

Supplementary Materials for

**Correlation of Local Effects of DNA Sequence and Position of Beta-Alanine
Inserts with Polyamide-DNA Complex Binding Affinities and Kinetics**

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Materials and Methods

Chemical Characterization of KA1055, dImImPyP γ P γ Im β P γ Py β Dp

HPLC/Mass Spectrometry (HRMS) ($\text{MS}^n \text{ ESI}^+$) calculated for $\text{C}_{54}\text{H}_{70}\text{N}_{21}\text{O}_{10} \text{ MH}^+$ 1172.56145; found 1172.55845. Elemental analysis calculated for KA1055·3TFA·7H₂O, C₆₀H₈₆N₂₁O₂₃F₉: C, 43.93%; H, 5.28%; F, 10.42; N, 17.93%; found: C, 44.20%; H, 5.21%; F, 10.00; N, 17.92%.

NMR conditions and descriptions: 500 or 600 MHz referenced to residual solvent, DMSO-d⁶ or MeOH-d⁴, temp (500 MHz = 27 °C, 600 MHz = 25°C), ex. indicate protons exchangeable in MeOH-d⁴ or D₂O.

¹H NMR (600 MHz, DMSO-d⁶) 10.33 (s, 1H, ex.), 10.32 (s, 1H, ex.), 9.93 (s, 1H, ex.), 9.88 (s, 1H, ex.), 9.83 (s, 1H, ex.), 9.75 (s, 1H, ex.), 9.23 (brs, 1H, ex.), 8.03 (m, 3H, ex.), 7.92 (t, J=5.9Hz, 1H, ex.), 7.58 (s, 1H), 7.50 (s, 1H), 7.47 (d, J=0.5Hz, 1H), 7.282 (d, J=1.8Hz, 1H), 2.276 (d, J=1.8Hz, 1H), 7.18 (d, J=1.7Hz, 1H), 7.15 (d, J=1.8Hz, 1H), 7.10 (d, J=1.7Hz, 1H), 7.09 (d, J=1.2Hz, 1H), 6.91 (d, J=1.8Hz, 2H), 6.90 (d, J=1.8Hz, 2H), 6.67 (d, J=2.3Hz, 1H), 4.016 (s, 3H), 4.014 (s, 3H), 3.94 (s, 3H), 3.85 (s, 3H), 3.82 (s, 3H), 3.81 (s, 3H), 3.78 (s, 3H), 3.52 (m, 2H), 3.36 (m, 2H), 3.21 (m, 2H), 3.10 (m, 2H), 2.99 (m, 2H), 2.73 (d, J=4.7Hz, 6H), 2.52 (t, J=6.4Hz, 2H), 2.33 (t, J=7.0Hz, 2H), 2.28 (t, J=7.1Hz, 2H), 1.79 (m, 2H), 1.73 (m, 2H).

¹H NMR (500 MHz, DMSO-d⁶) 10.35 (s, 1H, ex.), 10.33 (s, 1H, ex.), 9.94 (s, 1H, ex.), 9.89 (s, 1H, ex.), 9.84 (s, 1H, ex.), 9.74 (s, 1H, ex.), 9.23 (brs, 1H, ex.), 8.04 (m, 3H, ex.), 7.92 (t, J=6.0Hz, 1H, ex.), 7.58 (s, 1H), 7.50 (s, 1H), 7.47 (d, J=1.0Hz, 1H), 7.284 (d, J=1.9H, 1H), 7.281 (d, J=1.6Hz, 1H), 7.19 (d, J=1.9Hz, 1H), 7.16 (d, J=1.9Hz, 1H), 7.11 (d, J=1.9Hz, 1H), 7.09 (d,

J=1.0Hz, 1H), 6.91 (d, J=1.9Hz, 2H), 6.90 (d, J=1.9Hz, 2H), 6.67 (d, J=1.9Hz, 1H), 4.014 (s, 3H), 4.012 (s, 3H), 3.94 (s, 3H), 3.85 (s, 3H), 3.82 (s, 3H), 3.81 (s, 3H), 3.78 (s, 3H), 3.52 (m, 2H), 3.36 (m, 2H), 3.21 (m, 2H), 3.10 (m, 2H), 2.99 (m, 2H), 2.73 (d, J=4.7Hz, 6H), 2.33 (t, J=7.3Hz, 2H), 2.28 (t, J=7.3Hz, 2H), 1.78 (m, 2H), 1.72 (m, 2H).

¹H NMR (500 MHz, DMSO-*d*⁶ plus D₂O) 7.57 (s, 1H), 7.48 (s, 1H), 7.45 (d, J=0.7Hz, 1H), 7.27 (d, J=1.6Hz, 1H), 7.26 (d, J=1.9Hz, 1H), 7.17 (d, J=1.9Hz, 1H), 7.13 (d, J=1.9Hz, 1H), 7.10 (d, J=1.0Hz, 1H), 7.09 (d, J=1.9Hz, 1H), 6.90 (d, J=1.9Hz, 2H), 6.89 (d, J=1.9Hz, 2H), 6.66 (d, J=1.9Hz, 1H), 4.003 (s, 3H), 3.999 (s, 3H), 3.93 (s, 3H), 3.84 (s, 3H), 3.81 (s, 3H), 3.80 (s, 3H), 3.76 (s, 3H), 3.35 (m, 2H), 3.20 (m, 2H), 3.09 (m, 2H), 2.98 (m, 2H), 2.72 (s, 6H), 2.33 (t, J=7.0Hz, 2H), 2.28 (t, J=7.3Hz, 2H), 1.78 (m, 2H), 1.72 (m, 2H).

