

## Supplementary Information

# Sequence Dependence in Base Flipping: Experimental and Computational Studies

Lauren L O'Neil and Olaf Wiest\*

Department of Chemistry and Biochemistry, University of Notre Dame,

Notre Dame, Indiana 46556-5670 (USA)

[owiest@nd.edu](mailto:owiest@nd.edu)

### Table of Contents

**Figure S1.** Thymine maximum difference wavelength.

**Figure S2.** 5'-GGTGG-3' maximum difference wavelength.

**Figure S3.** Relative fluorescence of dansyl-cyclen in presence of thymine and guanosine monophosphate.

**Table S1.**  $R^2$  and  $F_{\max}$  values of data fit using one-site binding model.

**Figures S4 and S5.** Optimized geometry of anionic thymine bound to dansyl-cyclen.  
Cartesian coordinates of optimized geometry.

**Table S2.** Charges and atom types for anionic thymine/dansyl-cyclen.

Bond and angle parameters included in force field for anionic thymine/dansyl-cyclen.

**Figure S6.** RMSd vs. time, MD simulation of dansyl-cyclen bound to 5'-GGTGG-3'.

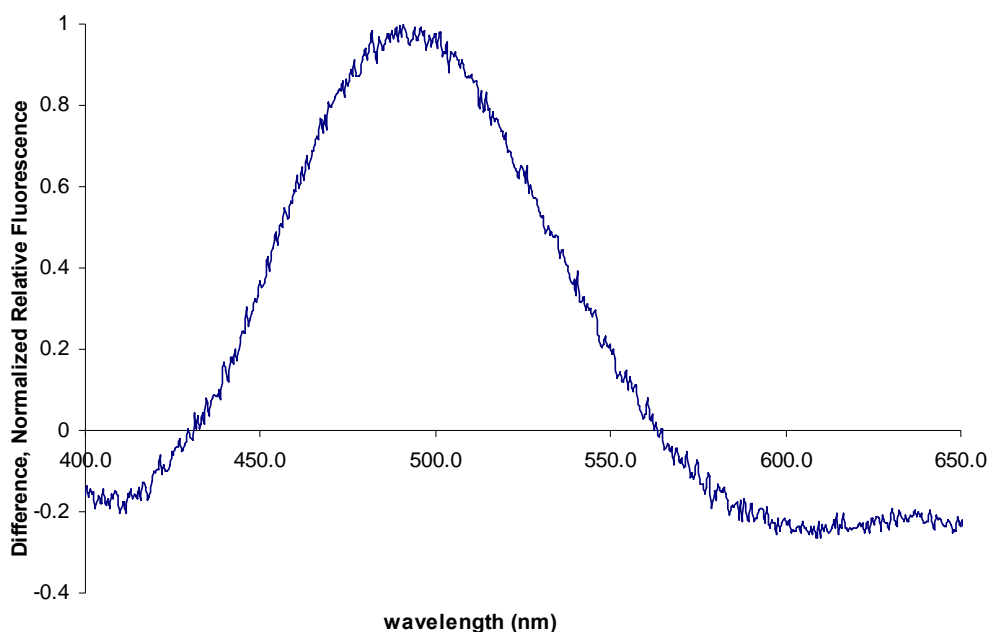
**Figure S7.** N1-H1-O3 angle vs. time for 5'-GGTGG-3' MD simulation.

