Electronic Supplementary Information

Conformational Changes of DNA Induced by *trans*-Azobenzene Derivative via Non-covalent Interactions

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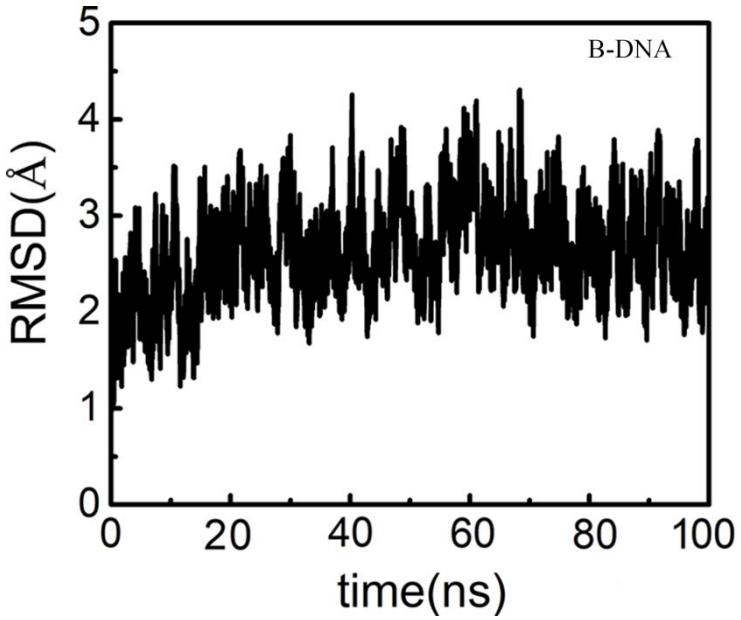

Fig. S1 Root-mean-square deviation (RMSDs) of heavy atoms of DNA for the last 100 ns simulation, using the initial structure as reference structures (native DNA).

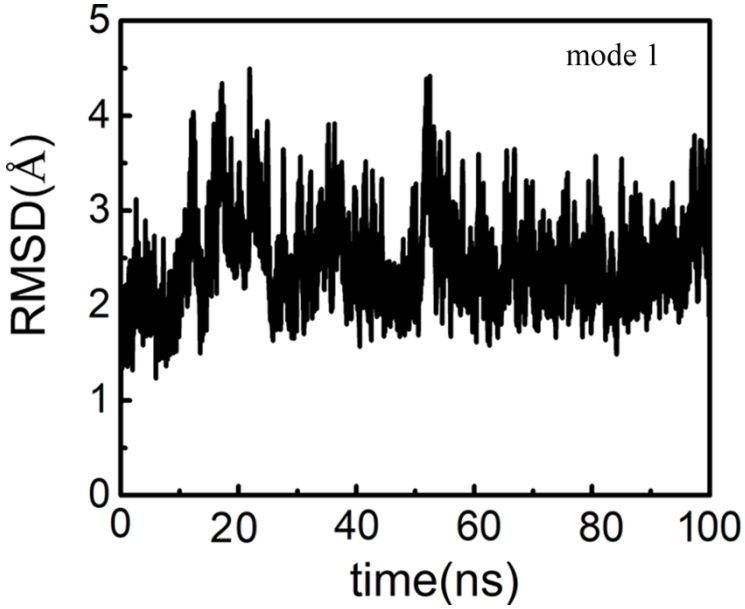

Fig. S2 Root-mean-square deviation (RMSDs) of heavy atoms of DNA for the last 100 ns simulation, using the initial structure as reference structures (mode1: the planar aromatic rings of *trans*-azobenzene intercalating from the minor groove).

