

## Supplementary Information

# Peptide-LNA Oligonucleotide Conjugates

I. Kira Astakhova,\*<sup>1,†</sup> Lykke Haastrup Hansen,<sup>‡</sup> Birte Vester,<sup>‡</sup> and Jesper Wengel<sup>†</sup>

<sup>†</sup>Nucleic Acid Center and the Biomolecular Nanoscale Engineering Center, Department of Physics, Chemistry and Pharmacy, University of Southern Denmark, Campusvej 55 DK-5230 Odense M, Denmark

<sup>‡</sup>Department of Biochemistry and Molecular Biology, University of Southern Denmark, Campusvej 55 DK-5230 Odense M, Denmark

## Contents

Analysis of oligonucleotides <b>ON1–ON3</b> (Table S1)	S2
IE HPLC retention times and MALDI-MS of <b>POC1–POC6</b> (Table S2, Figures S1-S2 )	S2-S3
Representative $T_m$ curves (Figure S3)	S4
Effect of single mismatches on binding affinities of modified POCs and reference oligonucleotides (Tables S3–S4)	S5-S6
Representative CD curves (Figure S4)	S7
Gel electrophoresis of 5'- <sup>32</sup> P-labeled oligonucleotides incubated with HS (Figure S5)	S8
Molecular model of duplex <b>POC2</b> :DNA (Figure S6)	S9

<sup>1</sup> Corresponding author. E-mail: [ias@sdu.dk](mailto:ias@sdu.dk)

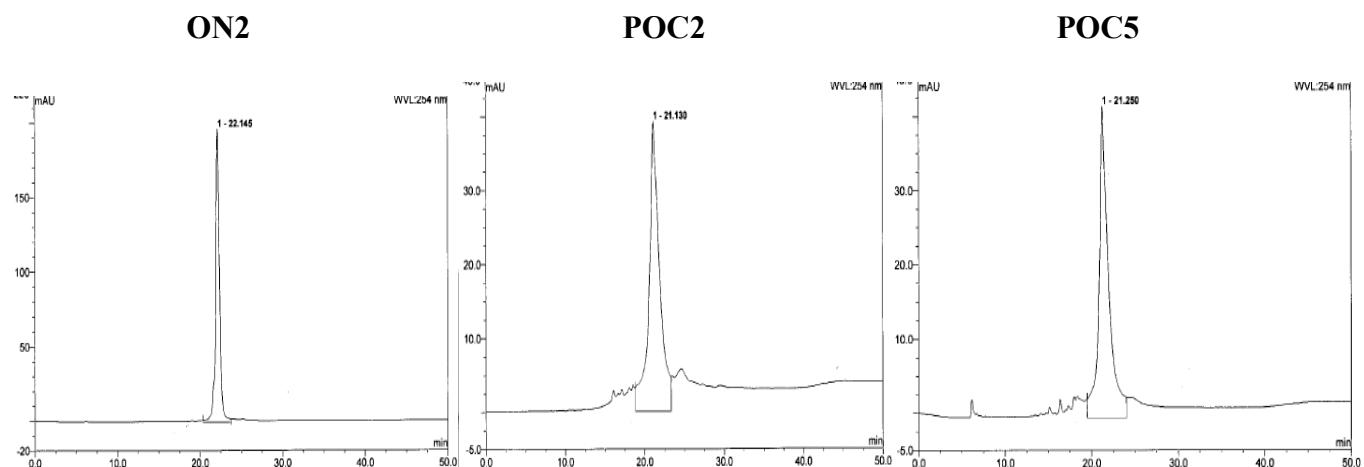
**Table S1.** IE HPLC retention times and MALDI-MS of purified oligonucleotides.

#	Sequence, 5'→3'	Ret. time, min	MALDI-MS	
			Found m/z [M-H] <sup>-</sup>	Calc. m/z [M-H] <sup>-</sup>
<b>ON1</b>	TGC ACT CTA <b>TG<u>M</u><sup>1</sup></b> CTG TAT CAT	24.04	6467	6468
<b>ON2</b>	TGC ACT CTA <b><u>M</u><sup>1</sup>GT CM<sup>1</sup>G</b> TAT CAT	22.14	6575	6575
<b>ON3</b>	TGC AC <u>M</u> <sup>1</sup> CTA TGT CTG <b>TAM<sup>1</sup></b> CAT	24.18	6572	6575