**Figure S8.** N2-H22-O4 angle vs. time for 5'-GGTGG-3' MD simulation.

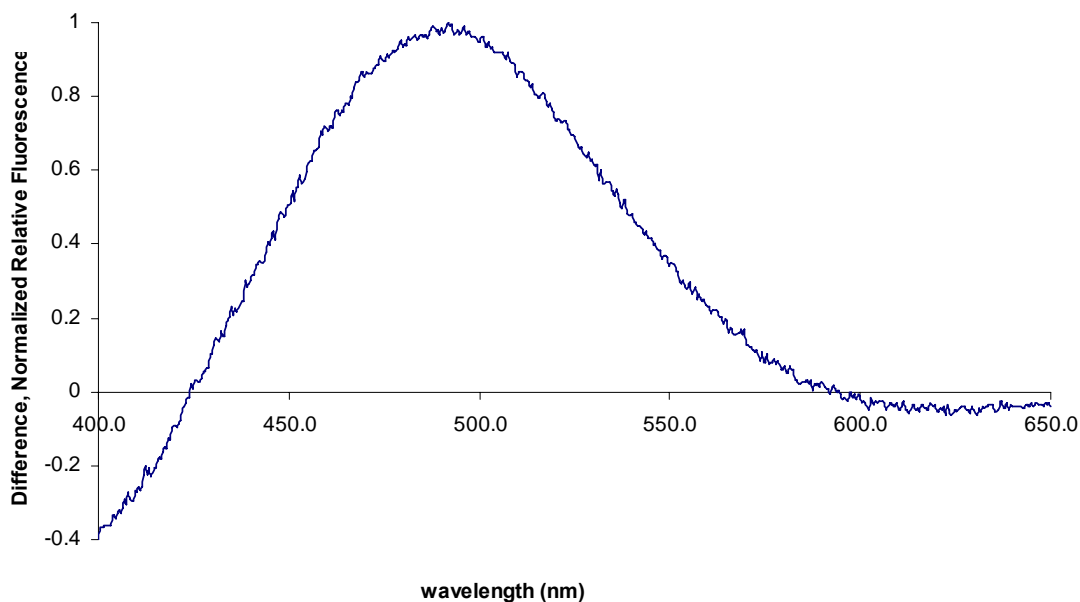
**Figure S9.** RMSd vs. time, MD simulation of dansyl-cyclen bound to 5'-CCTCC-3'.

**Figure S10.** Snapshot (3000 ps) of dansyl-cyclen bound to 5'-CCTCC-3'.

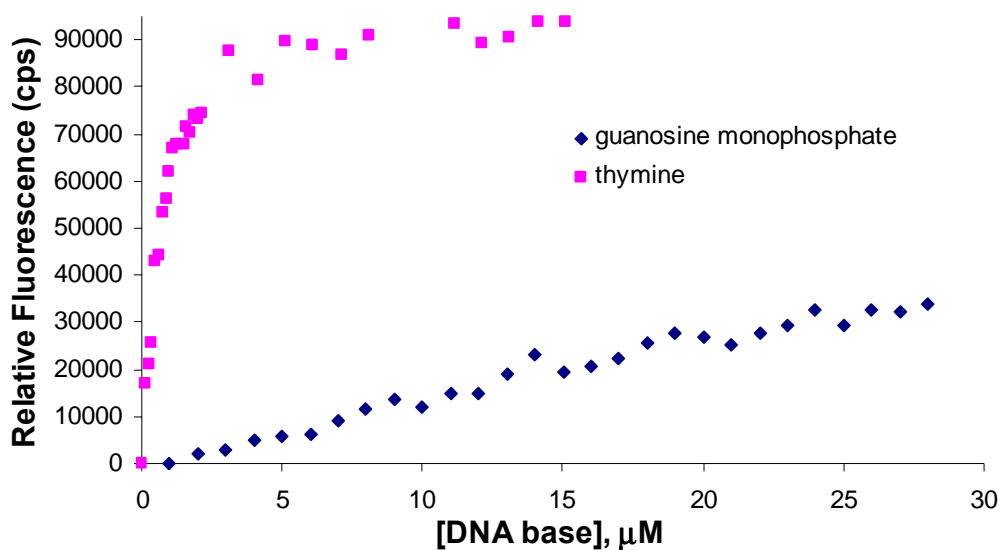
**Figure S11.** RMSd vs. time, MD simulation of duplex DNA bound to dansyl-cyclen.



**Figure S1.** Difference of the fluorescence of 1  $\mu\text{M}$  dansyl-cyclen in the presence of 10  $\mu\text{M}$  thymine and 1  $\mu\text{M}$  dansyl-cyclen in buffer.



**Figure S2.** Difference of the fluorescence of 1  $\mu\text{M}$  dansyl-cyclen in the presence of 11  $\mu\text{M}$  5'-GGTGG-3' and 1  $\mu\text{M}$  dansyl-cyclen in buffer. Fluorescence was corrected for the fluorescence of DNA strand by subtracting the fluorescence of a buffer solution containing 11  $\mu\text{M}$  5'-GGTGG-3'.



