

**Altering the Electrostatic Potential in the Major Groove:
Thermodynamic and Structural Characterization of 7-Deaza-2'-deoxyadenosine•dT Base
Pairing in DNA**

Ewa A. Kowal,¹ Manjori Ganguly,² Pradeep S. Pallan,³ Luis A. Marky,⁴ Barry Gold,² Martin Egli,³ and Michael P. Stone.^{1,3*}

Supporting Information

¹Department of Chemistry, Vanderbilt University, Nashville, TN 37235

²Department of Pharmaceutical Sciences, University of Pittsburgh, Pittsburgh, PA 15261

³Department of Biochemistry, Vanderbilt University, Nashville, TN 37232

⁴Department of Pharmaceutical Sciences, University of Nebraska Medical Center, Omaha, NE 68198

*To whom correspondence should be addressed

Telephone 615-322-2589

FAX 615-322-7591

e-mail michael.p.stone@vanderbilt.edu

Table S1. Parameters used to calculate differential water binding for dodecamers.^a

Oligodeoxynucleotide	NaCl (mM)	$\Delta H_{\text{cal}}/RT_M^2$ (°C)	$\partial T_M/\partial \log a_w$ (°C)	Δn_w (mol ⁻¹) DNA
DDD	10	0.62	7.49	-53.0 ± 5.0
	100	0.50		
	100 (EG)	0.40		
7-deaza-dA DDD	10	0.40	7.41	-26.0 ± 4.0
	100	0.32		
	100 (EG)	0.28		

^aThe slopes of T_M vs $\log a_w$ were obtained by least-square analysis. The values of $\Delta H/RT_M^2$ represent an average of three determinations in each salt concentration while $\partial T_M/\log a_w$ was determined at 100mM sodium phosphate buffer (pH 7.0)

EG : 1.4 m ethylene glycol

Table S2. Parameters Used to Calculate Differential Counterion Binding for Dodecamers.^a

Oligodeoxynucleotide	NaCl (mM)	$\Delta H_{\text{cal}}/RT_M^2$ (°C)	$\partial T_M/\partial \log[\text{Na}^+]$ (°C)	Δn_{Na^+} (mol ⁻¹) DNA
DDD	10	0.62	7.49	-2.3 ± 0.15
	100	0.50		-1.8 ± 0.12
7-deaza-dA DDD-1	10	0.40	7.41	-1.4 ± 0.14
	100	0.32		-1.1 ± 0.12

^aData obtained in 10 mM sodium phosphate at pH 7.0 adjusted to the desired ionic strength with NaCl.

