

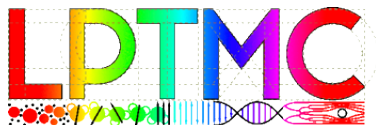
ON THE TOPOLOGY OF CHROMATIN FIBERS

Maria Barbi

Multiscale modeling of living matter (M3V) group

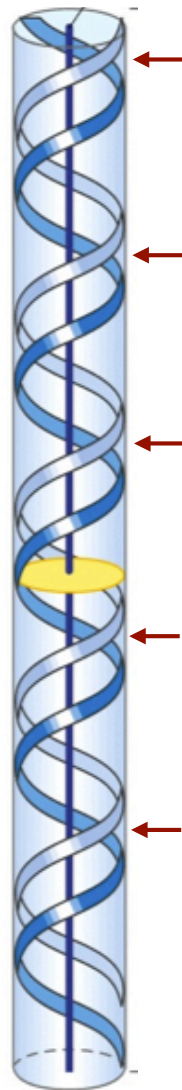
Laboratoire de Physique Théorique de la Matière Condensée
(LPTMC),
CNRS-Université Paris VI, France

collaboration experimental group:
Jean-Louis Viovy, Institut Curie, Paris

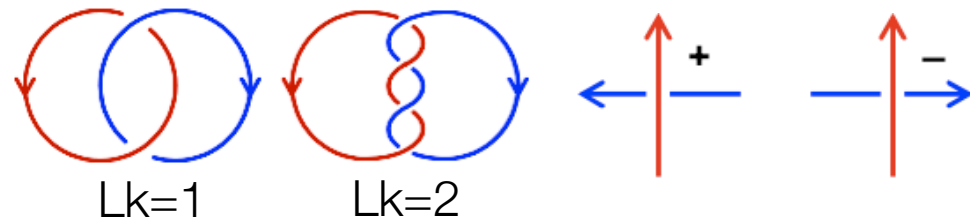


TOPOLOGY OF DNA

DNA
double helix

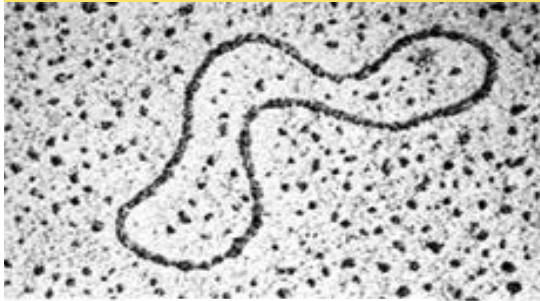


linking number Lk of two curves

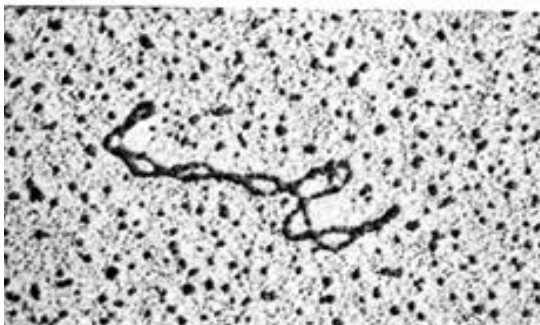
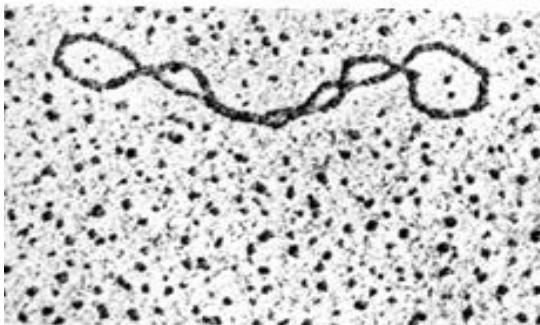
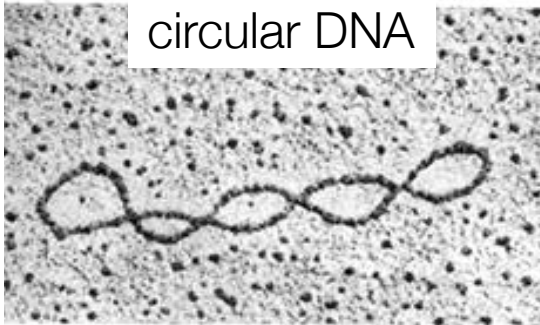


unconstrained B-DNA:
 $Lk_0 = +1/10.5$ turns/basepairs (bps)
(right handed double helix)