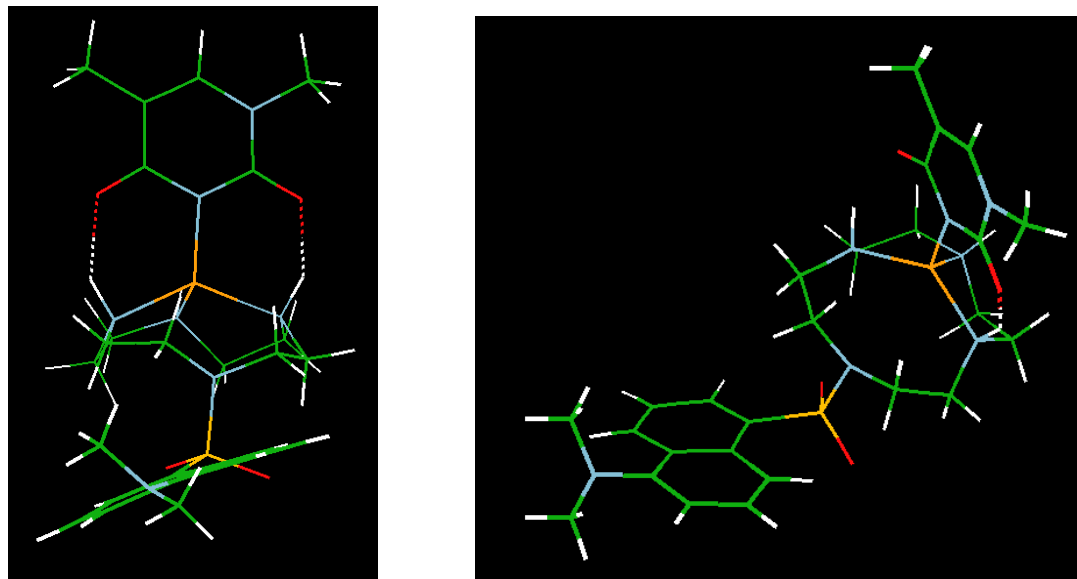
**Figure S3.** Relative fluorescence of dansyl-cyclen in the presence of thymine and guanosine monophosphate. Fluorescence has not been normalized in order to show the difference in signal between the two titrations.

**Table S1.**  $R^2$  and  $F_{\max}$  values of data fit using one-site binding model.

$$y = \frac{Fx}{K + x}$$

| System   | $R^2$   |         |         | $F_{\max}$ |           |            |
|--|---------|---------|---------|------------|-----------|------------|
|  | Trial 1 | Trial 2 | Trial 3 | Trial 1    | Trial 2   | Trial 3    |
| Thymine  | 0.98363 | 0.97348 | 0.97458 | 1.05±0.01  | 0.99±0.02 | 1.06±0.02  |
| Thymidine monophosphate                                  | 0.96251 | 0.92456 | 0.95749 | 1.00±0.02  | 1.07±0.04 | 1.081±0.02 |
| Guanosine monophosphate                                  | 0.97626 |         |         | 135±61     |           |            |
| 5'-AATAA-3'  | 0.97744 | 0.92067 | 0.92045 | 1.01±0.02  | 1.10±0.05 | 1.03±0.04  |
| 5'-GGTGG-3'  | 0.96771 | 0.89706 | 0.91119 | 1.00±0.02  | 0.91±0.02 | 0.91±0.03  |
| 5'-CCTCC-3'  | 0.97658 | 0.95983 | 0.94509 | 1.06±0.03  | 1.20±0.06 | 1.14±0.06  |
| 5'-GCACGAATAACGACG-3'<br>3'-CGTGCTTXXTTGCTGC-5' <i>a</i> | 0.9687  | 0.9664  | 0.9361  | 1.00±0.01  | 0.99±0.02 | 0.99±0.02  |
| 5'-GCACGGGTGGCGACG-3'<br>3'-CGTGCCXCCGCTGC-5'            | 0.95835 | 0.9124  | 0.95781 | 1.06±0.04  | 1.09±0.05 | 1.01±0.02  |
| 5'-GCACGCCTCCGACG-3'<br>3'-CGTGCGGXGGGCTGC-5'            | 0.96342 | 0.93164 | 0.95988 | 1.15±0.05  | 1.02±0.04 | 0.97±0.02  |
| 5'-GCACGTTTTTCGACG-3'<br>3'-CGTGCAAXAAGCTGC-5'           | 0.97787 | 0.96633 | 0.95501 | 1.00±0.02  | 1.10±0.02 | 0.99±0.03  |

*a* As previously reported in ref. 5.