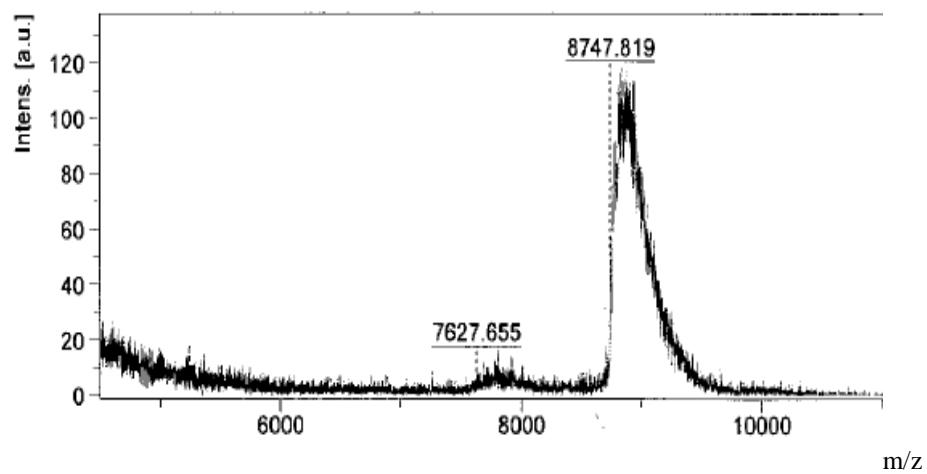
**Table S2.** IE HPLC retention times and MALDI-MS of **POC1–POC6**.

#	Sequence, 5'→3'	Ret. time, min	MALDI-MS	
			Found m/z [M-H] <sup>-</sup>	Calc. m/z [M-H] <sup>-</sup>
<b>POC1</b>	TGC ACT CTA <b>TG<u>M</u><sup>2</sup></b> CTG TAT CAT	22.91	7550	7551
<b>POC2</b>	TGC ACT CTA <b><u>M</u><sup>2</sup>GT CM<sup>2</sup>G</b> TAT CAT	21.13	8748	8741
<b>POC3</b>	TGC AC <u>M</u> <sup>2</sup> CTA TGT CTG <b>TAM<sup>2</sup></b> CAT	21.19	8745	8741
<b>POC4</b>	TGC ACT CTA <b>TG<u>M</u><sup>3</sup></b> CTG TAT CAT	23.54	7533	7533
<b>POC5</b>	TGC ACT CTA <b><u>M</u><sup>3</sup>GT CM<sup>3</sup>G</b> TAT CAT	21.25	8708	8705
<b>POC6</b>	TGC AC <u>M</u> <sup>3</sup> CTA TGT CTG <b>TAM<sup>3</sup></b> CAT	23.24	8706	8705

