

Supporting Information

Investigation of Dynamical flexibility of D5SIC-DNAM inside DNA duplex in Aqueous Solution: A Systematic Classical MD Approach

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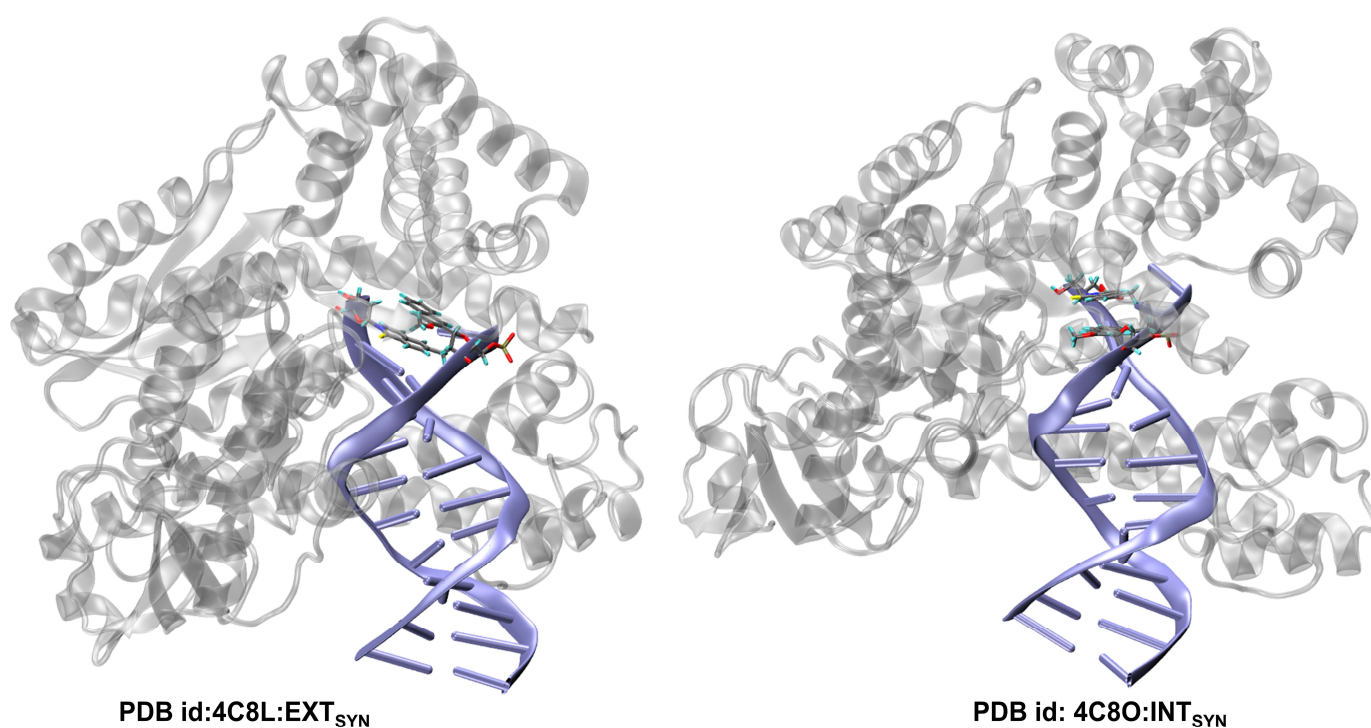


Figure S1. 3D representation of the crystal structures of DS-DN incorporated DNA in Taq polymerase in the post-insertion site.