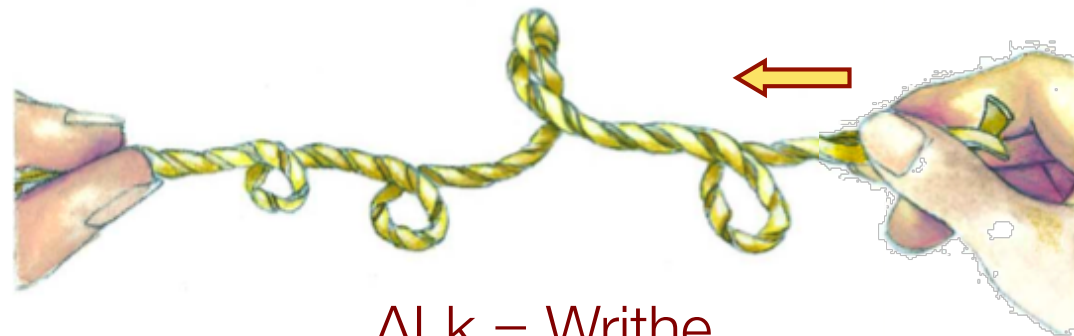
TOPOLOGY OF DNA



circular DNA



White-Fuller theorem



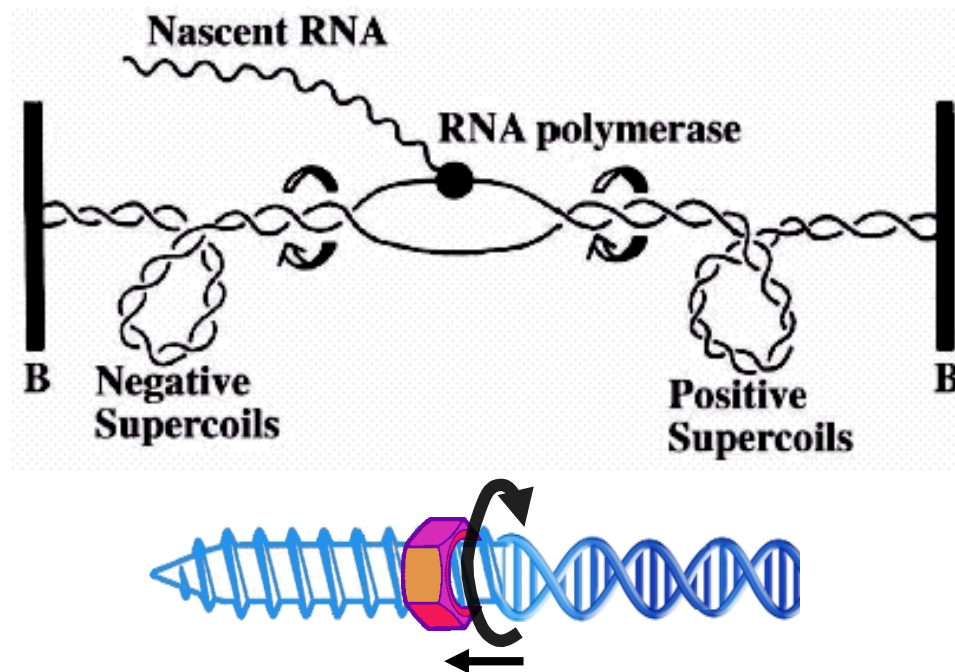
$$\Delta Lk = Tw + Wr$$

conserved quantity for
closed curves or fixed ends

SUPERCOILING *IN VIVO* AND *IN VITRO*

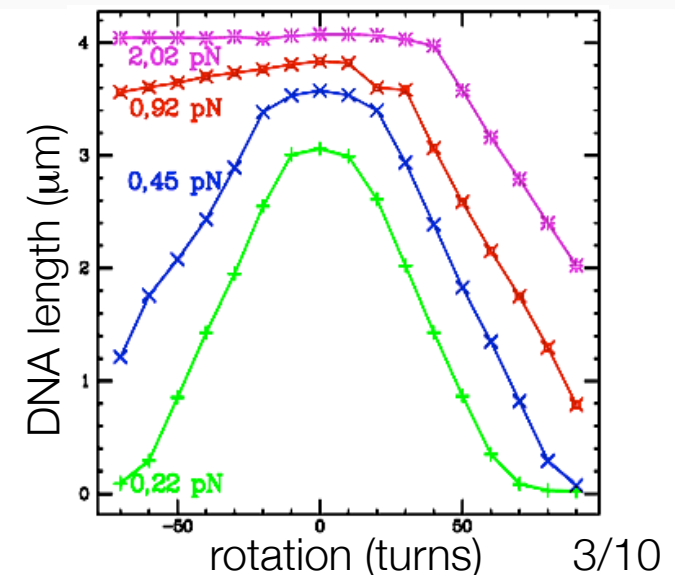
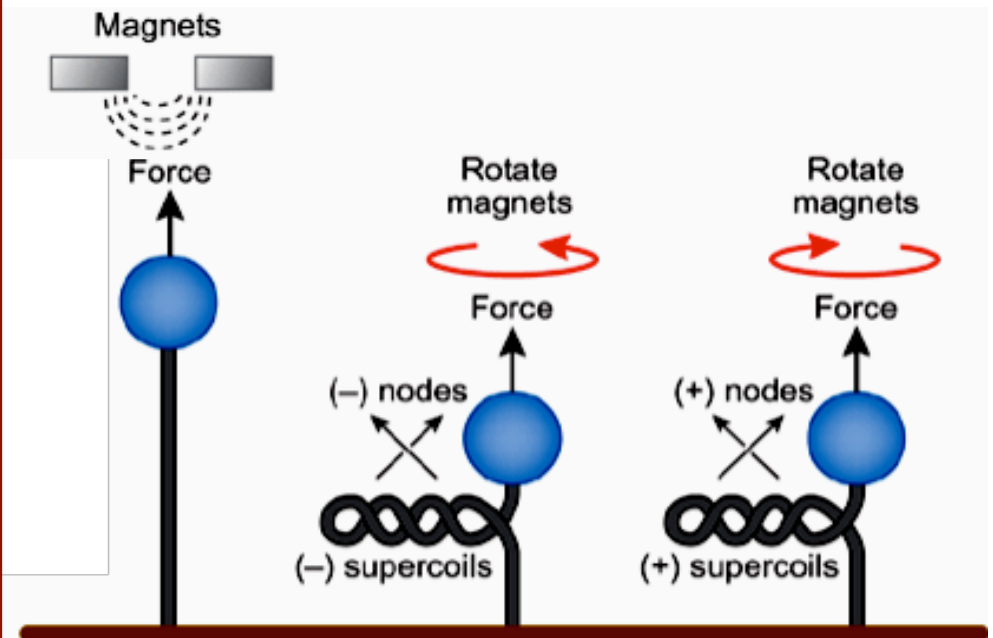
in vivo - transcription

twin supercoiled domains
(Liu Wang 1987)



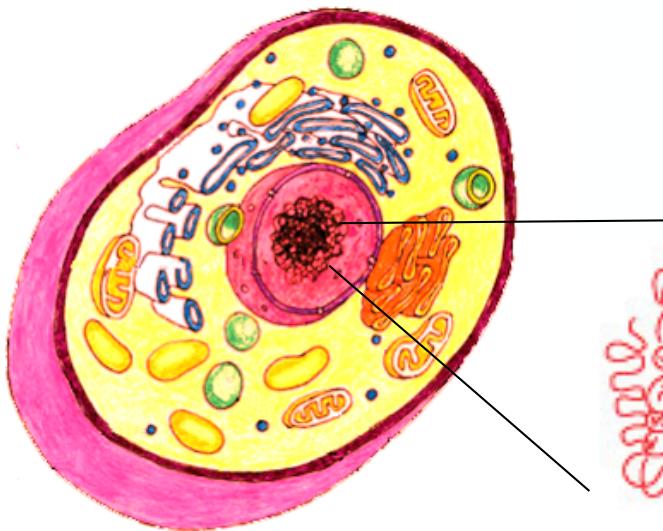
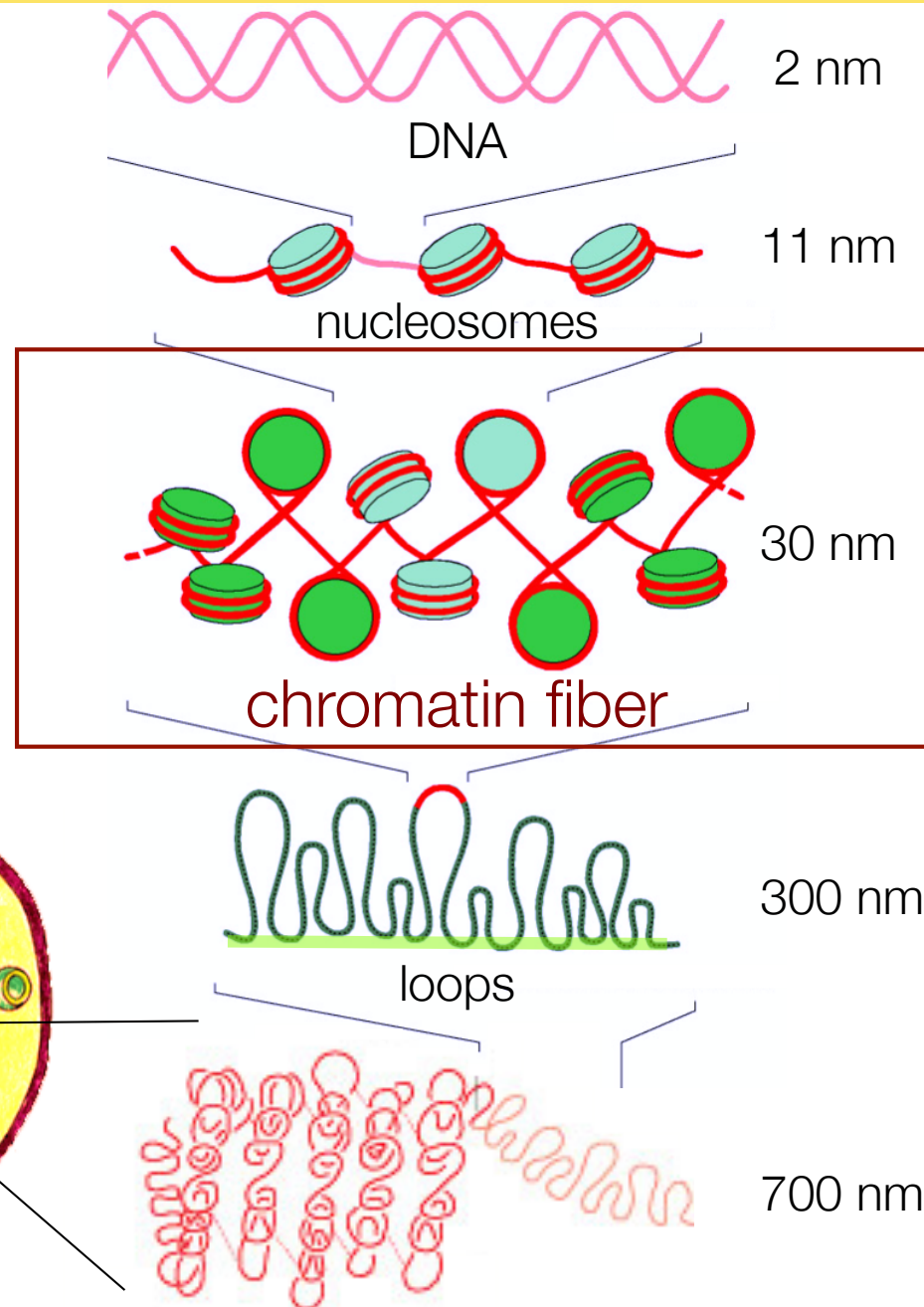
$V \sim 20$ bps/sec
 $\omega_0 \sim 2$ turns/sec
 torque $> +5$ pN·nm
 (Harada 2001)