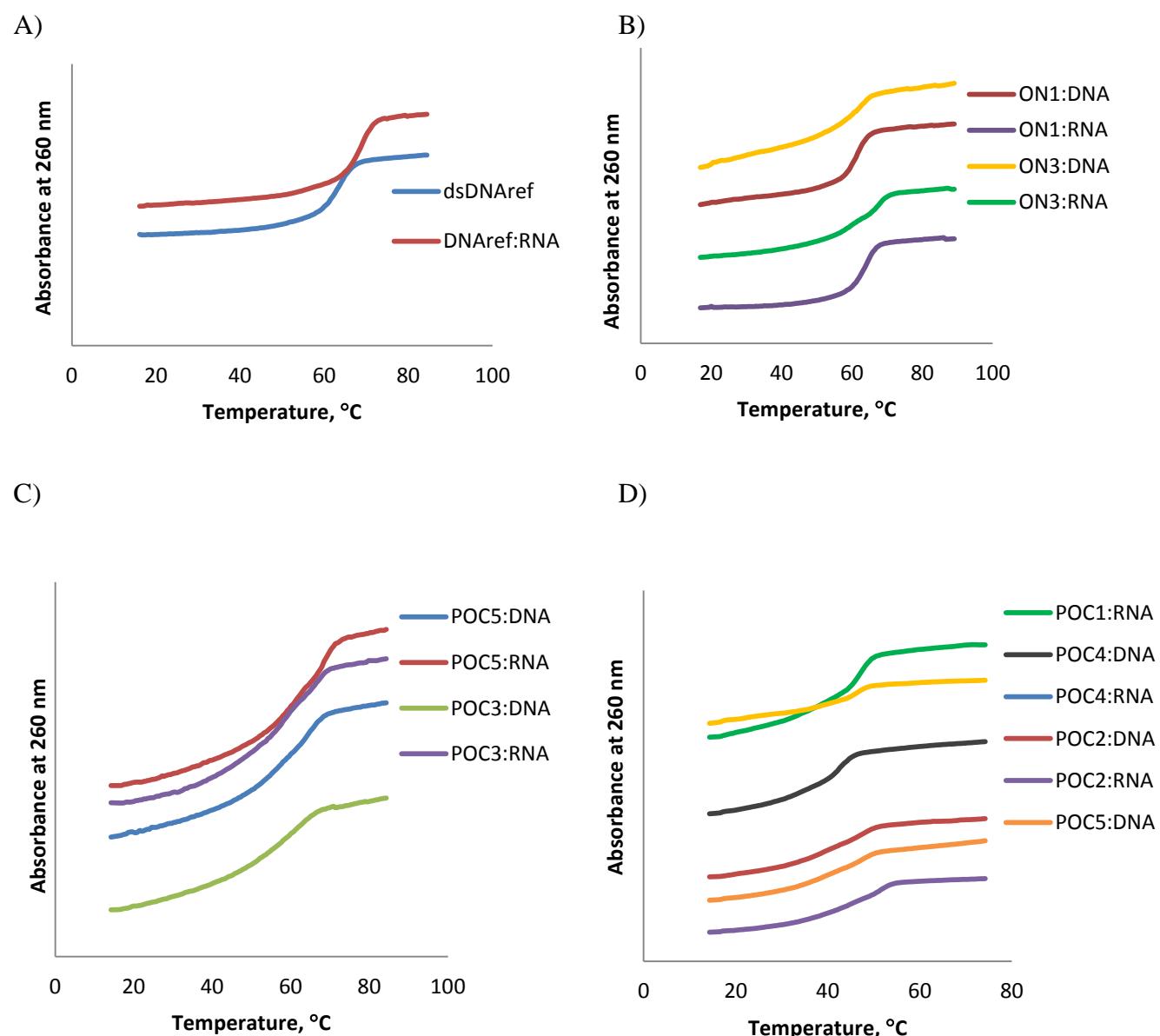
**Figure S1.** Representative IE HPLC traces of modified oligonucleotides prepared in this study.



**Figure S2.** Representative MALDI-MS spectrum of peptide-oligonucleotide conjugate **POC2**.



**Figure S3.** Representative  $T_m$  curves.



The melting curves were recorded in a medium salt (A–C) and low salt (D) phosphate buffer using 0.5  $\mu$ M concentration of complementary strands.

**Table S3.** Effect of single mismatches on binding affinities of single-labeled **ON1**, **POC1** and **POC2** to DNA/RNA targets in a medium salt phosphate buffer.<sup>a</sup>

Conjugate:Target	$\text{X} =$	$T_m$ (°C)							
		DNA target				RNA target			
		A	C	T	G	A	C	U	G
<b>(ON1)</b>									
5'- TGC ACT CTA TGM <sup>1</sup> CTG TAT CAT		50.5	62.0 <sup>cc</sup>	53.5	53.0	54.5	65.0 <sup>cc</sup>	56.0	57.0
3'- ACG TGA GAT AXA GAC ATA GTA									
<b>(ON1)</b>									
5'- TGC ACT CTA TGM <sup>1</sup> CTG TAT CAT		62.0 <sup>cc</sup>	53.0	54.0	54.0	65.0 <sup>cc</sup>	54.5	55.0	58.0
3'- ACG TGA GAT ACX GAC ATA GTA									
<b>(ON1)</b>									
5'- TGC ACT CTA TGM <sup>1</sup> CTG TAT CAT		49.0	49.0	49.0	62.0 <sup>cc</sup>	54.0	50.0	50.0	65.0 <sup>cc</sup>
3'- ACG TGA GAT ACA XAC ATA GTA									
<b>(POC1)</b>									
5'- TGC ACT CTA TGM <sup>2</sup> CTG TAT CAT		51.0	60.0 <sup>cc</sup>	55.0	53.0	53.0	63.5 <sup>cc</sup>	56.0	55.0
3'- ACG TGA GAT AXA GAC ATA GTA									
<b>(POC1)</b>									
5'- TGC ACT CTA TGM <sup>2</sup> CTG TAT CAT		60.0 <sup>cc</sup>	52.0	52.0	53.0	63.5 <sup>cc</sup>	54.0	55.0	57.0
3'- ACG TGA GAT ACX GAC ATA GTA									
<b>(POC1)</b>									
5'- TGC ACT CTA TGM <sup>2</sup> CTG TAT CAT		50.0	50.0	51.0	60.0 <sup>cc</sup>	52.5	49.0	49.5	63.5 <sup>cc</sup>
3'- ACG TGA GAT ACA XAC ATA GTA									
<b>(POC2)</b>									
5'- TGC ACT CTA TGM <sup>3</sup> CTG TAT CAT		45.0	62.0 <sup>cc</sup>	43.0	40.0	53.0	64.5 <sup>cc</sup>	55.0	55.5
3'- ACG TGA GAT AXA GAC ATA GTA									
<b>(POC2)</b>									
5'- TGC ACT CTA TGM <sup>3</sup> CTG TAT CAT		62.0 <sup>cc</sup>	55.0	50.0	52.0	64.5 <sup>cc</sup>	55.0	55.0	57.5
3'- ACG TGA GAT ACX GAC ATA GTA									
<b>(POC2)</b>									
5'- TGC ACT CTA TGM <sup>3</sup> CTG TAT CAT		52.5	51.0	53.0	62.0 <sup>cc</sup>	52.0	50.0	50.5	64.5 <sup>cc</sup>
3'- ACG TGA GAT ACA XAC ATA GTA									

