

## Supporting Information

### Base Pair Fraying in Molecular Dynamics Simulations of DNA and RNA

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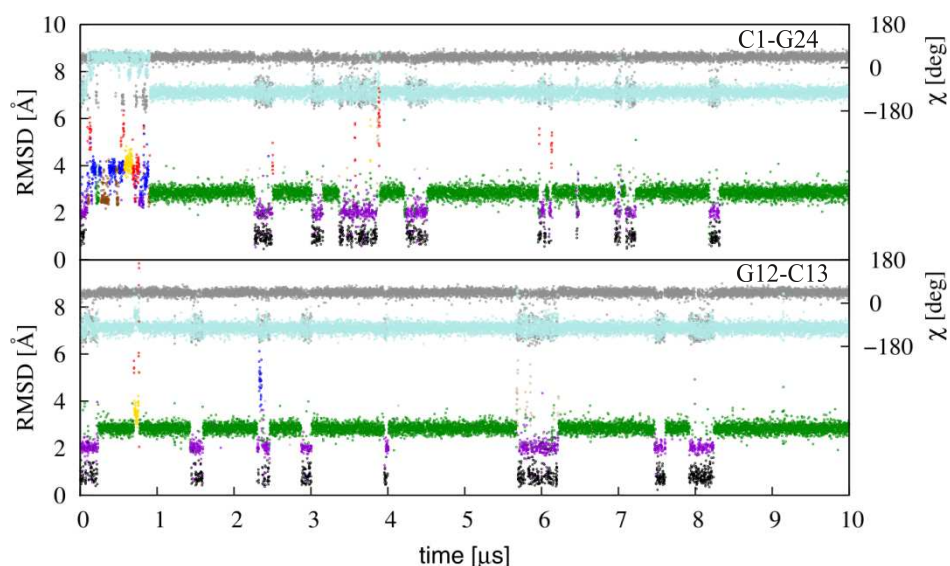
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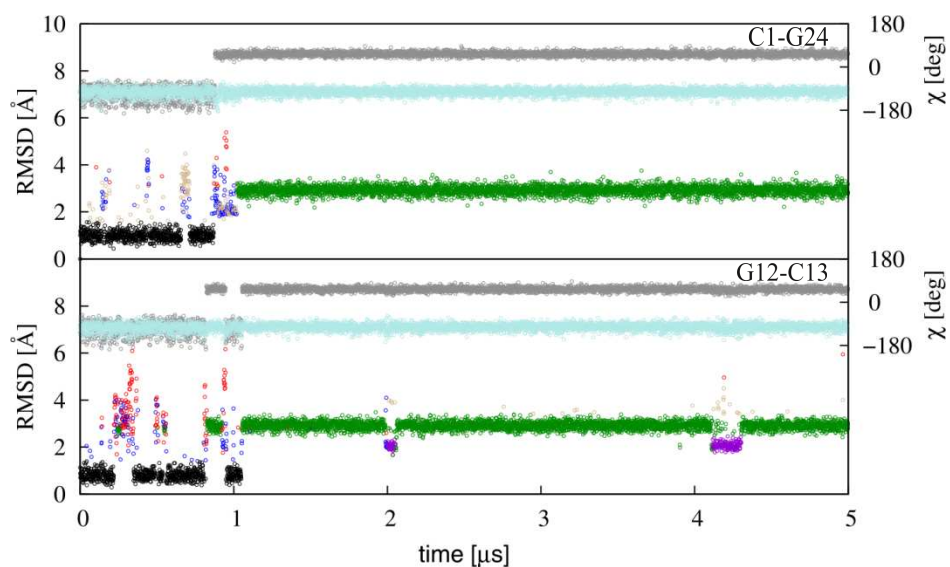


## 1) Simulations of DD dodecamer

**Figure S1.** Fraying of the C1-G24 (top) and G12-C13 (bottom) terminal base pairs in MD simulation of the DD dodecamer with the ff99bsc0 force field (10  $\mu$ s, TIP3P) characterized by the RMSD of the terminal pairs and torsion angles  $\chi$  for the terminal residues (gray – C1, C13; light blue – G12, G24). The colors in the RMSD plot correspond to different end structures: WC (black), tWC/SE (green), distorted WC (violet), ‘CH’/Ho (brown), stacked (blue), frayed (red) and 5’C adhered to the major groove, 5’C-MG (yellow) and other (tan).



