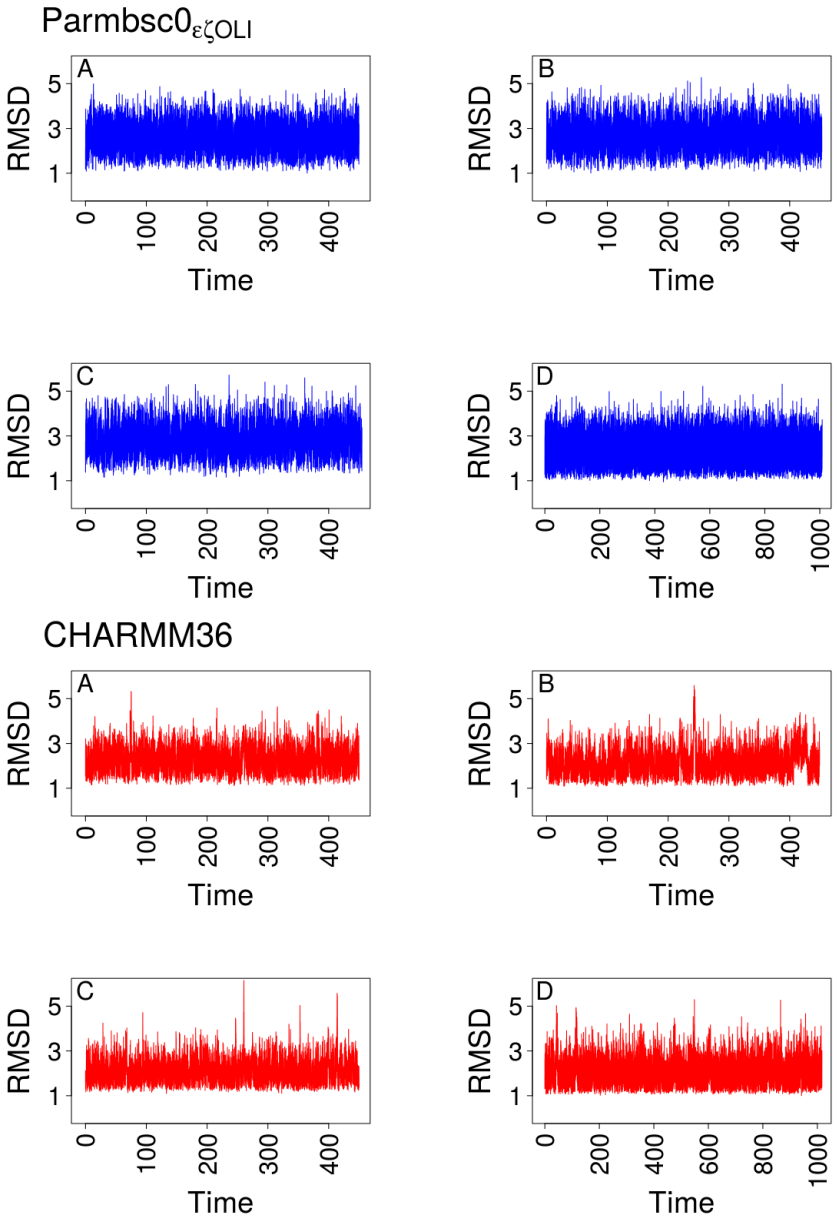
S1 Fig. RMSD along the trajectories with Parmbsc0$_{\varepsilon\zeta OLI}$ and CHARMM36.



The Root Mean Square Deviations (RMSD, Å) are plotted in function of time (ns) for four DNA dodecamers (A: Oligo1; B: Oligo 2; C: Oligo 3; D: Oligo 4) simulated with either Parmbsc0$_{\varepsilon\zeta OLI}$ (top panels, in blue) or CHARMM36 (bottom panels, in red) force fields. RMSDs were calculated on the heavy atoms of the simulated structures -discarding the first and last base-pairs- and reference canonical B-DNAs generated by AMBER.

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