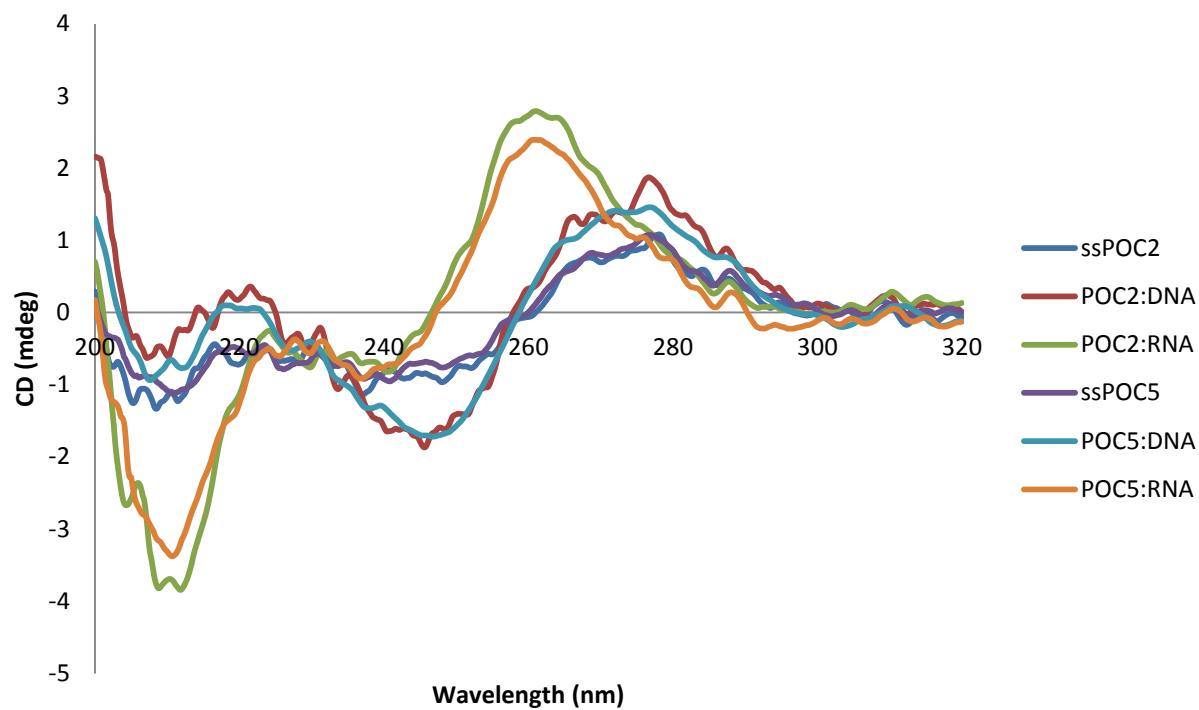
<sup>a</sup> Sequences of DNA target variants are presented; *cc* = complementary complex.

