Electronic Supplementary Material (ESI) for Organic & Biomolecular Chemistry

Supplementary information

Synthesis and properties of 2'O-neopentyl modified oligonucleotides

[a,b]Gérald Mathis, [c]Stéphane Bourg, [a]Samia Aci-Sèche, [b]Jean-Christophe Truffert, and *[a]Ulysse Asseline

[a]Centre de Biophysique Moléculaire, UPR 4301CNRS, conventionnée avec l'Université Orléans, Rue Charles Sadron - 45071 Orléans Cedex 02, France
[b]NucleoSyn Pépinières d'entreprises – Centre Innovation 16, Rue Léonard de Vinci 45074 Orleans Cedex 2, France
[c]Institut de Chimie Organique et Analytique, Université d'Orléans, UMR 7311 CNRS, rue de Chartres, 45067 Orléans cedex 2, France

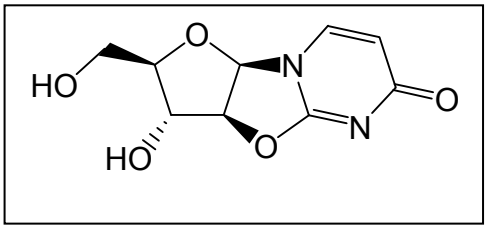
[*a] E-mail: ulysse.asseline@cnrs-orleans.fr
Fax : +33-2-38-63-15-17

^{1H}NMR, ^{13C}NMR and ^{31P}NMR spectra

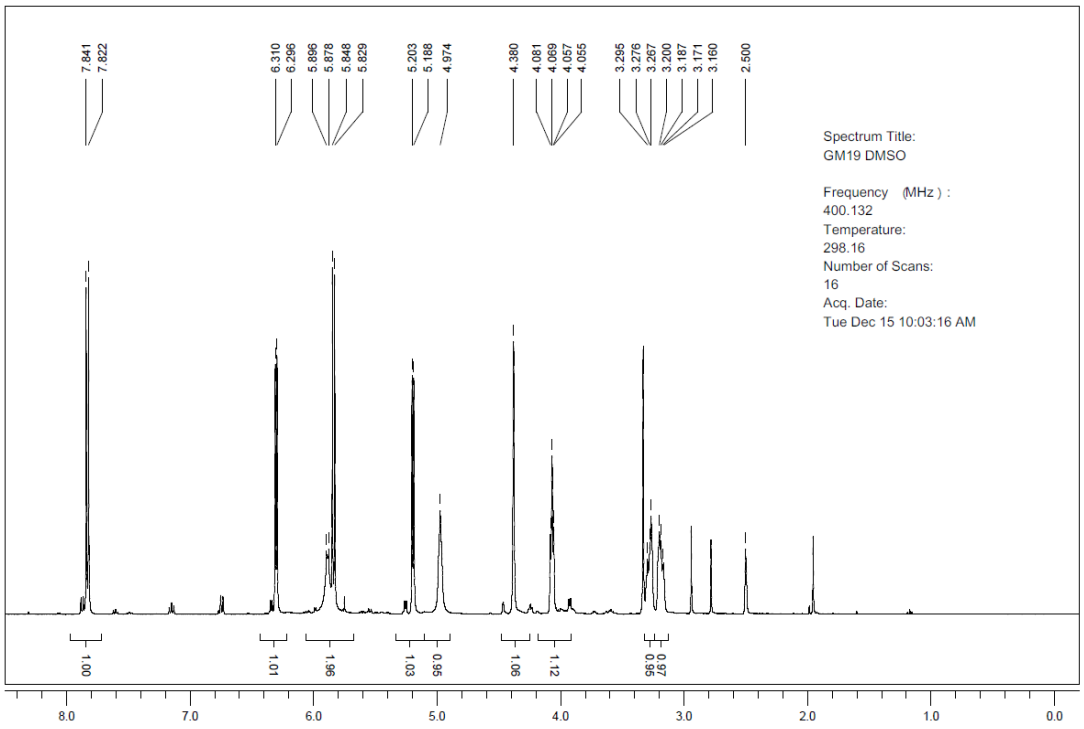
Reversed-phase HPLC and MS analyses of modified oligonucleotides 4-7

Molecular dynamics simulations

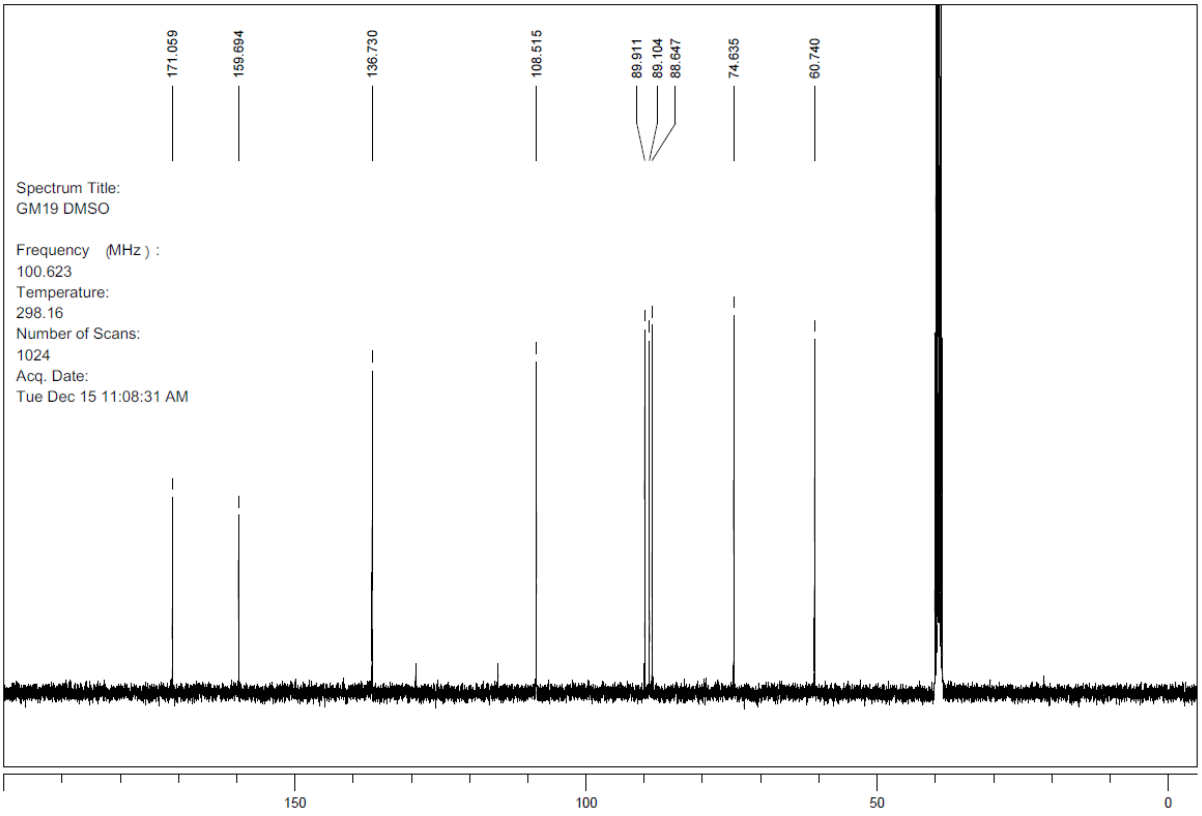
2,2'-anhydrouridine **13**



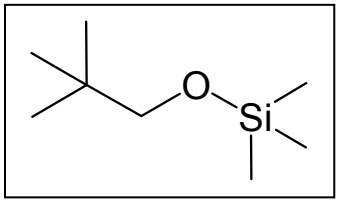
^{1}H NMR spectrum (400 MHz, DMSO-d_6) of **13**



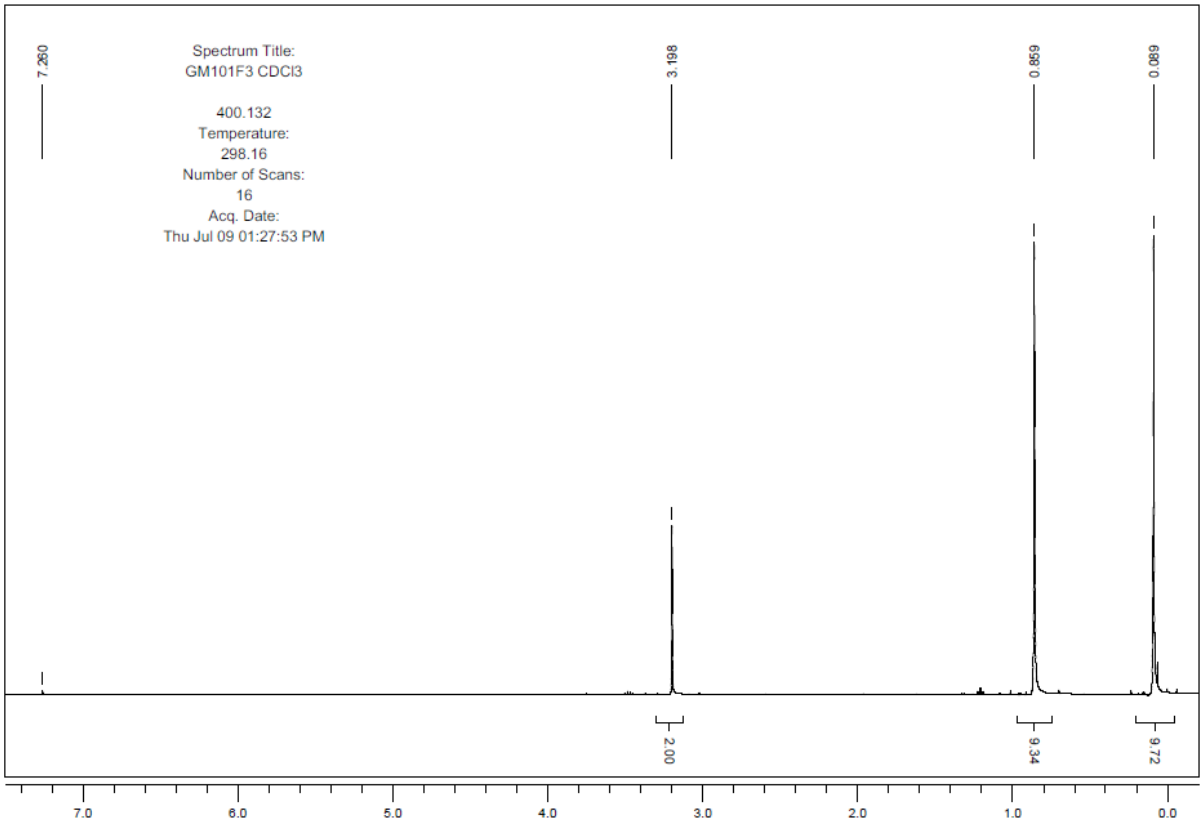
^{13}C NMR spectrum (100 MHz, DMSO-d_6) of **13**



