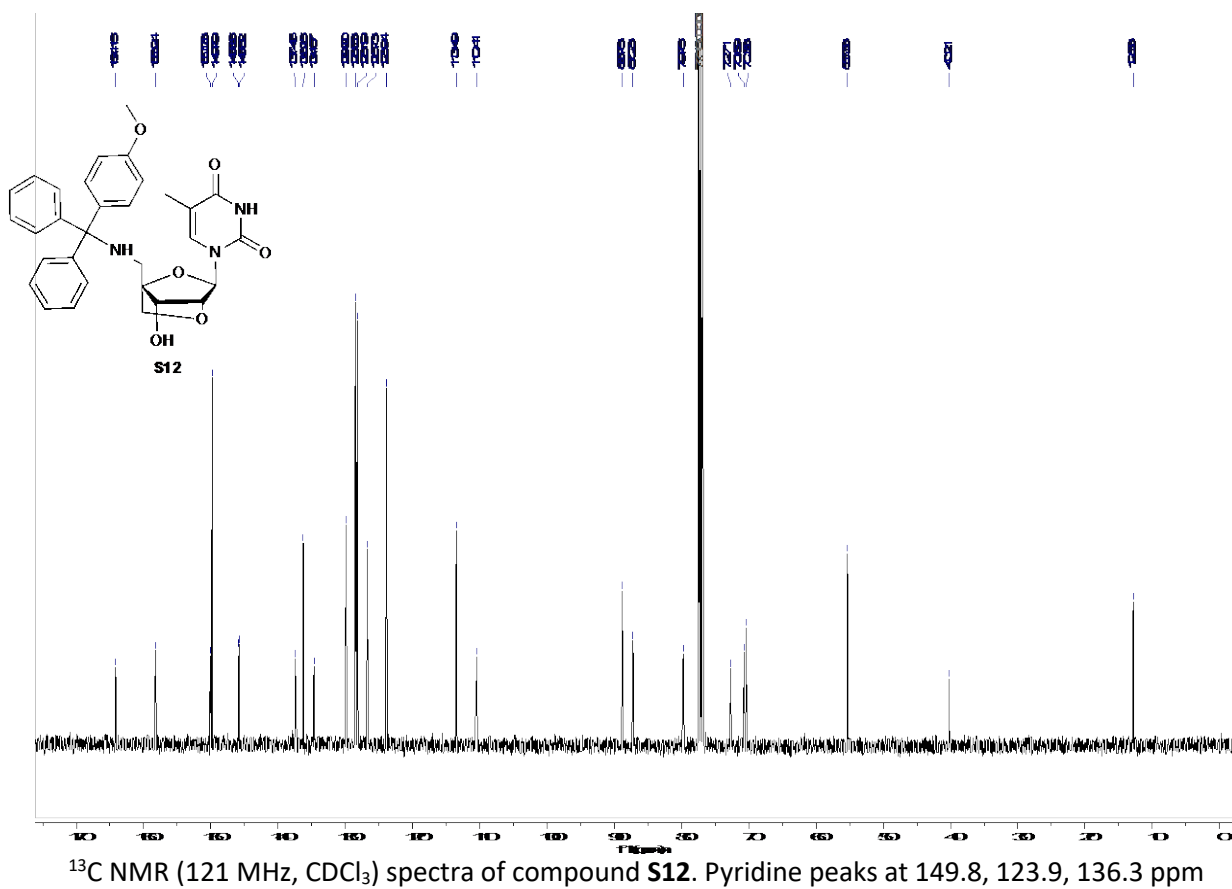
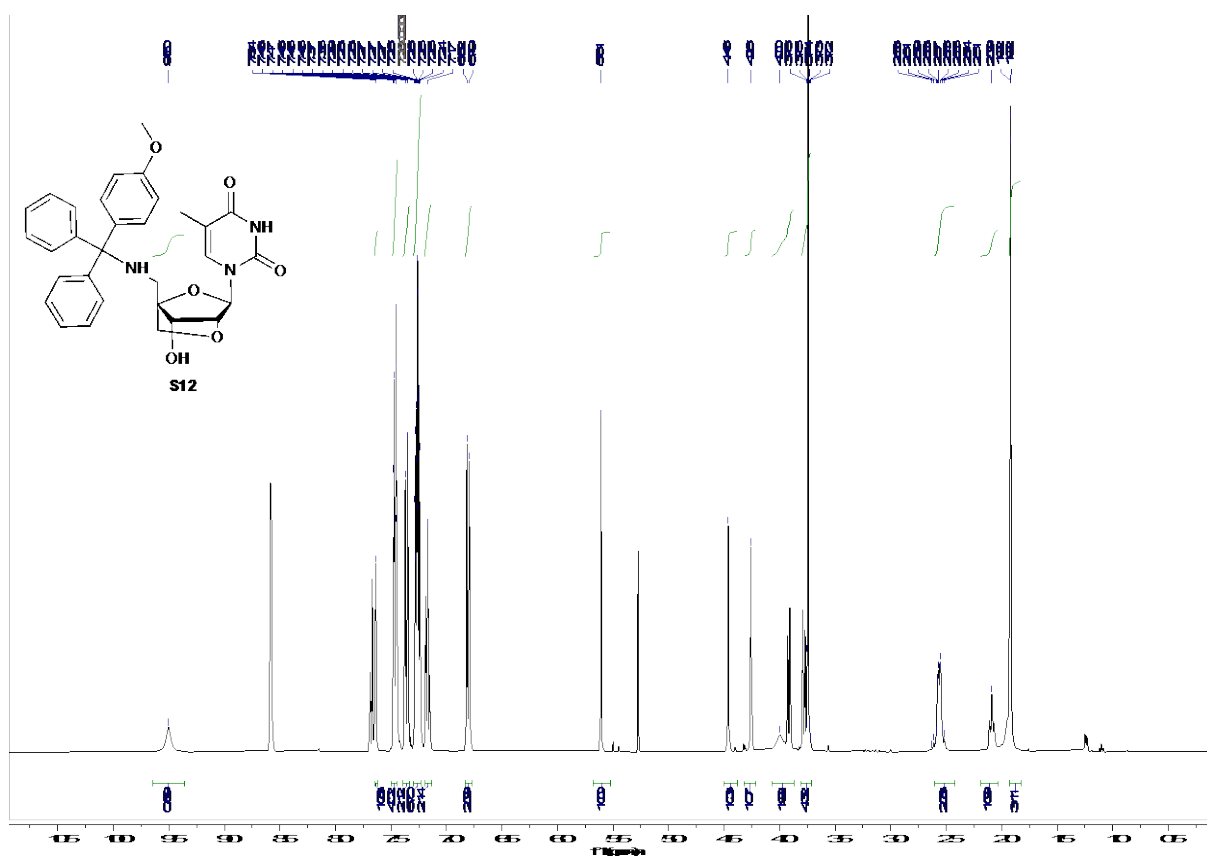


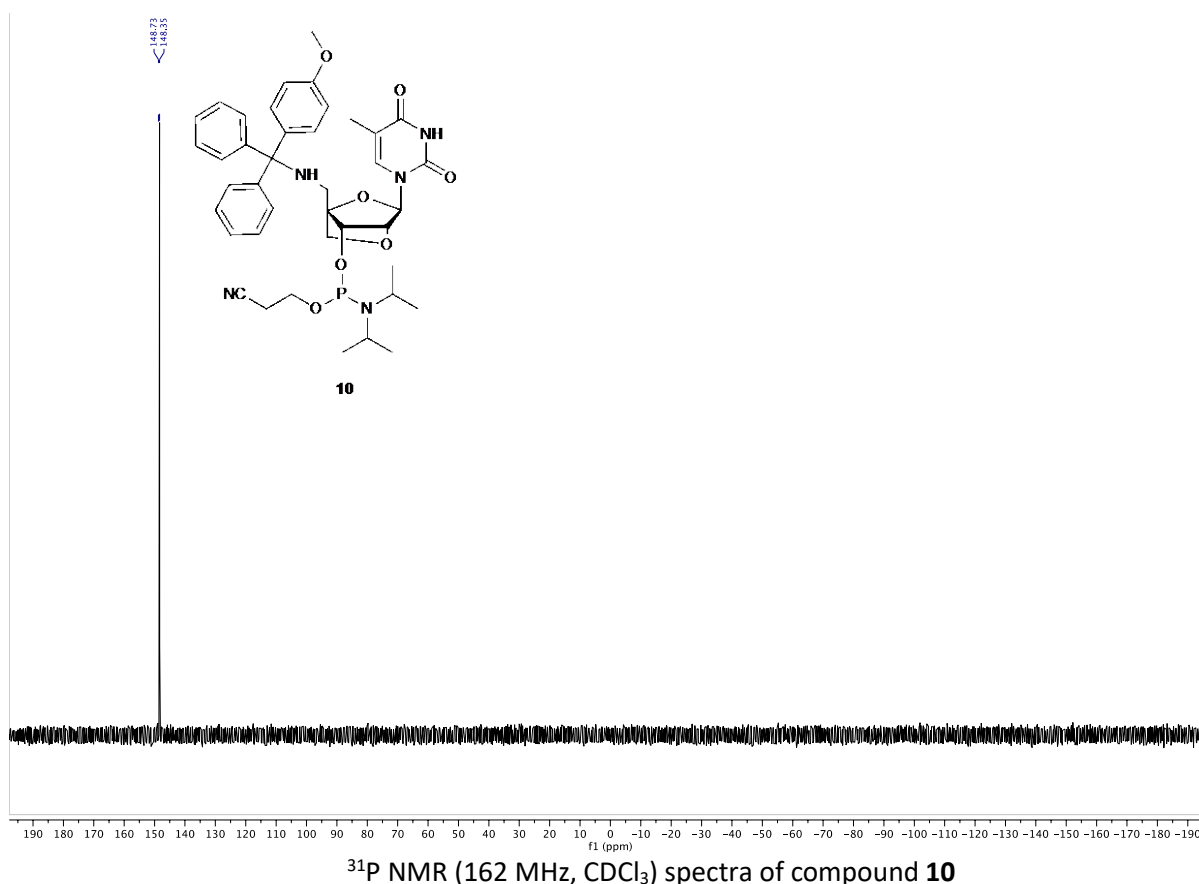












References

1. Thorpe, C., Epple, S., Woods, B., El-Sagheer, A.H. & Brown, T. Synthesis and biophysical properties of carbamate-locked nucleic acid (LNA) oligonucleotides with potential antisense applications. *Org. Biomol. Chem.* **17**, 5341-5348 (2019).