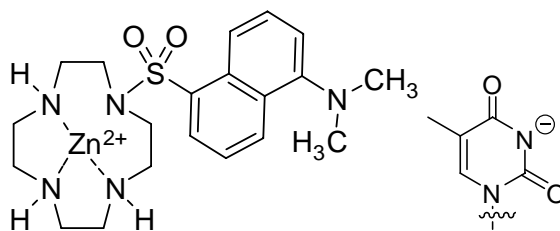
**Figures S4 (left) and S5 (right).** Optimized geometry of anionic thymine bound to dansyl-cyclen.

Cartesian coordinates of optimized geometry of anionic thymine-cyclen complex

|    |            |             |             |
|----|------------|-------------|-------------|
| N  | 4.45705500 | 2.95374600  | 0.99781800  |
| C  | 4.90470200 | 3.41067200  | -0.22292400 |
| H  | 5.44676900 | 4.35013600  | -0.18887100 |
| C  | 4.69532600 | 2.74837100  | -1.38741600 |
| C  | 5.18329200 | 3.23571800  | -2.72175500 |
| H  | 5.85189400 | 2.50168000  | -3.18516500 |
| H  | 4.34802500 | 3.37969900  | -3.41627200 |
| H  | 5.72183500 | 4.18322800  | -2.62639700 |
| C  | 3.95571900 | 1.49648200  | -1.31716800 |
| O  | 3.70885200 | 0.79850200  | -2.32140600 |
| N  | 3.51684600 | 1.07620700  | -0.06927100 |
| C  | 3.75538300 | 1.75899400  | 1.09517600  |
| O  | 3.37306700 | 1.35276500  | 2.20646300  |
| C  | 4.72073400 | 3.68696300  | 2.24009700  |
| H  | 3.78032200 | 3.93601100  | 2.73664300  |
| H  | 5.31879500 | 3.07578300  | 2.92027500  |
| H  | 5.26170900 | 4.60244500  | 1.99708600  |
| Zn | 2.53561300 | -0.61320400 | -0.05818700 |
| H  | 2.58788600 | -3.16758800 | 2.79384300  |
| C  | 2.96314100 | -2.56590000 | 1.95926300  |
| H  | 4.02775800 | -2.38162800 | 2.14624800  |
| C  | 2.79168500 | -3.32522100 | 0.63644700  |
| H  | 3.27578300 | -4.30826500 | 0.68202300  |

|   |             |             |             |
|---|-------------|-------------|-------------|
| H | 1.72655200  | -3.48098400 | 0.43576400  |
| N | 2.26572100  | -1.25265200 | 1.88478800  |
| H | 2.82955900  | -0.50878800 | 2.31784200  |
| N | 3.35155100  | -2.49072900 | -0.46051500 |
| H | 4.36929900  | -2.52467100 | -0.41021800 |
| C | 0.93165400  | -1.22547500 | 2.54602900  |
| H | 1.05724000  | -0.98116300 | 3.60798400  |
| H | 0.48326800  | -2.21816200 | 2.49073000  |
| C | 2.93648300  | -2.83059700 | -1.84915000 |
| H | 3.67782900  | -2.37533900 | -2.51296700 |
| H | 2.95031500  | -3.91454700 | -2.01839900 |
| C | 1.53997400  | -2.28163600 | -2.16706100 |
| H | 0.76541300  | -2.82996700 | -1.62790300 |
| H | 1.35253100  | -2.40590100 | -3.24123300 |
| C | -0.01770500 | -0.20782700 | 1.90798300  |
| H | -0.85834200 | -0.04279900 | 2.58792200  |
| H | 0.49700300  | 0.75164300  | 1.79348900  |
| N | -0.46673400 | -0.63051000 | 0.56577700  |
| N | 1.43033200  | -0.85068300 | -1.76988800 |
| H | 2.06696500  | -0.29123500 | -2.35356300 |
| C | 0.05392200  | -0.29000900 | -1.87609000 |
| H | -0.62758400 | -1.07298000 | -2.21323900 |
| H | 0.04376900  | 0.49819500  | -2.63673400 |
| C | -0.44831700 | 0.31847600  | -0.56011800 |
| H | -1.43646500 | 0.76472200  | -0.73555500 |
| H | 0.21592700  | 1.13830500  | -0.26753000 |
| S | -1.62843700 | -1.90227900 | 0.51807700  |
| O | -1.85862100 | -2.28355400 | 1.91568200  |
| O | -1.09241100 | -2.90709200 | -0.41588300 |
| C | -3.12098600 | -1.22919400 | -0.22971200 |
| C | -3.92091700 | -0.23001100 | 0.42066500  |
| C | -3.45728700 | -1.75254000 | -1.46509000 |
| C | -3.70758400 | 0.23443100  | 1.74488900  |
| C | -5.03468600 | 0.29244900  | -0.32729100 |
| C | -4.61409000 | -1.30127200 | -2.12824900 |
| H | -2.84340000 | -2.53241300 | -1.90030000 |
| C | -4.54511300 | 1.18500300  | 2.28438900  |
| H | -2.93921900 | -0.21577500 | 2.35808000  |
| C | -5.83676100 | 1.35371300  | 0.23199800  |
| C | -5.37329800 | -0.29518600 | -1.57290200 |
| H | -4.90531400 | -1.75698000 | -3.06927200 |
| C | -5.59003100 | 1.75951200  | 1.53397800  |
| H | -4.39101500 | 1.51386000  | 3.30843300  |
| H | -6.27830000 | 0.04186100  | -2.06506500 |
| H | -6.19481400 | 2.53818600  | 1.98470300  |
| N | -6.87466600 | 1.90176100  | -0.55442200 |