¹H NMR (500 MHz, MeOH-*d*⁴) 7.53 (s, 1H), 7.36 (s, 1H), 7.31 (d, J=1.0Hz, 1H), 7.27 (d, J=1.9Hz, 1H), 7.15 (d, J=1.6Hz, 1H), 7.12 (d, J=1.0Hz, 1H), 7.08 (d, J=1.9Hz, 1H), 7.04 (d, J=1.9Hz, 1H), 6.92 (d, J=1.9Hz, 1H), 6.87 (d, J=1.9Hz, 1H), 6.79 (d, J=1.9Hz, 1H), 6.72 (d, J=1.9Hz, 1H), 4.08 (s, 6H), 3.97 (s, 3H), 3.91 (s, 3H), 3.87 (s, 3H), 3.85 (s, 3H), 3.82 (s, 3H), 3.62 (t, J=6.6 Hz, 2H), 3.55 (t, J=6.6Hz, 2H), 3.40 (t, J=6.6Hz, 2H), 3.25 (t, J=6.6Hz, 2H), 3.06 (m, 2H), 2.82 (s, 6H), 2.59 (t, J=6.5Hz, 2H), 2.47 (t, J=6.6Hz, 2H), 2.41 (t, J=7.0Hz, 2H), 1.98 (m, 2H), 1.86 (m, 2H).

Reverse Phase HPLC/mass spectrometry and NMR data are shown for KA1055 (Figures S1-9): Agilent 1100 HPLC; MSD ESI⁺ and diode array detection; column: 70 × 4.6 mm Macherey-

Nagel Nucleodur C18 column; 5 μ particles; gradient: 5-60% MeCN/water with 0.1% formic acid at 0.5 mL/min; retention time 11.3 min (300 nm).

Figure Legends

Figure S1. HPLC/MS of KA1055: UV/Vis traces at 254, 300 and 220 nm, Total Ion Current (TIC).

Figure S2. HPLC/MS of KA1055: Area % at 300 nm

Figure S3. Mass spectrum of KA1055 from ESI⁺ HPLC/MS showing mono- and di-protonated species, [M+H]⁺ and [M+2H]²⁺.

Figure S4. Expansion of the mass spectrum of KA1055 for [M+H]⁺.

Figure S5. Further expansion of the mass spectrum of KA1055 for [M+H]⁺.

Figure S6. ¹H NMR (600 MHz, DMSO-*d*⁶) of KA1055.

Figure S7. ¹H NMR (500 MHz, DMSO-*d*⁶) of KA1055.

Figure S8. ¹H NMR (500 MHz, DMSO-*d*⁶ plus D₂O) of KA1055.

Figure S9. ¹H NMR (500 MHz, MeOH-*d*⁴) of KA1055.

Figure S10. Thermal melting curves of the DNA hairpin duplex containing the TGGCTT site in the absence and presence of KA1002, KA1007, KA1055 and KA1039 at 0.5:1, 1:1, 1.5:1 and 2:1 molar ratios of compound to DNA.

Figure S11. Mutant DNA sequences of TGGCTT with the hairpin loop underlined.

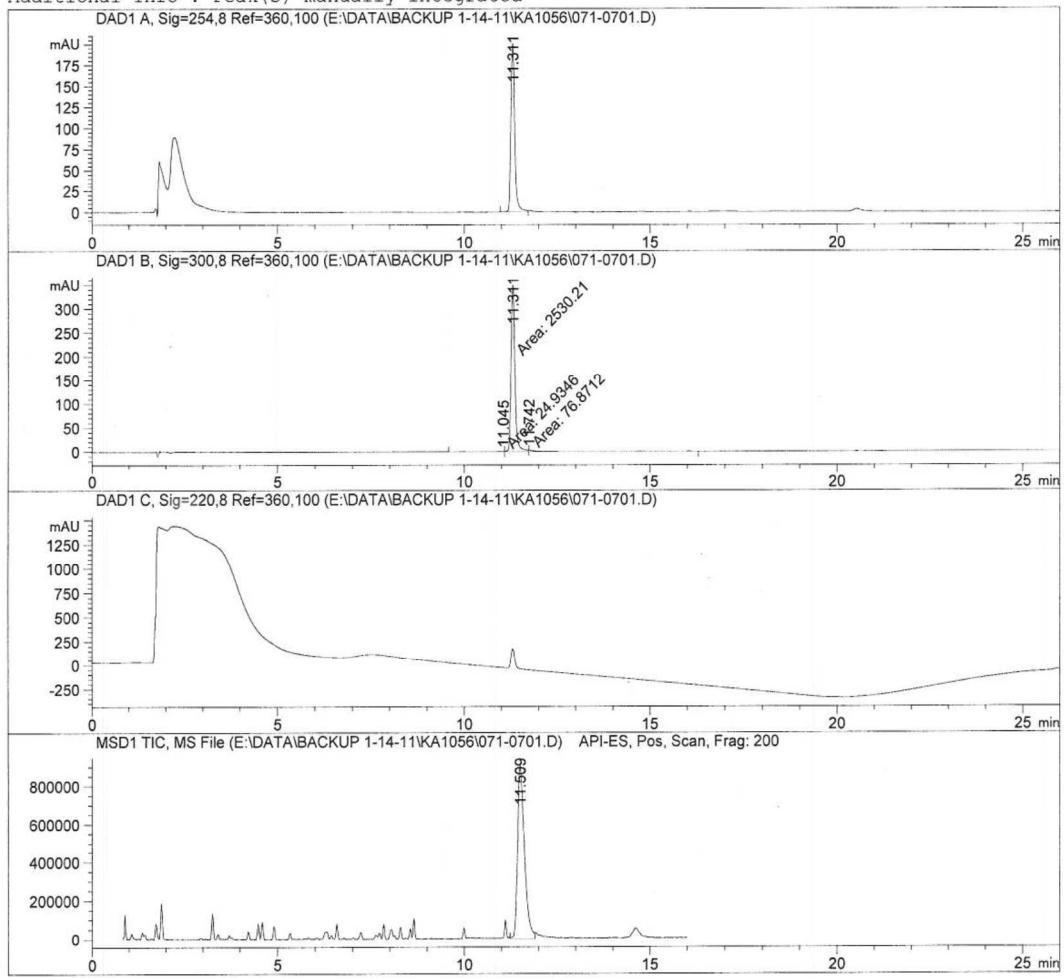
Figure S12. Models of PA binding induced DNA bending. (A) X-ray crystal structure of cyclic eight-ring PA bound to 5'-CCAGTACTGG-3' (PDB 3OMJ, ref. 39.) (B) Docking models of B-

DNA, Glucocorticoid receptor DNA-binding domain (GRDBD)+DNA, PA+DNA and PA+DNA+GRDBD based on the X-ray crystal structures PDB 3G6P and PDB 3OMJ (ref. 41).