2. Koshkin, A.A., Fensholdt, J., Pfundheller, H.M. & Lomholt, C. A Simplified and Efficient Route to 2'-O, 4'-C-Methylene-Linked Bicyclic Ribonucleosides (Locked Nucleic Acid). *J. Org. Chem.* **66**, 8504-8512 (2001).
3. Obika, S., Nakagawa, O., Hiroto, A., Hari, Y. & Imanishi, T. Synthesis and properties of a novel bridged nucleic acid with a P3' → N5' phosphoramidate linkage, 5'-amino-2',4'-BNA. *Chem. Commun.*, 2202-2203 (2003).
4. Kopka, M.L., Lavelle, L., Han, G.W., Ng, H.-L. & Dickerson, R.E. An Unusual Sugar Conformation in the Structure of an RNA/DNA Decamer of the Polypurine Tract May Affect Recognition by RNase H. *J. Mol. Biol.* **334**, 653-665 (2003).
5. Winter, G. & McAuley, K.E. Automated data collection for macromolecular crystallography. *Methods* **55**, 81-93 (2011).
6. Winter, G. et al. DIALS: implementation and evaluation of a new integration package. *Acta Crystallogr. D Struct. Biol.* **74**, 85-97 (2018).
7. Winter, G. xia2: An Expert System for Macromolecular Crystallography Data Reduction. *J. Appl. Crystallogr.* **43**, 186-190 (2010).
8. Lebedev, A.A. et al. JLigand: a graphical tool for the CCP4 template-restraint library. *Acta Crystallogr. D Biol. Crystallogr.* **68**, 431-440 (2012).
9. Rossmann, M.G. The molecular replacement method. *Acta Crystallogr. A* **46 (Pt 2)**, 73-82 (1990).
10. McCoy, A.J. et al. Phaser crystallographic software. *J. Appl. Crystallogr.* **40**, 658-674 (2007).
11. Murshudov, G.N., Vagin, A.A. & Dodson, E.J. Refinement of macromolecular structures by the maximum-likelihood method. *Acta Crystallogr. D Biol. Crystallogr.* **53**, 240-255 (1997).

12. Murshudov, G.N. et al. REFMAC5 for the refinement of macromolecular crystal structures. *Acta Crystallogr. D Biol. Crystallogr.* **67**, 355-367 (2011).
13. Liebschner, D. et al. Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallogr. D Struct. Biol.* **75**, 861-877 (2019).
14. Long, F. et al. AceDRG: a stereochemical description generator for ligands. *Acta Crystallogr. D Struct. Biol.* **73**, 112-122 (2017).
15. Winn, M.D. et al. Overview of the CCP4 suite and current developments. *Acta Crystallogr. D Biol. Crystallogr.* **67**, 235-242 (2011).
16. Evans, P.R. An introduction to data reduction: space-group determination, scaling and intensity statistics. *Acta Crystallogr. D Biol. Crystallogr.* **67**, 282-292 (2011).
17. Kang, S.-H., Cho, M.-J. & Koe, R. Up-Regulation of Luciferase Gene Expression with Antisense Oligonucleotides: Implications and Applications in Functional Assay Development. *Biochemistry* **37**, 6235-6239 (1998).
18. Palatinus, L. & Chapuis, G. SUPERFLIP— a computer program for the solution of crystal structures by charge flipping in arbitrary dimensions. *J. Appl. Crystallogr.* **40**, 786-790 (2007).
19. Parois, P., Cooper, R.I. & Thompson, A.L. Crystal structures of increasingly large molecules: meeting the challenges with CRYSTALS software. *Chem. Cent. J.* **9**, 30 (2015).
20. Cooper, R.I., Thompson, A.L. & Watkin, D.J. CRYSTALS enhancements: dealing with hydrogen atoms in refinement. *J. Appl. Crystallogr.* **43**, 1100-1107 (2010).