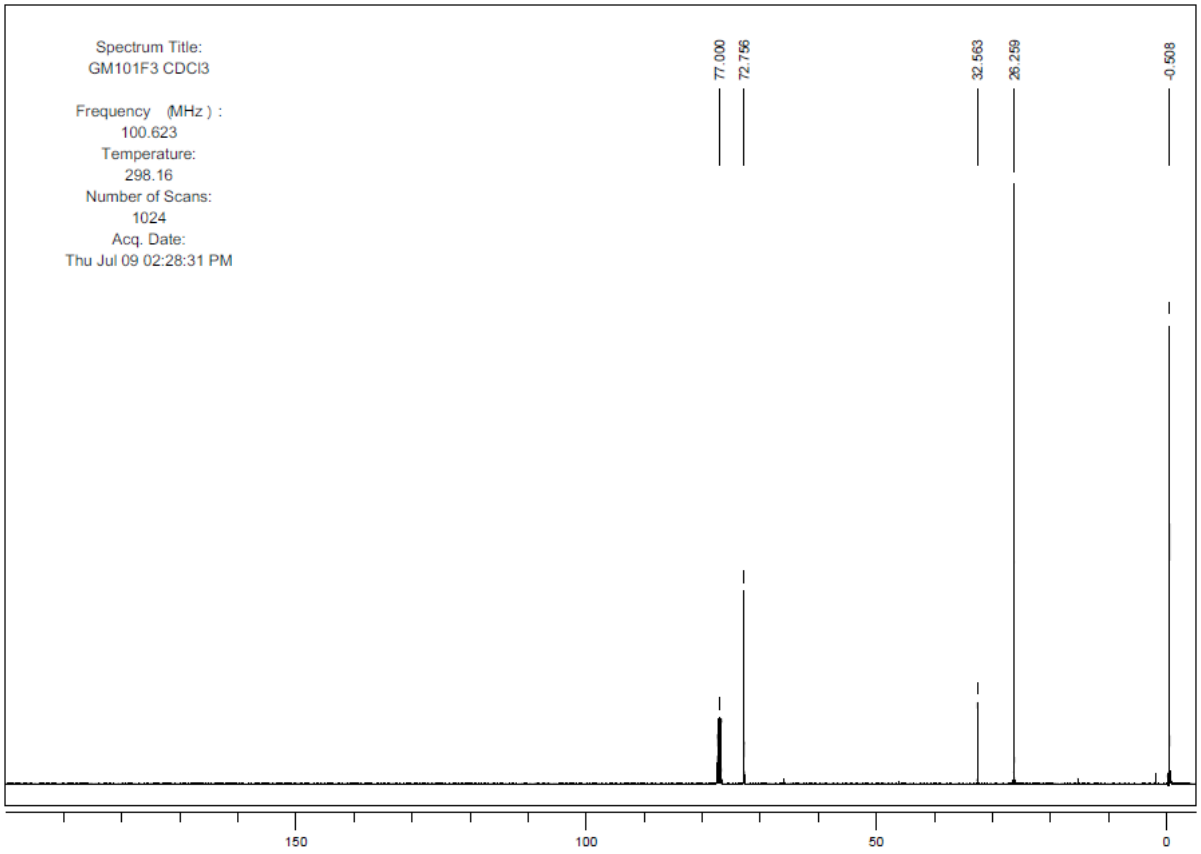
1-Trimethylsilyloxy-2,2-dimethypropane 15



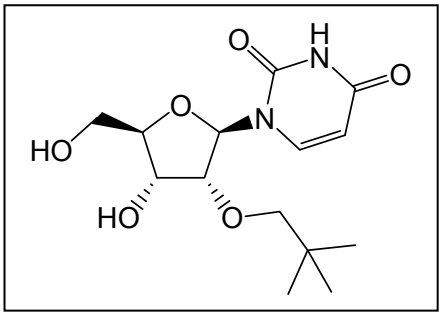
^{1}H NMR spectrum (400 MHz, $CDCl_3$) of **15**



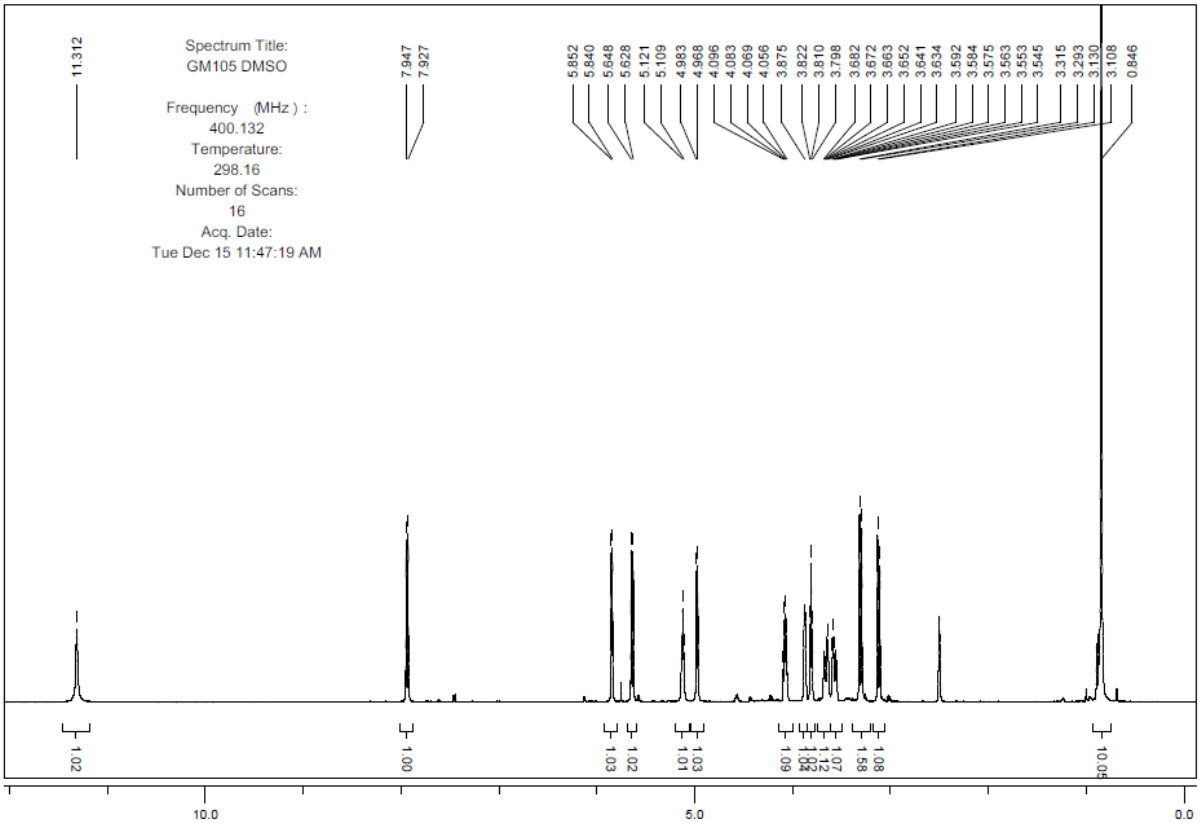
^{13}C NMR spectrum (100 MHz, $CDCl_3$) of **15**



