SUPPORTING INFORMATION

DNA-DNA interactions in bacteriophage capsids are responsible for the observed DNA knotting

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Polar and apolar cholesteric interactions: effects on DNA packaging

As discussed in the main paper, the symmetry of the DNA double-helix required the consideration of an *apolar* cholesteric potential which introduced a bias for the twist angle, α, formed by two contacting DNA strands. Using the same notation of the main paper, the twist angle is defined as:

$$\tan\alpha = [(\vec{b}_i \times \vec{b}_j) \cdot \vec{d}_{ij}]/[(\vec{b}_i \cdot \vec{b}_j)|\vec{d}_{ij}|] \ . \tag{1}$$

The apolar character of the bias is evident from the consideration that the reversal of the contacting segments, $\vec{b}_i \to -\vec{b}_i$ and/or $\vec{b}_j \to -\vec{b}_j$ leaves α unchanged.

While this yields the correct treatment for DNA, as the double helix cannot be oriented, it is interesting to consider the case of a *polar* interaction, which is simply obtained by replacing the previous definition of α with:

$$\tan\alpha = [(\vec{b}_i \times \vec{b}_j) \cdot \vec{d}_{ij}]/[|\vec{b}_i \cdot \vec{b}_j||\vec{d}_{ij}|], \tag{2}$$

which is not invariant anymore under the reversal of only one of the contacting strands.

To this purpose we carried out several hundreds packaging simulations of the P4-half genome under the chiral potential. The polar character of the interaction changes a number of important aspects of the DNA organization while leaving other unchanged. In particular, the order at the surface is preserved, but virtually no inversion of the winding direction is found. While, consistent with a theorem by Alexander which says that every knot can be drawn as a braid with no change of winding direction [1] the systematic winding directionality does not rule out *per se* the occurrence of twist or achiral knots, the knot spectrum was found to be still biased towards torus and chiral knots. For example the 3_1, 5_1, 7_1, 8_{19} and 9_1 torus knots account for $\sim 40\%$ of non-trivial (possible composite) knots of less than 10 crossings. The data pertain to a set of 1000 packaging simulations carried out for $k_c = 0.25\, K_B T$, Δ=5nm and $\alpha_0 = 1^\circ$).

The differences are aptly summarised in SI Figure 1 which shows typical configurations for the *full* genome of P4 packaged under three different conditions: no cholesteric interaction, apolar cholesteric interation and polar cholesteric interaction. The cholesteric, twist, interaction strength, range and biasing angle are the same mentioned above.

References

1. Alexander, A (1923) A lemma on systems of knotted curves. *Proc. Natl. Acad. Sci. USA* 9:93-95

Legends for SI figures and videos

Supporting Information Figure 1. Sample configurations of the fully-loaded DNA generated with (a) no cholesteric interation, (b) with the apolar cholesteric interaction and (c) with the polar version of the interaction. The configurations pertain to the full P4 genome, which corresponds to 1360 beads. For clarity of representation the model DNA is not shown with a bead representation but as a tube. The tube diameter matches the diameter of the beads used in Fig. 2 of the main manuscript, which corresponds to the dsDNA hydration radius 2.5nm. The diameter of the enclosing spherical capsid (not shown) is $\sim$50nm. In each of the three panels the figures offer a top, front and sliced view of the configurations.

Supporting Information Figure 2. Projection view of the fully-packaged model P4 genome configuration shown in Fig. 2b of the main paper. The configuration is represented with its projected centerline so to highlight the arrangement of the chain in the capsid interior, in a fashion analogous to cryo-EM images (where signal comes from all packed layers at the same time).

Supporting Information Figure 3. (a) Distribution of the local density of DNA for fully-packaged configurations of the entire P4 genome in the absence of the cholesteric potential. (b) Distribution of the local density of DNA for fully-packaged configurations of the half P4 genome in the absence of the cholesteric potential. In both cases a non neglibile part of the chain is packed at densities inside the cholesteric range $160-380$ mg/ml. This result indicates the necessity of considering a cholesteric interaction between DNA strands. With reference to locally hexagonal arrangements of dsDNA strands, the $160-380$ mg/ml density range corresponds to DNA interaxial distances going respectively from 4.9nm to 3.2nm, so that the typical separation of neighbouring DNA portions in both (a) and (b) is above 3nm.

Supporting Information Figure 4. Spectrum of the simplest knot types of fully-packaged half P4 genome obtained for $k_c = 1\,K_BT$, Δ=5nm and for three different values of the reference twist angle: (a) $\alpha_0 = 0°$; (b)$\alpha_0 = 1°$ deg; (c) $\alpha_0 = 10°$. The total knot population size for the three cases are (a) 200, (b) 250 and (c) 380. The error bars denote the statistical uncertainty computed using the Poissonian statistics. The spectra of case (a) and (b) are fully compatible within statistical uncertainty. All three spectra indicate a preferential bias towards the formation of torus knots.

Supporting Information Figure 5. Fraction of left-handed and right-handed knots among the set of torus knots. Analyzed configurations included knots of up to 16 crossings after simplification that were either prime torus knots or prime components of composite knots where all factors were torus knots. The three panels are associated to various values of the reference twist angle: (a) $\alpha_0 = 0°$; (b)$\alpha_0 = 1°$; (c) $\alpha_0 = 10°$. For all cases $k_c = 1\,K_BT$ and Δ=5nm.

