Symbol	Description		Value (simulation units)
Δt	time step of numerical integration of Eq. (S1)		0.01 τ_{LJ}
T	total run time of each simulation		8×10^4 τ_{LJ}
m_i	mass of bead i	chromatin bead	1
		protein complex	1
γ_i	friction coefficient	chromatin bead	2
		protein complex	2
d_{ii}	diameter of bead i	chromatin bead	σ
		protein complex	σ
R_0	equilibrium FENE bond length for chromatin beads		1.6 σ
K_{FENE}	energy of the FENE bonds		30 k_BT
K_{BEND}	energy of the bending interaction for the chromatin fibre		4 k_BT
r_{cut}	cut-off for Lennard-Jones interaction between protein complex and protein binding chromatin bead		1.4 σ
ε	energy for the interaction between protein complexes and binding chromatin beads		5.39 k_BT ($\varepsilon' = 10\ k_BT$)
r_{contact}	separation below which two chromatin beads are defined as being "in contact", i.e. we assume the beads are interacting in a way analogous to that which would give a signal in a 3C experiment		2.75 σ (44 nm)

Additional file 15: Table S1: **List of all simulation parameters.** Parameters are given in simulation units; see Additional file 2: Supplementary Methods for details of how these relate to physical units.