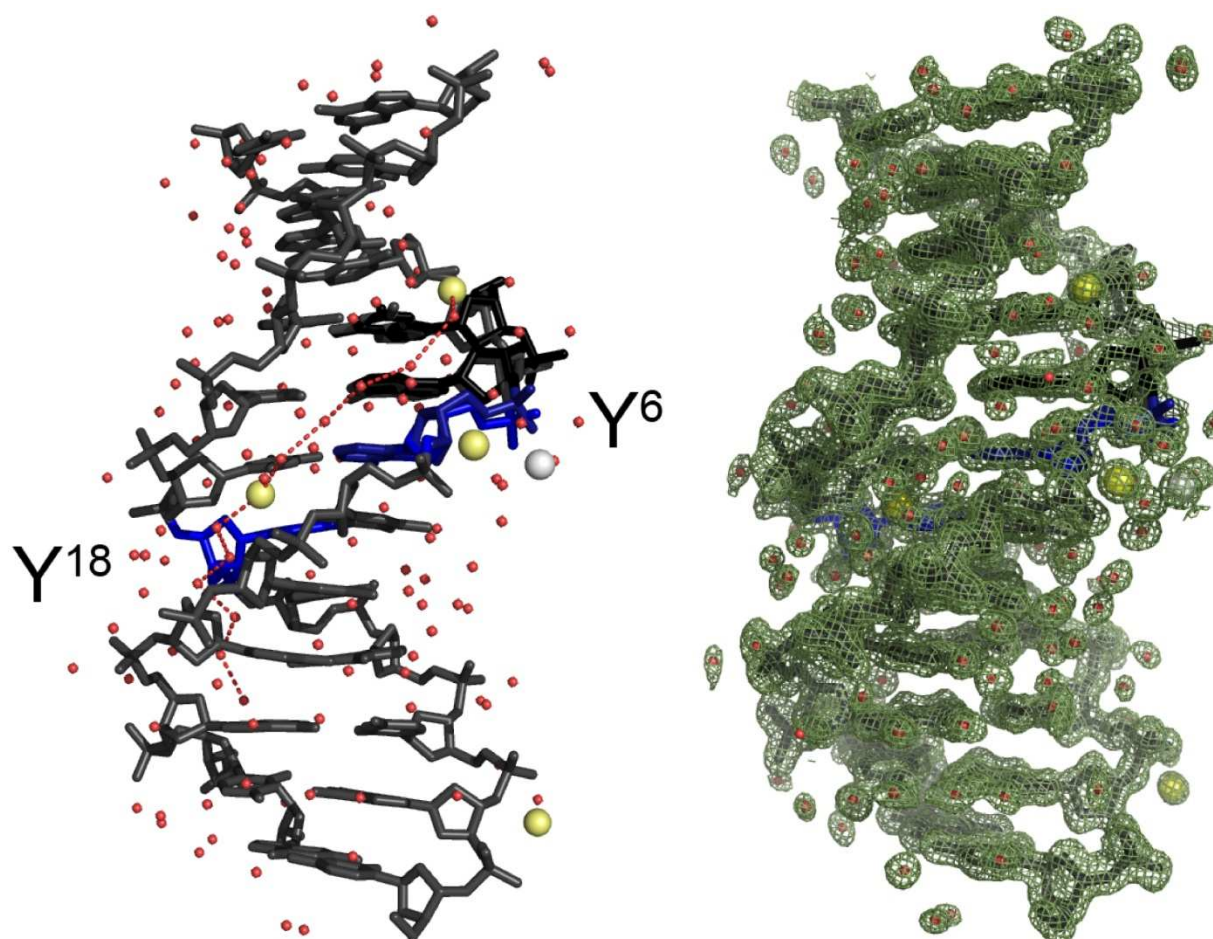


Figure S1. Stick model of the crystal structure of 7-deaza-dA modified DDD-1 (left side) and electron density shown at 1.0σ level around the duplex (right side). Modified bases Y^6 and Y^{18} are shown in blue, Mg^{2+} ion is shown as white sphere, 133 water molecules are shown as red spheres and four Na^+ ions as yellow spheres. Red dash line shows water inner spine in the minor groove of DNA duplex. It contains water and sodium molecules (from the bottom end): HOH 426, HOH 444, HOH 438, HOH 442, HOH 412, HOH 441, NA 400, HOH 450, HOH 413, HOH 451, HOH 432, HOH 519, NA 402.