**Table S4.** Effect of single-base mismatch on binding affinity of **ON2–ON3** to DNA/RNA targets in a medium salt phosphate buffer.<sup>a</sup>

ON:TARGET	$\text{X} =$	DNA target					$T_m$ (°C)			
		A	C	T	G		A	C	U	G
5' - TGC ACT CTA M <sup>1</sup> GT CM <sup>1</sup> G TAT CAT 3' - ACG TGA GAT ACA GAX ATA GTA		54.0	63.5 <sup>cc</sup>	57.0	54.0		57.0	69.0 <sup>cc</sup>	61.0	59.0
5' - TGC ACT CTA M <sup>1</sup> GT CM <sup>1</sup> G TAT CAT 3' - ACG TGA GAT ACA GXC ATA GTA		63.5 <sup>cc</sup>	50.0	57.0	57.0		69.0 <sup>cc</sup>	61.0	60.0	64.0
5' - TGC ACT CTA M <sup>1</sup> GT CM <sup>1</sup> G TAT CAT 3' - ACG TGA GAT XCA GAC ATA GTA		63.5 <sup>cc</sup>	55.0	56.0	57.0		69.0 <sup>cc</sup>	62.0	62.0	65.0
5' - TGC ACT CTA M <sup>1</sup> GT CM <sup>1</sup> G TAT CAT 3' - ACG TGA GAX ACA GAC ATA GTA		55.5	55.0	63.5 <sup>cc</sup>	59.5		62.0	60.0	69.0 <sup>cc</sup>	65.0
5' - TGC ACM <sup>1</sup> CTA TGT CTG TAM <sup>1</sup> CAT 3' - ACG TGA GAT ACA GA ATA XTA		54.0	53.0	55.0	63.0 <sup>cc</sup>		59.0	55.0	60.0	68.0 <sup>cc</sup>
5' - TGC ACM <sup>1</sup> CTA TGT CTG TAM <sup>1</sup> CAT 3' - ACG TGA GAT ACA GA ATX GTA		63.0 <sup>cc</sup>	53.0	54.0	55.0		68.0 <sup>cc</sup>	60.0	60.0	62.0
5' - TGC ACM <sup>1</sup> CTA TGT CTG TAM <sup>1</sup> CAT 3' - ACG TGA GAT ACX GA ATA BTA		63.0 <sup>cc</sup>	52.0	53.0	55.0		68.0 <sup>cc</sup>	58.8	58.8	63.0
5' - TGC ACM <sup>1</sup> CTA TGT CTG TAM <sup>1</sup> CAT 3' - ACG TGA XAT ACA GA ATA BTA		50.0	52.0	50.0	63.0 <sup>cc</sup>		55.0	53.0	56.0	68.0 <sup>cc</sup>

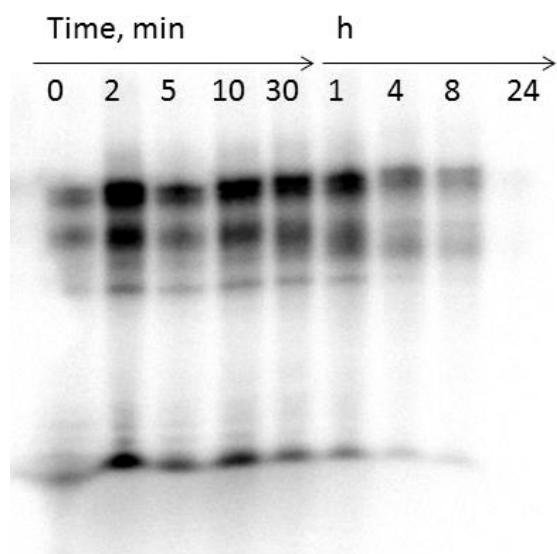
<sup>a</sup> Sequences of DNA target variants are presented; *cc* = complementary complex.