in vitro - magnetic tweezers



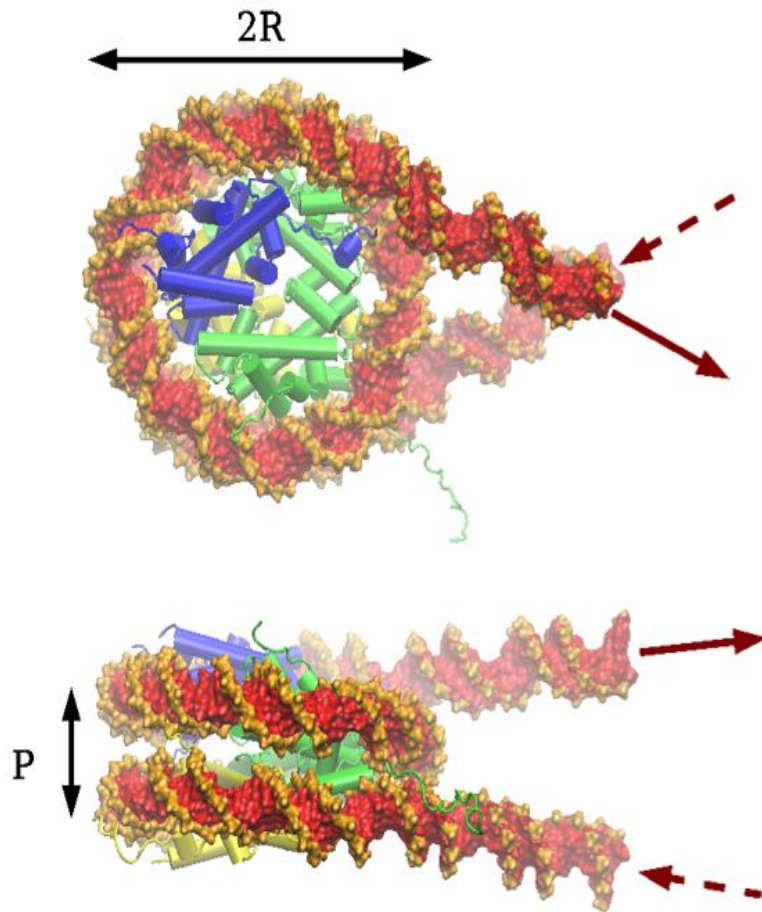
CHROMATIN FIBER

DNA in the
nucleus:
chromatin
a multiscale
functional
structure



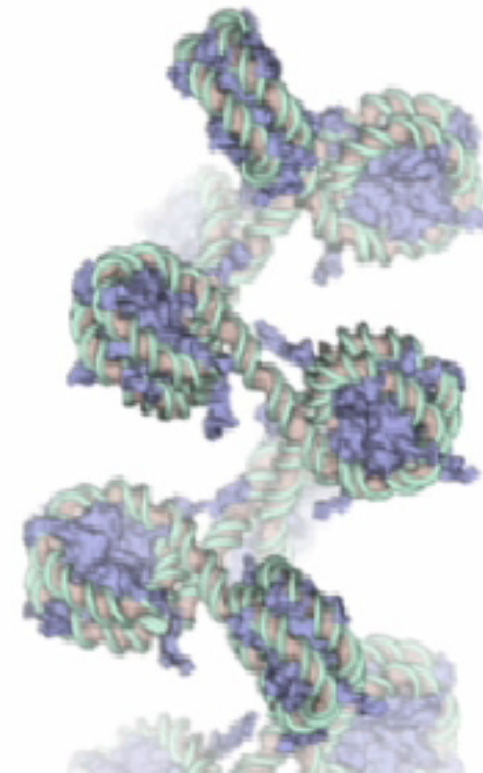
CHROMATIN FIBER

a closer view



nucleosome

a left handed superhelix
(crystallographic structure)



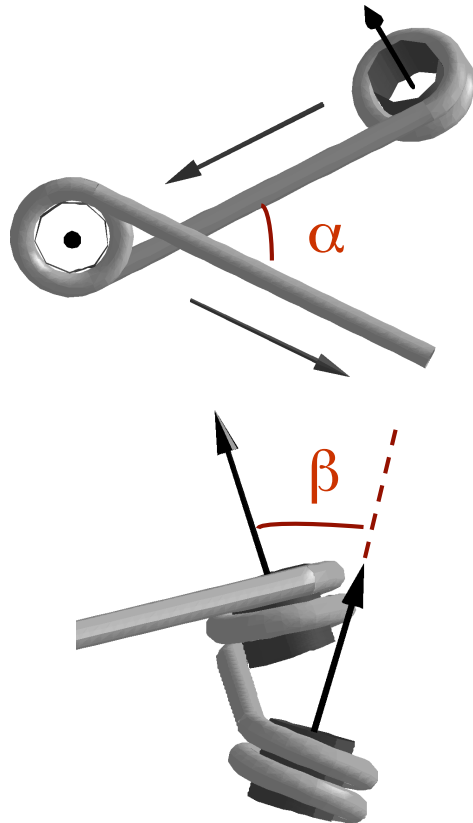
fiber

key accordable structure in
regulating DNA accessibility

movie by Hua Wong

CHROMATIN FIBER TOPOLOGY

how to calculate the DNA twist and writhe in the fiber?