The error bars denote the uncertainty obtained using the binomial statistics. A highly significant bias is observed for $\alpha_0 = +10°$.

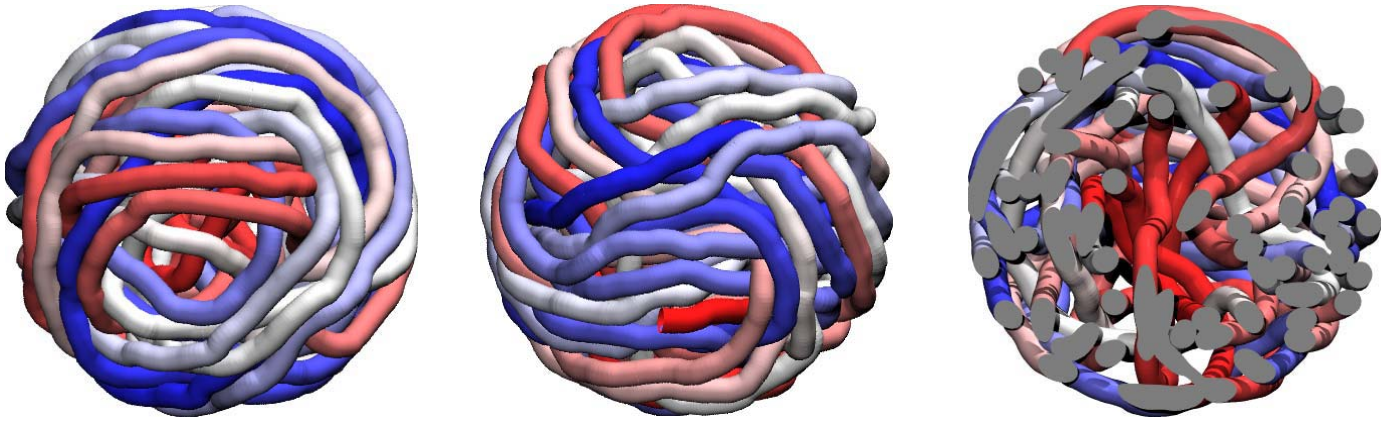
Supporting Information Figure 6. Average internal energy (with omission of the contribution from the chain connectivity, FENE, potential) as a function of the topological complexity of the configurations of the fully-loaded P4 half-genome. The topological complexity is conveyed by the minimal number of crossings after geometrical simplification of the closed configurations. On average, knots with 3, 5 and 7 crossings (which are dominated by torus knots) appear energetically favoured over non-torus knot types with comparable complexity.

Supporting Information Figure 7. Breakup of the internal energy of the DNA still inside the capsid during spontaneous ejection. The bending energy and cholesteric energy provide the dominant ejection force compared to the repulsive self-interaction.

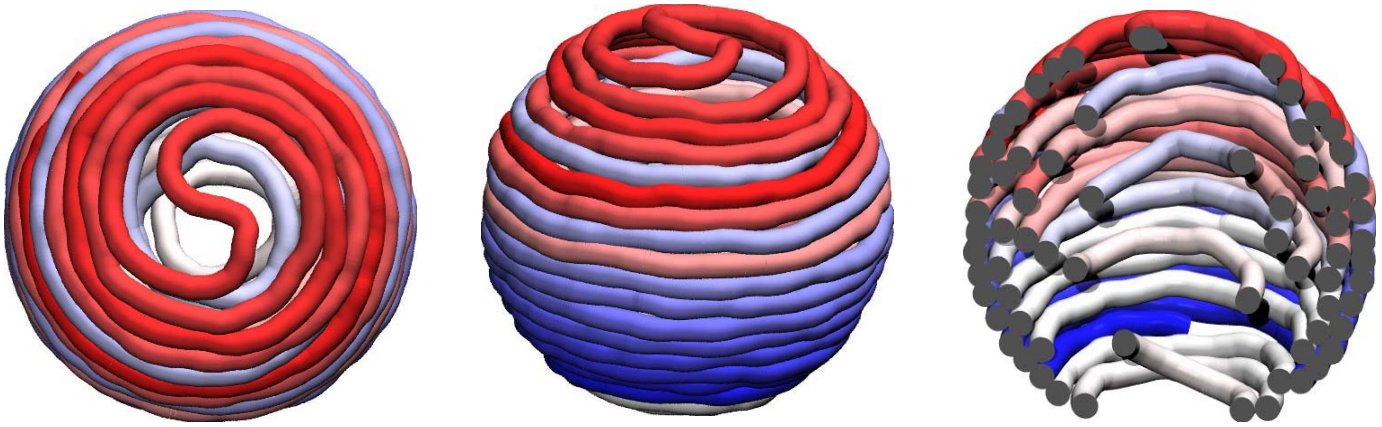
Supporting Information Video 1. The video illustrates three packaging simulations of the half-P4 genome.

Supporting Information Video 2. The video illustrates three ejection simulations of the half-P4 genome. The initial conformations correspond respectively to: an unknot, a 9_1 knot and a complex knot with 23 crossings after simplification. All ejection processed are followed up to release of 50% of the genome. Beyond this stage, the chain portion still inside the capsid is manifestly disentangled and is ejected without any significant geometrical or topological hindrance.