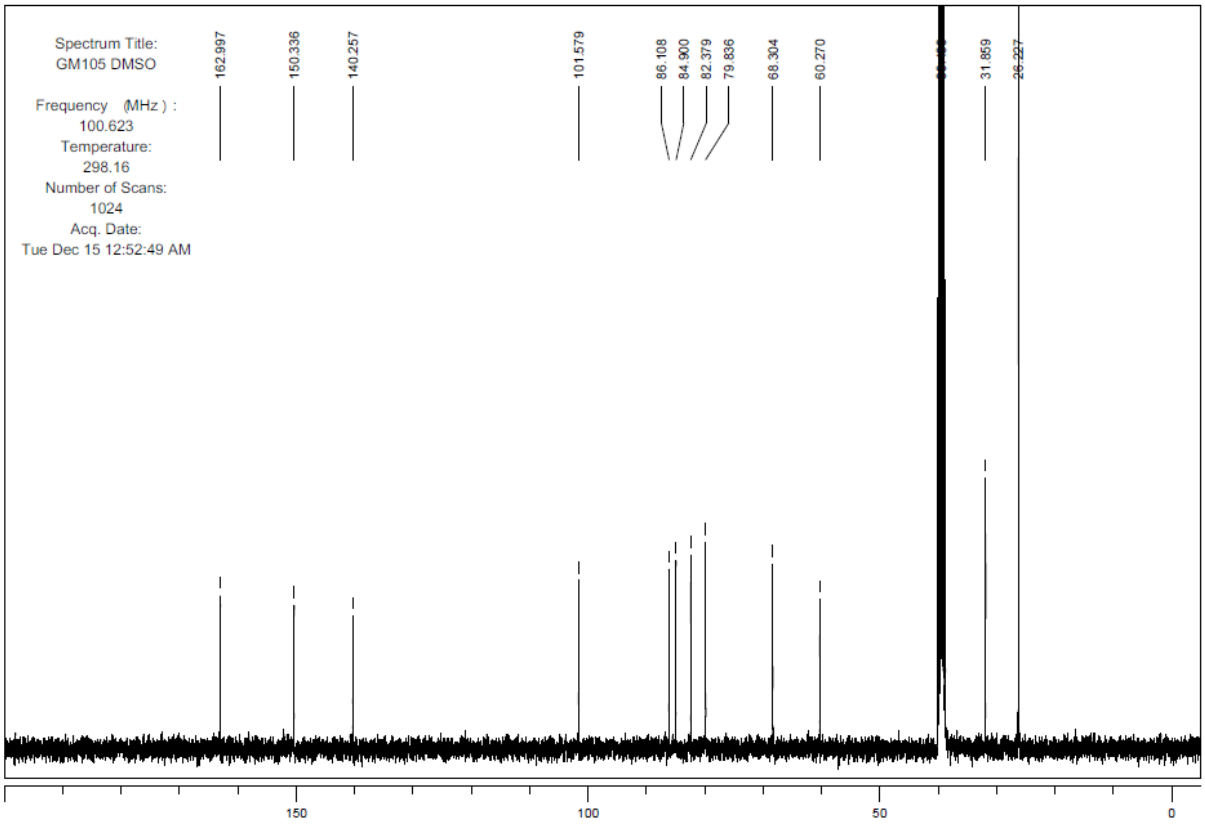
2'-*O*-Neopentyluridine 16



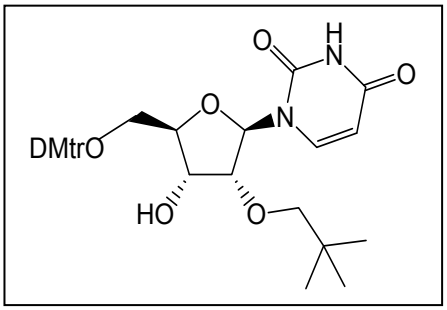
^{1}H-NMR spectrum (400 MHz, DMSO-d_6) of **16**



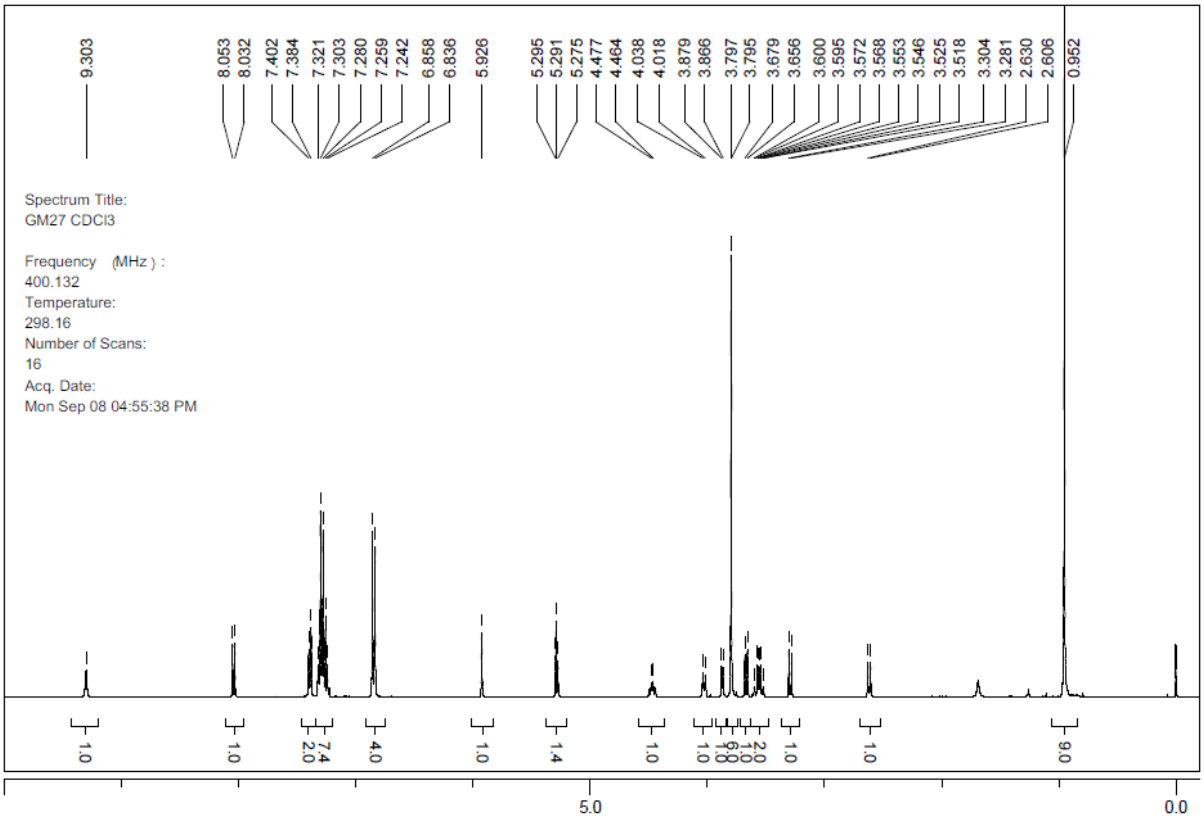
^{13}C-NMR spectrum (100 MHz, DMSO-d_6) of **16**



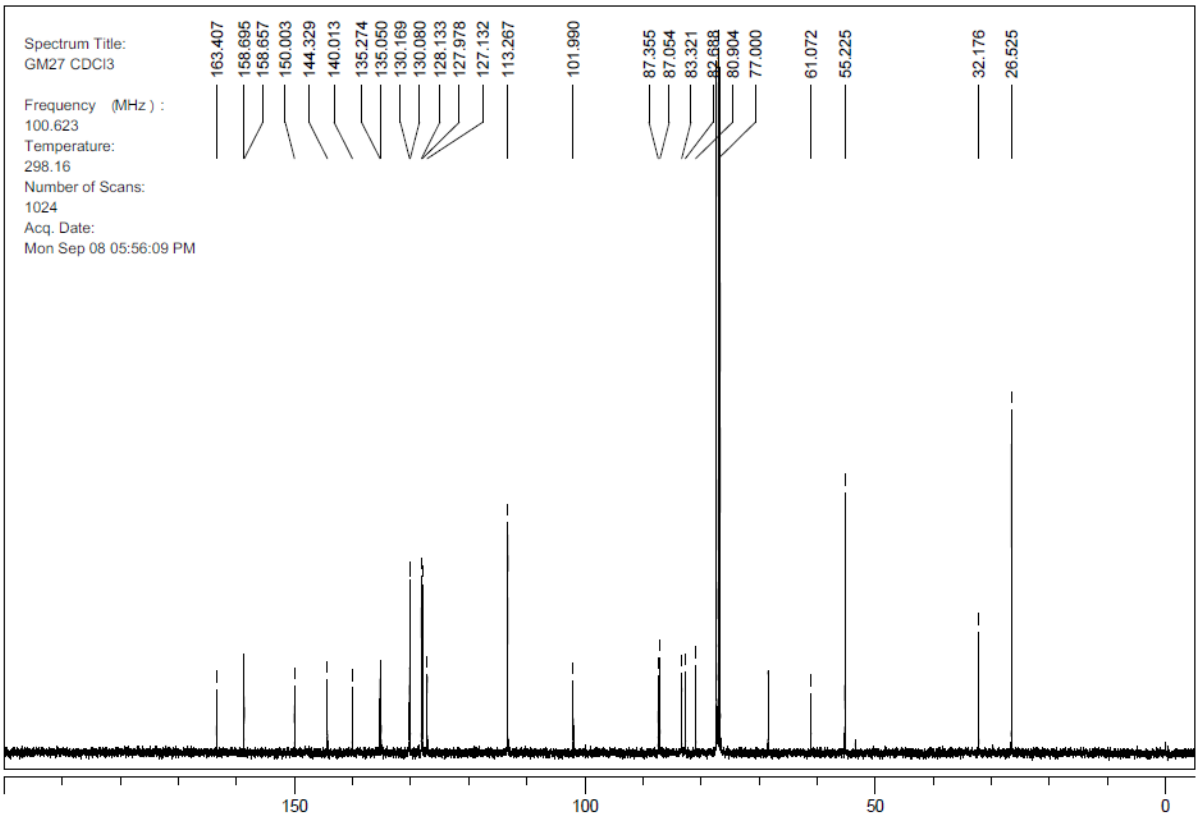
5'-*O*-Dimethoxytrityl-2'-*O*-neopentyluridine 17



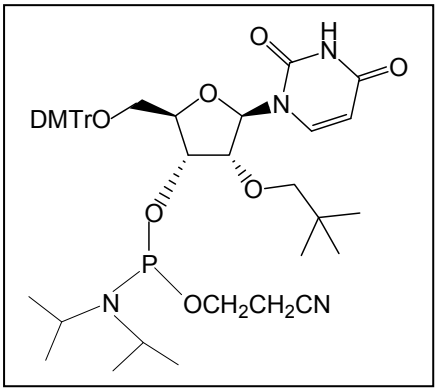
^{1}H NMR spectrum (400 MHz, $CDCl_3$) of **17**



