Nucleic acid structural principles

September 29, 2009
Chemical make-up of nucleic acids
Nucleic acids are linear polymers made up of concatenated sugars, phosphates, and bases. The sugars and phosphates alternate along the chain backbone and the bases are laterally attached to the sugars.
The furanose sugars are of two types: ribose in RNA and 2′-deoxyribose in DNA.
The phosphodiester linkage is directional. The 3' -oxygen of nucleotide $i$ is joined to the 5' -oxygen of nucleotide $i+1$. (Here: guanine)
The sugar-base (glycosidic) linkage is stereo specific. The base is attached to the same side of the sugar ring as the exocyclic C5′ atom.
The heterocyclic bases fall into two categories: purines \((R = A \text{ or } G)\) and pyrimidines \((Y = T/U \text{ or } C)\).

The 5-methyl group of T in DNA is replaced by H in RNA.
Watson-Crick hydrogen-bonding and double-helical DNA structure
The heterocyclic bases associate as hydrogen-bonded pairs, the most common of which are the canonical Watson-Crick A·T (A·U) and G·C pairs.

The comparable size of the R·Y pairs makes them isosteric, allowing for their interchange and rearrangement in nucleic acid structures.
The regular repetition of paired nucleotide units generates double-helical structures, such as the right-handed A and B forms. 

\[ dG_{20} \cdot dC_{20} \text{ and } dA_{20} \cdot dT_{20} \text{ in canonical A and B forms.} \]

w3DNA.rutgers.edu
The hydrogen bonding distances are independent of double-helical form.

<table>
<thead>
<tr>
<th></th>
<th>N6⋯O4</th>
<th>N1⋯N3</th>
<th>O6⋯N4</th>
<th>N2⋯O2</th>
</tr>
</thead>
<tbody>
<tr>
<td>A·T</td>
<td>2.90</td>
<td>2.88</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A-DNA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B-DNA</td>
<td>2.95</td>
<td>2.88</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G·C</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2.85</td>
<td>2.83</td>
<td>2.81</td>
<td></td>
</tr>
<tr>
<td></td>
<td>2.85</td>
<td>2.85</td>
<td>2.85</td>
<td></td>
</tr>
</tbody>
</table>
The interstrand virtual distances and angles between the paired bases are also independent of helical form.

<table>
<thead>
<tr>
<th></th>
<th>$\lambda_R$</th>
<th>$\lambda_Y$</th>
<th>$C1^{'} \cdots C1^{'}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>54.3</td>
<td>54.3</td>
<td>10.7</td>
</tr>
<tr>
<td>B DNA</td>
<td>54.2</td>
<td>54.2</td>
<td>10.7</td>
</tr>
</tbody>
</table>
The intrastrand virtual distances between successive P and C1´ atoms along the same strand differ in the two helical forms.

<table>
<thead>
<tr>
<th></th>
<th>P…P</th>
<th>C1´…C1´</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>5.5</td>
<td>5.4</td>
</tr>
<tr>
<td>B DNA</td>
<td>6.6</td>
<td>4.9</td>
</tr>
</tbody>
</table>
The cylindrical (helical) parameters differ in the two forms.

<table>
<thead>
<tr>
<th></th>
<th>base-pair inclination</th>
<th>helical twist</th>
<th>helical rise</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>20.6</td>
<td>32.7</td>
<td>2.6</td>
<td>11</td>
</tr>
<tr>
<td>B DNA</td>
<td>-0.2</td>
<td>36</td>
<td>3.4</td>
<td>10</td>
</tr>
</tbody>
</table>
Groove widths and depths also differ in the two helical forms.

<table>
<thead>
<tr>
<th></th>
<th>minor groove</th>
<th>Major groove</th>
<th>r_{c1}</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>16.7</td>
<td>11.1</td>
<td>6.9</td>
</tr>
<tr>
<td>B DNA</td>
<td>11.7</td>
<td>17.2</td>
<td>1.9</td>
</tr>
</tbody>
</table>
The overlap of successive base pairs depends on duplex form.

Top-down “stacking diagrams” of $dG_2 \cdot dC_2$ and $dA_2 \cdot dT_2$ units in canonical A and B forms.
Whereas the overlap of base rings is comparable, the overlap of side groups differs in the two helical forms.