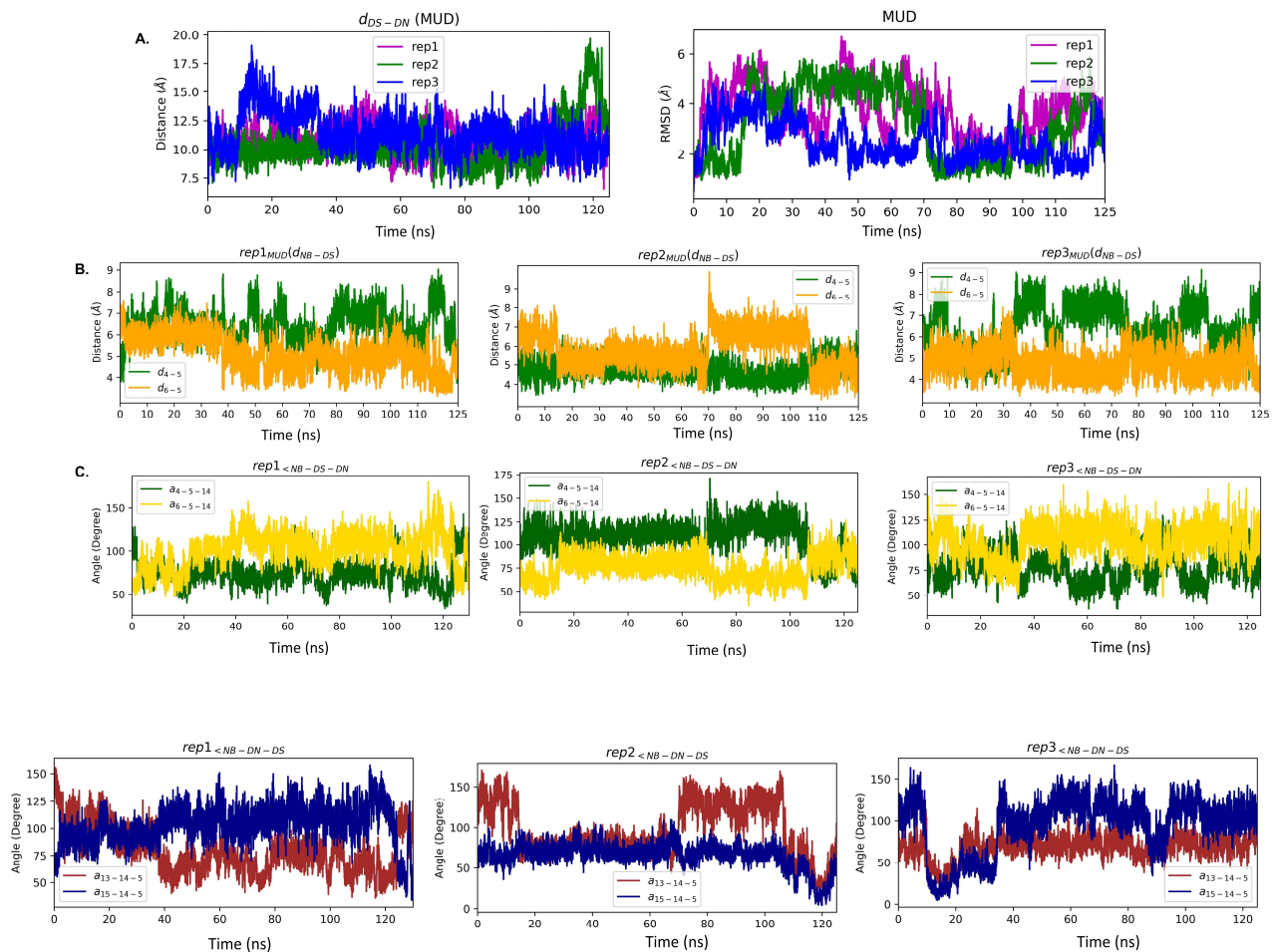


Figure S2. A. DS-NB (left), RMSD (right) B. NB-DS, C. <UB-NB-NB> values obtained from AMOEBA force fields.