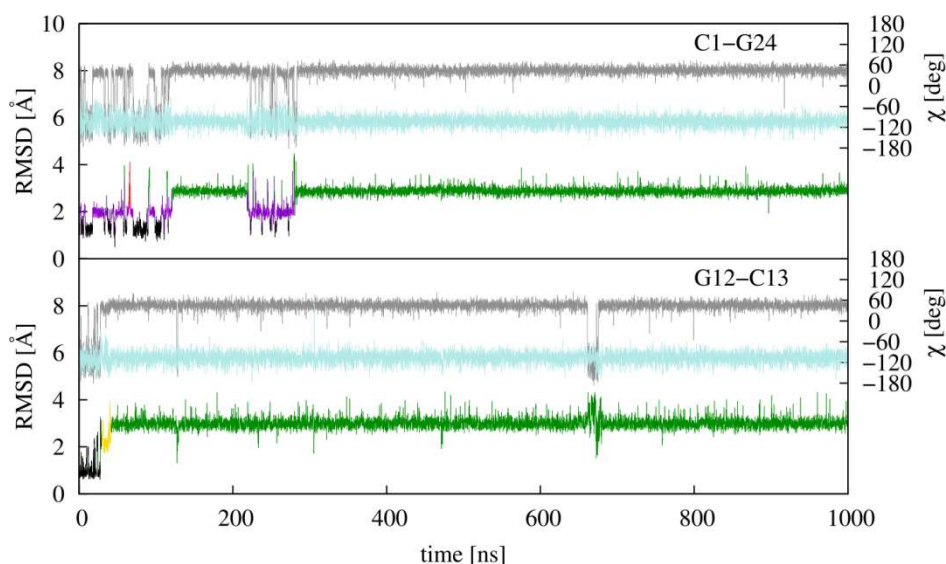
**Figure S2.** Fraying of the C1-G24 (top) and G12-C13 (bottom) terminal base pairs in MD simulation of the DD dodecamer with the ff99bsc0 $\chi_{OL4}$  force field (5  $\mu$ s, TIP3P) characterized by the RMSD of the terminal pairs and torsion angles  $\chi$  for the terminal residues (gray – C1, C13; light blue – G12, G24). The colors in the RMSD plot correspond to different end structures: WC (black), tWC/SE (green), distorted WC (violet), ‘CH’/Ho (brown), stacked (blue), frayed (red) and 5’C adhered to the major groove, 5’C-MG (yellow) and other (tan).



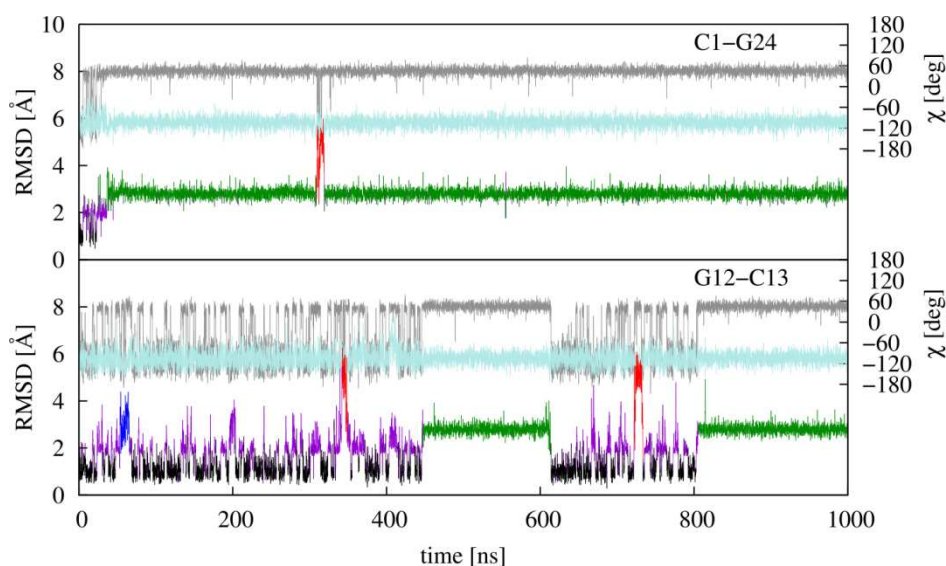


## 2) Additional DNA sequences terminated with the CG//CG step

**Figure S3.** Fraying in the A6 sequence (PDB ID 1D89) with the ff99bsc0 force field. Opening of the C1-G24 (top) and G12-C13 (bottom) terminal base pair in MD simulation of A6 structure (1  $\mu$ s, TIP3P water model, neutralizing  $\text{Na}^+$ ). Opening is characterized by the RMSD of the terminal pairs, and torsion angle  $\chi$  for the terminal residues (gray – terminal cytosines C1, C13; light blue – terminal guanines G24, G12). The colors in the RMSD plot correspond to different end structures: frayed (red), stacked structure (blue), tWC/SE (green), distorted WC (violet), and 5'C MG (yellow).