<table>
<thead>
<tr>
<th>Ring overlap</th>
<th>( i_{R1}-i_{R2} )</th>
<th>( i_{R1}-j_{Y2} )</th>
<th>( j_{Y1}-i_{R2} )</th>
<th>( j_{Y1}-j_{Y2} )</th>
<th>total</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>2.4</td>
<td>0.0</td>
<td>0.0</td>
<td>0.1</td>
<td>2.4</td>
</tr>
<tr>
<td>B DNA</td>
<td>2.0</td>
<td>0.0</td>
<td>0.0</td>
<td>0.2</td>
<td>2.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>“All-atom” overlap</th>
<th>( i_{R1}-i_{R2} )</th>
<th>( i_{R1}-j_{Y2} )</th>
<th>( j_{Y1}-i_{R2} )</th>
<th>( j_{Y1}-j_{Y2} )</th>
<th>total</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>3.8</td>
<td>0.0</td>
<td>0.0</td>
<td>1.0</td>
<td>4.8</td>
</tr>
<tr>
<td>B DNA</td>
<td>3.6</td>
<td>0.0</td>
<td>0.0</td>
<td>5.8</td>
<td>9.4</td>
</tr>
</tbody>
</table>
The differences in A vs. B groove widths, base-pair displacement and inclination, base-stacking overlap, and residues per turn are evident in molecular models.

dG_{20} \cdot dC_{20} and dA_{20} \cdot dT_{20} in canonical A and B forms.

w3DNA.rutgers.edu
Torsional preferences in double-helical A- and B-DNA structures
Nucleotide conformation is defined by seven torsion angles.
The canonical A- and B-DNA structures show large differences in three of the seven repeated nucleotide torsion angles.

<table>
<thead>
<tr>
<th></th>
<th>α</th>
<th>β</th>
<th>γ</th>
<th>δ</th>
<th>ε</th>
<th>ζ</th>
<th>χ</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>-52</td>
<td>175</td>
<td>42</td>
<td>79</td>
<td>-148</td>
<td>-75</td>
<td>-157</td>
</tr>
<tr>
<td>B DNA</td>
<td>-30</td>
<td>136</td>
<td>31</td>
<td>143</td>
<td>-141</td>
<td>-161</td>
<td>-98</td>
</tr>
</tbody>
</table>

α: $O3'(i-1)-P-O5'-C5'$
β: $P-O5'-C5'-C4'$
γ: $O5'-C5'-C4'-C3'$
δ: $C5'-C4'-C3'-O3'$
ε: $C4'-C3'-O3'-P(i+1)$
ζ: $C3'-O3'-P(i+1)-O5'(i+1)$

χ pyrimidines (Y): $O4'-C1'-N1-C2$
χ purines (R): $O4'-C1'-N9-C4$
The sugar ring adopts two distinct conformational states (N or S, C3′-endo or C2′-endo) in the canonical A- and B-DNA duplexes.

<table>
<thead>
<tr>
<th></th>
<th>( v_0 )</th>
<th>( v_1 )</th>
<th>( v_2 )</th>
<th>( v_3 )</th>
<th>( v_4 )</th>
<th>( P )</th>
<th>( \tau_m )</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>8</td>
<td>-34</td>
<td>44</td>
<td>-40</td>
<td>21</td>
<td>8</td>
<td>44.5</td>
</tr>
<tr>
<td>B DNA</td>
<td>-33</td>
<td>45</td>
<td>-40</td>
<td>23</td>
<td>6</td>
<td>154</td>
<td>44.7</td>
</tr>
</tbody>
</table>

\( v_0 \): C4′-O4′-C1′-C2′
\( v_1 \): O4′-C1′-C2′-C3′
\( v_2 \): C1′-C2′-C3′-C4′
\( v_3 \): C2′-C3′-C4′-O4′
\( v_4 \): C3′-C4′-O4′-C1′

\( \tau_m \): pseudorotation amplitude
\( P \): pseudorotation phase angle
The differences in the sugar-base torsion angles (the backbone sugar torsion $\delta$ or the pseudorotation parameters $P$ and $\tau_m$ and the glycosyl torsion $\chi$) give rise to characteristic intrastrand $P\cdots P$ distances that distinguish A from B DNA.

\[ C3'\text{-endo} \quad P \approx \pi/10 \]
\[ C2'\text{-endo} \quad P \approx 9\pi/10 \]

$P\cdots P$ distances cited here are average values found in high-resolution crystal structures.
The sugar and glycosyl torsion angles are the best chemical-level discriminators of high resolution A-DNA and B-DNA structures.