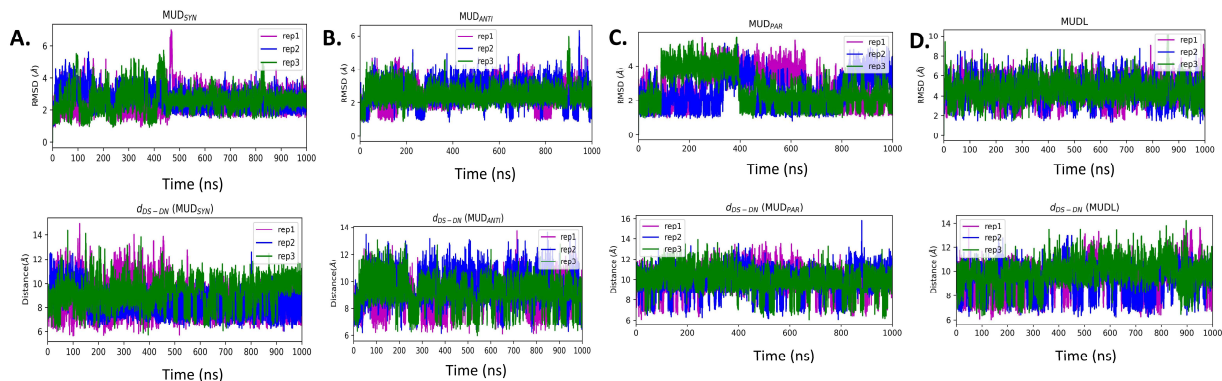


Figure S3. DS-DN distance and RMSD values for A. MUD_{SYN}, B. MUD_{ANTI}, C. MUD_{PAR} and D. MUD_L structures obtained from 1 μ s simulation employing AMBER force fields.

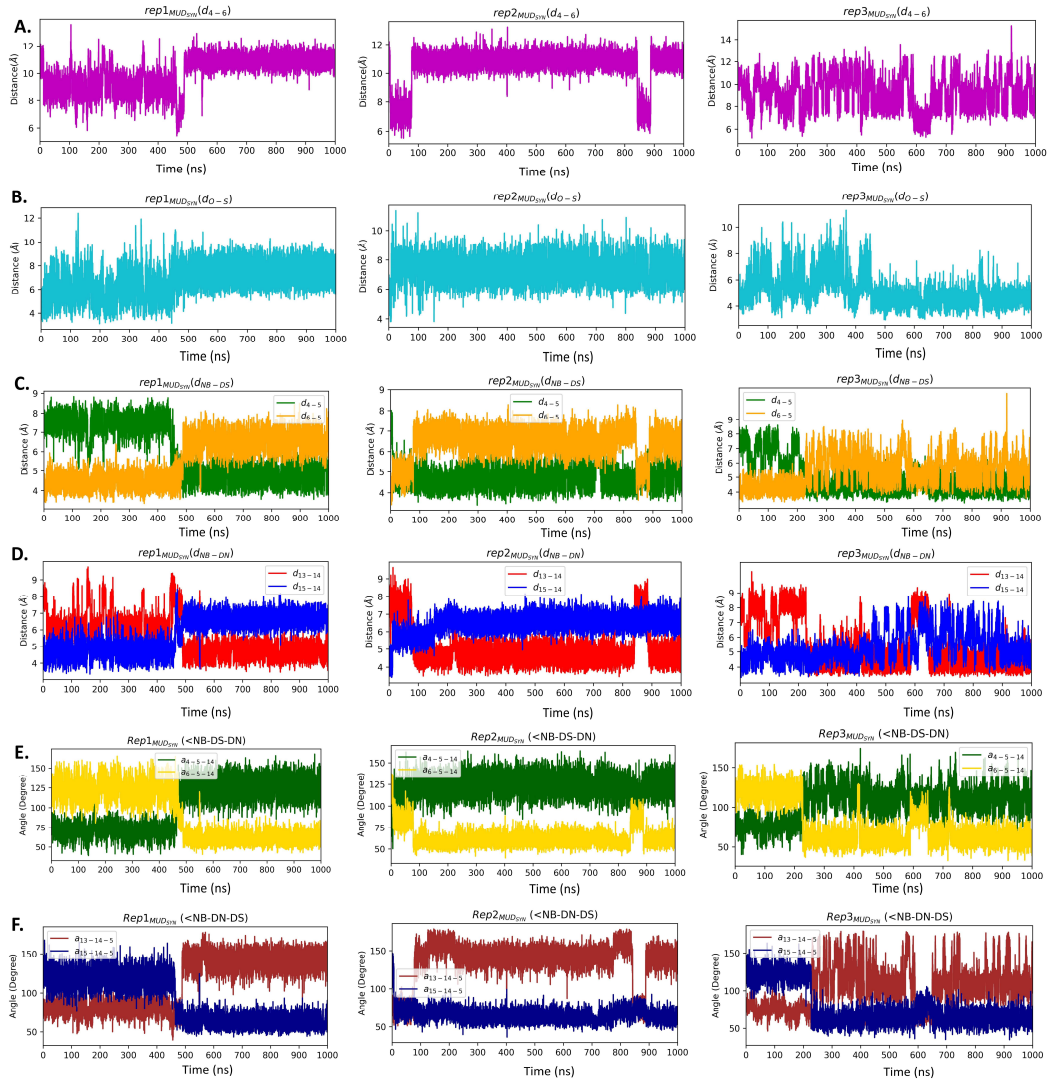


Figure S4. A) d_{4-6} , B) O-S, C) DS-NB, D) DN-NB, E) $\langle NB-DS-DN \rangle$, F) $\langle NB-DN-DS \rangle$ values for MUD_{SYN} obtained from AMBER force fields.