|   |             |            |             |
|---|-------------|------------|-------------|
| C | -7.99376800 | 2.50672000 | 0.16036600  |
| H | -7.75458300 | 3.49112900 | 0.59869000  |
| H | -8.81934700 | 2.64905700 | -0.54418900 |
| H | -8.33204800 | 1.83879700 | 0.95645800  |
| C | -6.44918400 | 2.73157800 | -1.68890400 |
| H | -7.28095700 | 2.83774200 | -2.39310800 |
| H | -6.13938000 | 3.73970900 | -1.36504000 |
| H | -5.61065800 | 2.26933300 | -2.21236400 |



**Table S2.** Atom types and charges for anionic thymine/dansyl-cyclen complex as used in Amber 8.0. Thymine atom types are first, starting with glycosidic nitrogen and continuing clockwise. Cyclen atom types start with Zinc, move into the cyclen ring with the sulfonamide nitrogen and move counter-clockwise. Dansyl atom types start with the sulfur, move into the naphthalene ring and begin by moving away from ring junction, continuing around entire ring and ending with tertiary amine.

| Table Entry | Atom Type | RESP Charge |
|-------------|-----------|-------------|
| 1           | N*        | -0.0048     |
| 2           | CM        | -0.2066     |
| 3           | H4        | 0.2012      |
| 4           | CM        | 0.0168      |
| 5           | CT        | -0.3957     |
| 6           | HC        | 0.1289      |
| 7           | HC        | 0.1289      |
| 8           | HC        | 0.1289      |
| 9           | C         | 0.6096      |
| 10          | O         | -0.5279     |
| 11          | N         | -0.7929     |
| 12          | C         | 0.6662      |
| 13          | O         | -0.5997     |
| 14          | Zn        | 0.7475      |
| 15          | n         | -0.2358     |
| 16          | c3        | 0.0103      |
| 17          | h1        | 0.0507      |
| 18          | h1        | 0.0507      |
| 19          | c3        | -0.0201     |
| 20          | h1        | 0.0610      |
| 21          | h1        | 0.0610      |
| 22          | n3        | -0.1318     |
| 23          | hn        | 0.2452      |
| 24          | c3        | -0.1831     |
| 25          | h1        | 0.1050      |
| 26          | h1        | 0.1050      |
| 27          | c3        | 0.0864      |
| 28          | h1        | 0.0770      |
| 29          | h1        | 0.0770      |
| 30          | n3        | -0.5801     |

