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Supporting Material

Title: Twist propagation in dinucleosome arrays

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Table S1: Table of physical parameters in the MC model.

Parameter	Description	Value
l_0	Equilibrium DNA segment length	3.0 nm
κ_{str}	DNA stretching constant	100 $k_{\mathrm{B}}T/l_0^2$
κ_{bend}	DNA bending constant	$L_{\mathrm{p}}k_{\mathrm{B}}T/l_0$
κ_{Tw}	DNA torsional rigidity constant	300 pN nm^2
κ_{ev}	Excluded volume interaction constant	0.001 $k_{\mathrm{B}}T$
σ	Excluded volume distance (all beads)	1.5 nm
L_{p}	DNA persistence length	50 nm
ϵ	Dielectric constant of solvent	80
κ_{DH}	Inverse Debye screening length	0.3319 nm^{-1}
T	Temperature	293 K

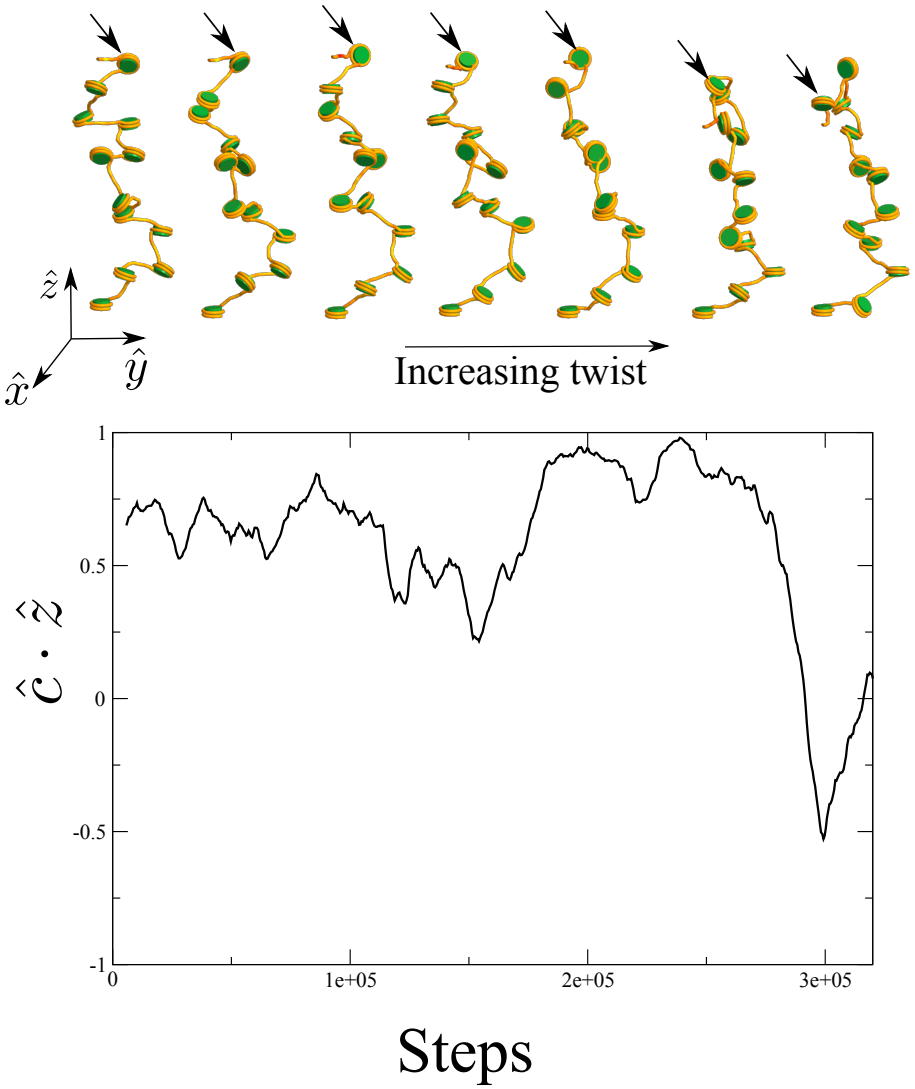

Figure S1: (Upper panel) Series of snapshots from a MC simulation of a 12-nucleosome array subjected to twist through the end linker (note that the first nucleosome is held fixed). With increasing applied twist, the last nucleosome, as indicated by the arrow, is observed to flip in a manner similar to that observed in dinucleosome arrays. (Lower panel) Plot of the dot product $\hat{c} \cdot \hat{z}$ as a function of time for the above nucleosome illustrating flipping. Here $\hat{c}$ represents a unit vector normal to the plane of the indicated nucleosome and $\hat{z}$ is a unit vector pointing along the z direction.

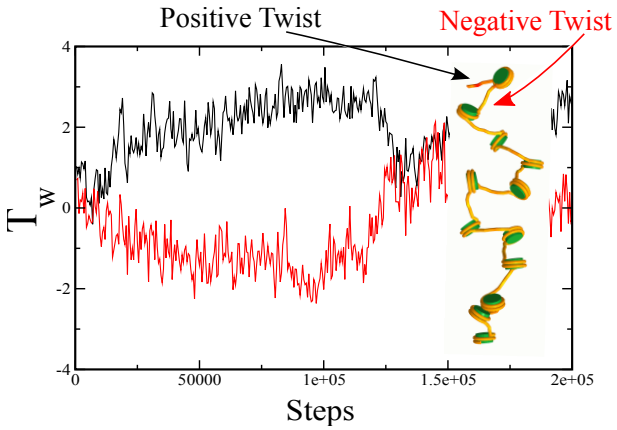

Figure S2: Twist inversion observed in a 12 nucleosome array subjected to twist. Application of twist (positive twist on linker is colored red) on the first linker leads to inverted twist in the second linker (negative twist on linker is colored yellow). The black and red lines show the time-evolution of the net twist observed in the first and second linkers, respectively.