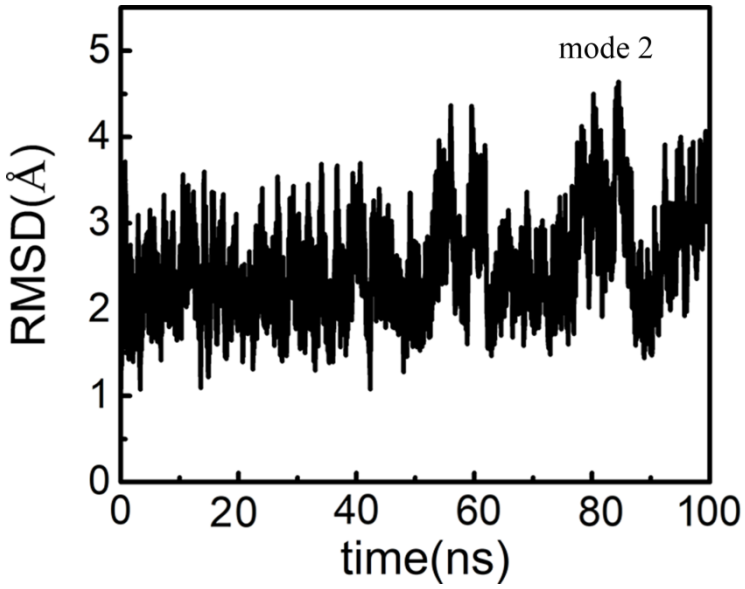

Fig. S3 Root-mean-square deviation (RMSDs) of heavy atoms of DNA for the last 100 ns simulation, using the initial structure as reference structures (mode 2: the planar aromatic rings of *trans*-azobenzene intercalating from the major groove).

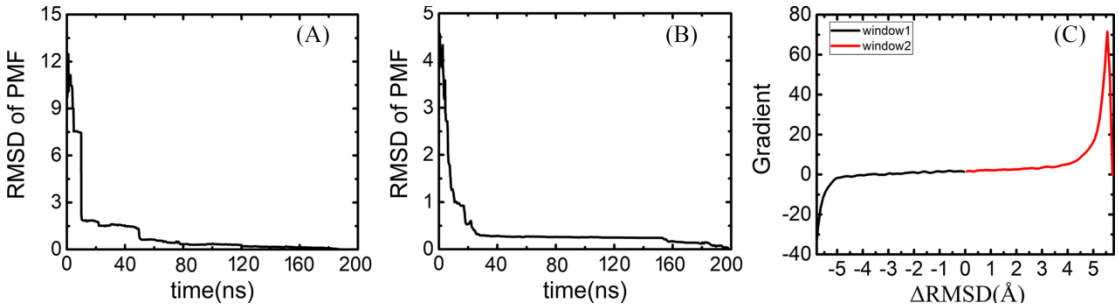

Fig. S4 (A and B) Time evolution of the root-mean-square deviation (RMSD) over the PMF depicting B- to A-DNA transition without azobenzene. (C) The gradients of the free-energy calculations in two windows.

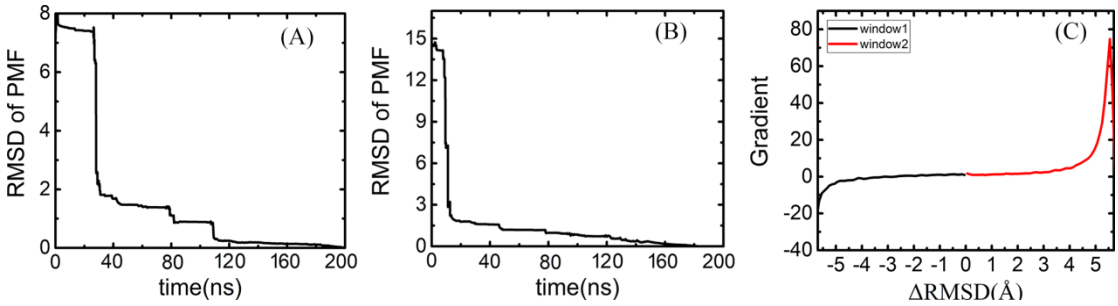

Fig. S5 (A and B) Time evolution of the root-mean-square deviation (RMSD) over the PMF depicting B- to A-DNA transition with *trans*-azobenzene intercalating from minor groove (mode 1). (C) The gradients of the free-energy calculations in two windows.