(a)



(b)



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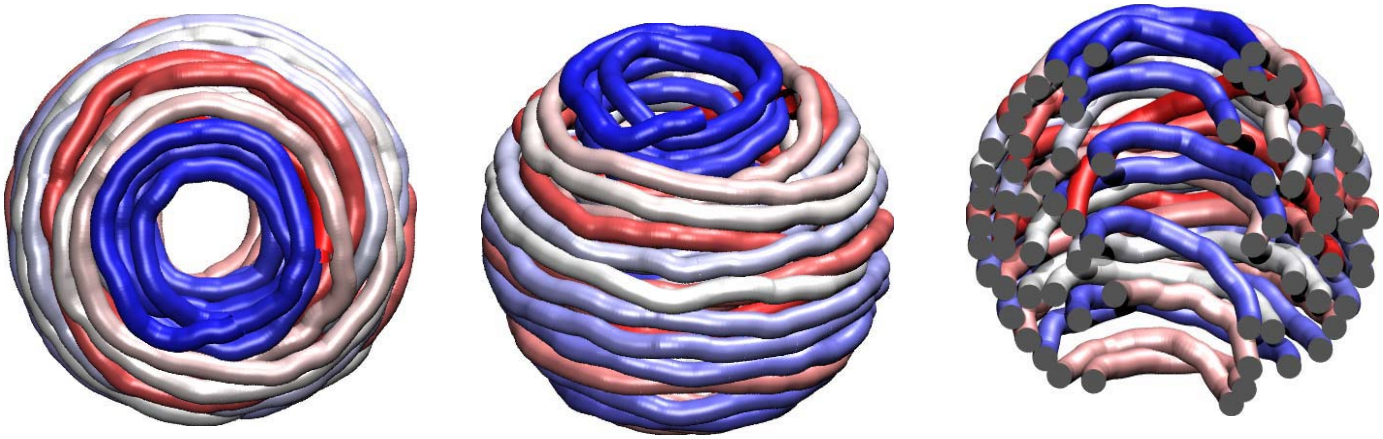