Data File E:\DATA\BACKUP 1-14-11\KA1056\071-0701.D
Sample Name: KA1055A

```
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Acq. Operator   : Aston          Seq. Line :    7
Acq. Instrument : Instrument 1 Location : Vial 71
Injection Date  : 10/29/2010 1:49:53 PM Inj :    1
                                                Inj Volume : 10.000 µl
Different Inj Volume from Sequence !      Actual Inj Volume : 5.000 µl
Acq. Method     : C:\CHEM32\1\METHODS\5_60ACN_26_500-2200
Last changed    : 10/28/2010 6:10:56 PM by Kevin
Analysis Method : C:\CHEM32\1\METHODS\5_60ACN_6_5_500-2200_ESI+.M
Last changed    : 6/12/2012 1:18:33 PM
                  (modified after loading)
Method Info     : 5 to 60% ACN/0.1% aq. formic acid over 4 min, 2.0 mL/min, 500-2200 MW,
                  ESI+, Analytical
Sample Info     : lyophilized combined lots of PA#3
```

Additional Info : Peak(s) manually integrated



LC1 6/14/2012 1:11:39 PM

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Figure S1

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                               Area Percent Report
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Sorted By          :      Signal
Multiplier:        :      1.0000
Dilution:         :      1.0000
Use Multiplier & Dilution Factor with ISTDs

Signal 1: DAD1 A, Sig=254,8 Ref=360,100

Peak RetTime Type  Width      Area       Height      Area
#   [min]      [min]    [mAU*s]    [mAU]      %
----|-----|---|-----|-----|-----|-----|
  1  11.311  BB    0.1101  1426.93359  200.44853 100.0000

Totals :           1426.93359  200.44853      -
```



```

Signal 2: DAD1 B, Sig=300,8 Ref=360,100

Peak RetTime Type  Width      Area       Height      Area
#   [min]      [min]    [mAU*s]    [mAU]      %
----|-----|---|-----|-----|-----|-----|
  1  11.045  MF    0.5239   24.93456  7.93263e-1  0.9474
  2  11.311  MF    0.1203  2530.20776  350.51517  96.1320
  3  11.742  FM    0.4155   76.87117   3.08343   2.9206

Totals :           2632.01349  354.39186      -
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Figure S2