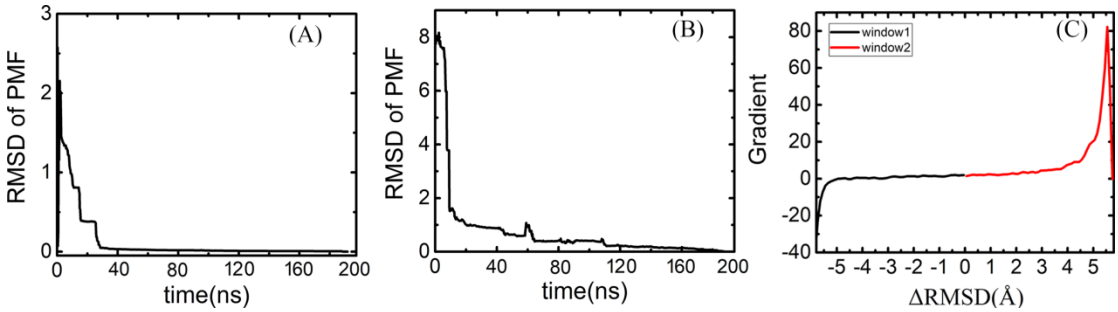

Fig. S6 (A and B) Time evolution of the root-mean-square deviation (RMSD) over the PMF depicting B- to A-DNA transition with *trans*-azobenzene intercalating from major groove (mode 2). (C) The gradients of the free-energy calculations in two windows.

Binding Modes of *cis*-azobenzene. To investigate the binding mode of *cis*-azobenzene, two preliminary simulations were performed. The results of the two 40-ns MD simulations for the DNA-azobenzene (*cis* form) complexes, wherein the ligand intercalates from the minor (mode 1) and the major (mode 2) grooves,

demonstrate that both of them cannot exist. As shown in Fig. S1A, for mode 1, the head benzene ring of *cis*-azobenzene separated from the nearest-neighboring base pairs in 40-ns MD simulations, while the azobenzene can stay in the minor groove. Additional 300-ns MD simulations show that minor-groove binding pattern is persistent. For mode 2, the azobenzene deviated from the base pairs and attached to DNA without specific binding site in 40-ns simulations. Compared with the planar *trans* form, non-planar *cis* form has a larger molecular size, acting as a steric hindrance to intercalate between two adjacent base pairs. Four main parameters are chosen to describe the conformational changes of DNA computed over the last 100-ns trajectories in the additional 300-ns simulations. As shown in Fig. S2, there are no appreciable changes compared with native DNA when combined with *cis*-azobenzene. It can be, therefore, inferred that *cis*-azobenzene can bind with DNA in minor groove, while there is no significant effect on the conformational changes of DNA.