The P atoms lie in two distinct locations in A and B duplex “steps”.

<table>
<thead>
<tr>
<th></th>
<th>$x_P$</th>
<th>$y_P$</th>
<th>$z_P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>-1.0</td>
<td>8.4</td>
<td>2.5</td>
</tr>
<tr>
<td>B DNA</td>
<td>-3.0</td>
<td>8.9</td>
<td>-0.6</td>
</tr>
</tbody>
</table>

Mean coordinates of P atoms in the local dimer frames.
Phosphorus displacement ($z_p$) differs in A-DNA and B-DNA dimer steps.

**A-DNA:** $GG·CC$ step from $d(GCCCCGGG)_{2}$ (adh038)

**B-DNA:** $AA·TT$ step from $d(CGCGAATTGCG)_{2}$ (bdl084)

Lu et al. (2000)
Phosphorus displacement discriminates A-DNA vs. B-DNA base-pair “steps”  
(Histograms of observed values of $z_p$ in high-resolution structures)

Lu et al. (2000)
Mechanisms of DNA bending
Proteins often bend DNA without disruption of the double-helical structure. Homing endonuclease I-PpoI bend DNA by ~60° (PDB_ID: 1ipp).

The sugar ring and glycosyl rotations appear to interconvert between A- and B-like forms in this complex.

\[ \delta: \quad C5'\text{-}C4'\text{-}C3'\text{-}O3' \quad (79^\circ \text{ A-DNA vs. } 143^\circ \text{ B-DNA}) \]

\[ \chi \text{ pyrimidines (Y): } O4'\text{-}C1'\text{-}N1\text{-}C2 \]

\[ \chi \text{ purines (R): } O4'\text{-}C1'\text{-}N9\text{-}C4 \]

\[ (203^\circ \text{ A-DNA vs. } 262^\circ \text{ B-DNA}) \]
The sugar ring and glycosyl torsions are strongly coupled.

\[ \delta: \quad C5'-C4'-C3'-O3' \quad (79° \text{ A-DNA vs. } 143° \text{ B-DNA}) \]

\[ \chi \text{ pyrimidines} (Y): \quad O4'-C1'-N1-C2 \]
\[ \chi \text{ purines} (R): \quad O4'-C1'-N9-C4 \]

(203° A-DNA vs. 262° B-DNA)
One of the phosphodiester rotations ($\zeta$) also appears to interconvert between A- and B-like forms (but in an opposite sense to $\delta$ and $\chi$).

\[ \varepsilon: \ C4'-C3'-O3'-P(i+1) \]
\[ \zeta: \ C3'-O3'-P(i+1)-O5'(i+1) \]
(285° A-DNA vs. 161° B-DNA)
The $\epsilon \zeta$ angle pair exhibits slight coupling.

$\epsilon$: $C4'-C3'-O3'-P(i+1)$
$\zeta$: $C3'-O3'-P(i+1)-O5'(i+1)$

($285^\circ$ A-DNA vs. $161^\circ$ B-DNA)
Although the $\alpha$ and $\gamma$ angles adopt similar values in the canonical A and B helices, they show large coupled changes in the I-$PpoI$-DNA complex.

$\alpha$: $O3'(i-1)-P-O5'-C5' \ (308^\circ \text{ A-DNA vs. } 330^\circ \text{ B-DNA})$

$\gamma$: $O5'-C5'-C4'-C3' \ (42^\circ \text{ A-DNA vs. } 31^\circ \text{ B-DNA})$
Although the $\alpha$ and $\gamma$ angles adopt similar values in the canonical A and B helices, they show large coupled changes in the I-PpoI-DNA complex.

$\alpha$: $O3'(i-1)-P-O5'-C5$ $^\circ$ (308$^\circ$ A-DNA vs. 330$^\circ$ B-DNA)
Although the $\alpha$ and $\gamma$ angles adopt similar values in the canonical A and B helices, they show large coupled changes in the I-PpoI-DNA complex.