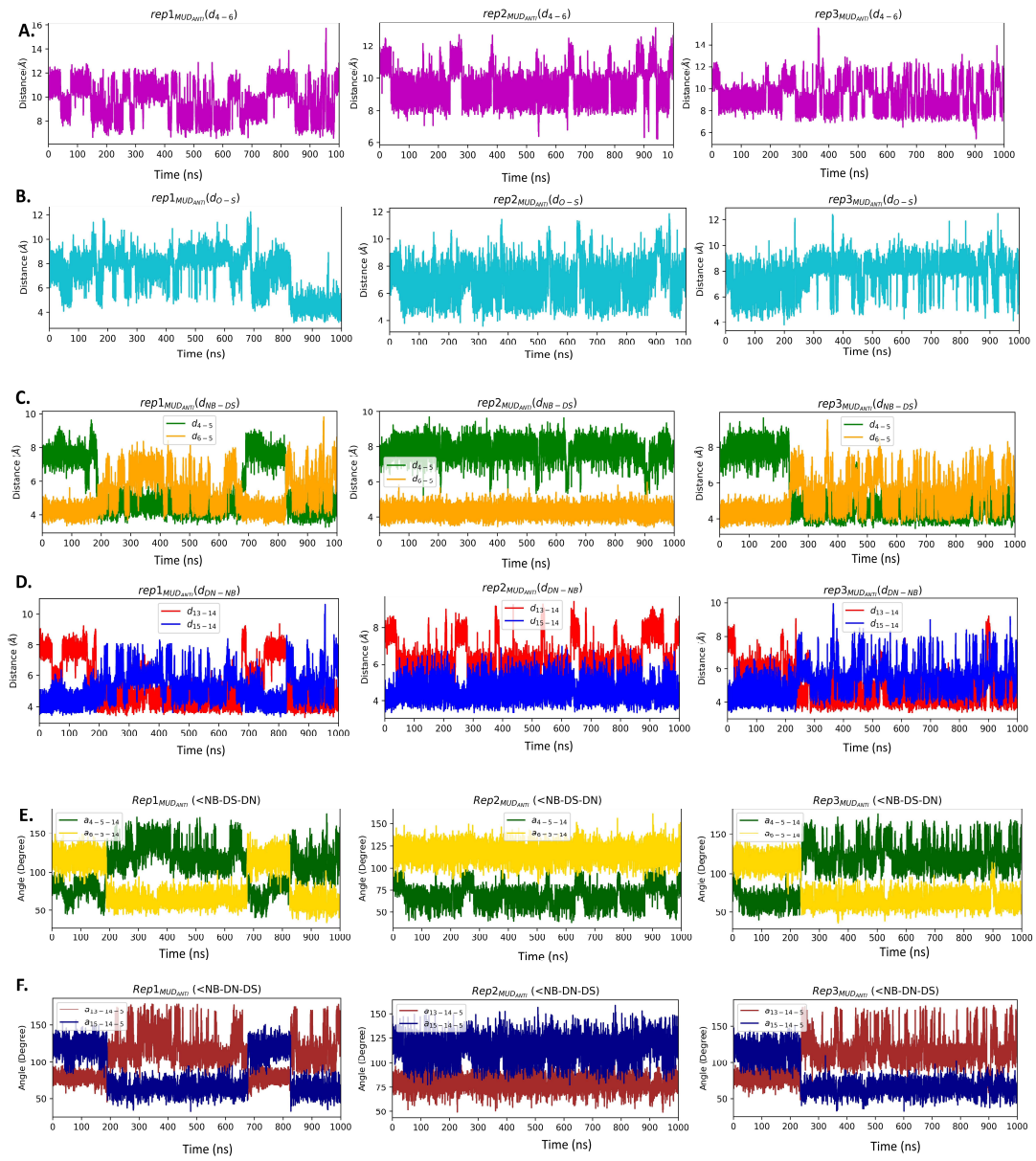


Figure S5. A) d_{4-6} , B) d_{O-S} , C) d_{NB-DS} , D) d_{DN-NB} , E) $\angle_{NB-DS-DN}$, F) $\angle_{NB-DN-DS}$ values for MUD_{ANTI} obtained from AMBER force fields.