|    |    |         |
|----|----|---------|
| 31 | hn | 0.3378  |
| 32 | c3 | 0.0864  |
| 33 | h1 | 0.0770  |
| 34 | h1 | 0.0770  |
| 35 | c3 | -0.1831 |
| 36 | h1 | 0.1050  |
| 37 | h1 | 0.1050  |
| 38 | n3 | -0.1318 |
| 39 | hn | 0.2452  |
| 40 | c3 | -0.0201 |
| 41 | h1 | 0.0610  |
| 42 | h1 | 0.0610  |
| 43 | c3 | 0.0103  |
| 44 | h1 | 0.0507  |
| 45 | h1 | 0.0507  |
| 46 | s4 | 0.7323  |
| 47 | o  | -0.4411 |
| 48 | o  | -0.4411 |
| 49 | ca | -0.0561 |
| 50 | ca | -0.0735 |
| 51 | ha | 0.1351  |
| 52 | ca | -0.1657 |
| 53 | ha | 0.1430  |
| 54 | ca | -0.0622 |
| 55 | ha | 0.1106  |
| 56 | ca | -0.0400 |
| 57 | ca | 0.2087  |
| 58 | ca | -0.1407 |
| 59 | ha | 0.1246  |
| 60 | ca | -0.0961 |
| 61 | ha | 0.1357  |
| 62 | ca | -0.3262 |
| 63 | ha | 0.2040  |
| 64 | ca | 0.1709  |
| 65 | na | -0.2159 |
| 66 | c3 | -0.2221 |
| 67 | h1 | 0.1058  |
| 68 | h1 | 0.1058  |
| 69 | h1 | 0.1058  |
| 70 | c3 | -0.2221 |
| 71 | h1 | 0.1058  |
| 72 | h1 | 0.1058  |
| 73 | h1 | 0.1058  |

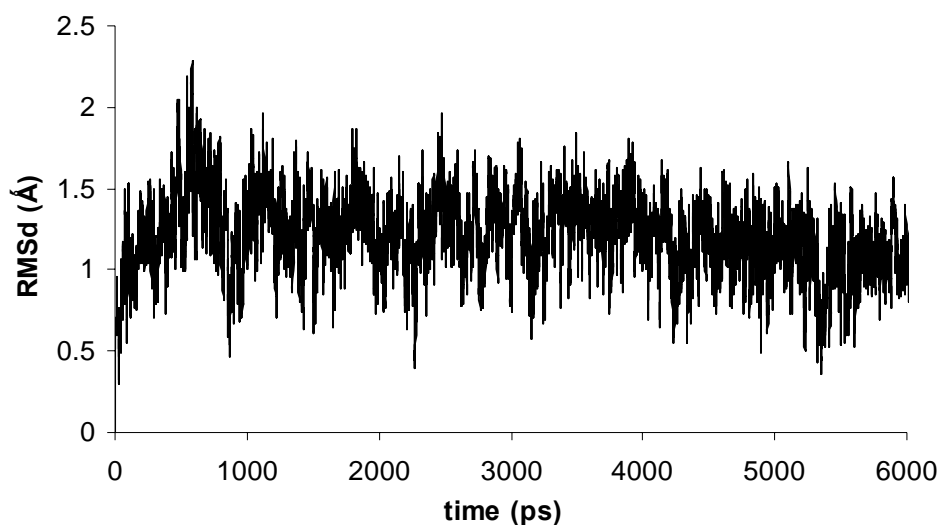


Bond Parameters

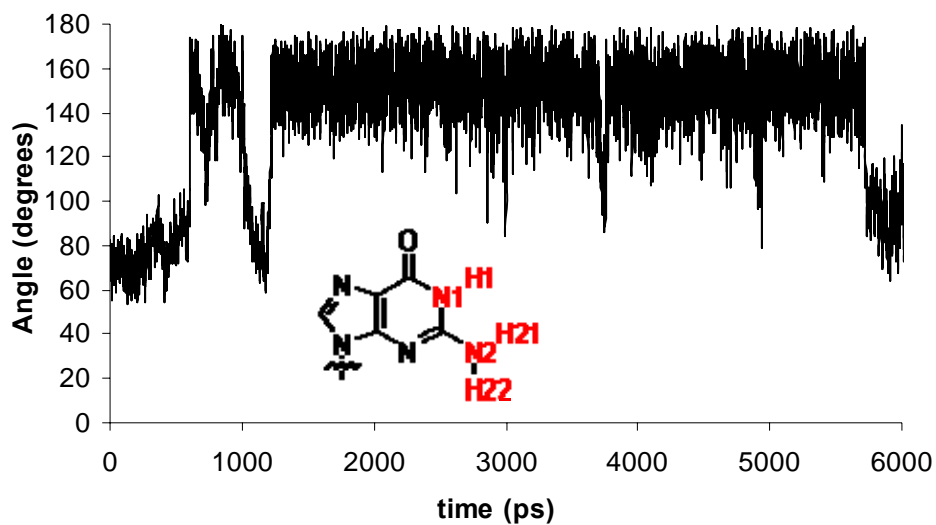
|       |       |       |
|-------|-------|-------|
| N-CT  | 337.0 | 1.449 |
| Zn-n3 | 250.0 | 2.053 |
| N-Zn  | 250.0 | 2.150 |

