Biophysics

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AIMS Biophysics, 2(4): 613-629.
DOI: 10.3934/biophy.2015.4.613
Received date 27 September 2015,
Accepted date 28 October 2015,
Published date 03 November 2015

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*Research article*

# Topological diversity of chromatin fibers: Interplay between nucleosome repeat length, DNA linking number and the level of transcription

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## Supplementary

For L = 20 bp, our structure has the inclination angle $\rho = -45°$ and rise = 27 Å. The "direct" model by Schalch et al. [7] is based on the X-ray tetranucleosome structure; it has inclination about −50°/−40° and low rise = 17 Å. Note, however, that this model has "steric overlaps" [7]; the authors suggest that these overlaps can be relieved by increasing the separation of tetranucleosomes. On the other hand, using the EM images for L = 20 bp [9,16], one can estimate the rise to be ~ 25 Å, which is close to 27 Å in our energetically optimal fiber (**A**).

For L = 30 bp, Song et al. [8] built the high-resolution model based on the Cryo-EM data, with the inclination angle $\rho \approx -60°$ and rise = 24 Å (**E**). Our optimal structure is very close to this model: $\rho = -60°$ and rise = 25 Å (**B**).

For L = 40 bp, the Cryo-EM-based model has $\rho \approx -60°$ and rise = 22.5 Å, compared to $\rho = -70°$ and rise = 20 Å in our optimal structure (**C**). Note that in both the theoretical (**B, C**) and the Cryo-EM-based models (**E, F**) the linker increase from L = 30 to 40 bp is accompanied by a decrease in superhelical rise and increase in the diameter of fibers.

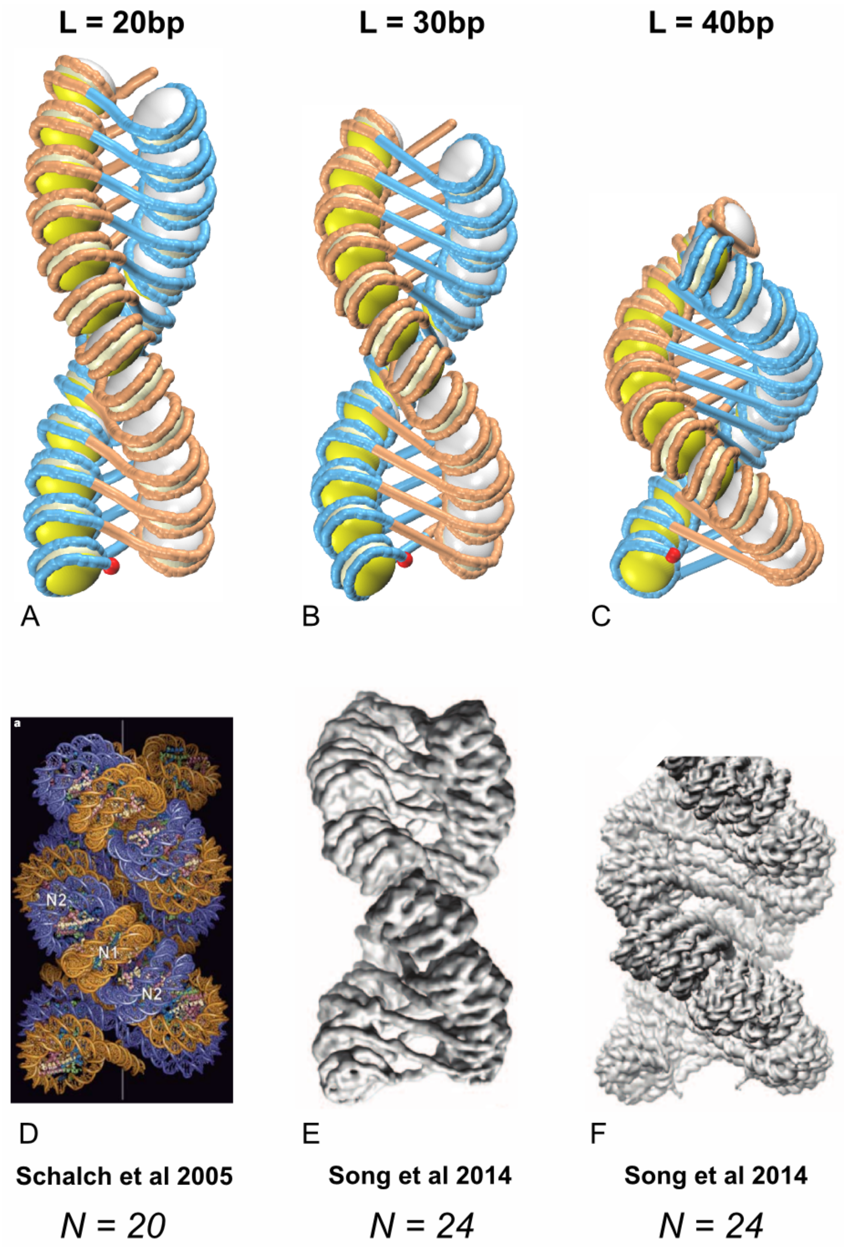

**Figure S1. Comparison of the energetically optimal fibers with the experiment-based models.** The computed structures for L=20, 30, 40 bp (A, B, C) are the same as shown in Figure 3. In each case, the number of nucleosomes, *N*, is 24. (D–F) The published experiment-based models are shown for comparison, with the *N* values given below.