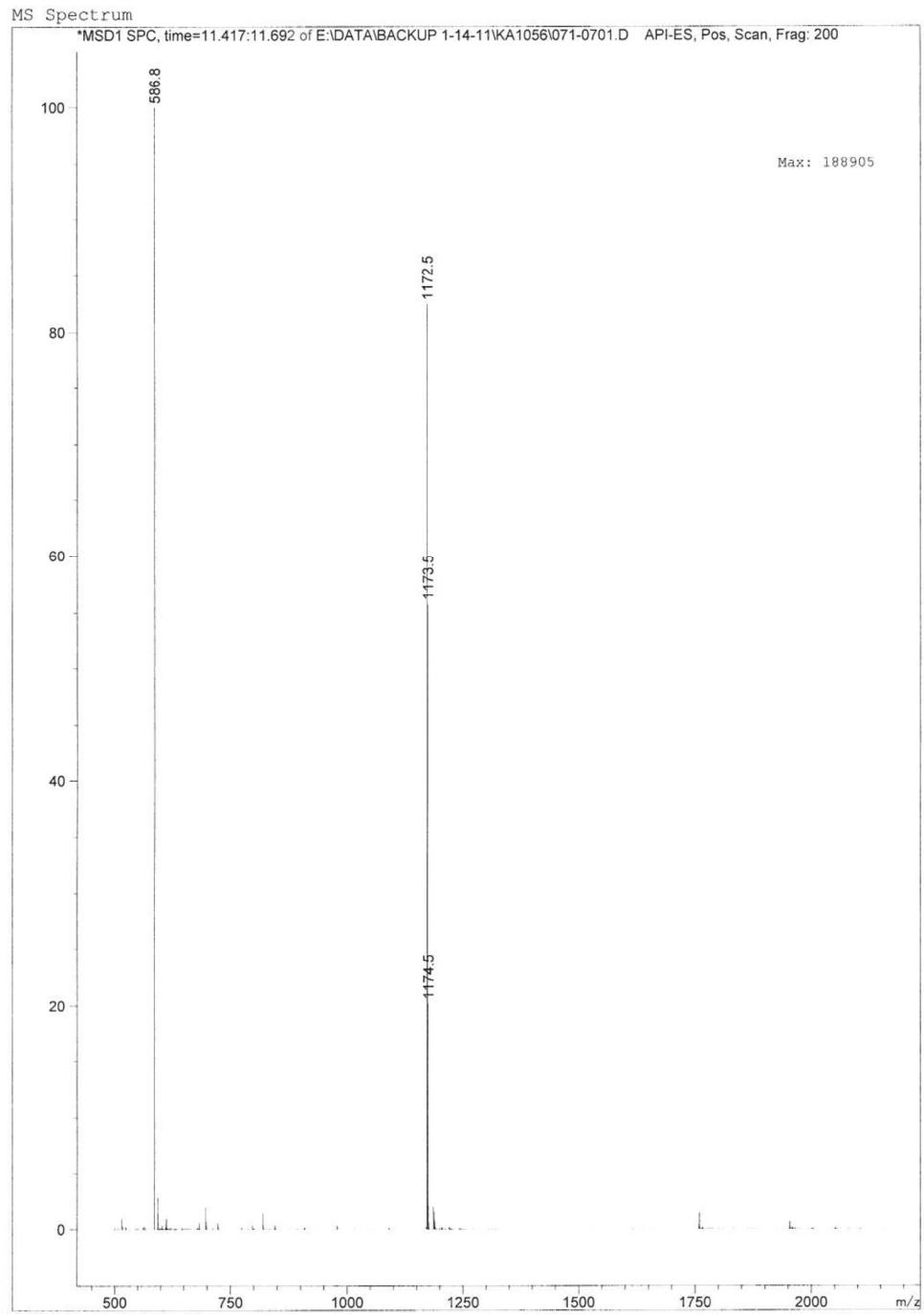


Figure S3

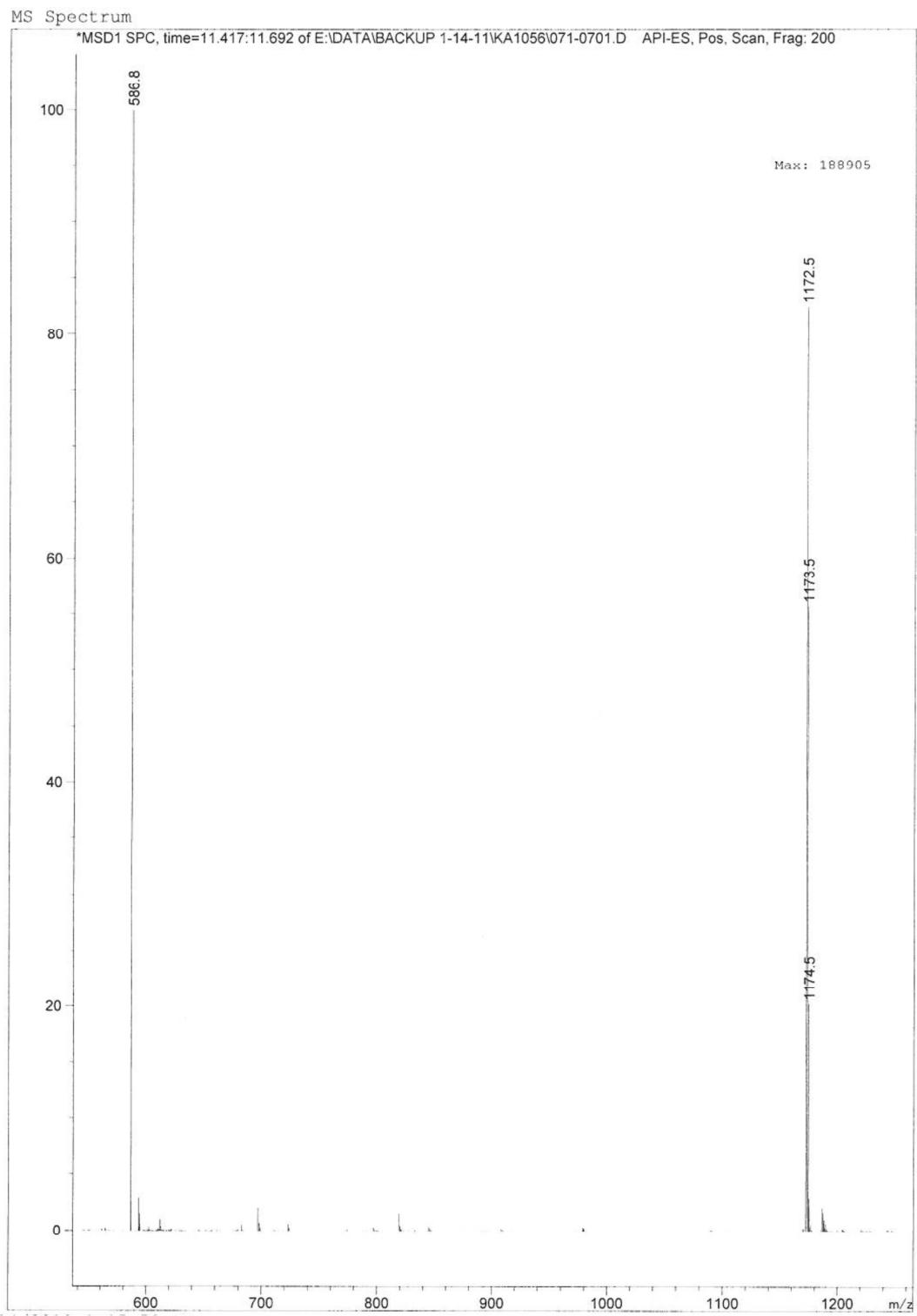


Figure S4

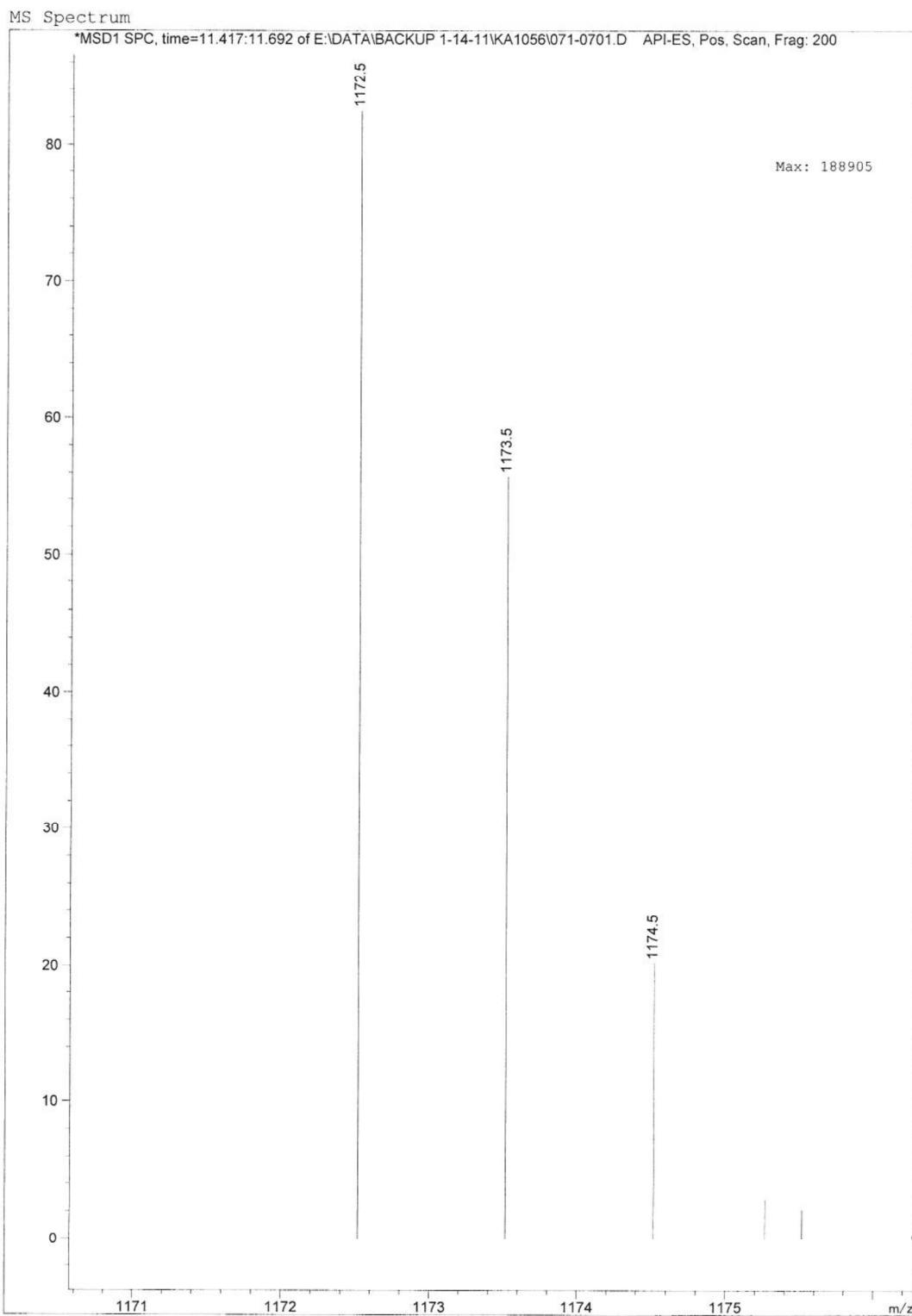


Figure S5

desImImPyPyGammaPyImBetaPyBetaDp

Gradient Shimming

Acquisition Time (sec)	1.7039	Comment	Gradient Shimming	Date	Jul 26 2012
Date Stamp	Jul 26 2012	File Name	\\$t\\$\\$um.edu\dept\share\sh_nmrdatal\Ag\ben160\bashkin\KA2056-G-072612.1dd\1d		
Frequency (MHz)	599.78	Nucleus	1H	Number of Transients	64
Points Count	16384	Pulse Sequence	s2puI	Receiver Gain	50.00
Spectrum Offset (Hz)	3609.1106	Spectrum Type	STANDARD	Sweep Width (Hz)	9615.38