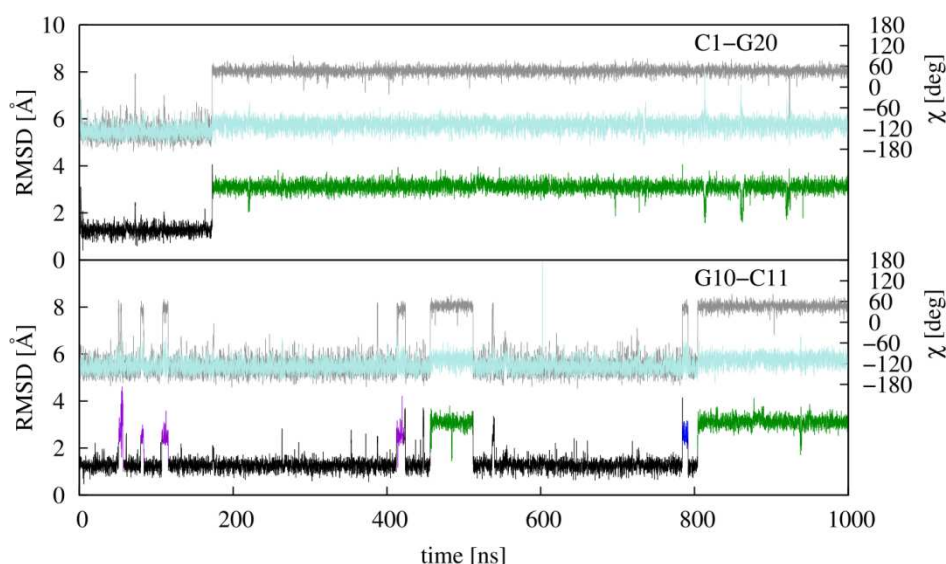
**Figure S4.** Fraying in the 3AT sequence with the ff99bsc0 force field. Opening of the C1-G24 (top) and G12-C13 (bottom) terminal base pair in MD simulation of 3AT structure (1  $\mu$ s, TIP3P water model, neutralizing  $\text{Na}^+$ ). Opening is characterized by the RMSD of the terminal pairs and torsion angle  $\chi$  for the terminal residues (gray – terminal cytosines C1, C13; light blue – terminal guanines G24, G12). The colors in the RMSD plot correspond to different end structures: frayed (red), stacked structure (blue), tWC/SE (green), and distorted WC (violet).