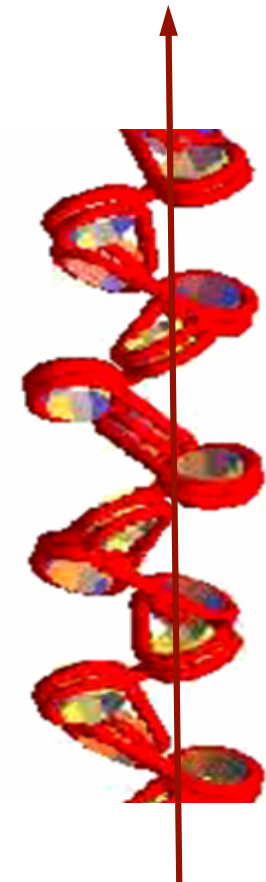


“two angle model”:
linker DNA between
2 nucleosomes are
assumed to be straight

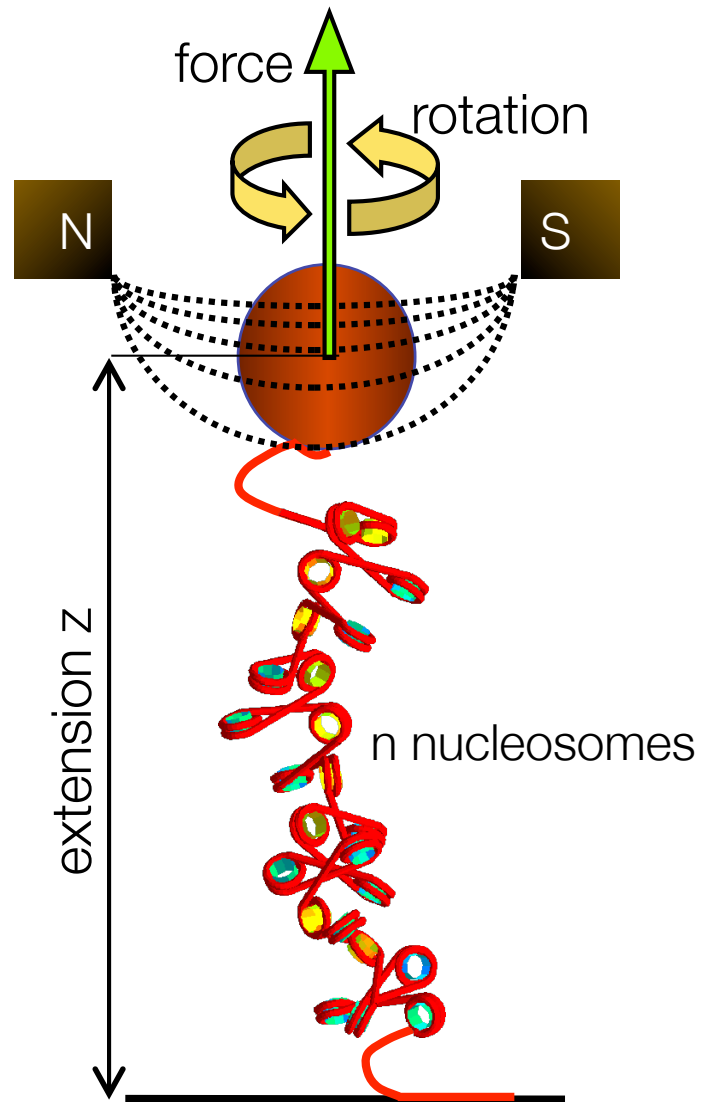
twist is additive, *writhe is not!*

but

regular fiber → Tw, Wr, Lk contribution *per nucleosome*

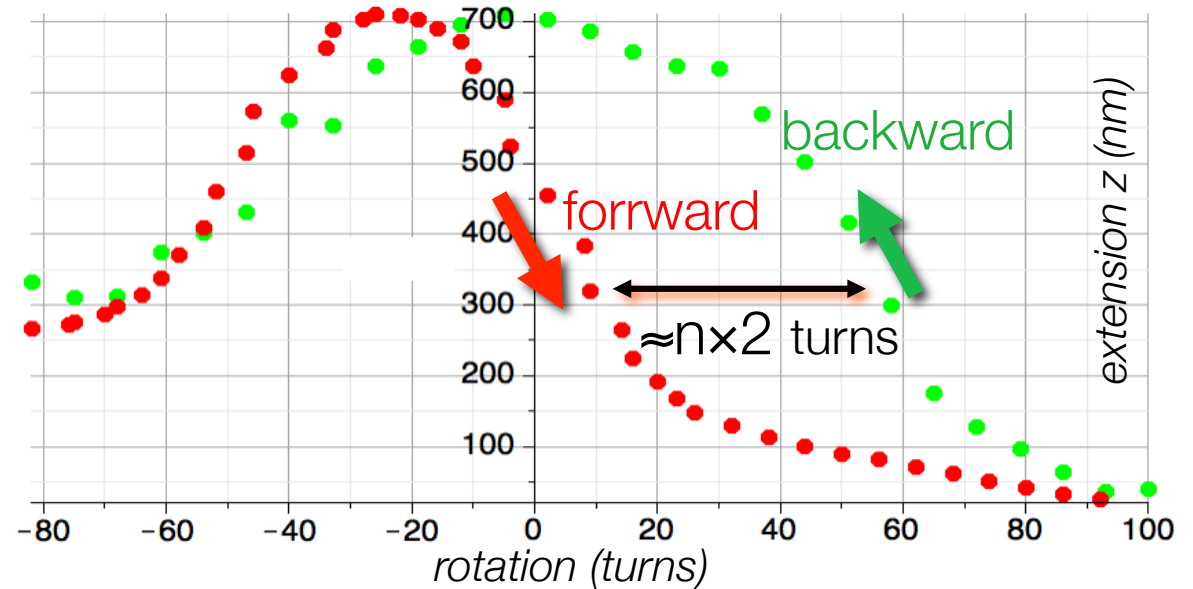


FIBER UNDER MAGNETIC TWEEZERS



experiments by JL Viovy
Institut Curie, Paris

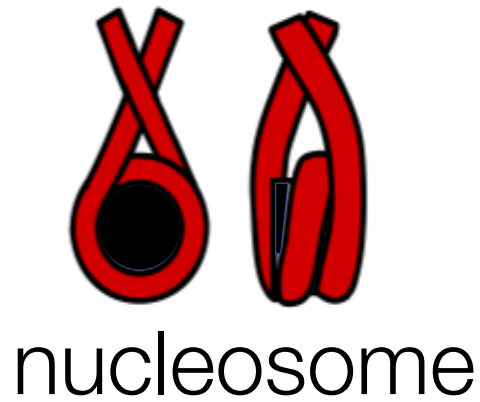
hysteresis (high positive torsion)



NUCLEOSOME CHIRAL INVERSION

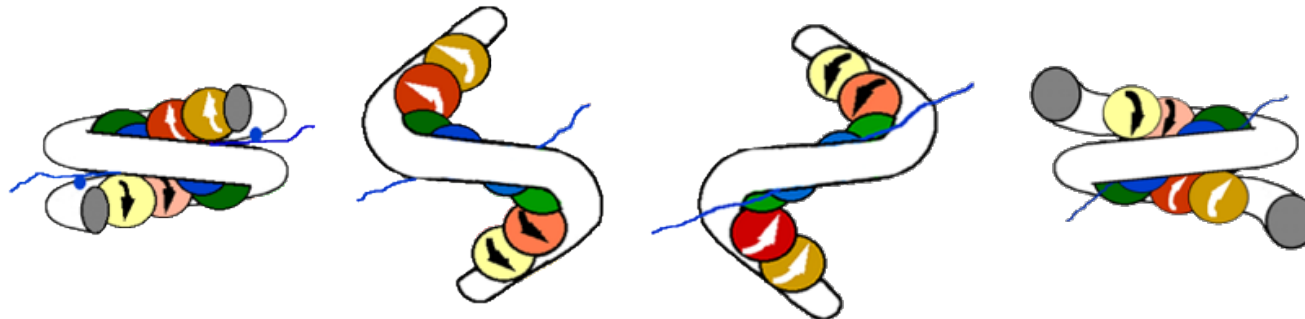
a plastic nucleosome!