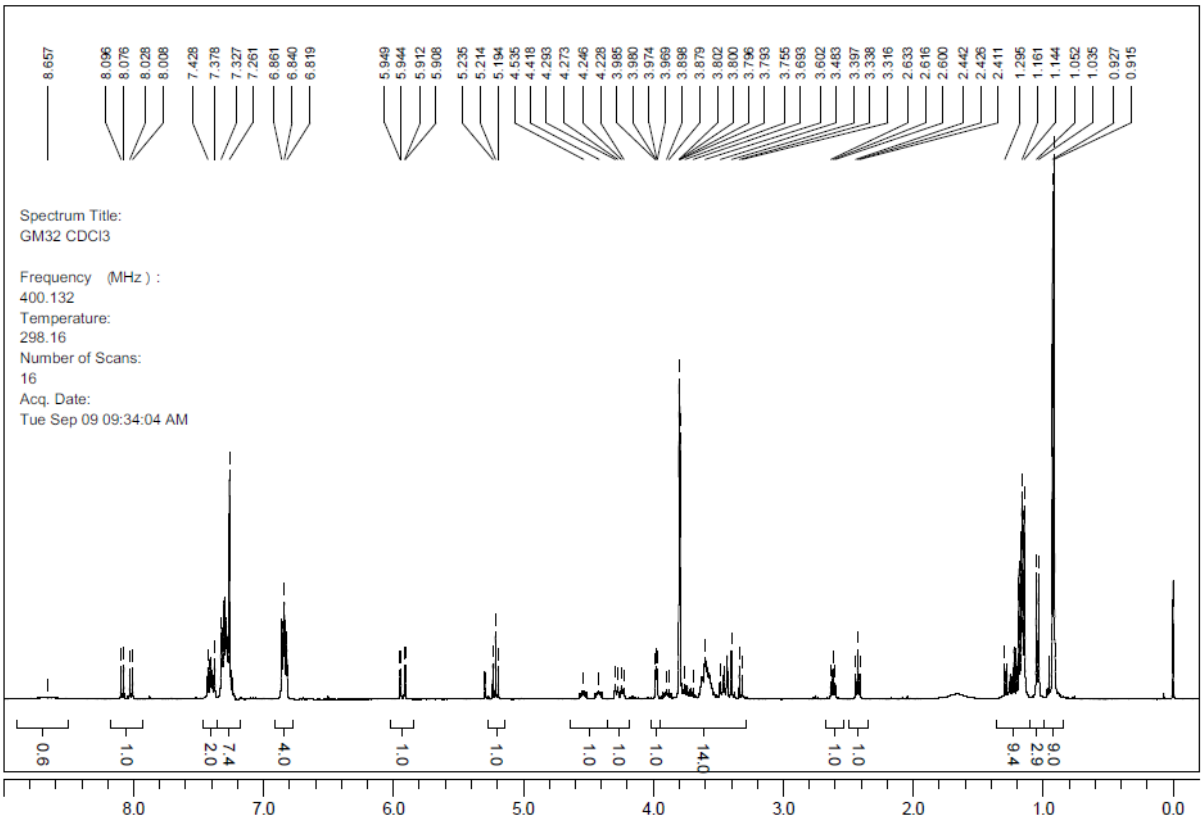
^{13}C NMR spectrum (100 MHz, $CDCl_3$) of **17**



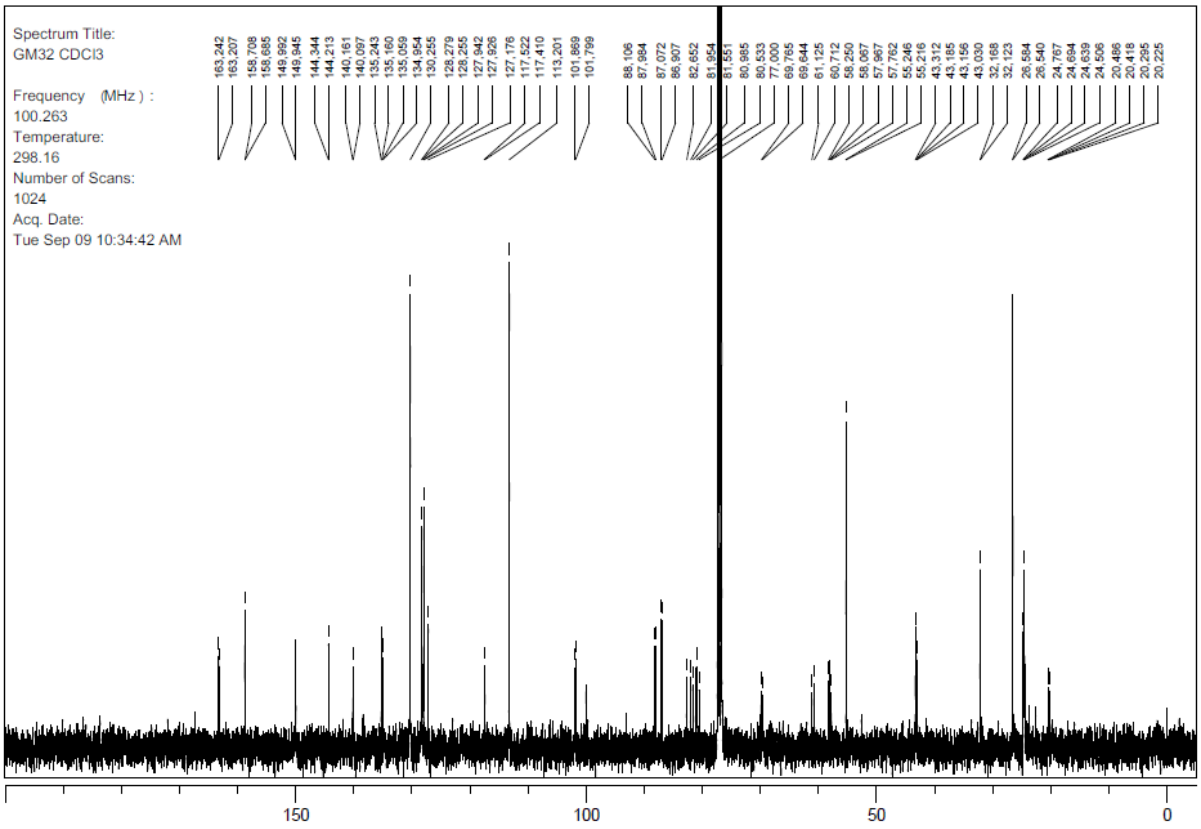
5'-*O*-Dimethoxytrityl-3'-*O*-(2-cyanoethyl-N,N'-diisopropylphosphoramidite)-2'-*O*-neopentyluridine 18



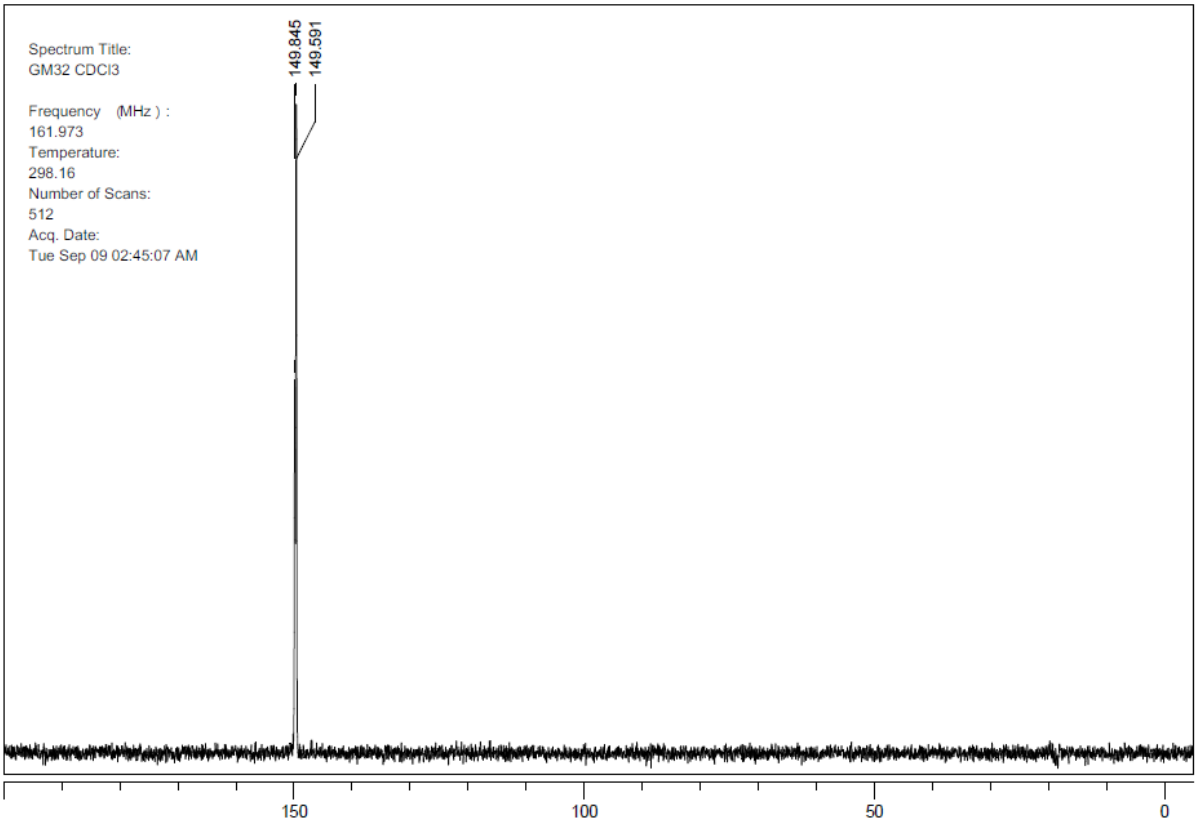
^{1}H NMR spectrum (400 MHz, $CDCl_3$) of **18**



