Synthesis, Chirality-dependent Conformational and Biological Properties of siRNAs Containing 5'-(*R*)- and 5'-(*S*)-*C*-Methyl-Guanosine

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Sr.	Code	^a Sequence	Ma	ass
No.		•	Calculated	Observed
1	$G_{PO}dT_{19}$	<u>G</u> dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6062.9	6076.9
2	$S_{\rm PO} dT_{19}$	G ^S dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6076.9	6076.3
3	$R_{\rm PO} dT_{19}$	G ^R dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6076.9	6076.3
4	G _{PS} dT ₁₉	₲●dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6078.9	6078.4
5	$R_{\rm PS} dT_{19}$	G ^R ●dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.4
6	$S_{\rm PS} dT_{19}$	G ^s ●dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.4
7	dT _{19PO} G	ϴͳͶͻͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧͲϧ	6062.9	6062.3
8	dT _{19PO} S	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.4
9	$dT_{19PO}R$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.4
10	$dT_{19PS}G$	dT	6078.9	6080.3
11	$dT_{19PS}S$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.3
12	$dT_{19PS}R$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6093.0	6092.3
13	$dT_{18}G_{PO}G$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTGG	6103.9	6103.3
14	$dT_{18}S_{PO}S$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTG ^S G ^S	6131.9	6131.4
15	$dT_{18}R_{PO}R$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTG ^R G ^R	6131.9	6131.4
16	$dT_{18}G_{PS}G$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTG • G	6119.9	6119.3
17	$dT_{18}S_{Ps}S$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTG ^S ●G ^S	6148.0	6147.4
18	$dT_{18}R_{PS}R$	dTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdTdT	6148.0	6147.4

Supplementary Table 1. MS (m/z) analysis of modified oligonucleotides for exonuclease assay

^a Modifications are indicated as follows: •, phosphorothioate (PS) linkage; dT, deoxy thymidine; $\mathbf{G}^{\mathbf{R}}$, 5'-(*R*)-*C*-methyl-guanosine; and $\mathbf{G}^{\mathbf{S}}$, (*S*)-*C*-methyl-guanosine.

Sr.No.	Target	Sense strand (top)	Modification	Calculated	Observed
		Antisense strand (bottom) ^a	position ^b	Mass	Mass
Si-1	TTR	A•a•CaGuGuUCUuGcUcUaUaAL		8590.2	8590.3
		u•U•aUaGaGcAagaAcAcUgUu•u•u		7595.9	7597.6
Si-2	TTR	A∙a•CaG ^R uGuUCUuGcUcUaUaAL	S-5	8602.2	8602.8
		u•U•aUaGaGcAagaAcAcUgUu•u•u		7595.9	7597.7
Si-3	TTR	A∙a•CaGu <mark>G^RuUCUuGcUcUaUaAL</mark>	S-7	8602.2	8602.9
		u•U•aUaGaGcAagaAcAcUgUu•u•u		7595.9	7596.9
Si-4	TTR	A•a•CaGuGuUCUuGcUcUaUaAL		8590.2	8590.7
		u•U•aUa <mark>G^RaGcAagaAcAcUgUu•u•</mark> u	AS-6	7608	7609.1
Si-5	TTR	A•a•CaGuGuUCUuGcUcUaUaAL		8590.2	8590.8
		u•U•aUaGa <mark>G^Rc</mark> AagaAcAcUgUu•u•u	AS-8	7608	7608.8
Si-6	TTR	A•a•Ca <mark>G^{\$}uGuUCUuGcUcUaUaAL</mark>	S-5	8602.2	8603.2
		u•U•aUaGaGcAagaAcAcUgUu•u•u		7595.9	7597.5
Si-7	TTR	A∙a•CaGu <mark>G^{\$}uUCUuGcUcUaUaAL</mark>	S-7	8602.2	8603
		u•U•aUaGaGcAagaAcAcUgUu•u•u		7595.9	7596.5
Si-8	TTR	A•a•CaGuGuUCUuGcUcUaUaAL		8590.2	8591
		u•U•aUa <mark>G^SaGcAagaAcAcUgUu•u•u</mark>	AS-6	7608	7608.2
Si-9	TTR	A•a•CaGuGuUCUuGcUcUaUaAL		8590.2	8591.3
		u•U•aUaGa <mark>G^ScAagaAcAcUgUu•u•u</mark>	AS-8	7608	7608.4
Si-10	F12	g•a•aacuCaAUAaagugcuuuaL		8756.6	8757.3
		u•A•aagCacuuuauUgAguuuc•u•g		7610	7610.8
Si-11	F12	G ^R •a•aacuCaAUAaagugcuuuaL	S-1	8756.6	8757.4
		u•A•aagCacuuuauUgAguuuc•u•g		7610	7610.6
Si-12	F12	G ^s •asaacuCaAUAaagugcuuuaL	S-1	8756.6	8757.3
		u•A•aagCacuuuauUgAguuuc•usg		7610	7611