				Temperature (degree C)	25.000

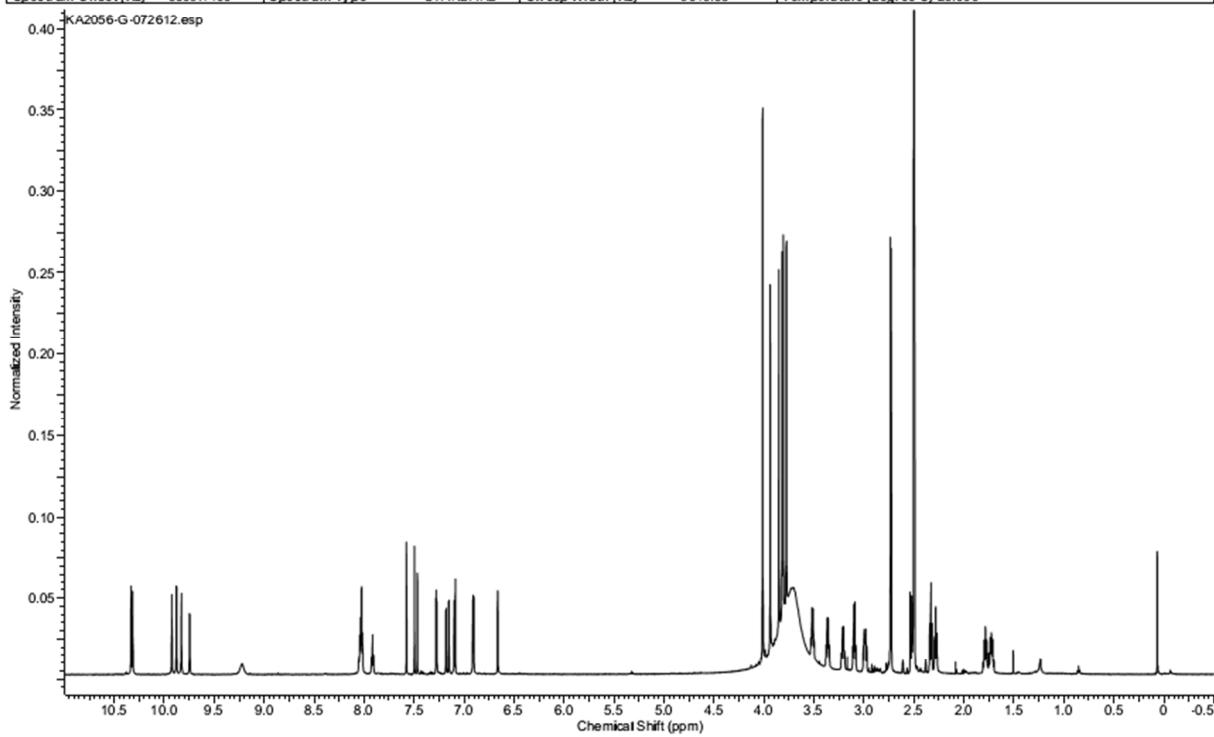


Figure S6

desImImPyPyGammaPyImBetaPyBetaDp

KA2056 G 5.5mg-0.6mL DMSO-d6

Acquisition Time (sec)	3.1457	Comment	KA2056G 5.5mg-0.6mL DMSO-d6	Date	25 Jun 2012 19:14:08
Date Stamp	25 Jun 2012 19:14:08		File Name	\134.124.122.67\data\ARX500\mr\KA2056G\11d	
Frequency (MHz)	500.13	Nucleus	1H	Number of Transients	531
Original Points Count	32768	Owner	root	Points Count	32768
Receiver Gain	2048.00	SW(cyclical) (Hz)	10416.67	Pulse Sequence	zg30
Spectrum Type	STANDARD	Sweep Width (Hz)	10416.35	Spectrum Offset (Hz)	3080.5850
				Temperature (degree C)	27.000