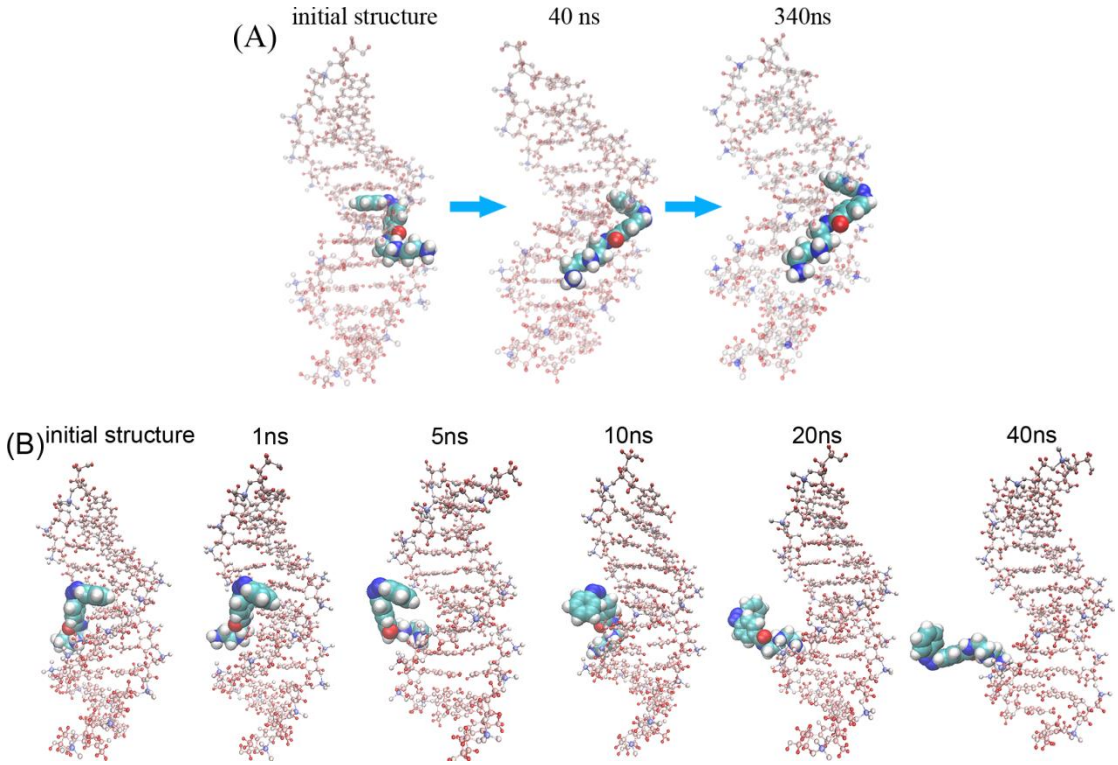

Fig. S7 MD simulations for two possible binding modes of *cis*-azobenzene intercalating into DNA. (A) Milestones of the structural changes of mode 1 (the head benzene ring of *cis*-azobenzene intercalats from the minor groove, leaving its cationic tail located in the minor groove) obtained from an MD simulation over a 340 ns period. (B) Milestones of the structural changes of mode 2 (the head benzene ring of *cis*-azobenzene intercalats from the major groove, leaving its cationic tail located in the major groove) obtained from a 40-ns MD simulation.

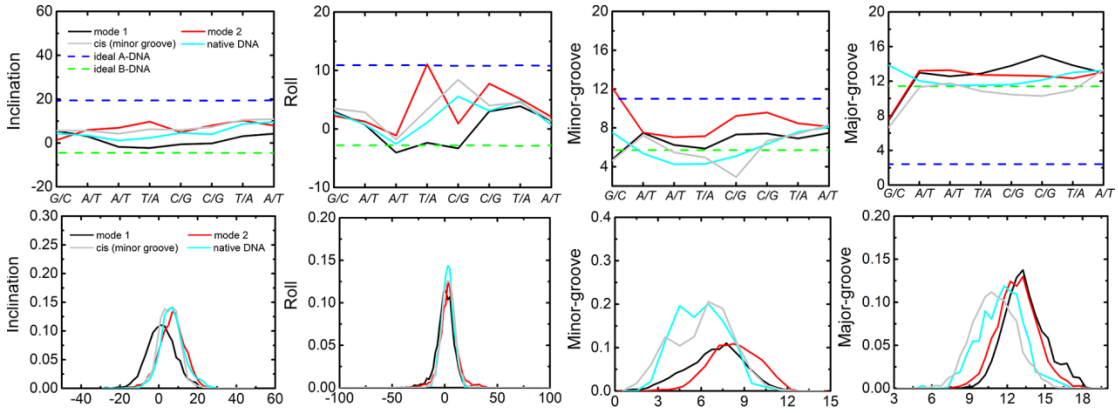

Fig. S8 Average values and populations of main parameters of DNA computed over the last 100 ns simulations for the minor-groove binding mode of the DNA-*cis*-azobenzene complexes.

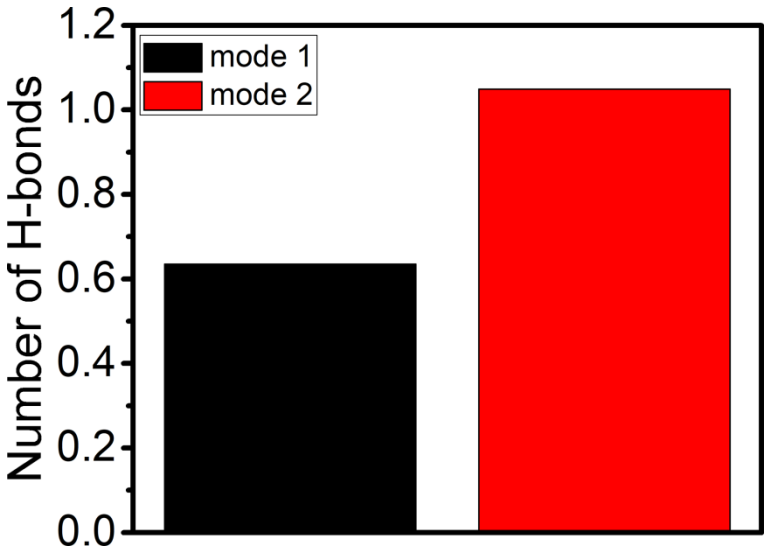

Fig. S9 Average values of the number of H-bonds between the DNA and *trans*-azobenzene for different binding mode. (mode 1: intercalating the planar aromatic rings from the minor groove, mode 2: intercalating the planar aromatic rings from the major groove)