$\gamma$: O5'-C5'-C4'-C3'  (42° A-DNA vs. 31° B-DNA)
The anticorrelation of the $\alpha \gamma$ torsions preserves the stacked geometry of DNA base pairs in the I-PpoI-DNA complex.
The excursions in the $\beta$ torsion in the I-\textit{PpoI}-DNA complex differ from the changes characteristic of changes from the canonical B to A forms.

$\beta$: $P\text{-O5'}-C5'-C4'$ (175° A-DNA vs. 136° B-DNA)
Multiple A/B junctions apparently contribute to the significant DNA bending in the I-PpoI-DNA complex.


Lu et al. (2000)
Analysis of the I-PpoI-DNA complex suggests that concatenation of A- and B-DNA helices generates a naturally curved structure.
If regularly repeated, the concatenation of A- and B-DNA helices generates a naturally curved structure.

\[ A_3G_5A_5G_5A_3\cdot T_3C_5T_5C_5T_3 \] miniduplex

B-like AA·TT and AG·TC steps

A-like GG·CC and GA·CT steps
The concatenation of short $A$- and $B$-DNA helices alters the groove structure at helix junctions.

$A_3G_5A_5G_5A_3\cdot T_3C_5T_5C_5T_3$ miniduplex

$B$-like $AA\cdot TT$ and $AG\cdot TC$ steps

$A$-like $GG\cdot CC$ and $GA\cdot CT$ steps
The angle between the base pairs at the termini of concatenated helices depends upon the length of the A-DNA segment.

\[ \cos^{-1}(\mathbf{n}_1 \cdot \mathbf{n}_{37}) = 83^\circ \]

\[ \cos^{-1}(\mathbf{n}_1 \cdot \mathbf{n}_{37}) = 27^\circ \]

\[ \cos^{-1}(\mathbf{n}_1 \cdot \mathbf{n}_{37}) = 67^\circ \]
DNA phase transitions
DNA phase transitions

- The ionic character of the sugar-phosphate backbone makes DNA especially sensitive to changes in its local environment, e.g., salt, alcohol.
- Interactions with other molecules, including proteins, may lead to a change of helical state.
The $A \rightarrow B$ transition: first known change of DNA double-helical state.

A-DNA base pairs inclined with respect to helical axis and untwisted cf. B DNA.

A-DNA minor groove wider and more shallow, major groove narrower and more deep cf. B DNA.

Base pairs displaced from A-DNA helical axis.
Base composition of A- & B-DNA structures depends on sequence.

<table>
<thead>
<tr>
<th>Dimer Step</th>
<th>A-DNA (2.0 Å)</th>
<th>All</th>
<th>B-DNA (2.0 Å)</th>
<th>All</th>
<th>ΔG_{B/A} † (kcal/mole)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA · TT</td>
<td>0</td>
<td>2</td>
<td>31</td>
<td>112</td>
<td>0.97</td>
</tr>
<tr>
<td>GG · CC</td>
<td>92</td>
<td>243</td>
<td>14</td>
<td>55</td>
<td>0.19</td>
</tr>
<tr>
<td>CA · TG</td>
<td>16</td>
<td>20</td>
<td>17</td>
<td>48</td>
<td>1.04</td>
</tr>
<tr>
<td>AC · GT</td>
<td>42</td>
<td>80</td>
<td>4</td>
<td>22</td>
<td>0.13</td>
</tr>
<tr>
<td>GA · TC</td>
<td>4</td>
<td>21</td>
<td>27</td>
<td>80</td>
<td>0.96</td>
</tr>
<tr>
<td>AG · CT</td>
<td>2</td>
<td>18</td>
<td>18</td>
<td>30</td>
<td>0.33</td>
</tr>
<tr>
<td>GC · GC</td>
<td>40</td>
<td>102</td>
<td>11</td>
<td>121</td>
<td>0.73</td>
</tr>
<tr>
<td>CG · CG</td>
<td>44</td>
<td>93</td>
<td>28</td>
<td>200</td>
<td>0.52</td>
</tr>
<tr>
<td>TA · TA</td>
<td>10</td>
<td>26</td>
<td>6</td>
<td>15</td>
<td>0.75</td>
</tr>
<tr>
<td>AT · AT</td>
<td>4</td>
<td>6</td>
<td>17</td>
<td>58</td>
<td>0.68</td>
</tr>
</tbody>
</table>