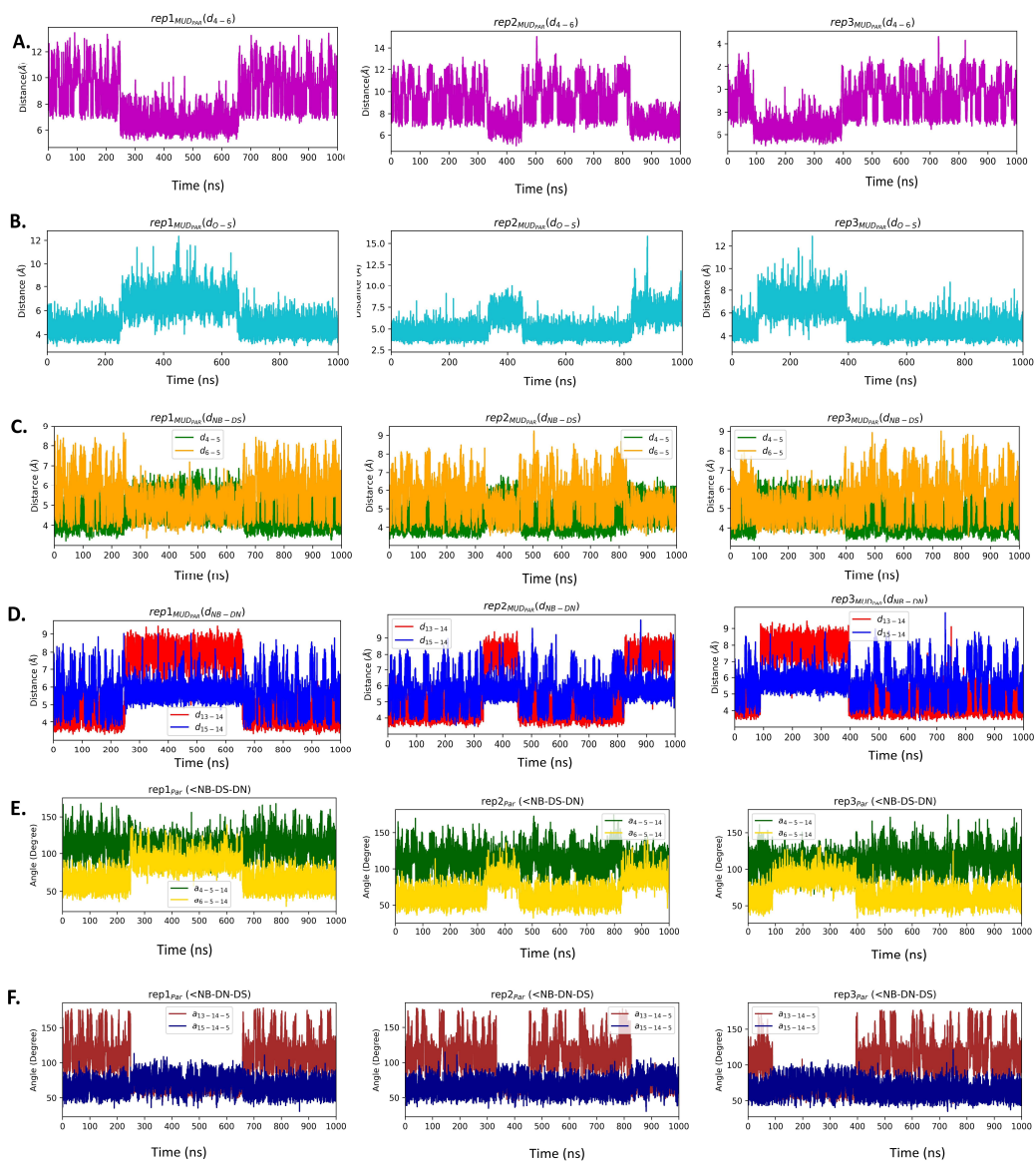


Figure S6. A) d_{4-6} , B) O-S, C) DS-NB, D) DN-NB, E) $\angle NB-DS-DN$, F) $\angle NB-DN-DS$ values for MUDPAR obtained from AMBER force fields