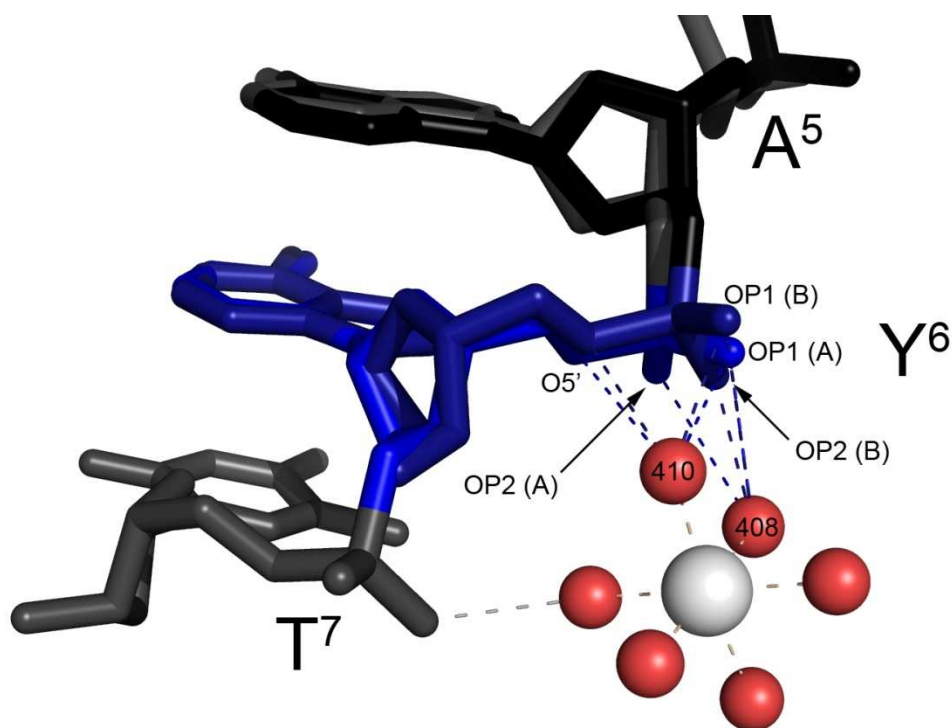


Figure S2. Interactions between Mg²⁺ ion and DDD-1 duplex are indicated by dash lines.

Modified base Y⁶ is in blue (one phosphate conformation, A) and navy (second phosphate group conformation, B). Mg²⁺ ion (white sphere) is coordinated by six water molecules (red spheres).

The Mg²⁺ ion interacts via coordinated waters with phosphate oxygens of two conformers of Y⁶ and T⁷ nucleotides. Distances between water molecules coordinated to Mg²⁺ ion and Y⁶

nucleotide are shown below:

HOH 410	OP1 (A)	3.55 Å
HOH 410	OP1 (B)	2.73 Å
HOH 410	O5' (A)	4.06 Å
HOH 410	O5' (B)	3.44 Å
HOH 408	OP1 (A)	2.85 Å
HOH 408	OP1 (B)	3.53 Å
HOH 408	OP2 (A)	4.04 Å