^{13}C NMR spectrum (100 MHz, $CDCl_3$) of **18**

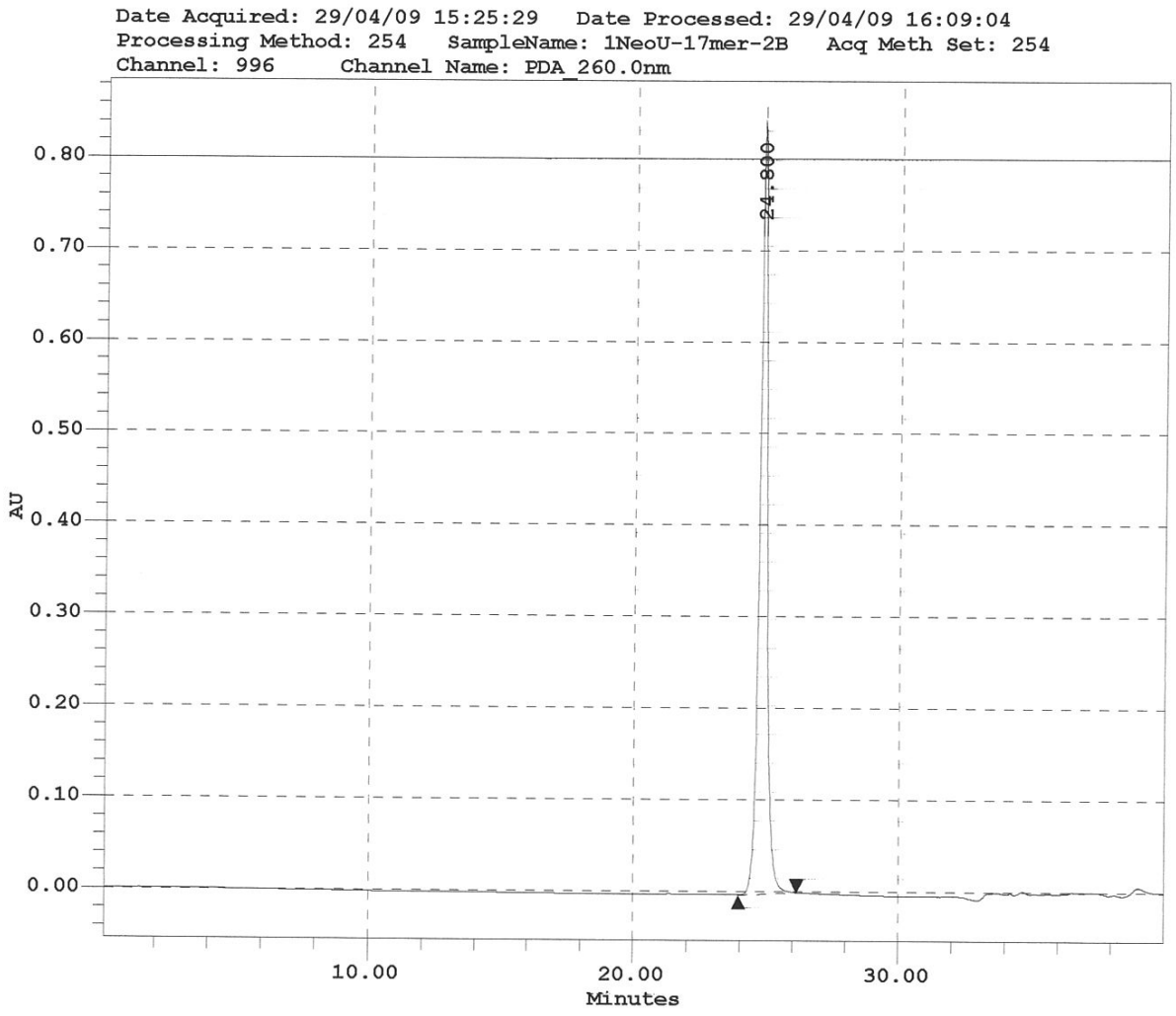


^{31}P NMR spectrum (100 MHz, $CDCl_3$) of **18**



Sequence 4: $^{5'}$d(**Un**TG TTA CCA GTT TTA GT)$^{3'}$

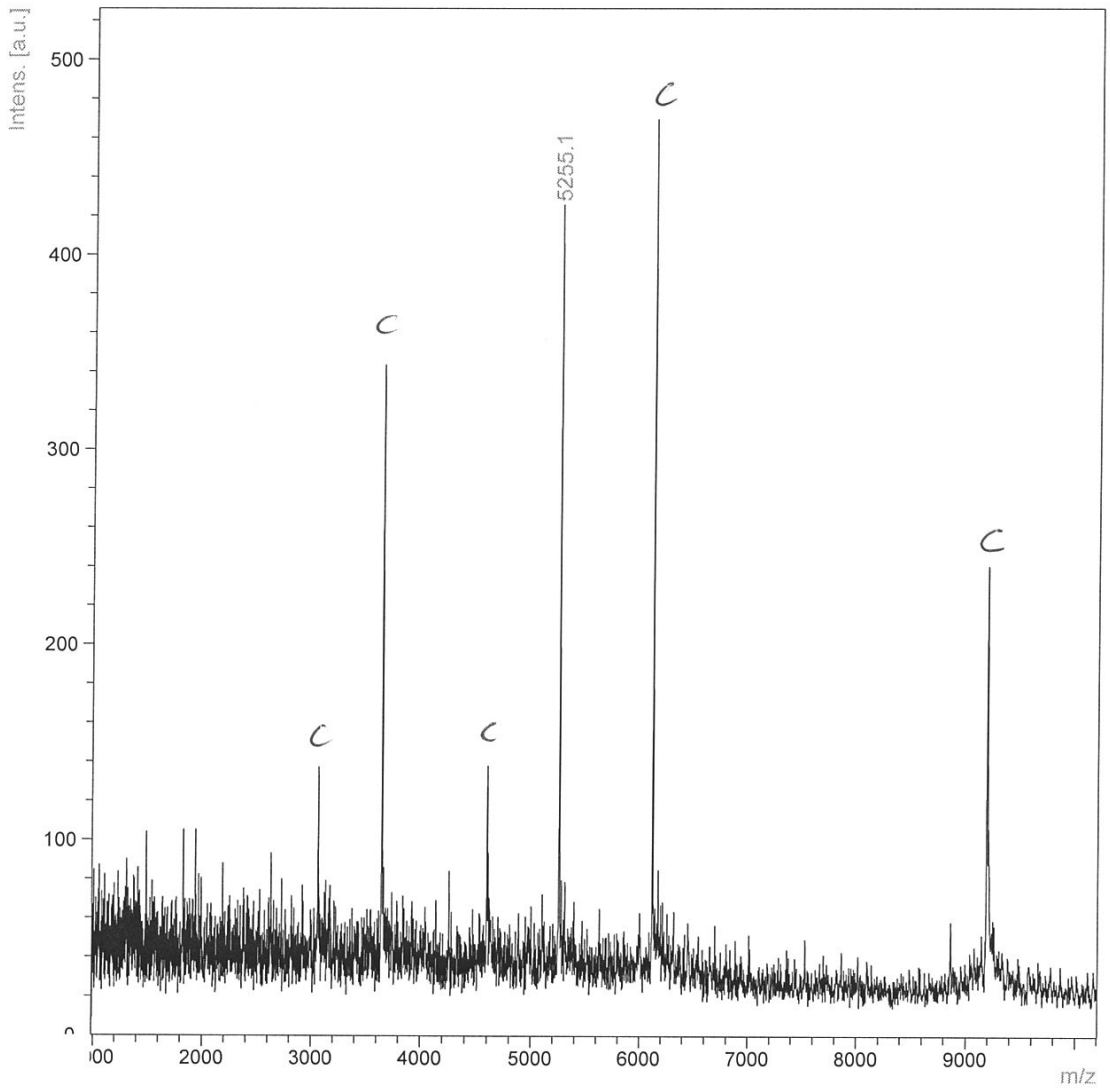
RP-HPLC chromatogram of ON **4**



MS analysis

MW = 5253.5 g.mol^{-1} for $C_{176}H_{222}O_{107}N_{54}P_{16}$

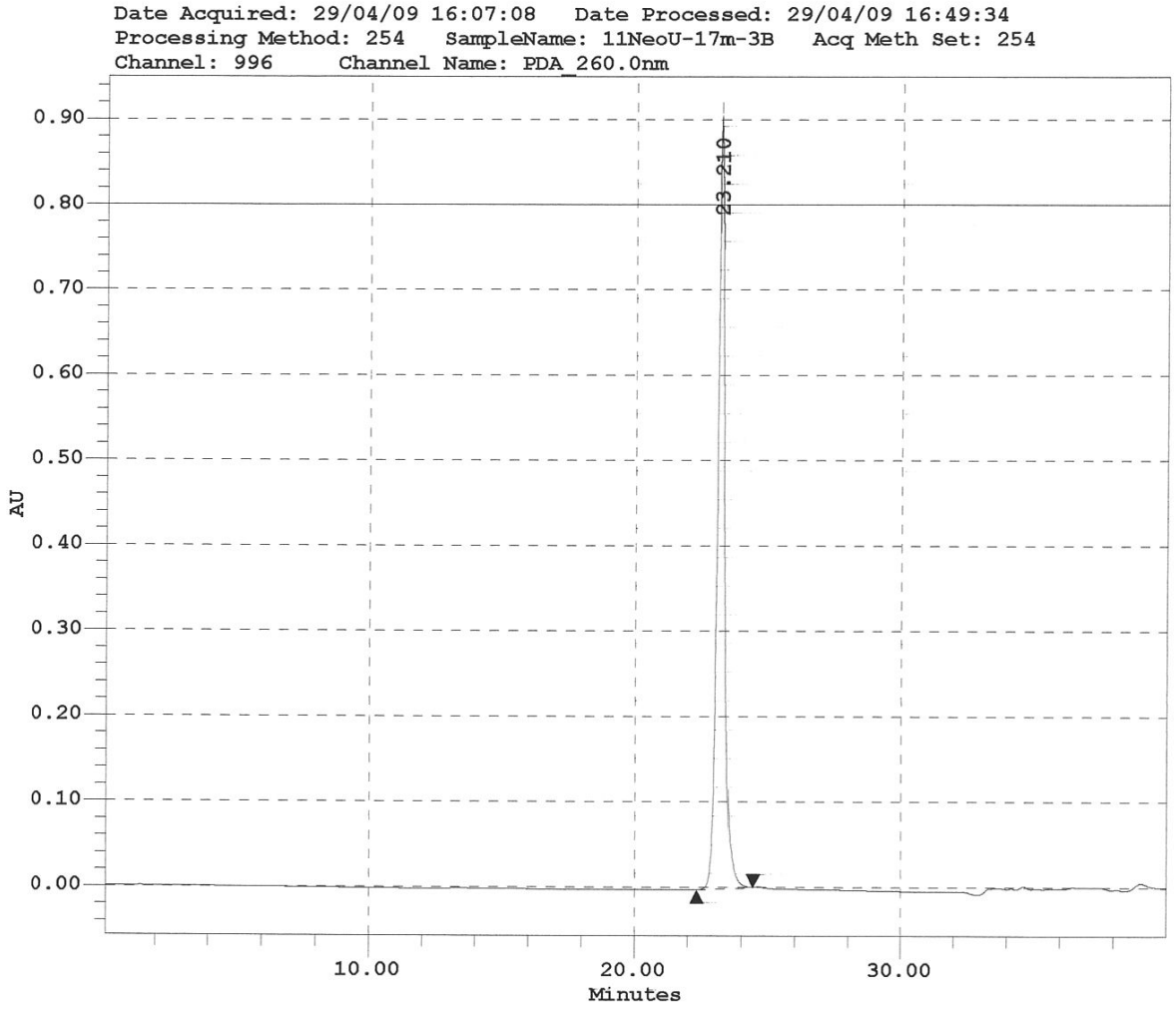
Mass spectrum (MALDI-TOF) of ON **4**