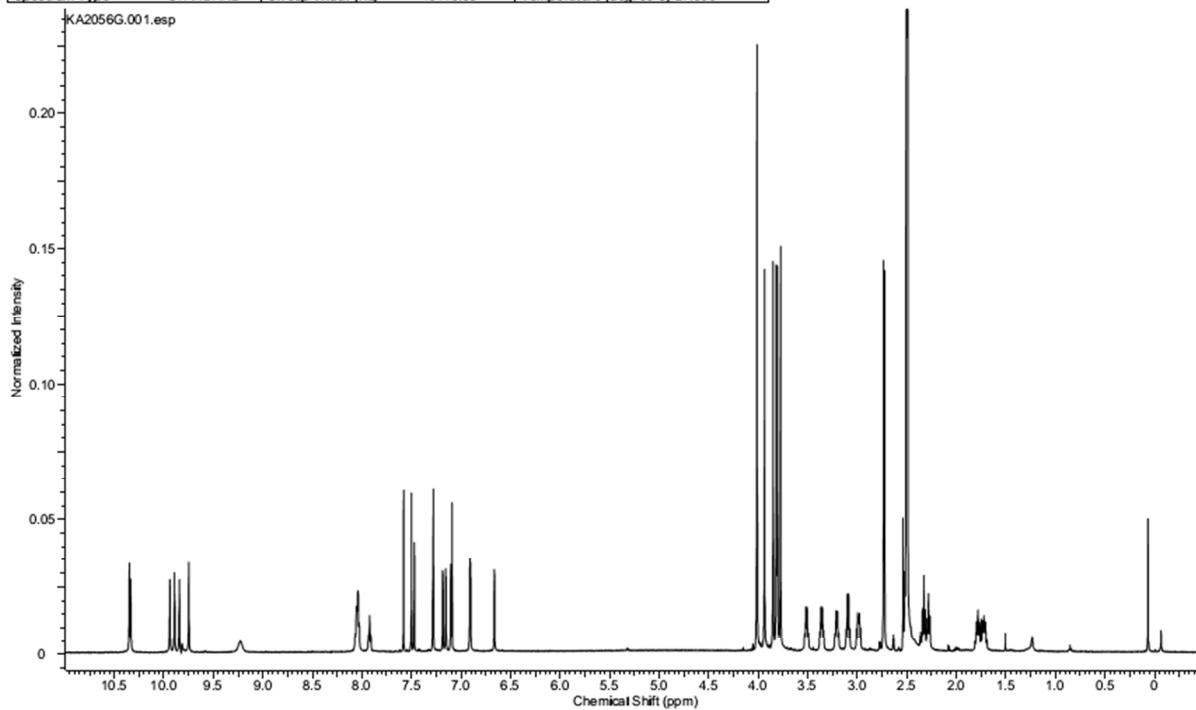


Figure S7

desImImPyPyGammaPyImBetaPyBetaDp

KA2056G 2uL D2O added

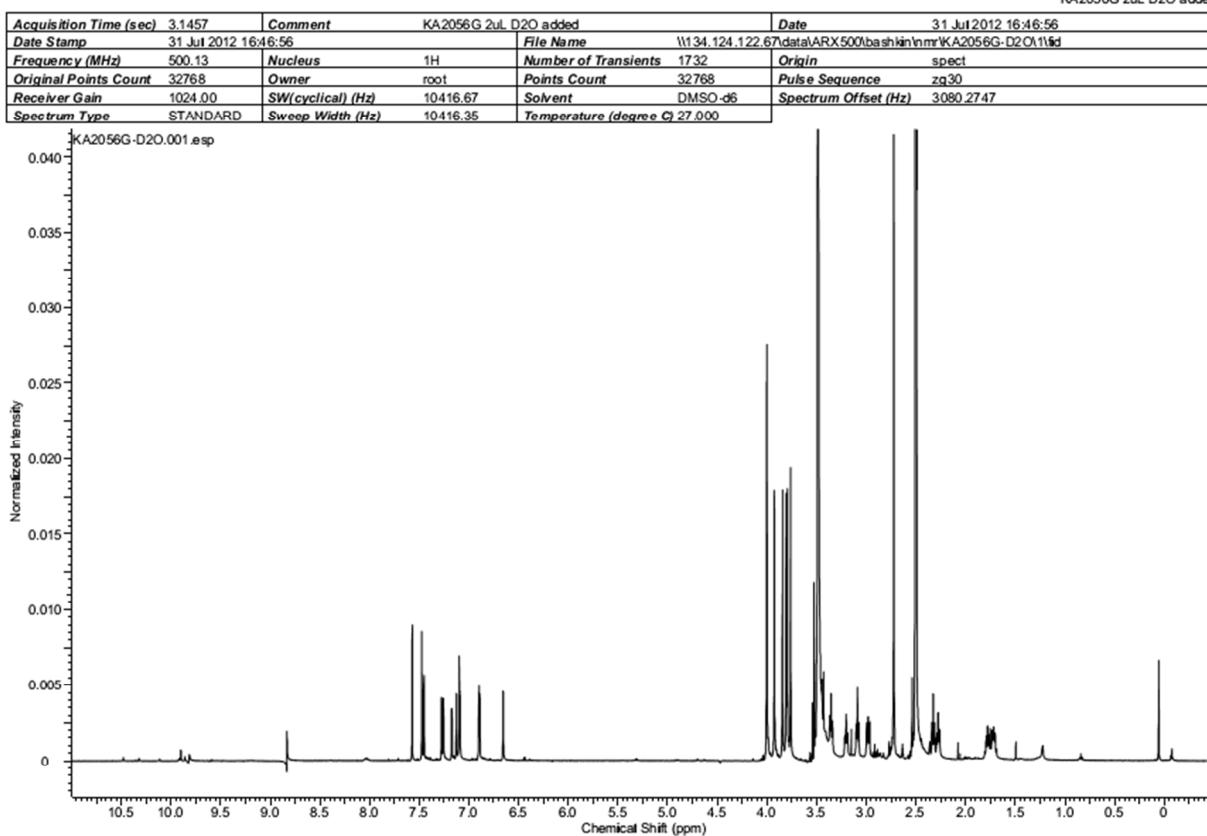


Figure S8

desImImPyPyGammaPyImBetaPyBetaDp

KA1055A run in CD3OD