HOH 408 OP2 (B) 2.77 Å

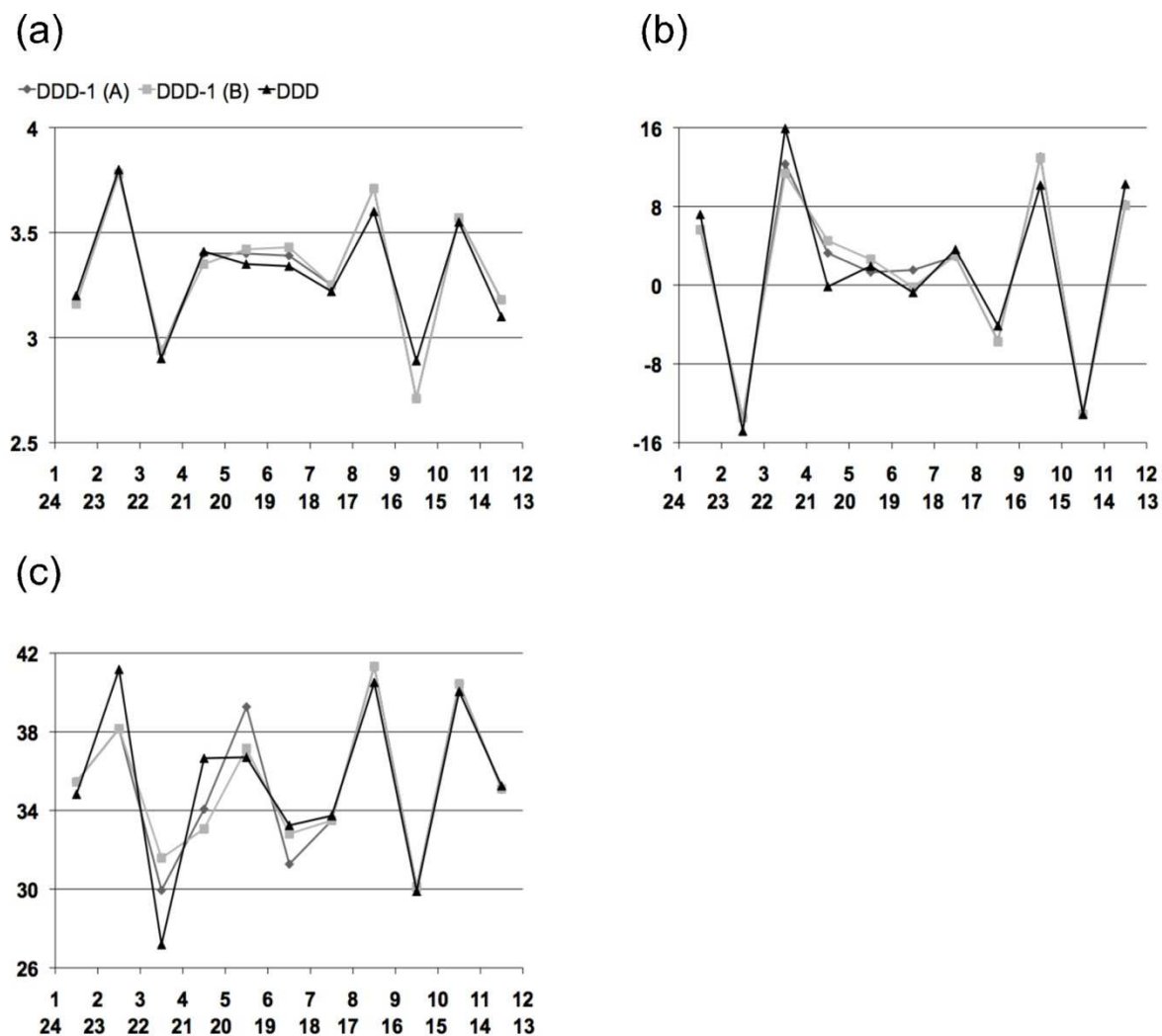


Figure S3. Interbase pair parameters: (a) helical rise, (b) roll and (c) twist for the DDD-1(A) (with one phosphate backbone conformation for the G⁴, A⁵ and Y⁶), DDD-1 (B) (with second phosphate conformation for the G⁴, A⁵ and Y⁶), DDD (PDB entry 355D) duplexes.