MS calcd for $[M+H]^+$ 5254.5 Da, found 5255.1 Da. C stand for calibrating ONs

Sequence 5: $^{5'}$d(TTG TTA CCA G**Un**T TTA GT)$^{3'}$

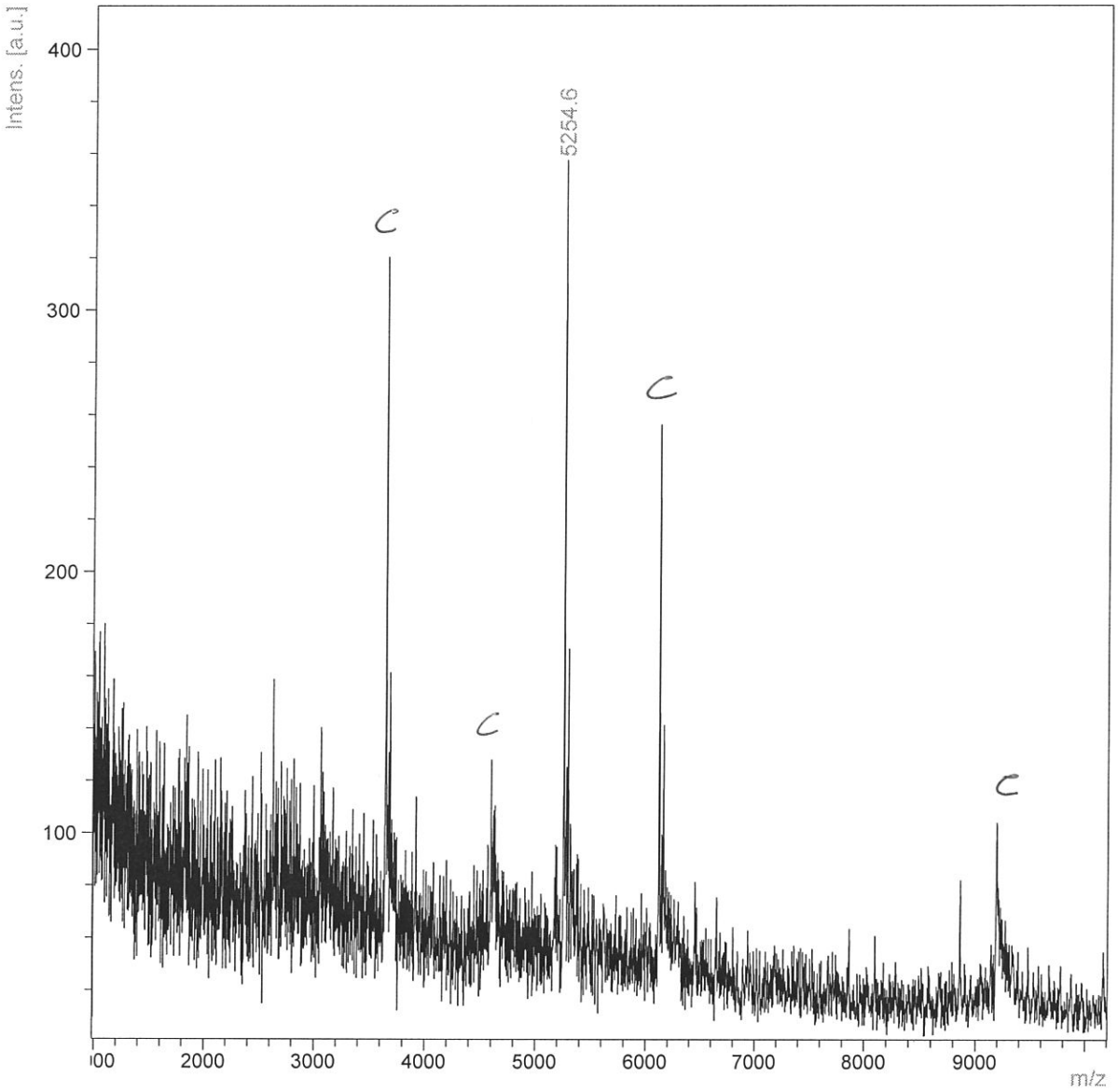
RP-HPLC chromatogram of ON **5**



MS analysis

MW = 5253.5 g.mol^{-1} for $C_{176}H_{222}O_{107}N_{54}P_{16}$

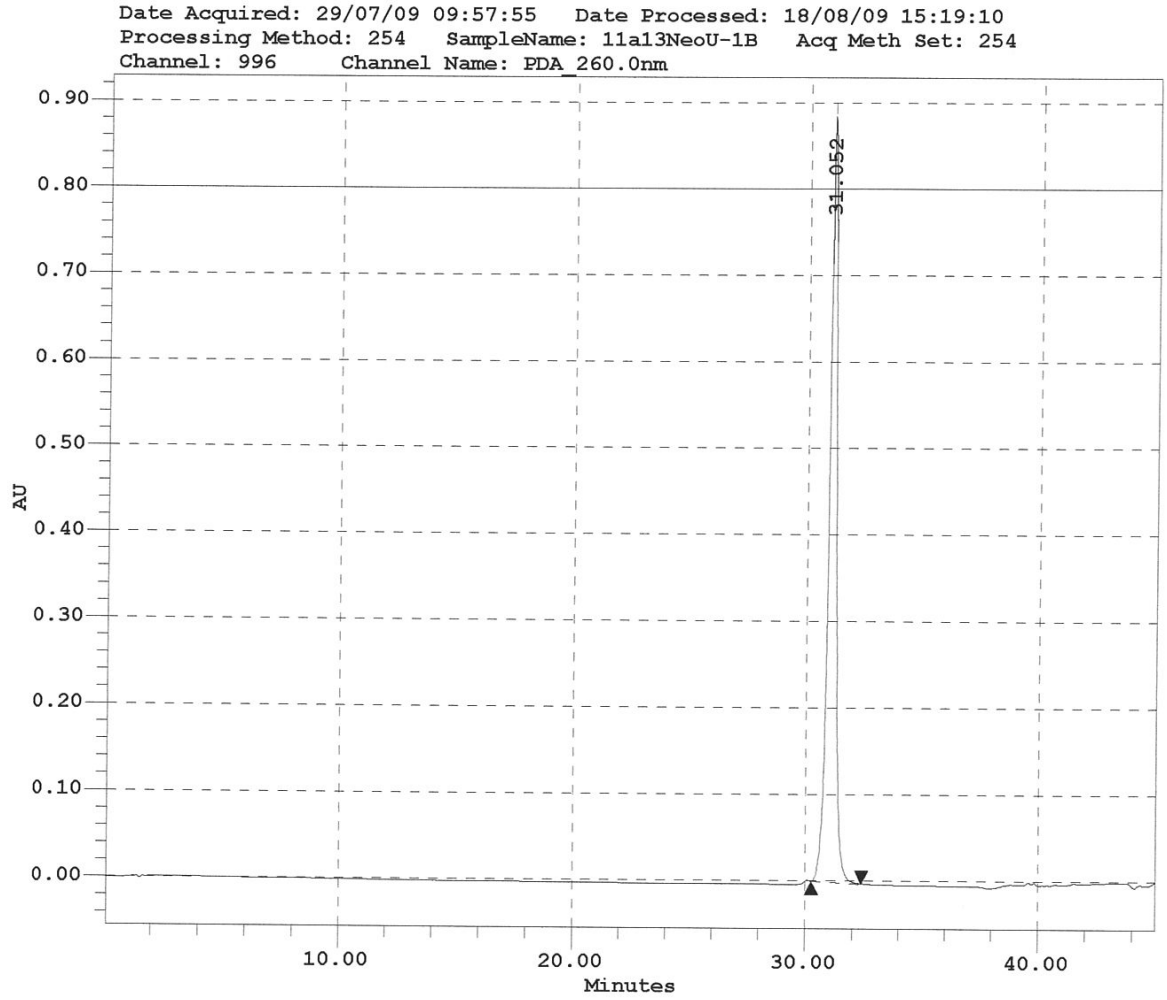
Mass spectrum (MALDI-TOF) of ON **5**



MS calcd for $[M+H]^+$ 5398.7 Da, found 5399.1 Da.