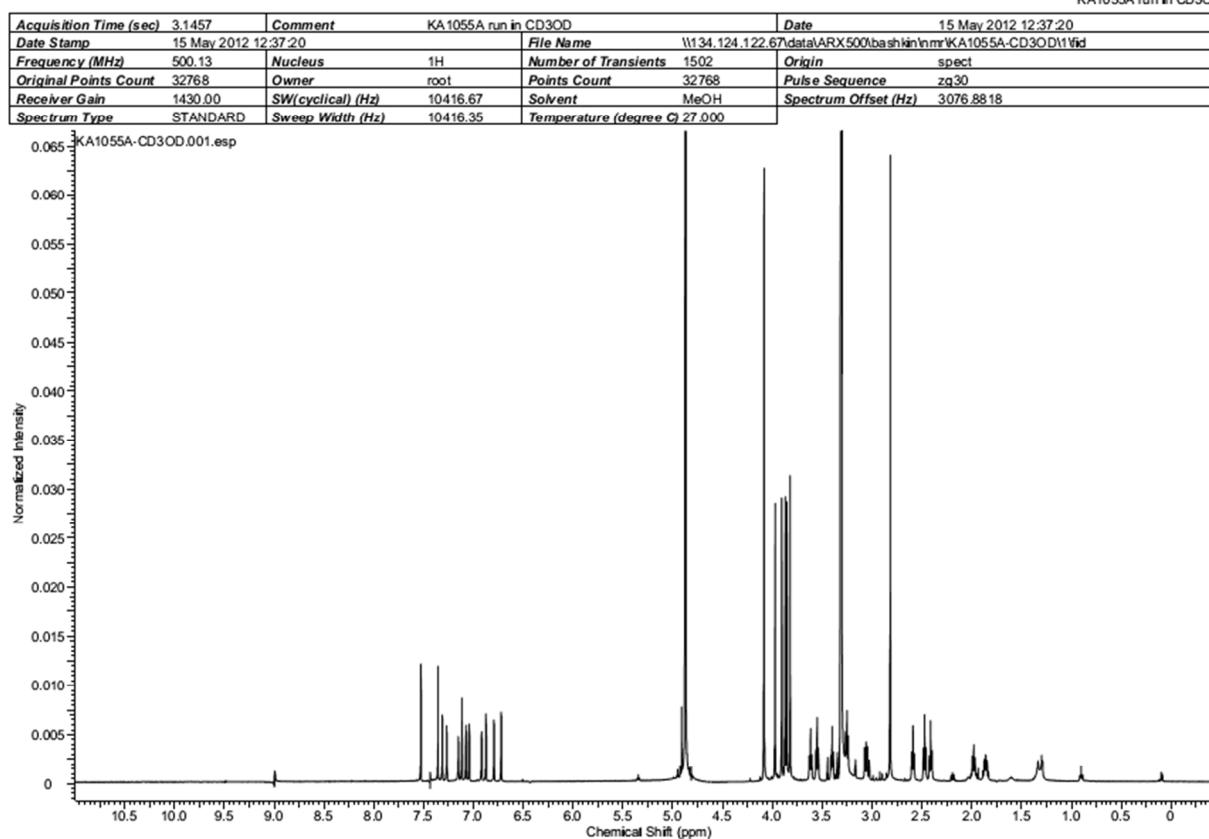


Figure S9

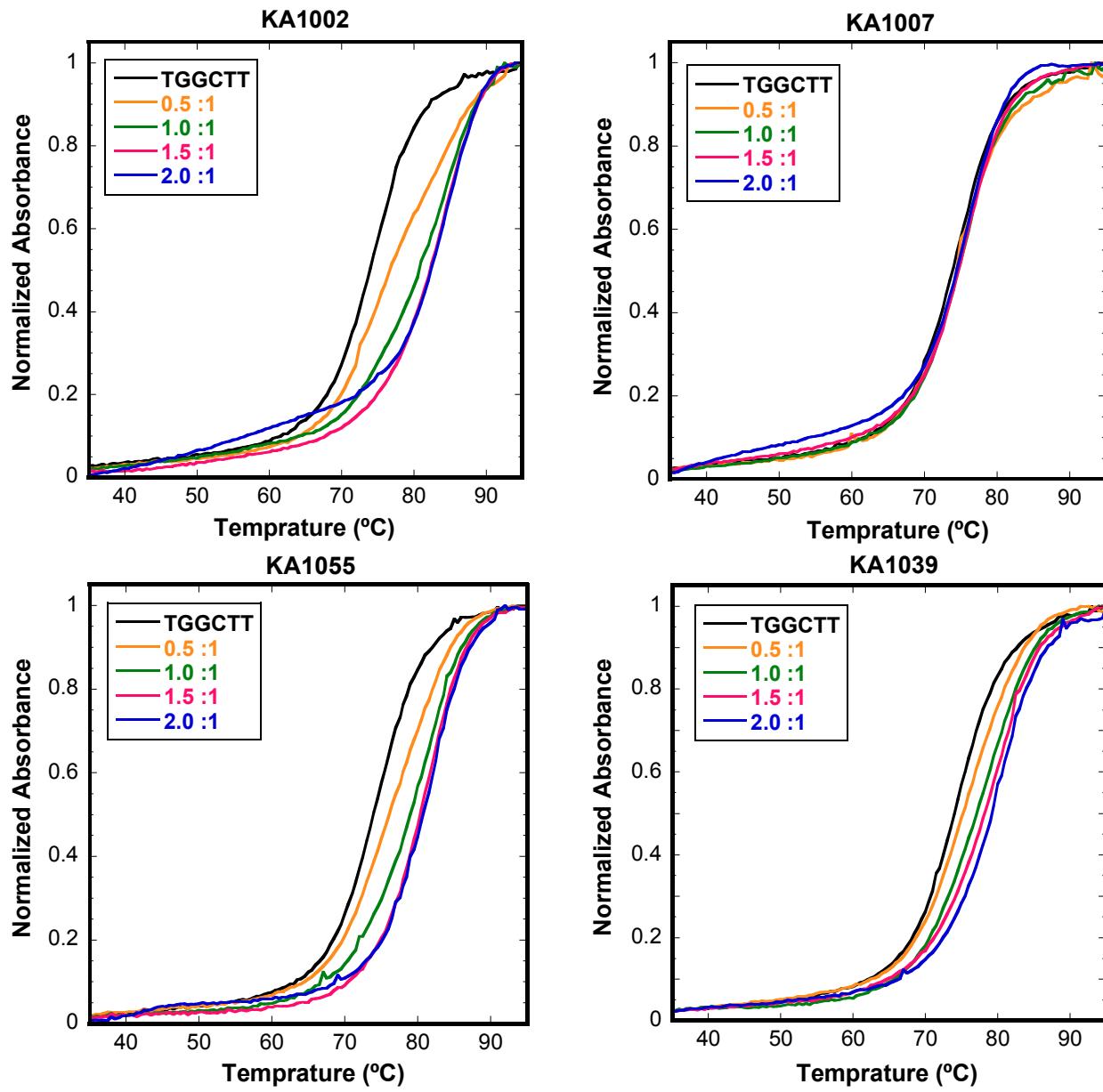


Figure S10

Original sequence:

5' -CCT**TGGCTT**CTTTGAAGCCAAGG-3'

Mutant sequences:

1. 5' -CCT**TGCCTT**CTTTGAAGGCAAGG-3'