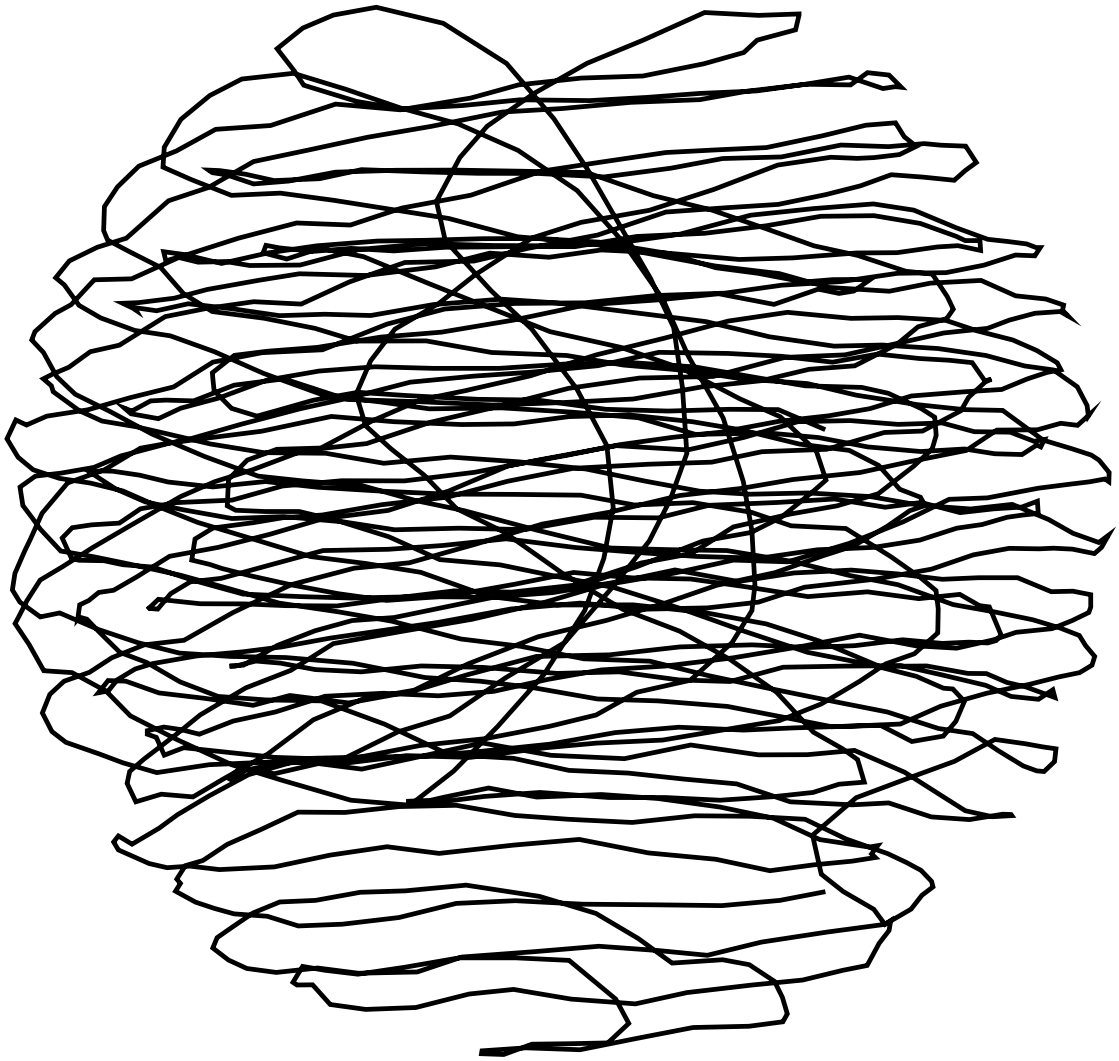

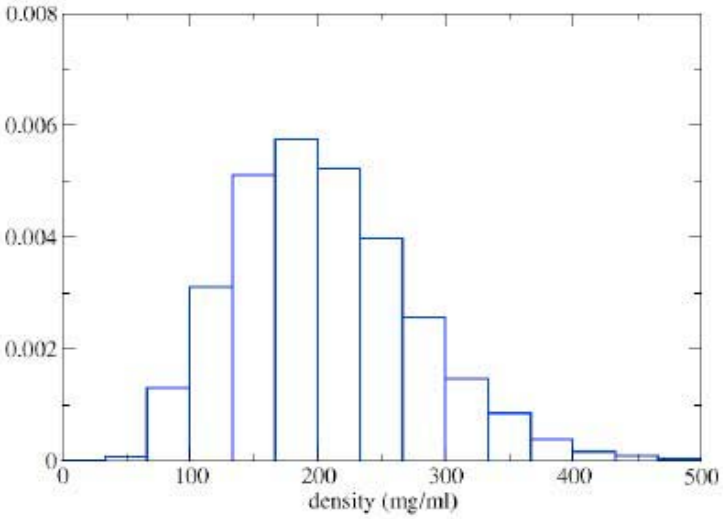
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0.004
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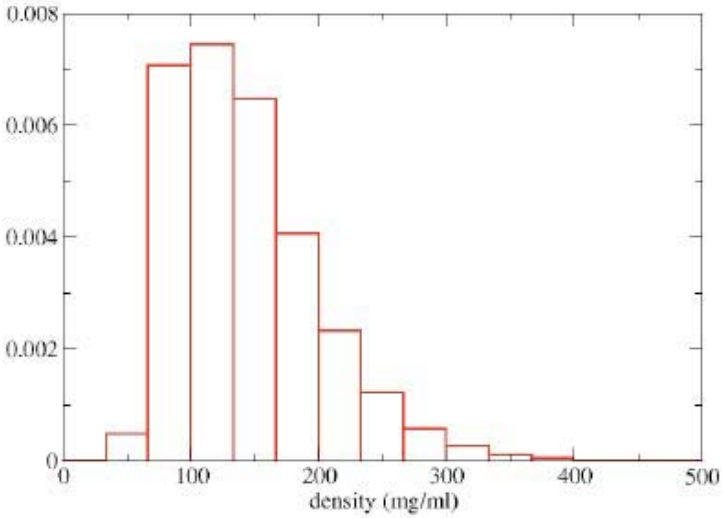
400
500
density (mg/ml)

(a)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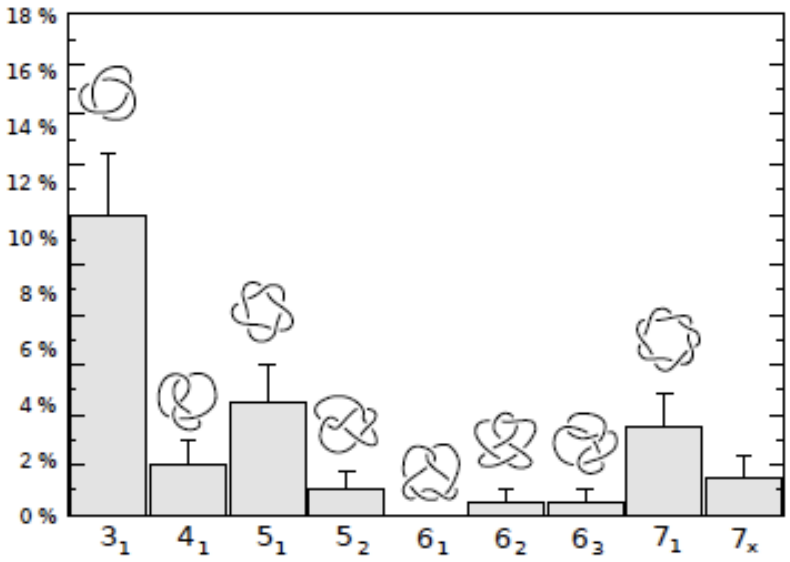
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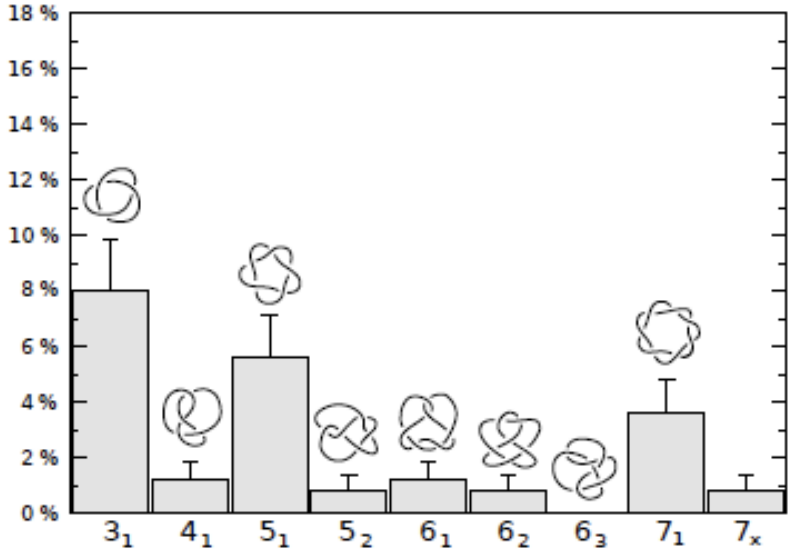
6 1
6 2
6 3
7 1
7 x