Angle Parameters

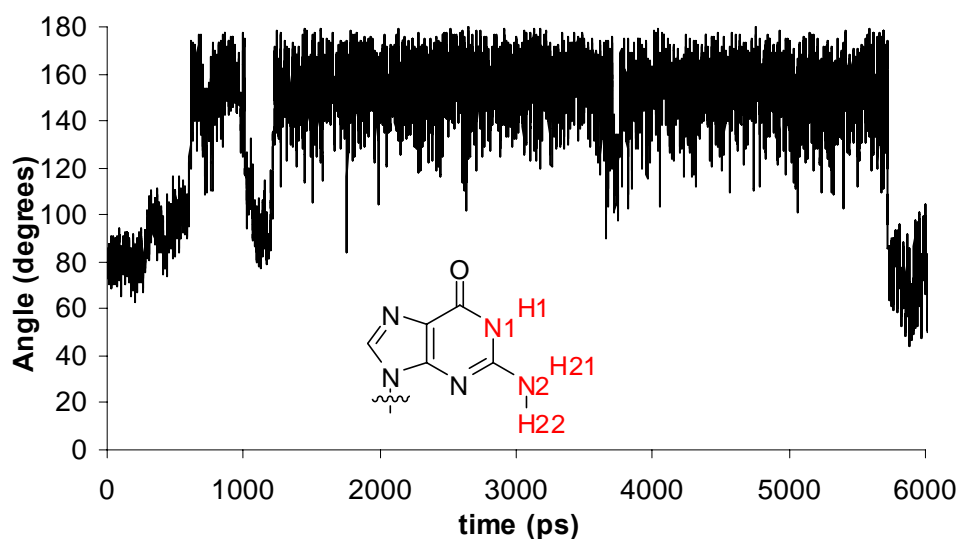
|          |      |       |
|----------|------|-------|
| Zn-N-C   | 20.0 | 115.9 |
| c3-n3-Zn | 20.0 | 115.9 |
| hn-n3-Zn | 20.0 | 106.8 |
| N-Zn-n3  | 20.0 | 101.4 |
| n3-Zn-n3 | 20.0 | 97.0  |
| CM-C-N   | 50.0 | 117.7 |
| N*-C-N   | 70.0 | 117.2 |
| n-s4-ca  | 64.3 | 117.6 |
| c3-n-s4  | 60.0 | 117.6 |



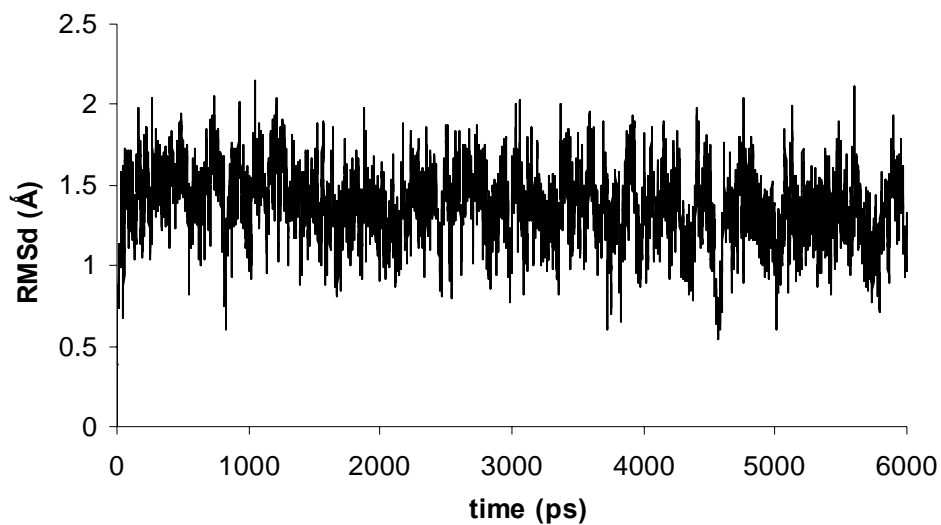
**Figure S6.** RMSd vs. time for dansyl-cyclen bound to 5'-GGTGG-3'. RMSd calculated from minimized, equilibrated structure over 6 ns of trajectory (data saved every 1 ps). "All atom" RMSd include all heavy atoms of DNA (C, N, O, P) but not hydrogens.