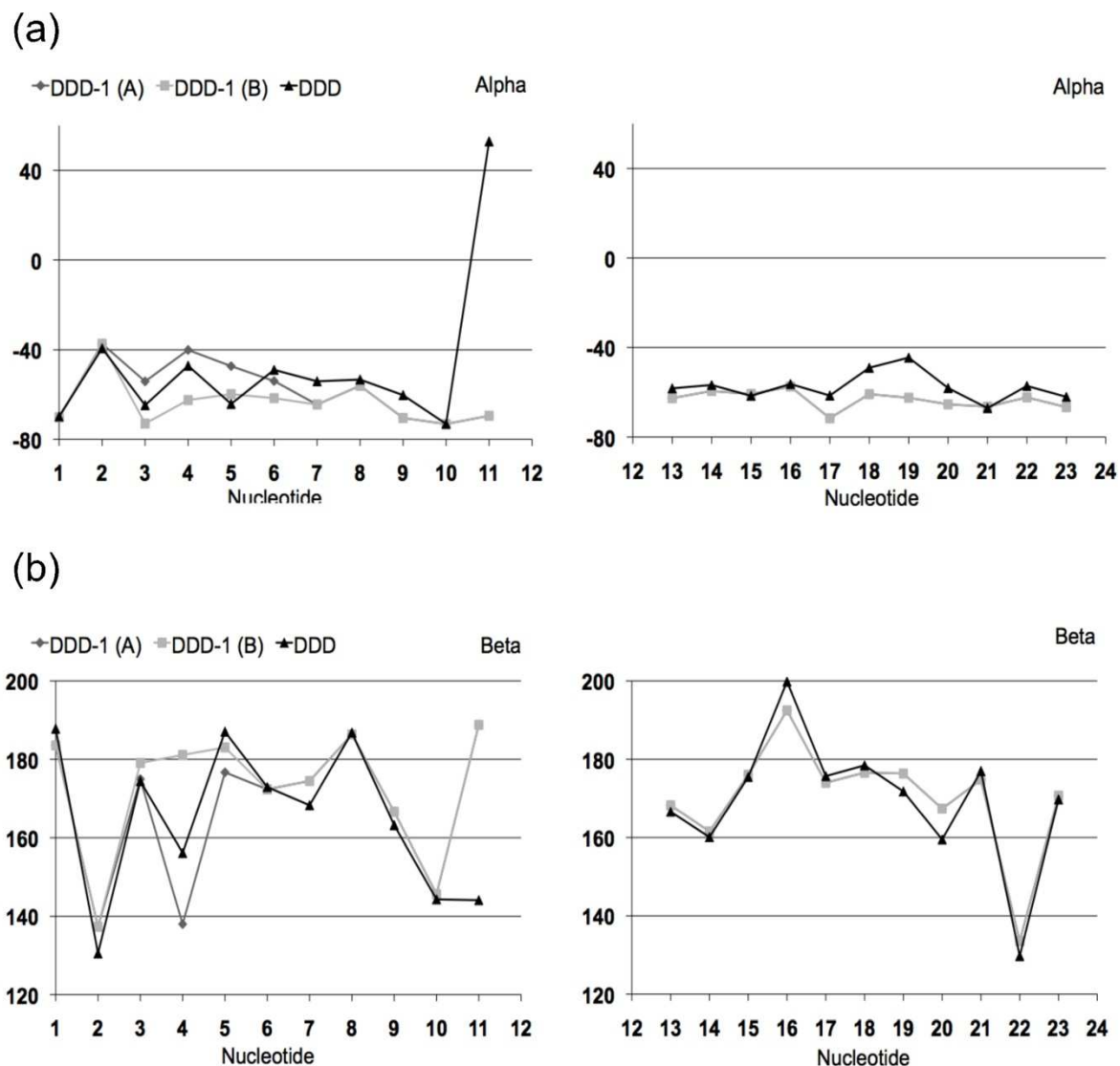
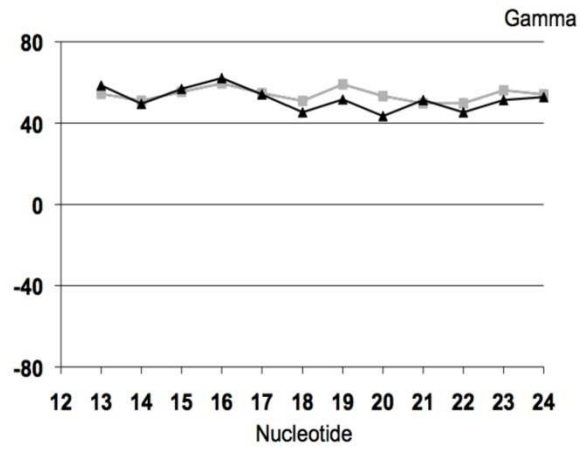
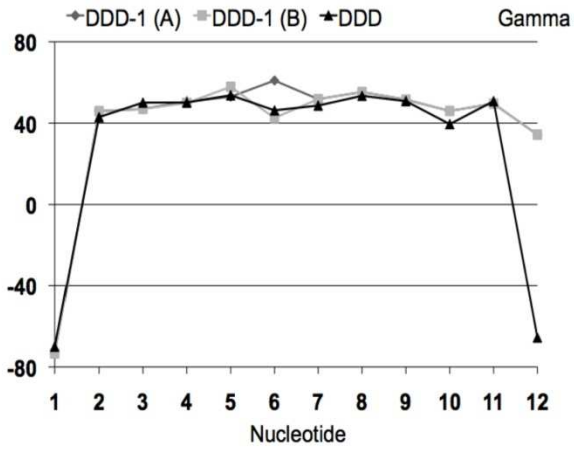