(a)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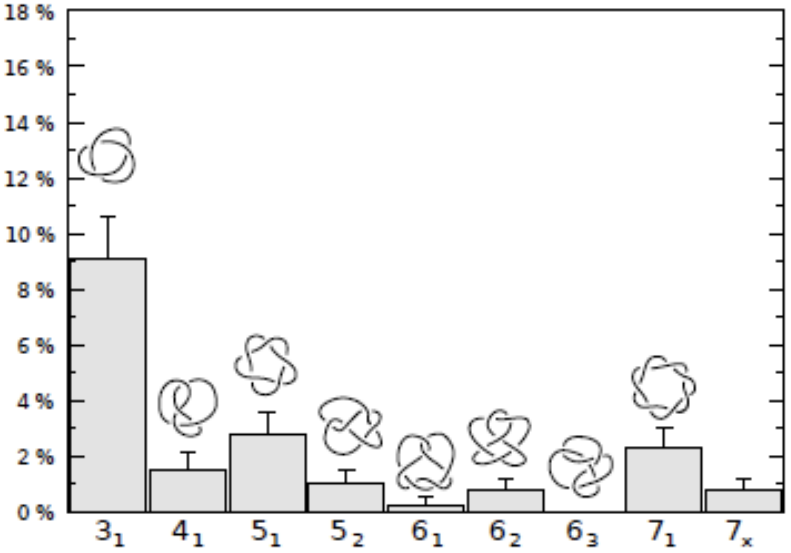
(b)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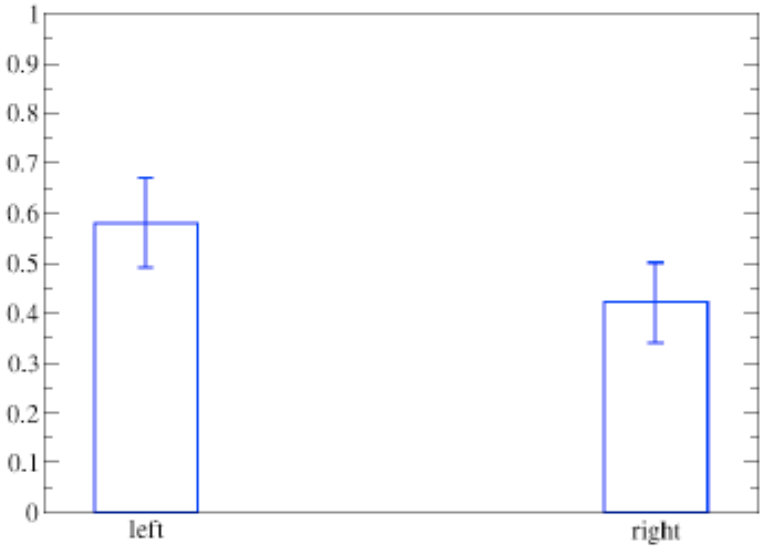
7 1
7 x

(c)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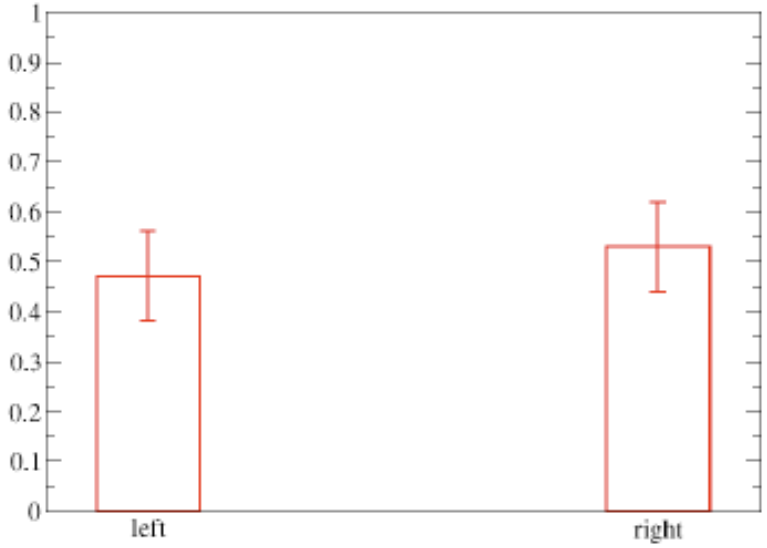
0.5
0.4
0.3
0.2
0.1
0
left
right