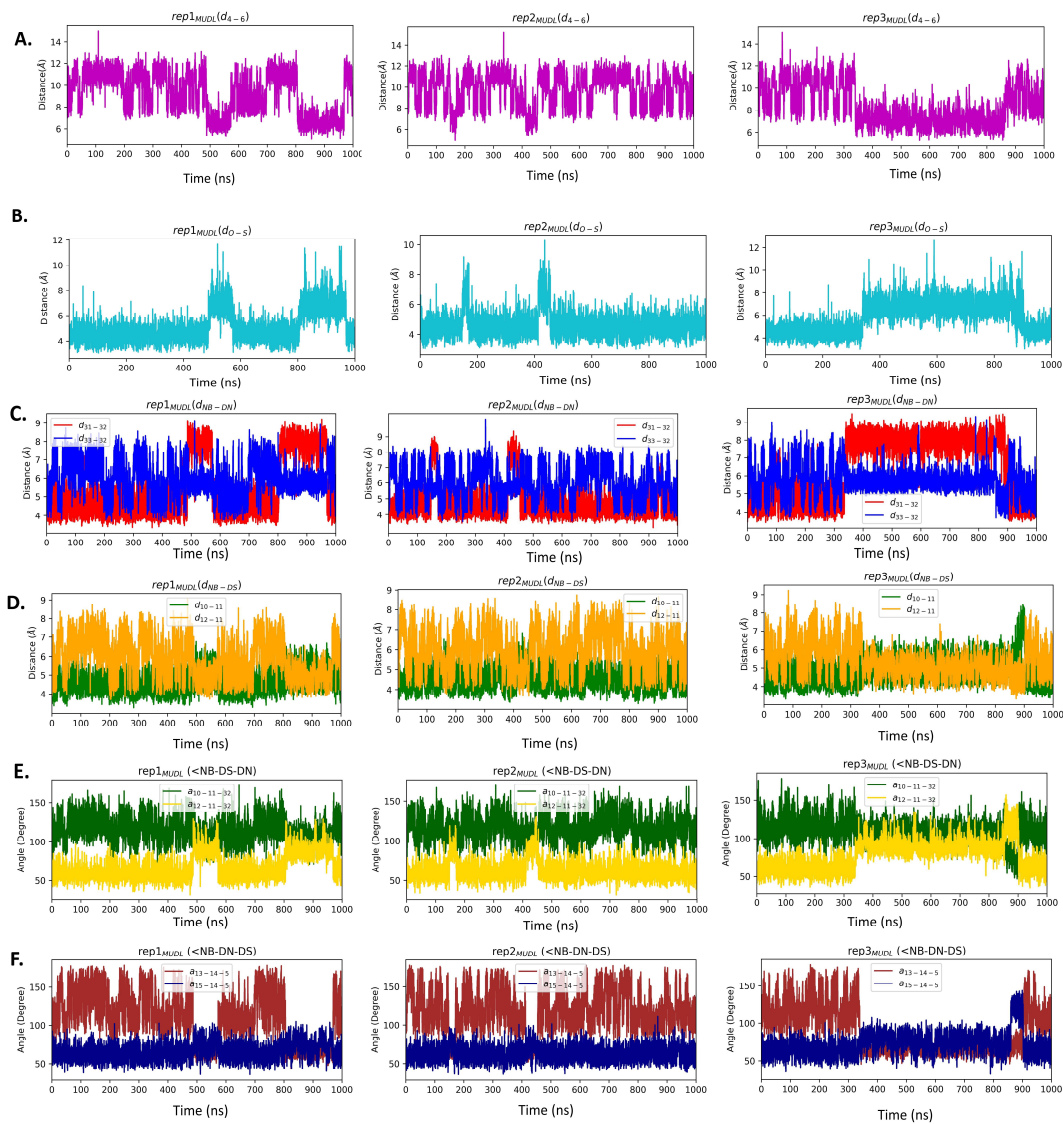


Figure S7. A) d_{4-6} , B) O-S, C) DS-NB, D) DN-NB, E) <NB-DS-DN, F) <NB-DN-DS values for MUDL obtained from AMBER force fields.