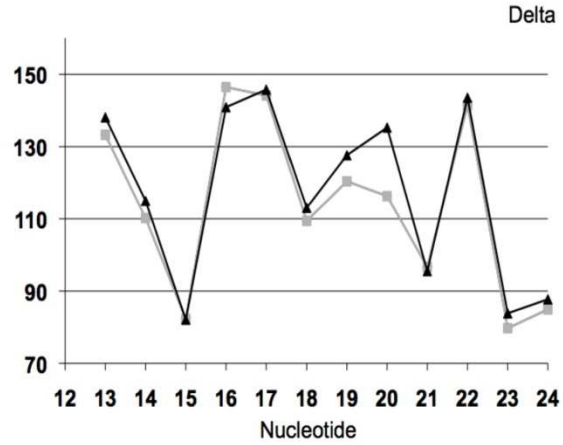
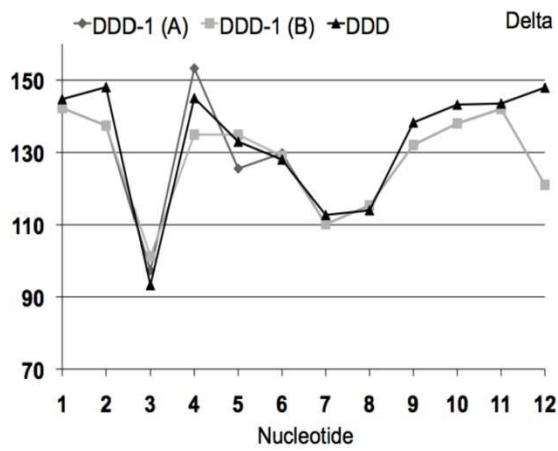