left
handed
 $\langle \Delta Lk \rangle \sim -1$

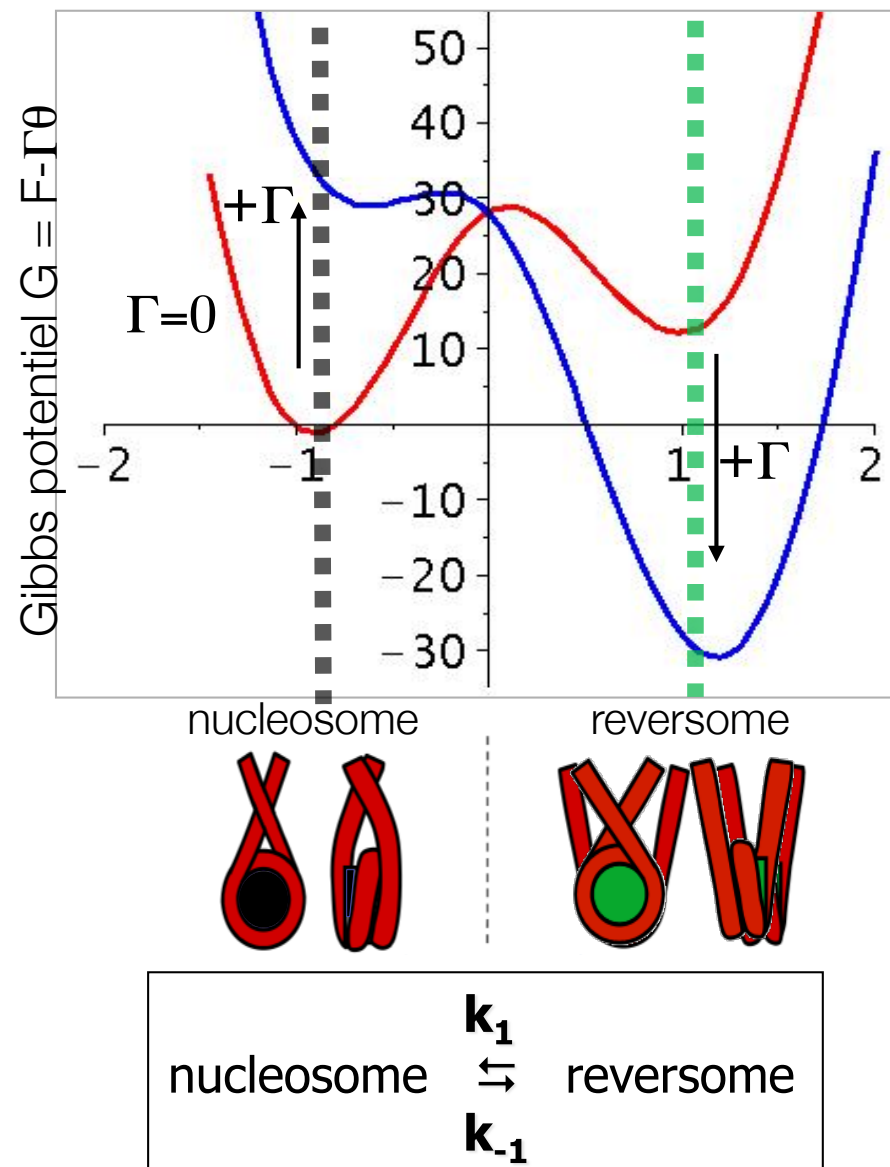


right
handed
 $\langle \Delta Lk \rangle \sim +1$

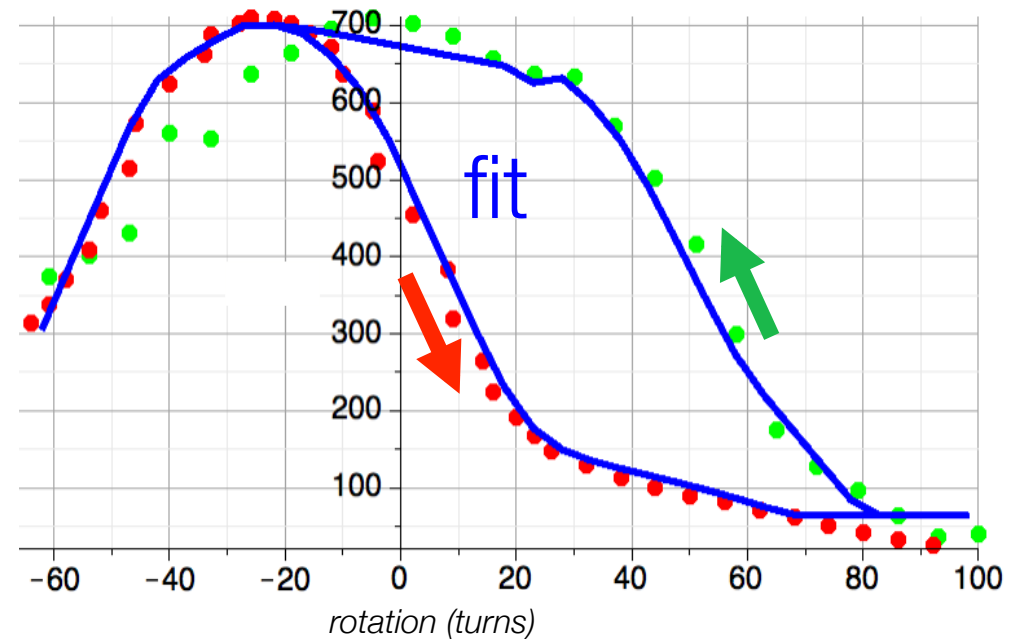
chiral transition



STATISTICAL MECHANICS AND THE FIT

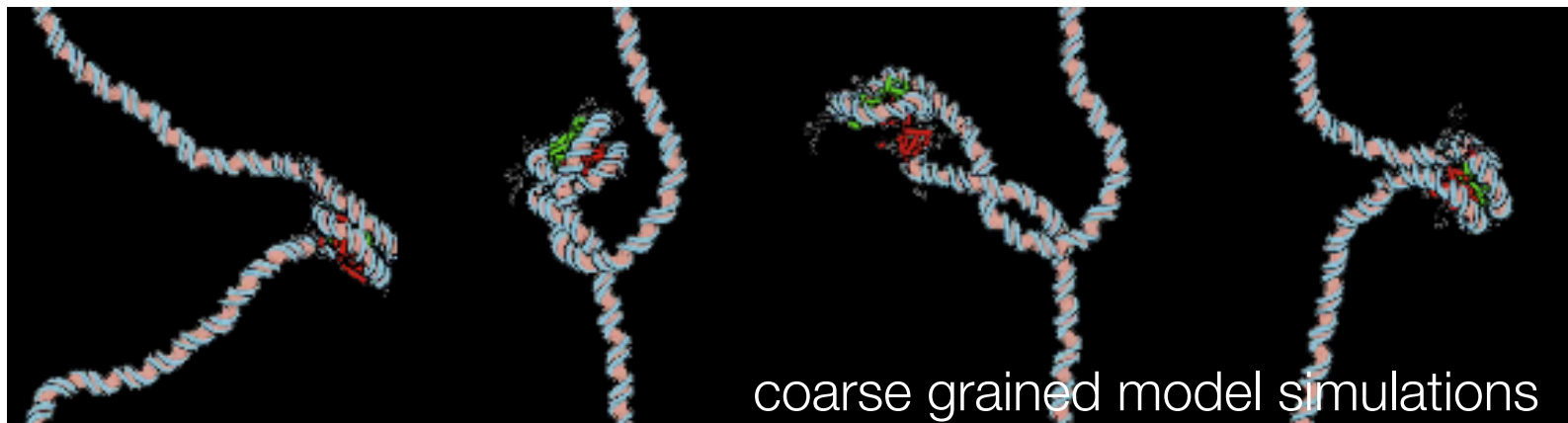
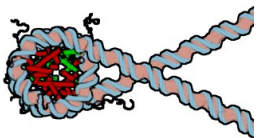


a torque-induced transition



REVERSOME: A TOPOLOGICAL BUFFER

absorbing torsion constraint trough transition to reversome



coarse grained model simulations

what about transcription? (next episode...)