Sequence 6: $^{5'}$d(TTG TTA CCA G**UnUn Un**TA GT)$^{3'}$

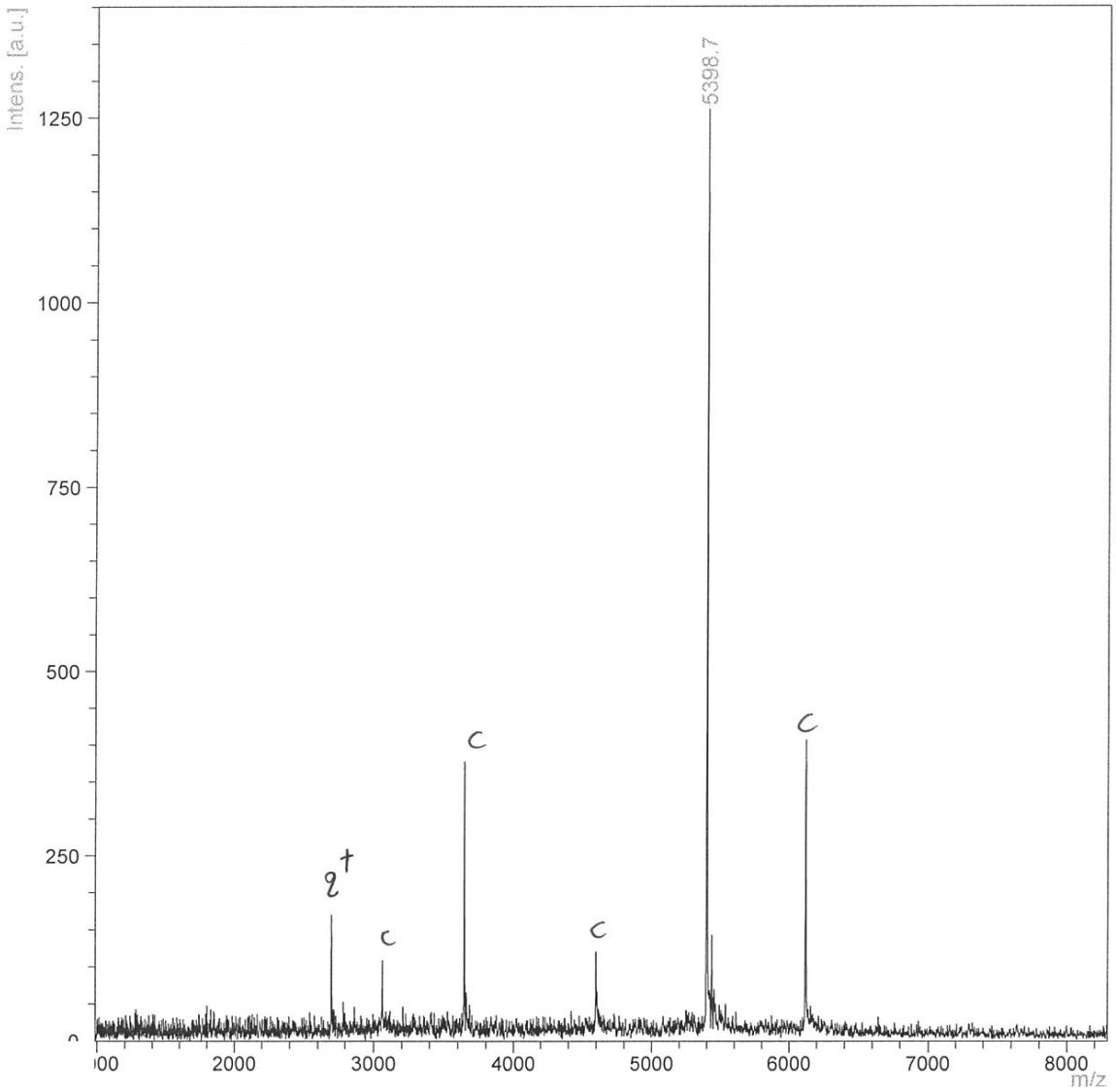
RP-HPLC chromatogram of ON **6**



MS analysis

MW = 5397.7 g.mol^{-1} for $C_{180}H_{238}O_{109}N_{54}P_{16}$

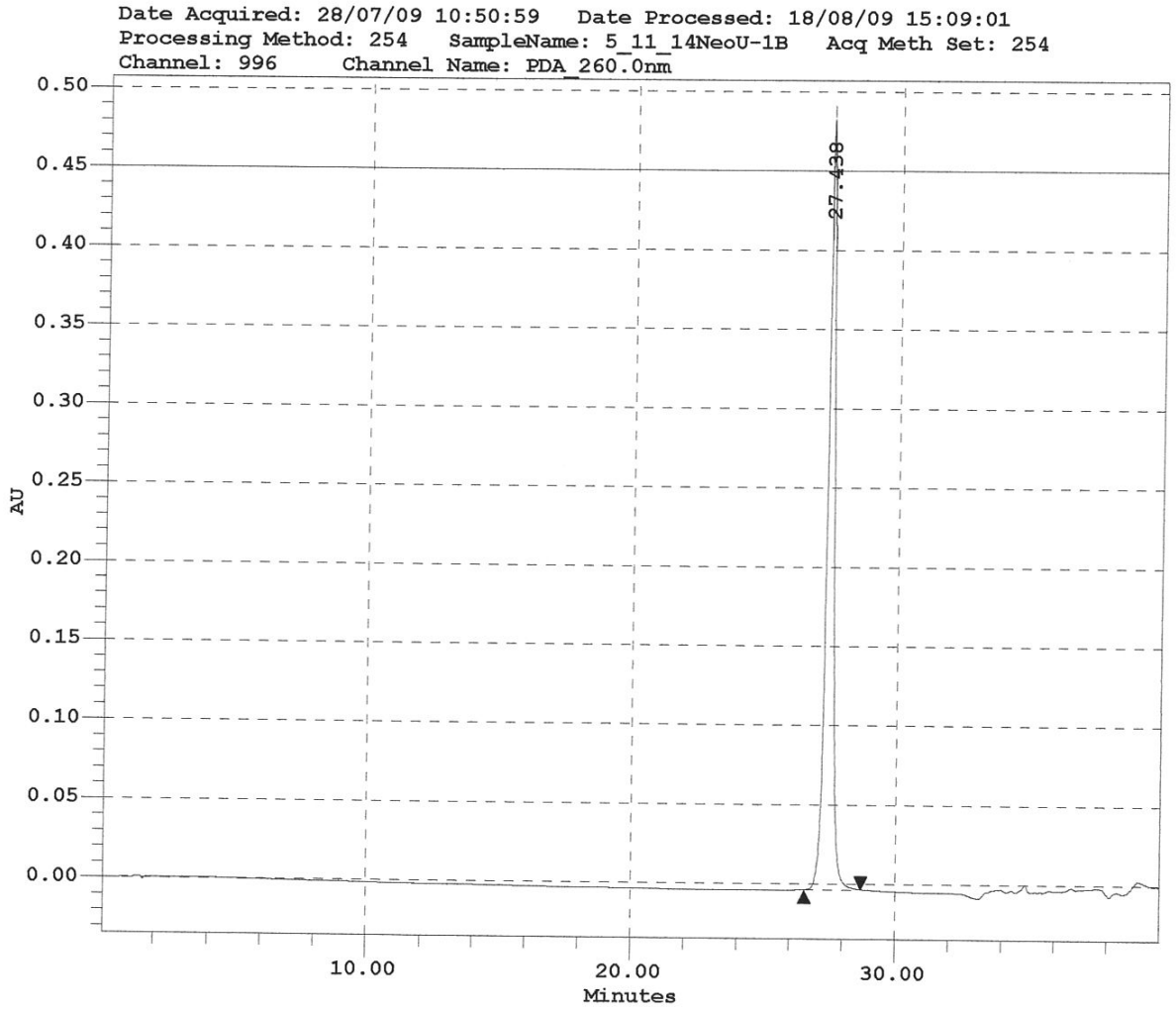
Mass spectrum (MALDI-TOF) of ON **6**



MS calcd for $[M+H]^+$ 5398.7 Da, found 5398.7 Da.