Figure S4. Comparison of backbone torsion angles (a) Alpha and (b) Beta in the crystal structures of the DDD-1(A) (with one phosphate backbone conformation for the G⁴, A⁵ and Y⁶), DDD-1 (B) (with second phosphate conformation for the G⁴, A⁵ and Y⁶), DDD (PDB entry 355D) duplexes.

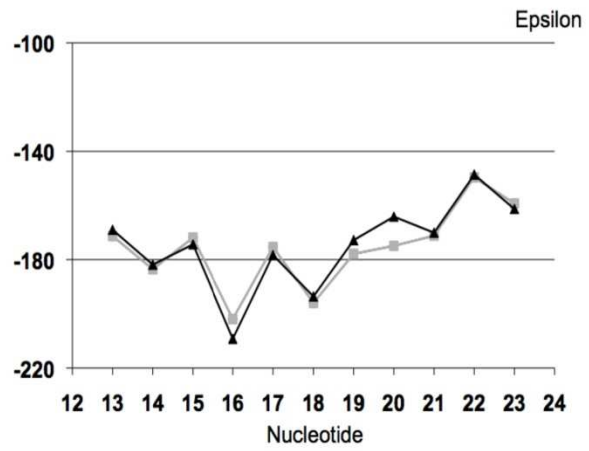
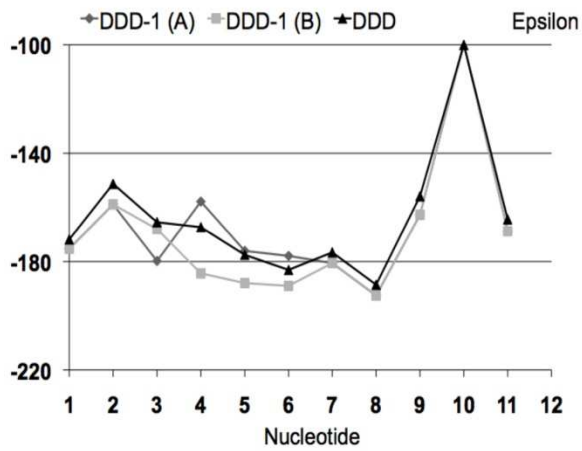
(a)