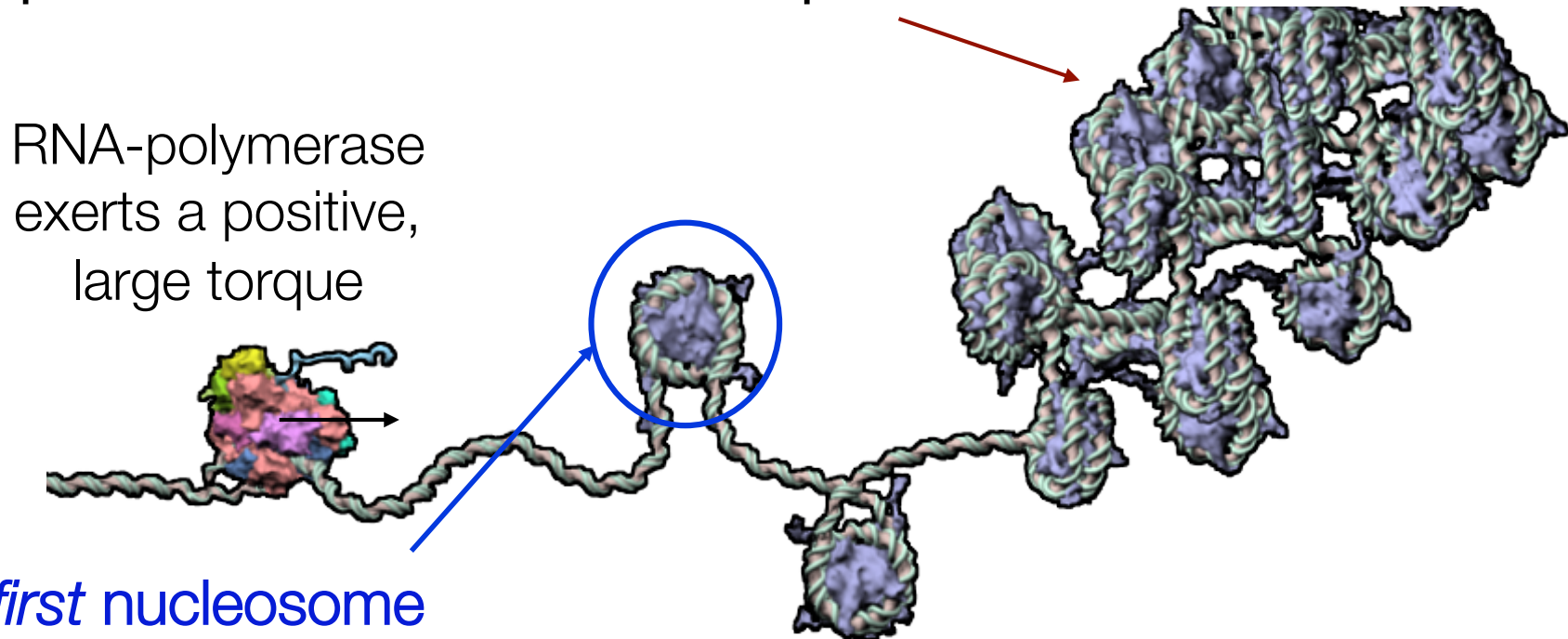
- Maria Barbi (UPMC)
- Annick Lesne (CNRS)
- Jean-Marc Victor (CNRS)
- Julien Mozziconacci (UPMC)
- Hua Wong (doc 2005–2008)
- Fabien Paillusson (doc 2007–2010)
- Christophe Bécavin (doc 2007–2010)
- Pascal Carrivain (doc 2008–2011)
- Christophe Lavelle (postdoc 2003–2004)

- M. Barbi et al. **How the chromatin fiber deals with topological constraints** Phys. Rev. E 2005
- J. Mozziconacci et al. **A Physical Model for the Condensation ...** FEBS letters 2006
- A. Bancaud et al. **Structural reorg. of chromatin fibers revealed by torsional nanomanipulation** NSMB 2006
- A. Bancaud et al. **Torsional manipulation of chromatin fibers reveals a highly flexible structure** Mol Cell 2007
- C. Lavelle **Transcription elongation through a chromatin template** Biochimie 2007
- C. Lavelle **Forces and torques in the nucleus: ...** Biochem. Cell Biol. 2009
- J. Zlatanova & JM. Victor **How are nucleosomes disrupted during transcription elongation?** HFSP J. 2009
- C. Bécavin et al. **Transcription within Condensed Chromatin: ...** Biophys J. 2009
- P. Recouvreux et al. **Linker histones incorporation maintains fiber plasticity** Biophys. J. 2011