(a)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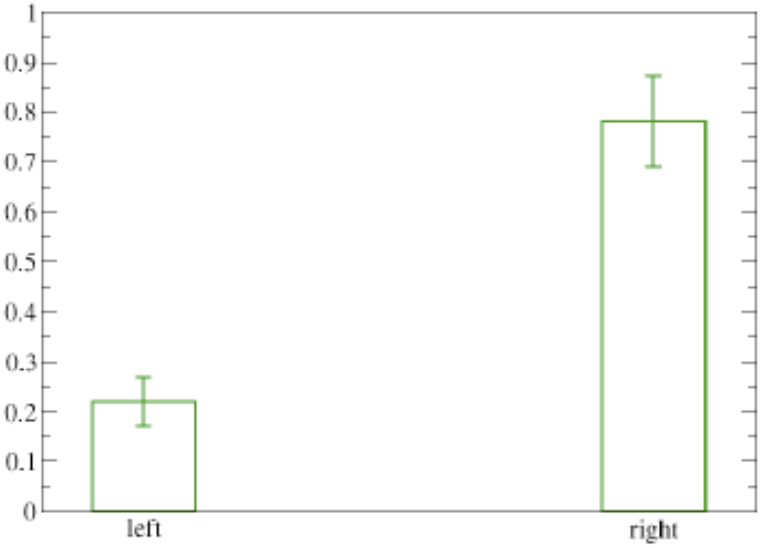
(b)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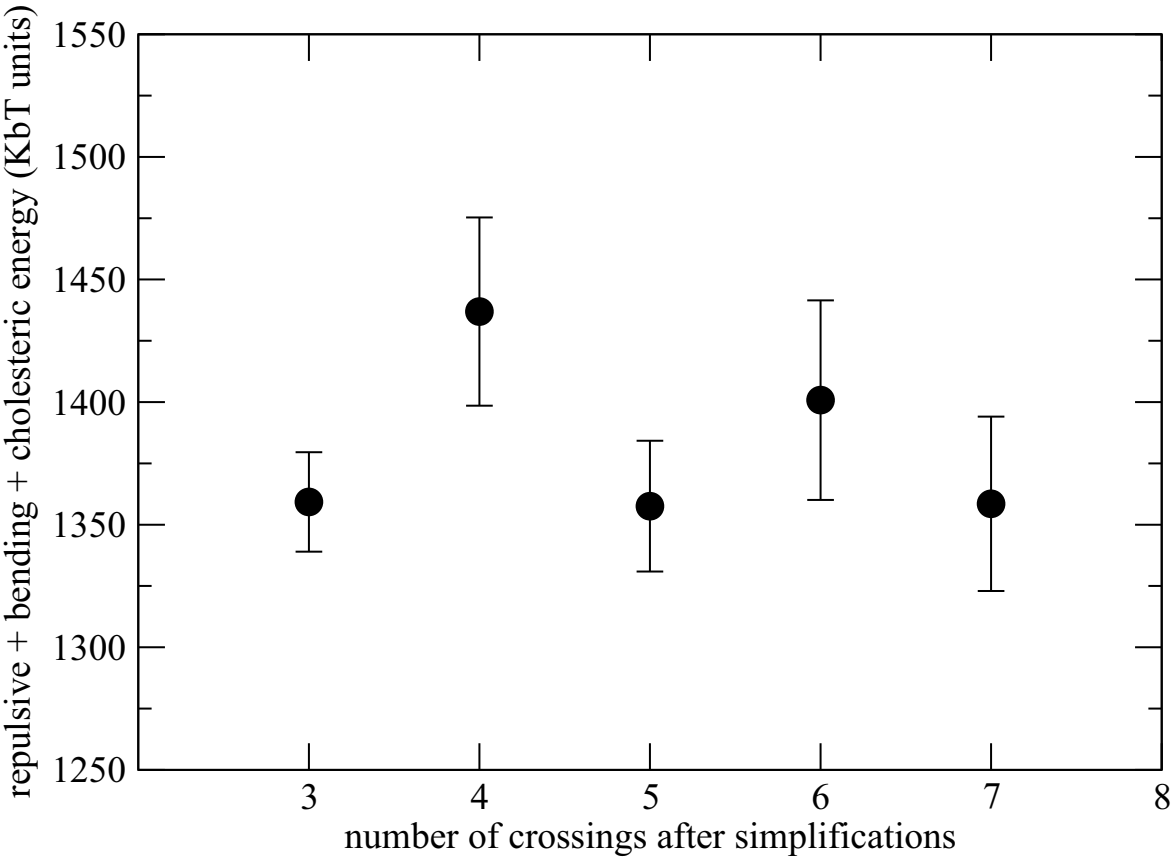
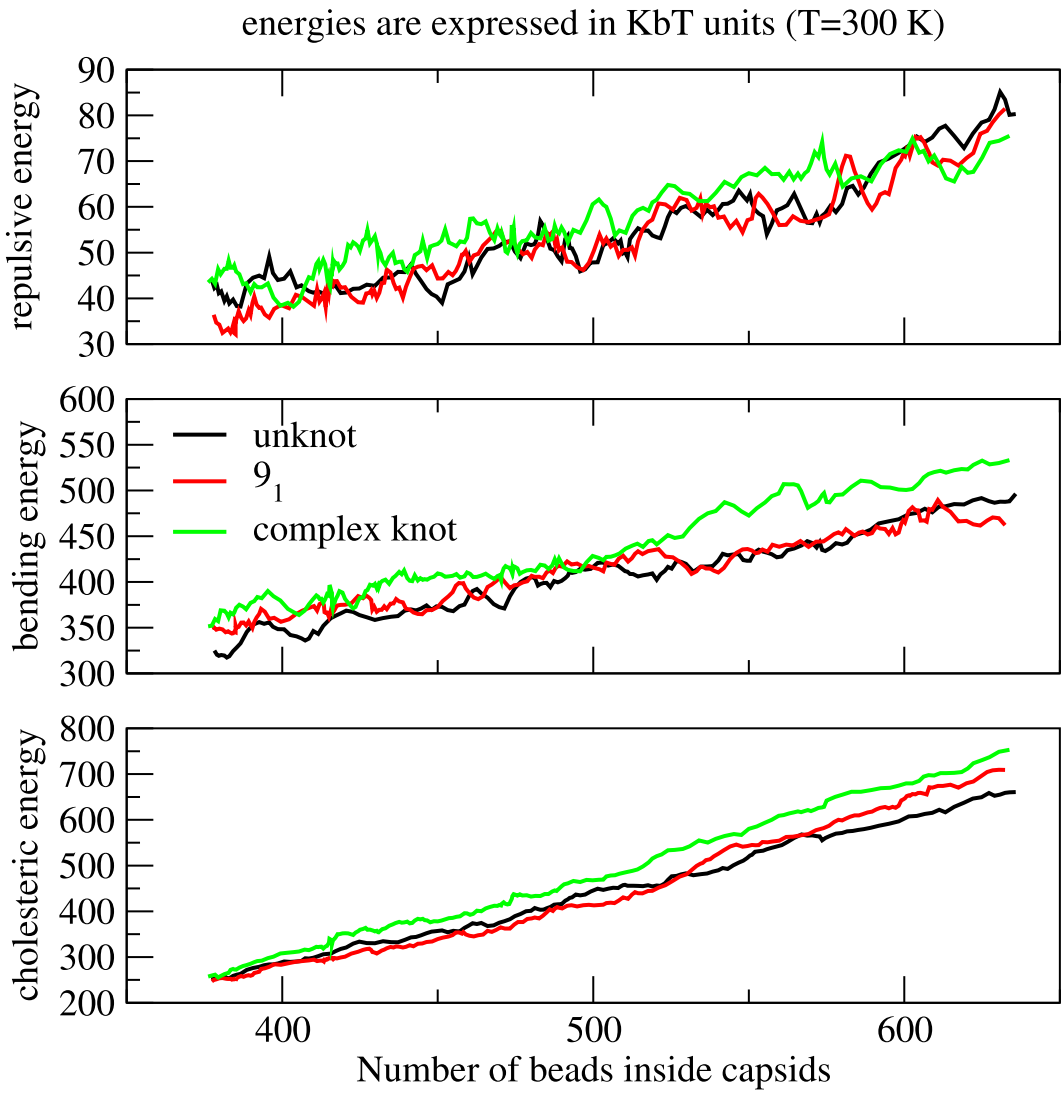
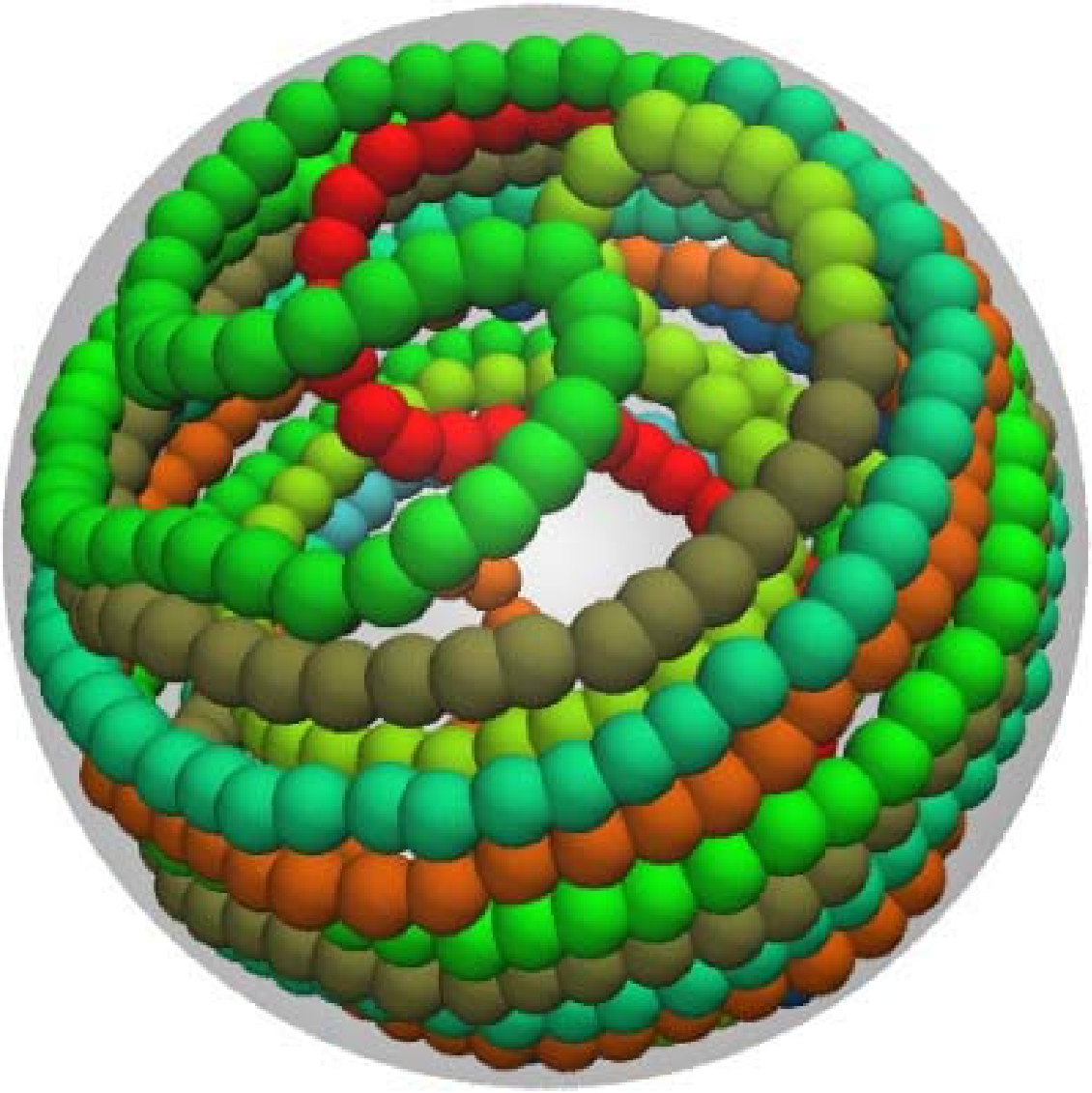
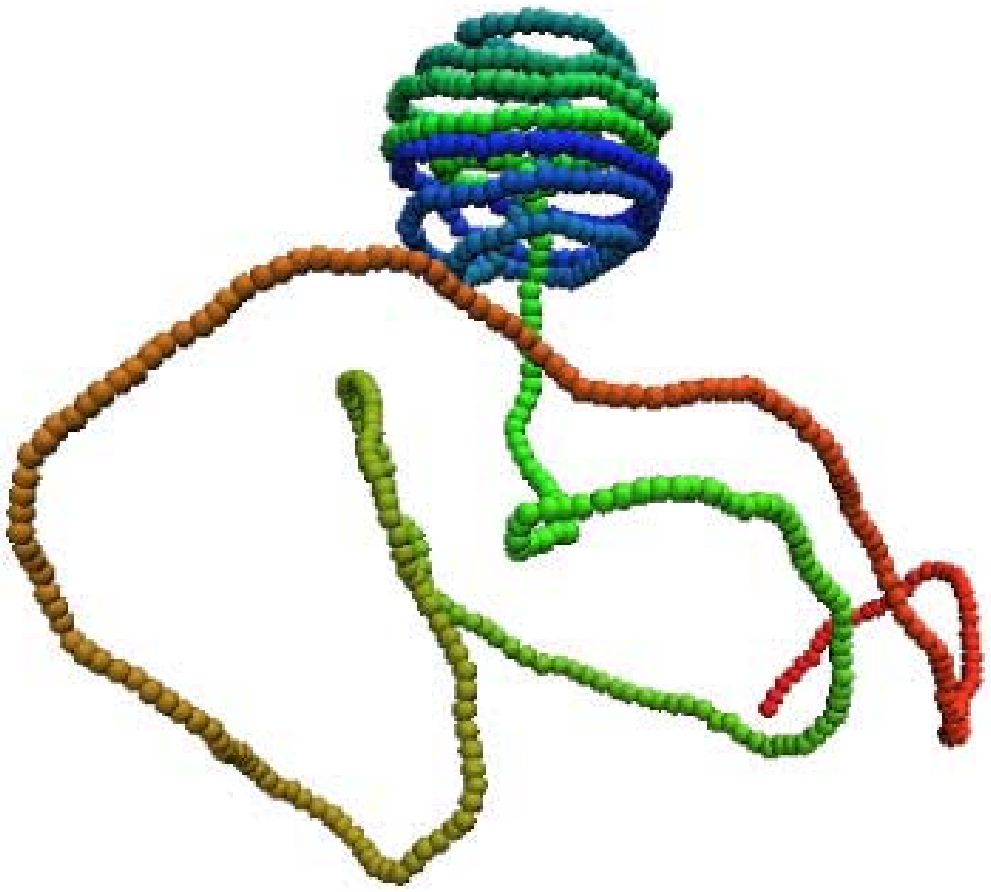
(c)


repulsive + bending + cholesteric energy (KbT units)
1550
1500
1450
1400
1350
1300
1250
3
4
5
6
7
8
number of crossings after simplifications


energies are expressed in KbT units (T=300 K)
repulsive energy
90
80
70
60
50
40
30
bending energy
600
550
500
450
400
350
300
unknot
9_1
complex knot
cholesteric energy
800
700
600
500
400
300
200
400
500
600
Number of beads inside capsids



Movie S1 (MOV). The video illustrates three packaging simulations of the half-P4 genome.



Movie S2 (MOV). The video illustrates three ejection simulations of the half-P4 genome. The initial conformations correspond respectively to: an unknot, a 9_1 knot and a complex knot with 23 crossings after simplification. All ejection processed are followed up to release 50% of the genome. Beyond this stage, the chain portion still inside the capsid is manifestly disentangled and is ejected without any significant geometrical or topological hindrance.