(b)



(c)



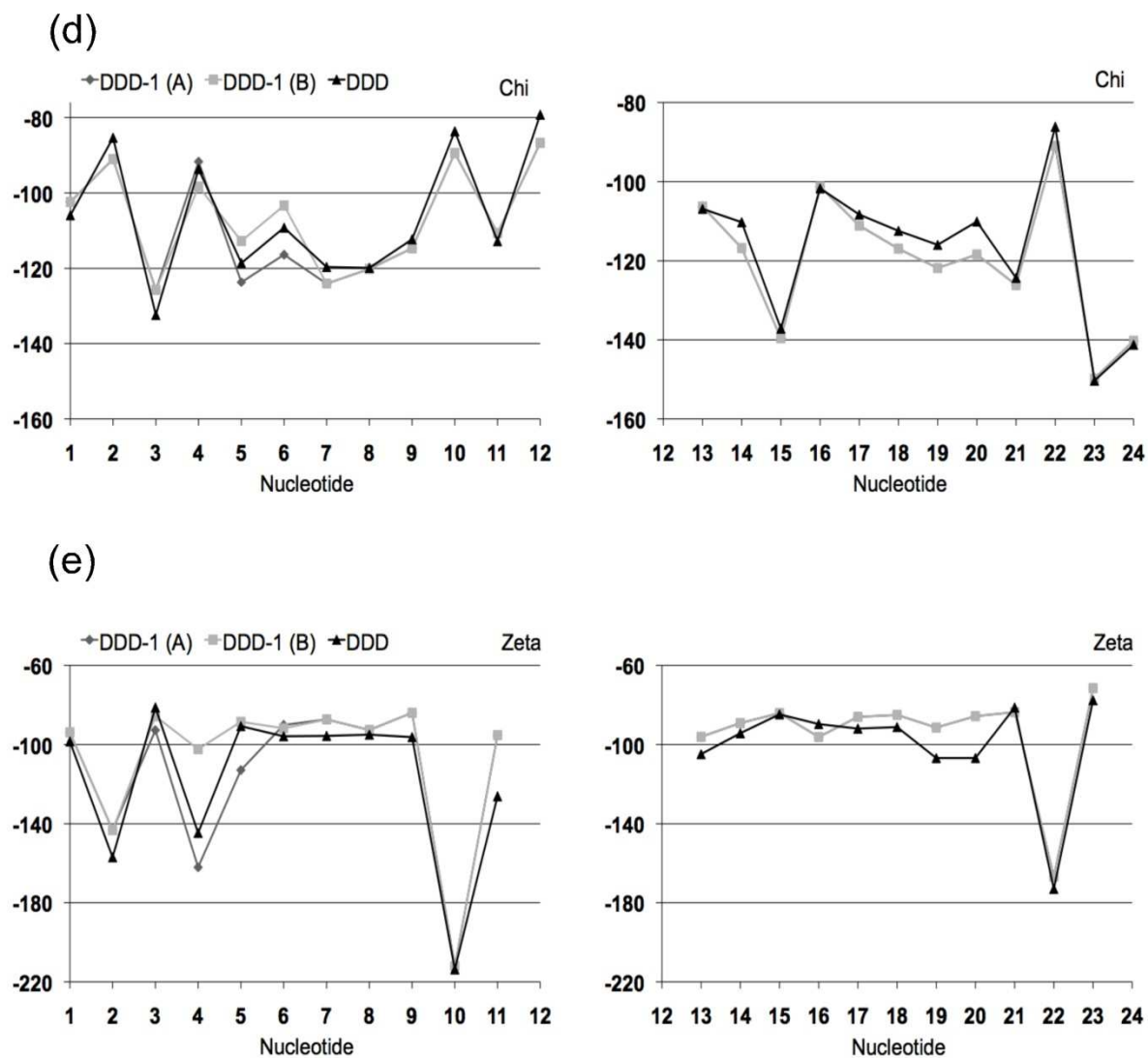


Figure S5. Comparison of (a) Gamma, (b) Delta, (c) Epsilon, (d) Chi and (e) Zeta angles in the crystal structures of the DDD-1(A) (with one phosphate backbone conformation for the G⁴, A⁵ and Y⁶), DDD-1 (B) (with second phosphate conformation for the G⁴, A⁵ and Y⁶), DDD (PDB entry 355D) duplexes.

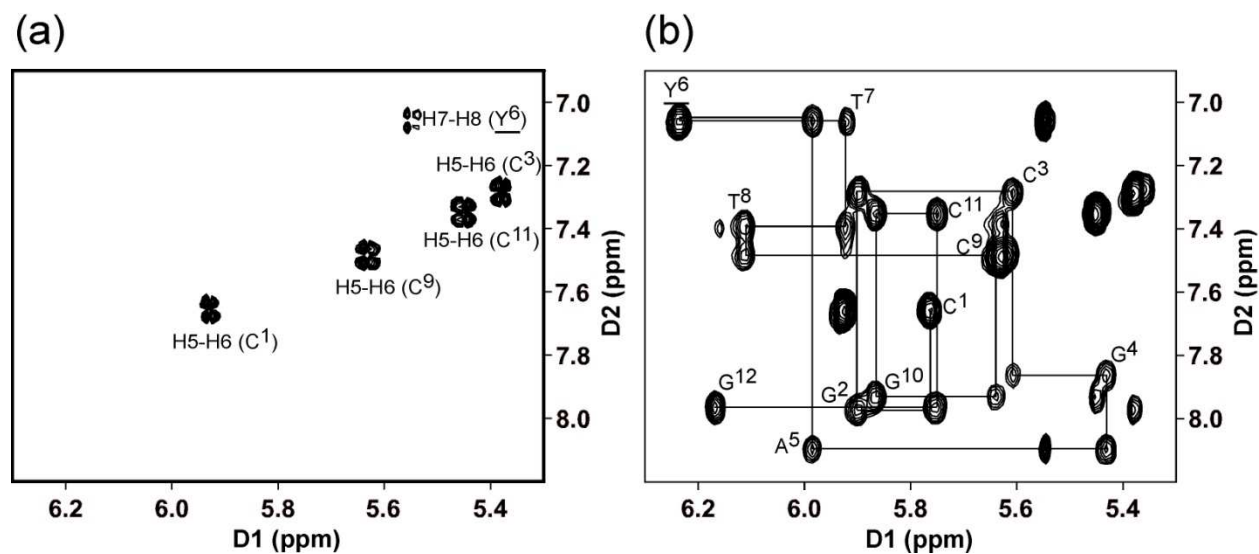


Figure S6. The 7-deaza-dA modified DDD-1 duplex. (a) The expanded plot of a DQF-COSY spectrum of DDD-1 duplex shows four cross peaks corresponding to four cytosine H5-H6 proton interactions (C¹, C³, C⁹, C¹¹) and one cross peak corresponding to the H7-H8 proton interactions of the 7-deaza-dA (b) The expanded plot of the NOESY spectrum of the DDD-1 duplex showing sequential NOEs between the aromatic and anomeric protons.