THE REVERSOME WAVE

back to *in vivo*: transcription in a compact fiber

compact fiber \Rightarrow steric hindrance prevents nucleosome transitions

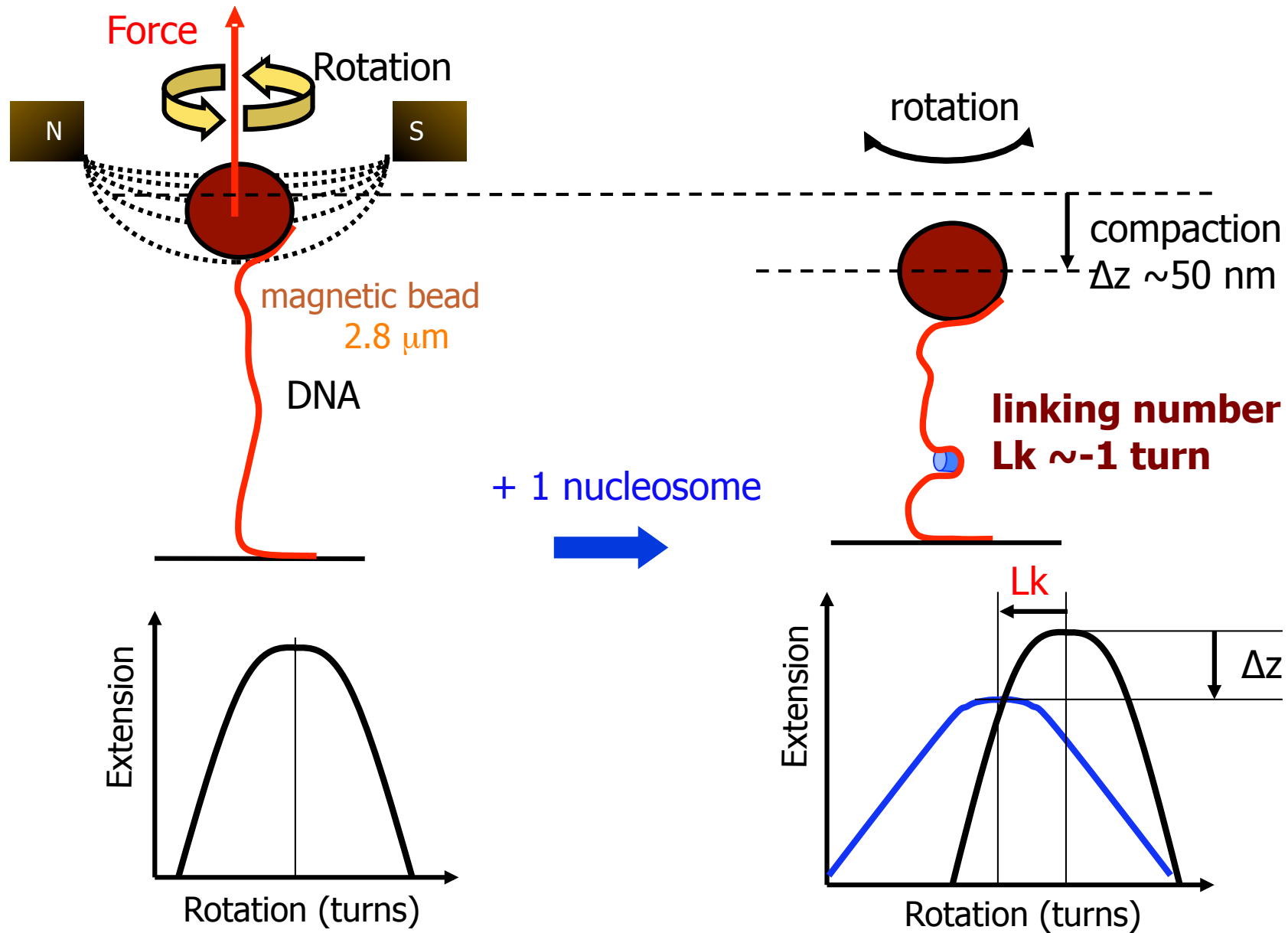


the *first* nucleosome
pass to reversome, then the second...

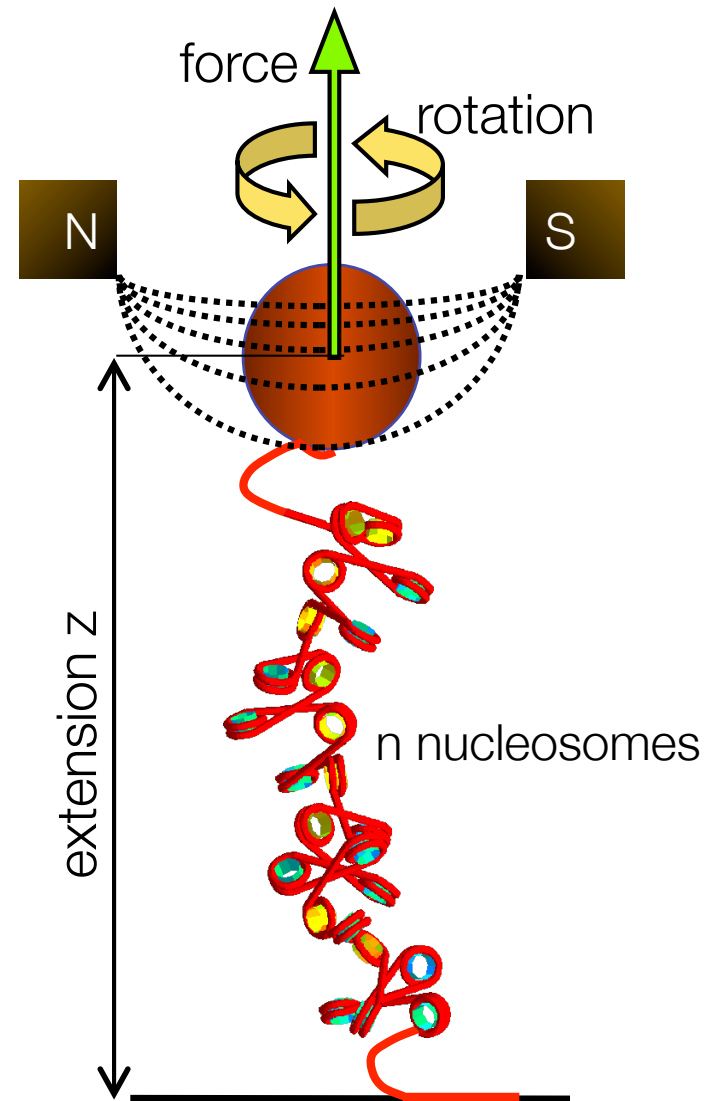
\Rightarrow creation of a “reversome front”

$$v_{\text{RNAPol}} = 20 \text{ bps/s} \rightarrow 2 \text{ turns/s} \rightarrow 1 \text{ reversome/s} \rightarrow v_{\text{front}} = 200 \text{ bps/s}$$