A/B helical motifs are common in complexes of DNA with enzymes that make or break the O3´-P phosphodiester linkage

<table>
<thead>
<tr>
<th>Enzyme/Complex</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tc3 transposase</td>
<td>A G G G G G G G T C C T A T A G A A C T T</td>
</tr>
<tr>
<td></td>
<td>T C C C C C C C A G G A T A T C T T T G A</td>
</tr>
<tr>
<td>I-PPOI homing endonuclease</td>
<td>T T G A C T C T C T T A A G A G A G A G T C A</td>
</tr>
<tr>
<td></td>
<td>A C T G A G A G A A T T C T C T C A G T T</td>
</tr>
<tr>
<td>PVUII restriction endonuclease</td>
<td>T G A C C A G C T G G T C</td>
</tr>
<tr>
<td></td>
<td>C T G G T C G A C C A G</td>
</tr>
<tr>
<td>Eco RV endonuclease</td>
<td>G G G A T A T C C C</td>
</tr>
<tr>
<td></td>
<td>C C C T A T A G G G</td>
</tr>
<tr>
<td>TAQ polymerase</td>
<td>G A C C A C G G C G C C</td>
</tr>
<tr>
<td></td>
<td>C T G G T G C C G G C C C</td>
</tr>
<tr>
<td>Bacillus polymerase I</td>
<td>G C A T G A T G C</td>
</tr>
<tr>
<td></td>
<td>C G T A C T A C G A</td>
</tr>
<tr>
<td>HIV-1 RT + FAB 28</td>
<td>G T C C C T G T T C G G G C G C C A</td>
</tr>
<tr>
<td></td>
<td>C A G G G A C A A G C C C G C G T A</td>
</tr>
</tbody>
</table>

Lu et al. (2000)
DNA helical form influences atomic exposure as well as global shape.

**A-DNA**
- 11 res/turn
- Roll > 0
- Slide < 0

**B-DNA**
- 10 res/turn
- Roll ≈ 0
- Slide ≈ 0

**C-DNA**
- 9 res/turn
- Roll < 0
- Slide > 0

Wide/shallow minor groove exposes O3' and base-pair edges

~12 Å minor groove exposes O5' vs. O3', partial base-pair edges

Deep/narrow minor groove exposes O5', hides base-pair edges

Pseudo-symmetric R(N3), Y(O2) proton-acceptor atoms of Watson-Crick base pairs
Transformations within the ABCD family of right-handed double helices affect:

(i) the inclination of Watson-Crick base pairs
(ii) the widths and exposure of atoms on the major and minor-groove edges
(iii) the overall helical extension.
Transformations within the ABCD family of structures also alter:

(i) the number of residues per helical turn;
(ii) the width of the solvent “channel” through the center of the duplex.

The tendency to adopt these helical forms depends upon sequence: poly dG·poly dC is “A philic”; repetition of A·T or I·C bases promotes formation of the C and D forms.
Sequence-dependent responses of DNA helical structure

\[
\begin{array}{ccc}
\text{A} \rightarrow \text{G} & \text{T} \rightarrow \text{A} & \text{C} \rightarrow \text{G} \\
\text{C} \rightarrow \text{T} & \text{G} \rightarrow \text{C} & \text{A} \rightarrow \text{T} \\
\text{G} \rightarrow \text{T} & \text{T} \rightarrow \text{G} & \text{A} \rightarrow \text{T} \\
\text{A} \rightarrow \text{G} & \text{T} \rightarrow \text{A} & \text{C} \rightarrow \text{G} \\
\end{array}
\]

- 20 H\textsubscript{2}O - 10 H\textsubscript{2}O - m H\textsubscript{2}O

\[
\begin{align*}
A_{11} & \quad B_{10} & \quad C_9 & \quad D_8 \\
2.6 & \quad 3.4 & \quad 3.2-3.3 & \quad 3.0
\end{align*}
\]

Mixed Sequence

Deformations toward the A and C forms bend DNA in the opposite sense.

Major (M), minor (m) groove edges lie on opposite faces of B→A vs. B→C induced curves.