**Figure S4.** Representative CD spectra of single-stranded (ss) POCs and their duplexes with complementary DNA/RNA.

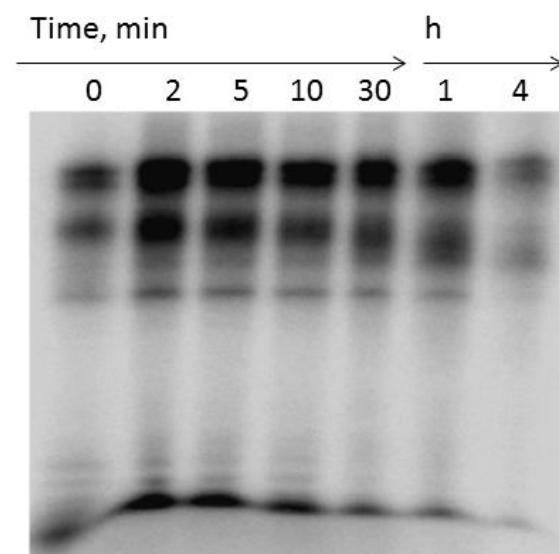


**Figure S5.** Gel electrophoresis of 5'-<sup>32</sup>P-labeled oligonucleotides incubated with HS.

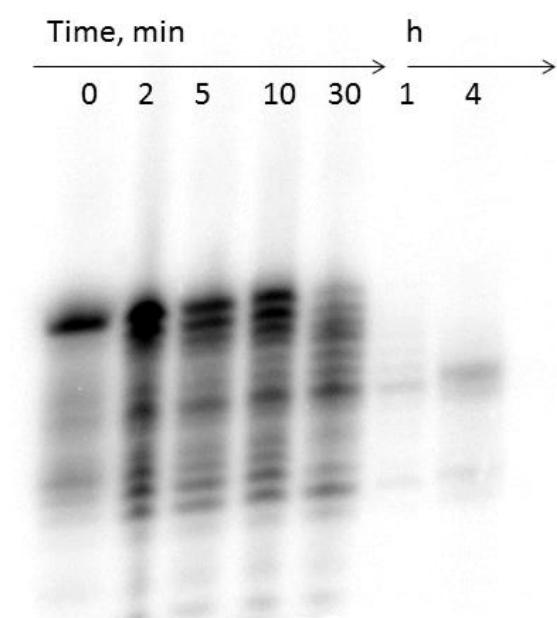
A) POC3



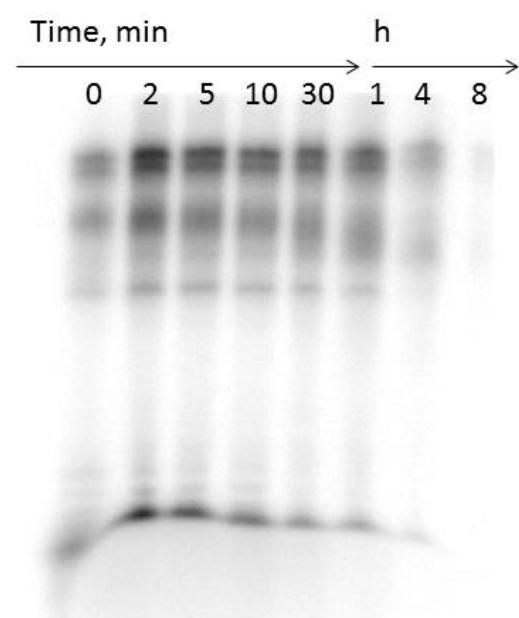
B) POC4



C) ON2

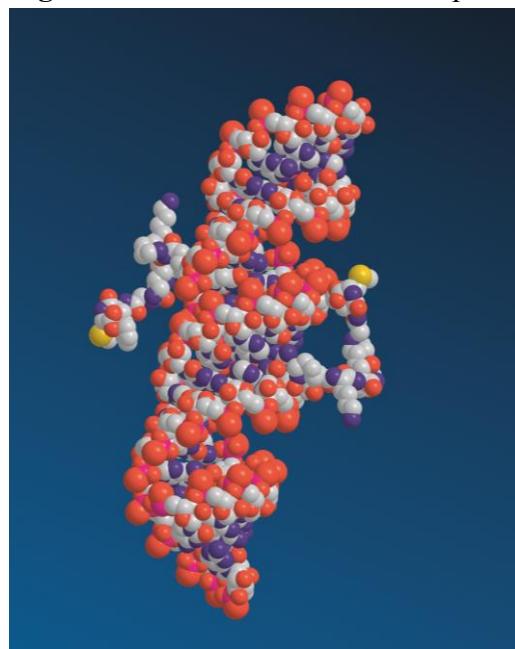


D) POC5



Assay conditions: (A–B) 90% HS in HBSS buffer; (C–D) 90% HS pre-treated with 1 mM paraoxon-ethyl, HBSS buffer.

**Figure S6.** Molecular model of duplex POC2:DNA.



White, red, pink, blue and yellow balls represent carbon, oxygen, phosphorus, nitrogen and sulphur atoms, respectively; hydrogen atoms are not shown.