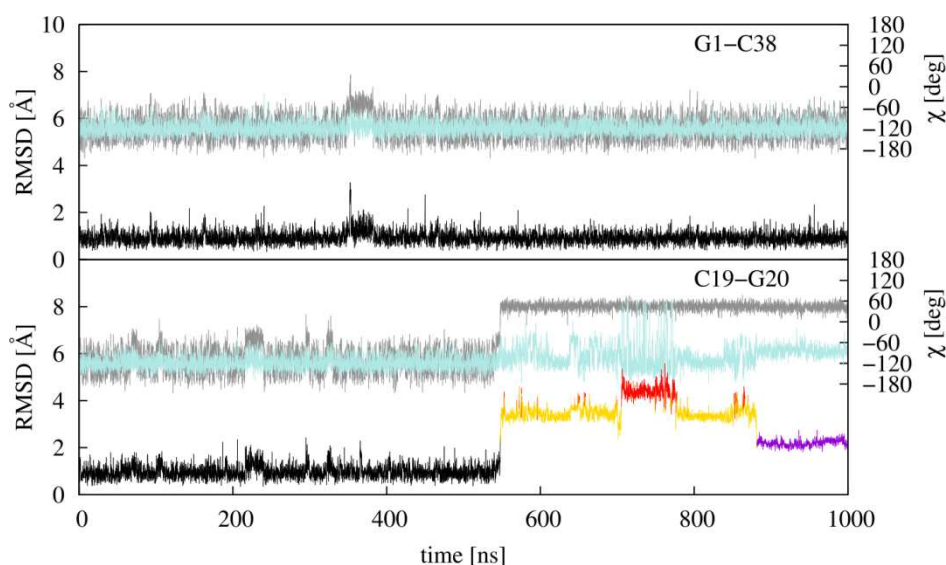


### 3) Influence of Neighboring Base Pairs - sequences terminated with CC//GG and GC//GC steps

**Figure S5.** Fraying in the 5C5G sequence with the ff99bsc0 force field. Opening of the C1-G20 (top) and G10-C11 (bottom) terminal base pair in MD simulation of 5C5G structure (1  $\mu$ s, TIP3P water model, neutralizing  $\text{Na}^+$ ). Opening is characterized by the RMSD of the terminal pairs, and torsion angle  $\chi$  for the terminal residues (gray – terminal cytosines C1, C11; light blue – terminal guanines G20, G10). The colors in the RMSD plot correspond to different end structures: frayed (red), stacked structure (blue), tWC/SE (green), and distorted WC (violet).



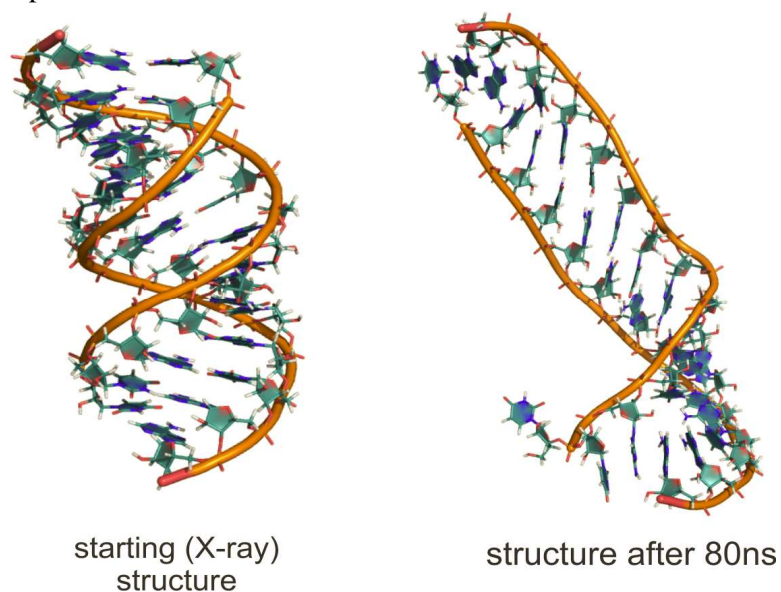
**Figure S6.** Fraying in the d(GCCAAGAAGCAGGAGTGGC)<sub>2</sub> sequence with the ff99bsc0 force field. Opening of the G1-C38 (top) and C19-G20 (bottom) terminal base pair in MD simulation of d(GCCAAGAAGCAGGAGTGGC)<sub>2</sub> structure (1  $\mu$ s, SPC/E water model, 150 mM KCl). Opening is characterized by the RMSD of the terminal pairs, and torsion angle  $\chi$  for the terminal residues (gray – terminal guanines G1, G20; light blue – terminal cytosine C38, C19). The colors in the RMSD plot correspond to different end structures: WC (black), distorted WC (violet), frayed (red), 3'C adhered to the major groove, 3'C-MG (yellow).