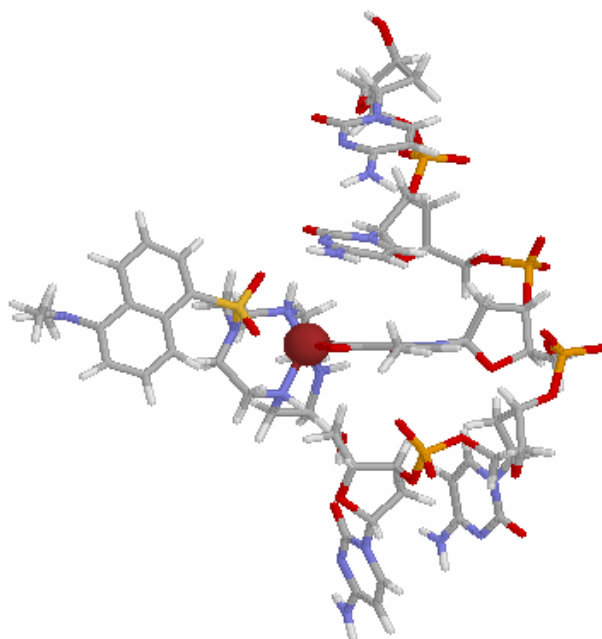
**Figure S7.** Plot of N1-H1-O3 (sulfonamide oxygen) angle over time for 5'-GGTGG-3' MD simulation calculated from data saved every 1 ps over 6 ns trajectory.



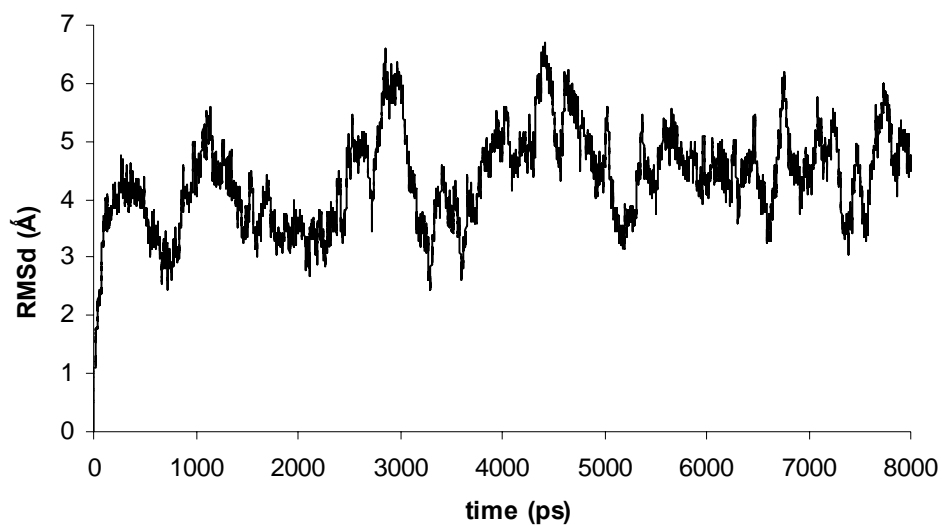
**Figure S8.** Plot of N2-H21-O4 (sulfonamide oxygen) angle over time for 5'-GGTGG-3' MD simulation calculated from data saved every 1 ps over 6 ns trajectory.



**Figure S9.** RMSd vs. time for dansyl-cyclen bound to 5'-CCTCC-3'. RMSd calculated from minimized, equilibrated structure over 6 ns of trajectory (data saved every 1 ps). "All atom" RMSd include all heavy atoms of DNA (C, N, O, P) but not hydrogens.



**Figure S10.** Snapshot at 3000 ps of dansyl-cyclen bound to 5'-CCTCC-3'.



**Figure S11.** RMSd vs. time for dansyl-cyclen bound to 5'-CGACGAATAAGCACG-3'/3'-GCTGCTTATTCGTGC-3'. RMSd calculated from minimized, equilibrated structure over 8 ns of trajectory (data saved every 1 ps). "All atom" RMSd include all heavy atoms of DNA (C, N, O, P) but not hydrogens.