Supplementary Table 2. MS (*m/z*) analysis of modified oligonucleotides for i*n vitro* assay

^a Chemical modifications are indicated as follows: •, PS linkage; lower case, 2'-OMe; upper case and italics, 2'-F; G^{R} , 5'-(*R*)-*C*-methyl-guanosine; G^{s} , 5'-(*S*)-*C*-methyl-guanosine; L, trivalent GalNAc. ^b S and AS indicates sense and antisense strand, and number indicates position of modification from 5' end. ; L indicate tri-GalNAc it is hydroxyprolynyl trivalent N-acetyl galactosamine ligand.¹⁶ **Supplementary Table 3.** Primer and template sequences used in the mitochondrial polymerase incorporation and inhibition assays.

		POLRMT	POLG
Primer		5'-Atto-425-UUUUGCCGCGCC-3'	5'-Atto-425-d[CGATATTCACAAAG]-3'
Template	G+	5'-d[GGGAATGTACGGCGCGGC]-3'	5'-d[CATGCTCTAACCCGCCTTTGTGAATATCG]-3'



Figure S1: Incorporation of native and 5'-C-methyl-guanosine triphosphates by POLRMT *in vitro*. Reaction conditions: 200 nM template, 50 nM primer, 300 nM enzyme, and 1 mM or 100 μ M NTP of interest, 30 min, 35 °C. Samples were run in duplicate and analysed using analytical HPLC using fluorescence detection. The red box marks the location of the non-extended primer.



Figure S2: Incorporation of native and 5'-C-methyl guanosine triphosphates by POLG *in vitro*. Reaction conditions: 200 nM template, 50 nM primer, 300 nM enzyme, and 1 mM or 100 µM NTP of interest, 30 min, 35 °C. Samples were run in duplicate and analysed using analytical HPLC using fluorescence detection. The red box marks the location of the non-extended primer.

Supplementary Table 4 Selected crystallographic data and data collection and refinement parameters for 5'-CCCCXGGG-3' (X=(*R*)-5'-*C*-Me-guanosine)

Space group	P61		
Unit cell constants a, b, c [Å]; α, β, γ [°]	37.92, 37.92, 57.85, 90, 90, 120		
Data Collection			
Wavelength [Å]	0.91833		
Resolution [Å]	21.72-1.56 (1.62-1.56) ^a		
No. of unique reflections	6,721 (627)		
Redundancy	18.5 (12.1)		
Ι/σ(Ι)	63.3 (1.33)		
Completeness [%]	99.3 (92.4)		
R-merge	0.063 (0.869)		
R-pim	0.015 (0.243)		
Refinement			
No. of reflections	6,392 (295)		
R-work [%]	0.177 (0.259)		
R-free [%]	0.244 (0.268)		
No. of RNA atoms	340		
No. of ions (Co3+)/waters	5/30		
R.m.s. deviations bonds [Å]	0.029		
R.m.s. deviations angles [°]	1.85		
Avg. B-factor, DNA atoms [Å2]	37.6		
Avg. B-factor, ions/water [Å2]	36.4/48.9		
PDB entry code	6VEM		

a Values in parentheses refer to the highest resolution shell

¹H, ¹³C and ³¹P NMR spectra of the new compounds

 1 H NMR spectrum of compound **3** in DMSO-d6



¹H NMR spectrum of compound **4** in DMSO-d6



¹H NMR spectrum of compound **5** in DMSO-d6



¹H NMR spectrum of compound **6** in DMSO-d6



¹H NMR spectrum of compound **7** in DMSO-d6



¹H NMR spectrum of compound **8** in DMSO-d6



¹H NMR spectrum of compound **9** in DMSO-d6





¹H NMR spectrum of compound 11 in CDCl₃



³¹P NMR spectrum of compound 11 in CDCl₃



¹³C NMR spectrum of compound 11 in CDCl₃



















¹H NMR spectrum of compound 21 in CDCl₃

8.8.6. 7.757 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.759 7.721 7.721 7.721 7.721 7.721 7.721 7.723 7



 ^{31}P NMR spectrum of compound 21 in CDCl_3



 ^{13}C NMR spectrum of compound 21 in CDCl_3







1.0

0

1.5

2.0

¹H NMR spectrum of compound 25 in DMSO-*d*6



¹H NMR spectrum of compound 26 in DMSO-*d*6







D