Sequence 7: $^{5'}$d(TTG TU$_n$A CCA GU$_n$T TU$_n$A GT)$^{3'}$

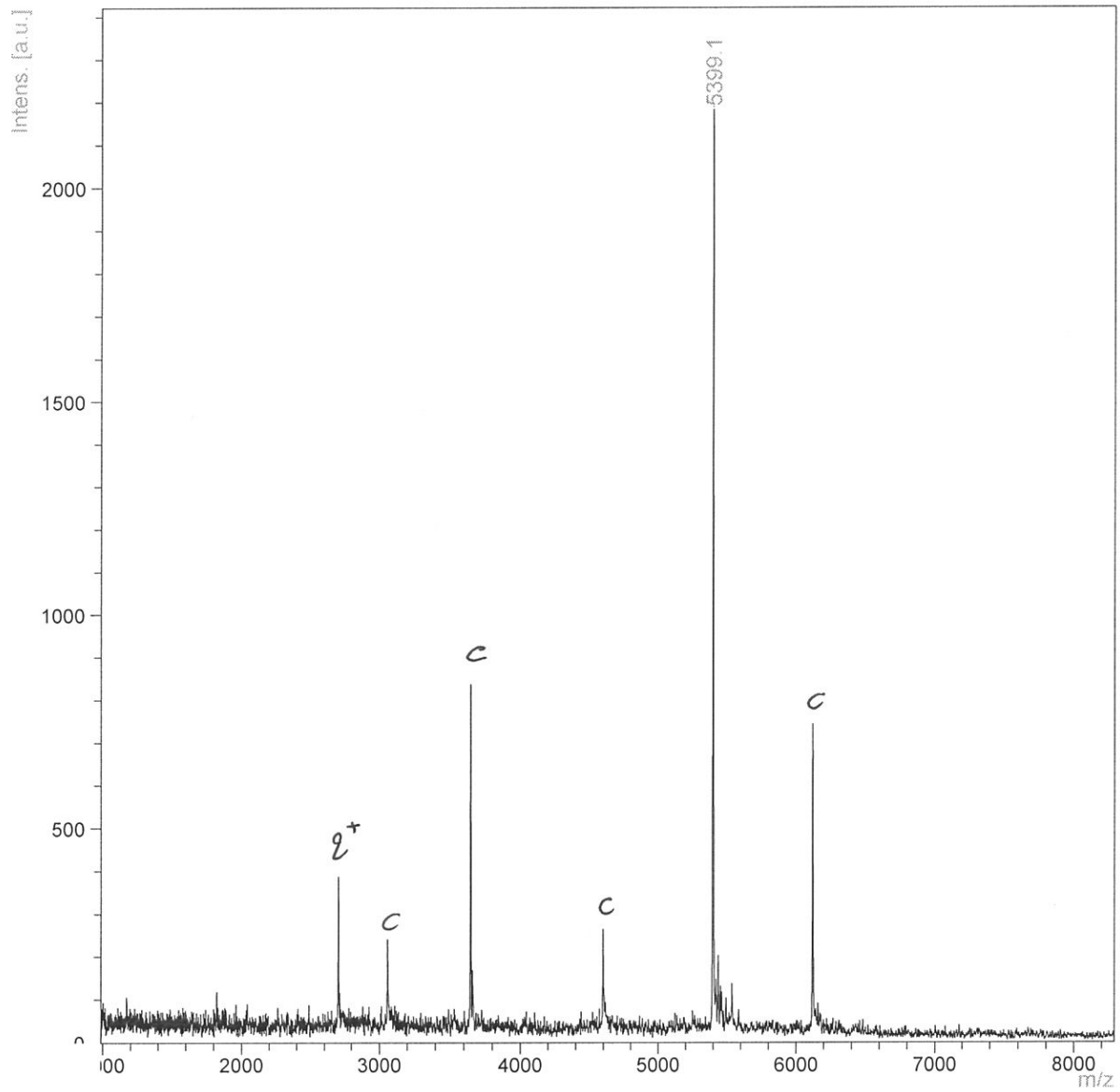
RP-HPLC spectrum of ON **7**



MS Analysis

MW = 5397.7 g.mol^{-1} for $C_{180}H_{238}O_{109}N_{54}P_{16}$

Mass spectrum (MALDI-TOF) of ON 7



MS calcd for $[M+H]^+$ 5398.7 Da, found 5399.1 Da.

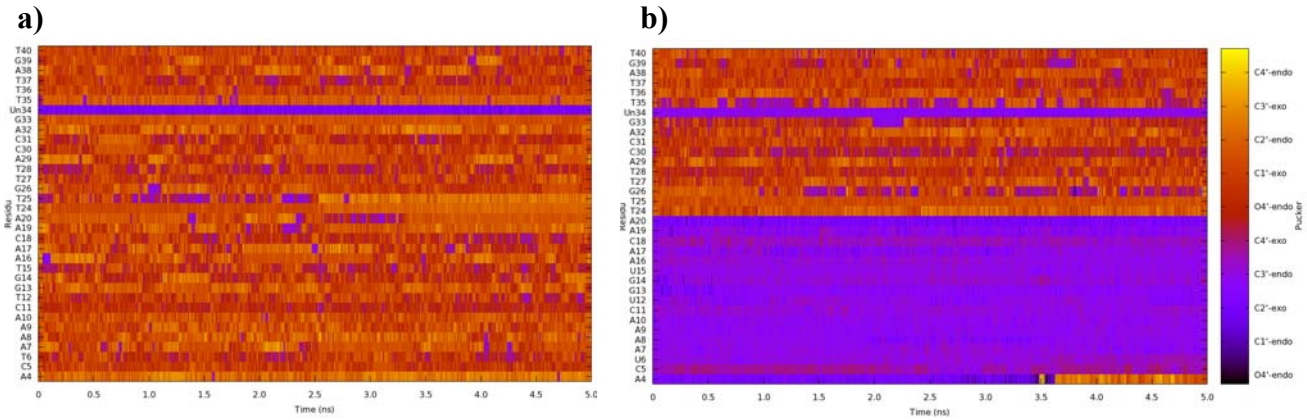


Fig 6. Heat maps of the variation of the sugar pucker conformation of each paired residue during the simulation: **a)** DNA/DNA duplex and **b)** DNA/RNA duplex, containing a single modified nucleoside Un. The numbering of the base-pairs for the unmodified DNA/DNA duplex is shown below and used for all the duplexes.

```
          1----- 4----------10---------- 16------ -20-----23
d-5′TACACTAAAACTGGTAACAACTC3′
   3′TGATTTTGACCATTGTT5′
   40----------  34---------- 28--------24
```

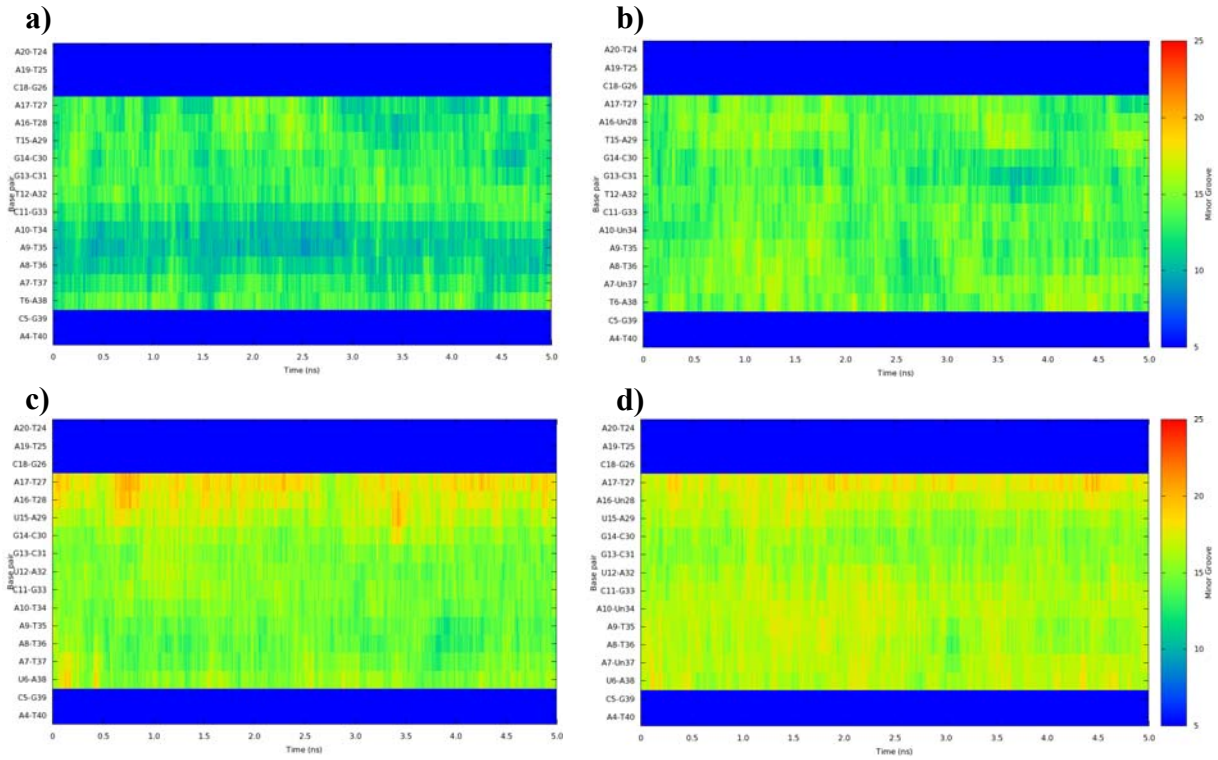


Fig 7 Heat maps of the minor groove width evolution of each base pair during the simulation for **a)** the unmodified DNA/DNA duplex, **b)** the DNA/DNA duplex containing three noncontiguous modified nucleoside Un, **c)** the unmodified DNA/RNA duplex and **d)** the DNA/RNA duplex containing three noncontiguous modified nucleoside Un. The deep-blue bands on the top and the bottom of the graph mean that the minor groove width of the first two base pairs and of the last three base pairs cannot be measured.

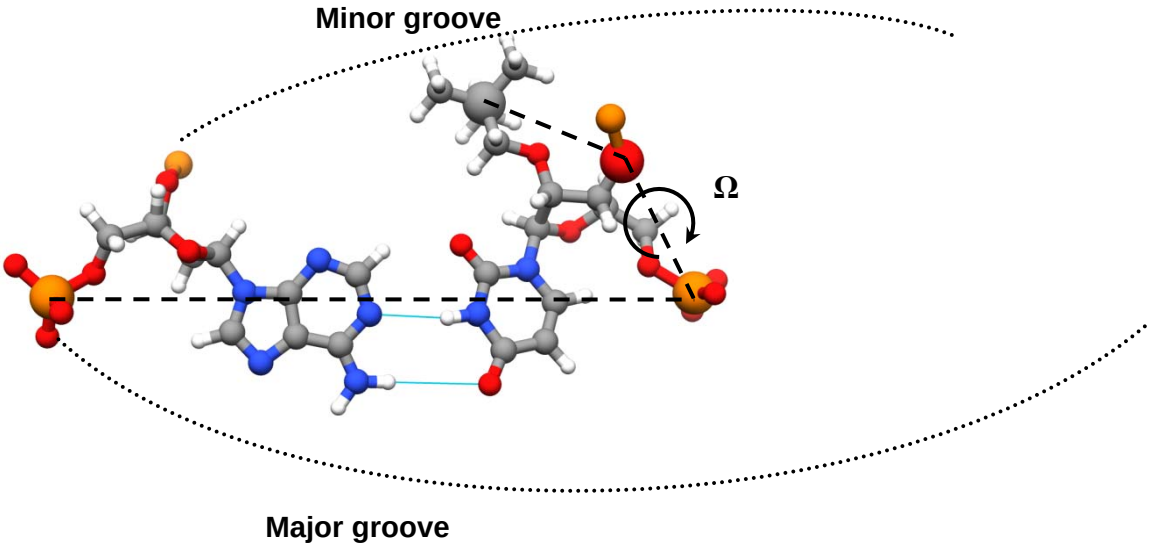


Fig 8 Definition of the Ω torsion angle used to evaluate the positioning of the neopentyl group into the minor groove.