A.R. Srinivasan
Combined $B\rightarrow A$ and $B\rightarrow C$ deformations tighten the bending of DNA:

Global bend: $360^\circ/75$ bp
left-handed superhelix

Combined $B\rightarrow A$ and $B\rightarrow C$ deformations tighten the bending of DNA:
Unusual DNA structures
DNA sequences of repeated CG dinucleotides crystallize in an unusual left-handed Z-DNA (zig-zag) double-helical form.
The conformational parameters of Z-DNA differ at YR vs. RY steps.

Z-DNA backbone torsion angles

<table>
<thead>
<tr>
<th></th>
<th>α</th>
<th>β</th>
<th>γ</th>
<th>δ</th>
<th>ε</th>
<th>ζ</th>
<th>χ</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>-140</td>
<td>-137</td>
<td>51</td>
<td>138</td>
<td>-97</td>
<td>82</td>
<td>-154</td>
</tr>
<tr>
<td>G</td>
<td>52</td>
<td>179</td>
<td>-174</td>
<td>95</td>
<td>-104</td>
<td>-65</td>
<td>59</td>
</tr>
</tbody>
</table>

α: O3'(i-1)-P-O5'-C5'
β: P-O5'-C5'-C4'
γ: O5'-C5'-C4'-C3'
δ: C5'-C4'-C3'-O3'
ε: C4'-C3'-O3'-P(i+1)
ζ: C3'-O3'-P(i+1)-O5'(i+1)
χ: pyrimidines (Y): O4'-C1'-N1-C2
χ: purines (R): O4'-C1'-N9-C4

Acyclic torsions of dimer steps noted by color coding: CpG GpC
Z-DNA base-pair steps progress in an opposite direction from those of the ABCD family.
Some DNA sequences can be locked in 4-way Holliday junctions.
DNA junctions are the design elements of novel nanomaterials.

DNA as a collection of rigid-body parameters
DNA sequence-dependent structure is easily understood at the base-pair level. (bd1084; Shui et al., 1998)
Complementary base-pair frame and parameters

Base-Pair Reference Frame

Shear

Buckle

Stretch

Propeller

Stagger

Opening
Nucleic acid base-pair “step” parameters

- Shift
- Tilt
- Slide
- Roll
- Rise
- Twist
Standard base-pair coordinate frame
Comparative DNA Twist Angles
Crystal vs. Solution Averages

Gorin et al. (1995)
Bending angles of base-pair “steps” in DNA crystal structures
Shear displacement of dimers in DNA crystal structures
Intrinsic coupling of Roll and Twist angles in DNA structures

Olson et al. (1998)
The canonical A- and B-DNA structures exhibit differences in three of the six base-pair step parameters.

<table>
<thead>
<tr>
<th></th>
<th>Tilt</th>
<th>Roll</th>
<th>Twist</th>
<th>Shift</th>
<th>Slide</th>
<th>Rise</th>
</tr>
</thead>
<tbody>
<tr>
<td>A DNA</td>
<td>0</td>
<td>12</td>
<td>30</td>
<td>0</td>
<td>-1.4</td>
<td>3.3</td>
</tr>
<tr>
<td>B DNA</td>
<td>0</td>
<td>2</td>
<td>36</td>
<td>0</td>
<td>0</td>
<td>3.4</td>
</tr>
</tbody>
</table>
The differences in Roll, Twist, and Slide in A and B DNA account for the observed differences in global helical structure.
Roll, Slide, Twist exhibit subtle, sequence-dependent behavior.

Sequence-dependent variation of the three base-pair 'step' parameters, which dominate the conformational variability in high-resolution protein-DNA structures.
CA·TG steps are naturally ‘soft’, allowing them to take up the deformations of structure responsible for the superhelical DNA path in the nucleosome.

341 CA·TG and 418 AC·GT steps from 239 protein-DNA crystal complexes of 2.5 Å or better resolution.
Schematic of the structural and deformational code embedded in DNA sequence.
Assignment (due Tuesday, October 13, 2009):

1. Compare the overlap of bases at YR and RY base-pair steps in A, B, vs. Z DNA helices.

2. How much global bending is induced by the insertion of A DNA helical fragments of 1, 5, 6, and 11 base-pair steps within a B-DNA helix?