2. 5' -CCT**TGTCTT**CTTTGAAGACAAGG-3'
3. 5' -CCT**TGGGTT**CTTTGAACCCAAGG-3'
4. 5' -CCT**TGGCCT**CTTTGAGGCCAAGG-3'
5. 5' -CCT**TGATTT**CTTTGAAATCAAGG-3'

Figure S11

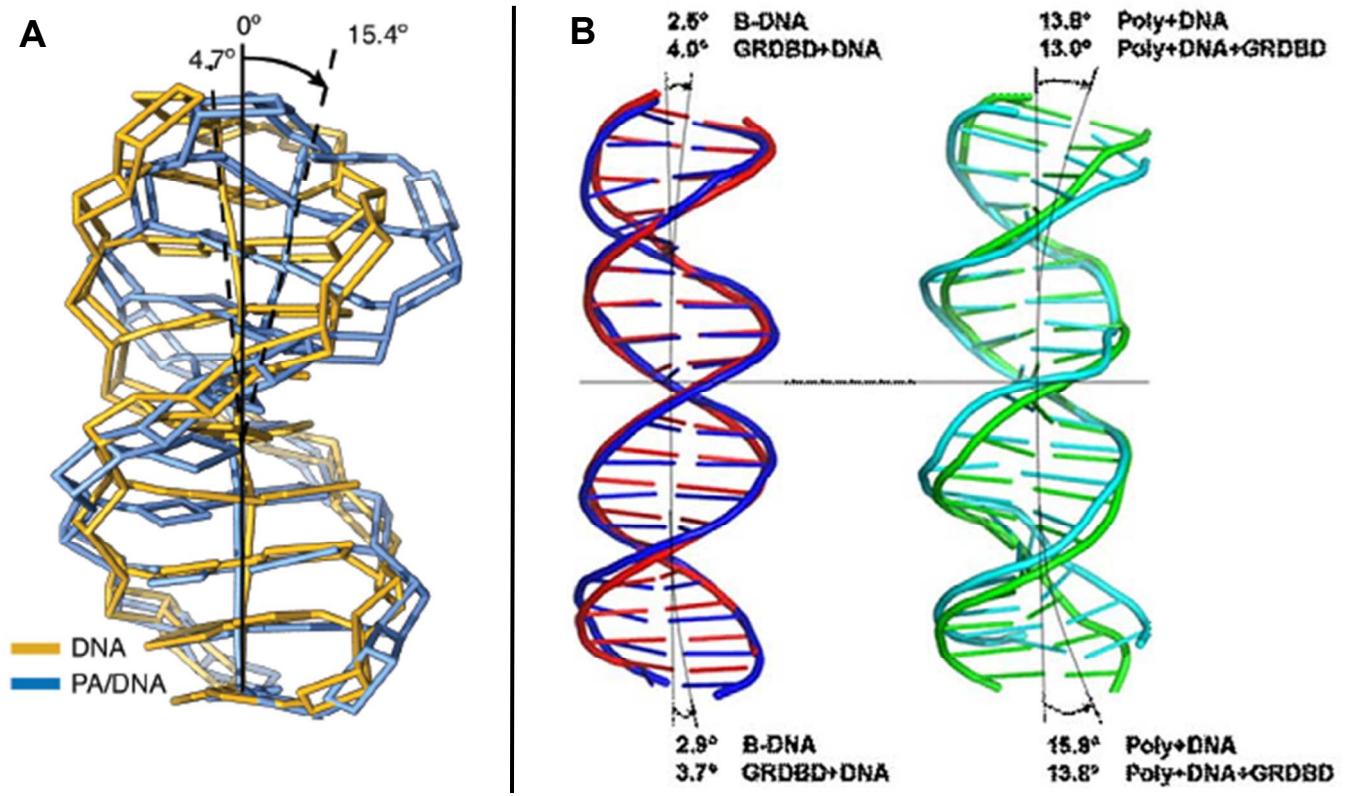


Figure S12