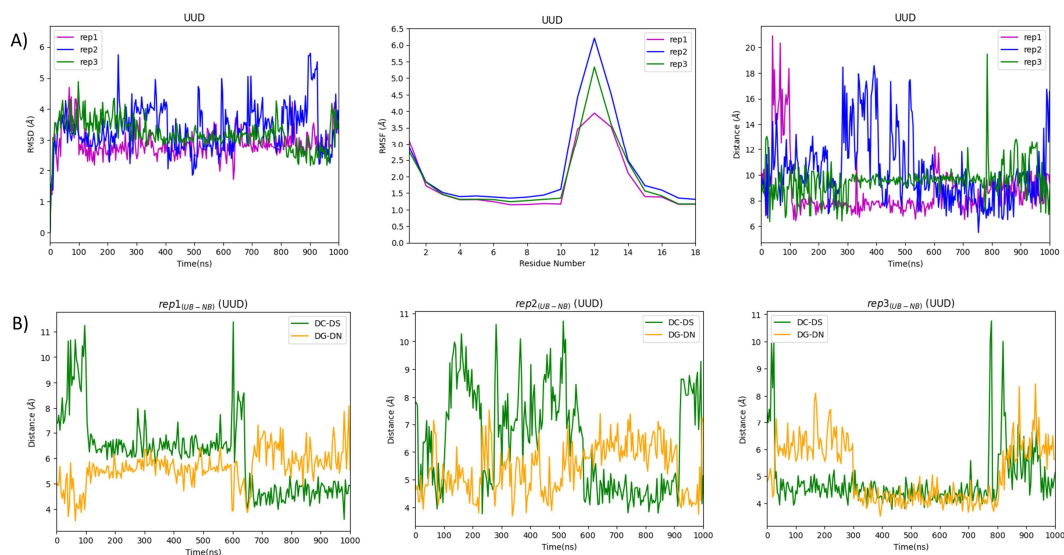


Figure S8. A) RMSD (left), RMSF (middle), d_{DS-DN} and B) d_{DS-NB} values of UUD structures obtained from obtained from 1 μ s simulation employing AMBER force fields.

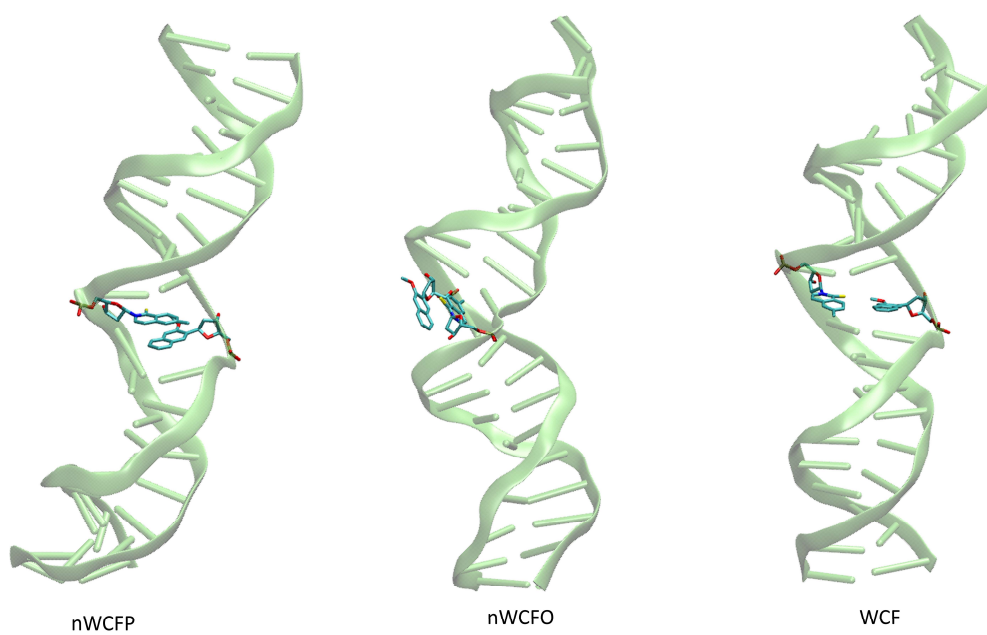


Figure S9. Different conformers obtained from long UBPs-incorporated DNA duplex.

Table S1. Fragmentation of energies at ω B97xD/ 6-311++G(d,p) between DS and DN. Energy values are given in kcal/mol.

UBP	Electrostatic	Dispersion	Induction	Exchange	Total
SYN	-8.8	-17.5	-3.3	18.9	-10.8
ANTI	-7.2	-15.3	-3.0	16.4	-9.1