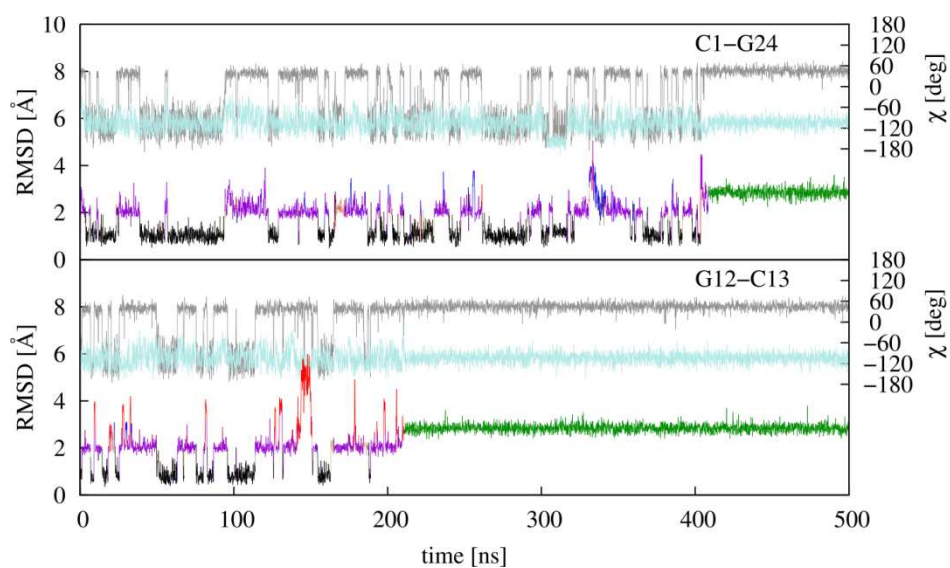
#### 4) AU Terminated RNA Duplex

**Figure S7.** Ladder-like structure formed in ff99bsc0 simulation of 1RNA after 80 ns of MD simulation. An example of a non-canonical terminal motif is shown at the lower end of the duplex.



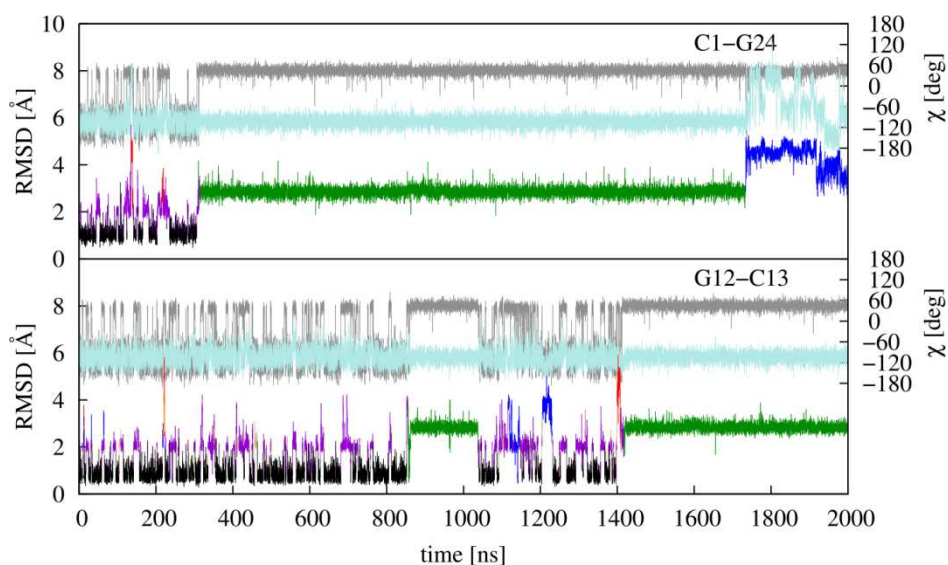
#### 5) Influence of Water Model and Salt Concentration

**Figure S8.** Fraying of the terminal base pairs in MD simulation of the DD dodecamer with the ff99bsc0 force field (500 ns, SPC/E) characterized by the RMSD of the terminal pairs and torsion angles  $\chi$  for the terminal residues (gray – C1, C13; light blue – G12, G24). The colors in the RMSD plot correspond to different end structures: WC (black), tWC/SE (green), distorted WC (violet), stacked (blue), and frayed (red).





**Figure S9.** Fraying of the C1-G24 and G12-C13 terminal base pairs in MD simulation of the DD dodecamer with the ff99bsc0 force field (2  $\mu$ s, SPC/E, 150 mM KCl) characterized by the RMSD of the terminal pairs and torsion angles  $\chi$  for the terminal residues (gray – C1, C13; light blue – G12, G24). The colors in the RMSD plot correspond to different end structures: WC (black), tWC/SE (green), distorted WC (violet), stacked (blue), frayed (red) and other (tan).



**Figure S10.** Fraying of the C1-G24 and G12-C13 terminal base pairs in MD simulation of the DD dodecamer with the ff99bsc0 $\chi_{OL4}$  force field (1.5  $\mu$ s, SPC/E, 150 mM KCl) characterized by the RMSD of the terminal pairs and torsion angles  $\chi$  for the terminal residues (gray – C1, C13; light blue – G12, G24). The colors in the RMSD plot correspond to different end structures: WC (black), tWC/SE (green), stacked (blue), frayed (red) and 5'C adhered to the major groove, 5'C-MG (yellow) and other (tan).