SIGNATURE OF NUCLEOSOMES

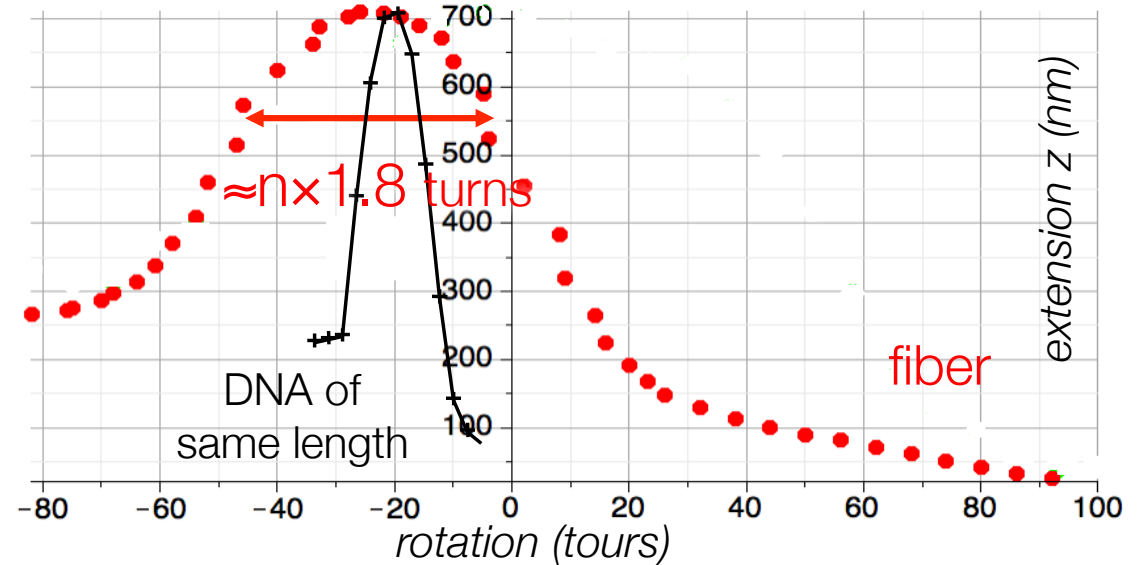


FIBER UNDER MAGNETIC TWEEZERS

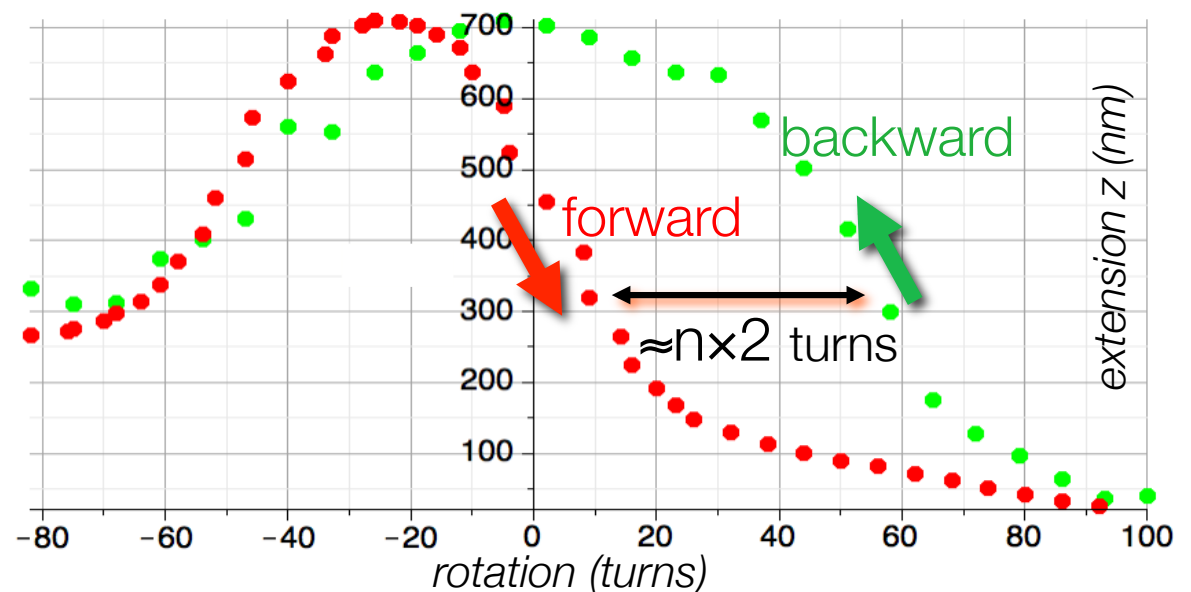


experiments by LJ Viovy
Institut Curie, Paris

1. torsional resilience

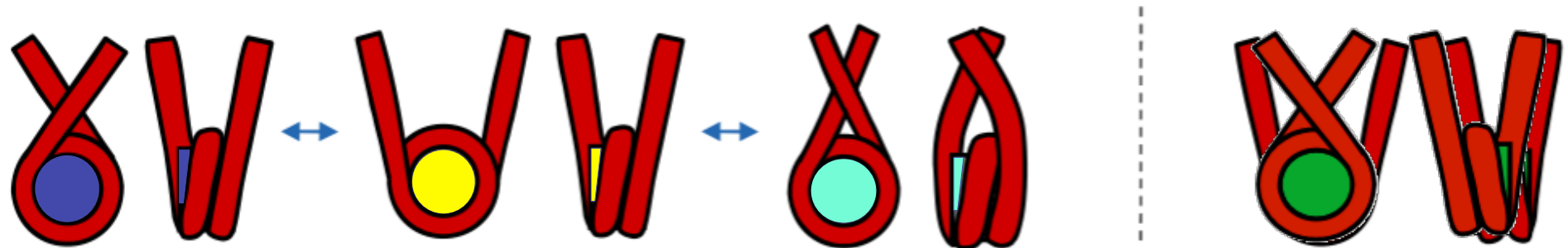


2. hysteresis (higher torsion)



4 NUCLEOSOME STATES

a plastic nucleosome!



negatively
crossed

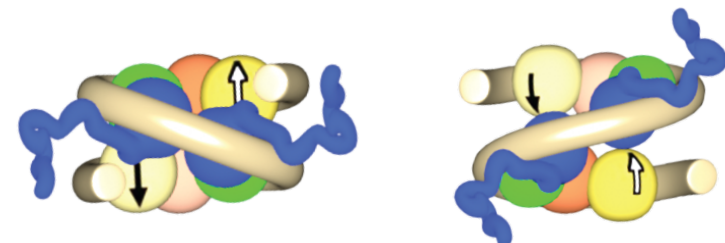
open

positively
crossed

reversome

chiral transition

state	Neg.	Open	Pos.	barrier	Rev.
α	54°	-30°	30°	/	30°
β	115°	90°	115°	/	80°
d (nm)	4.1	8.3	2.8	/	2.0
ΔLk per nuc.	-1.4	-0.4	-0.2	-0.15	+0.9
E (kT)	0.7	0	2	28	10



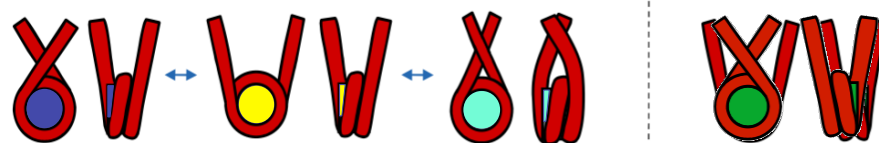
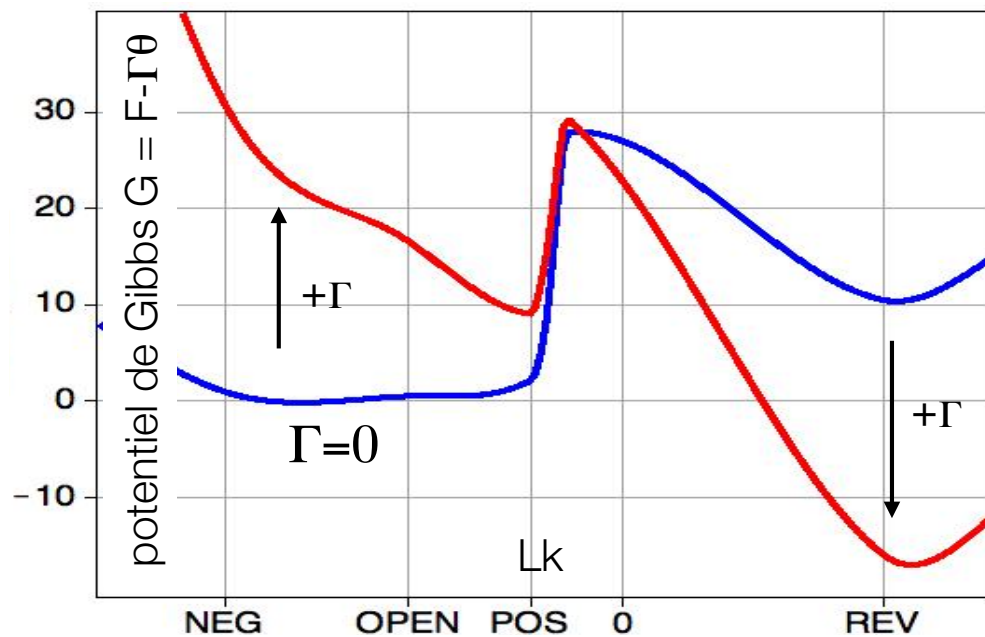
left
 $\langle \Delta Lk \rangle \sim -1$

$+\Gamma$

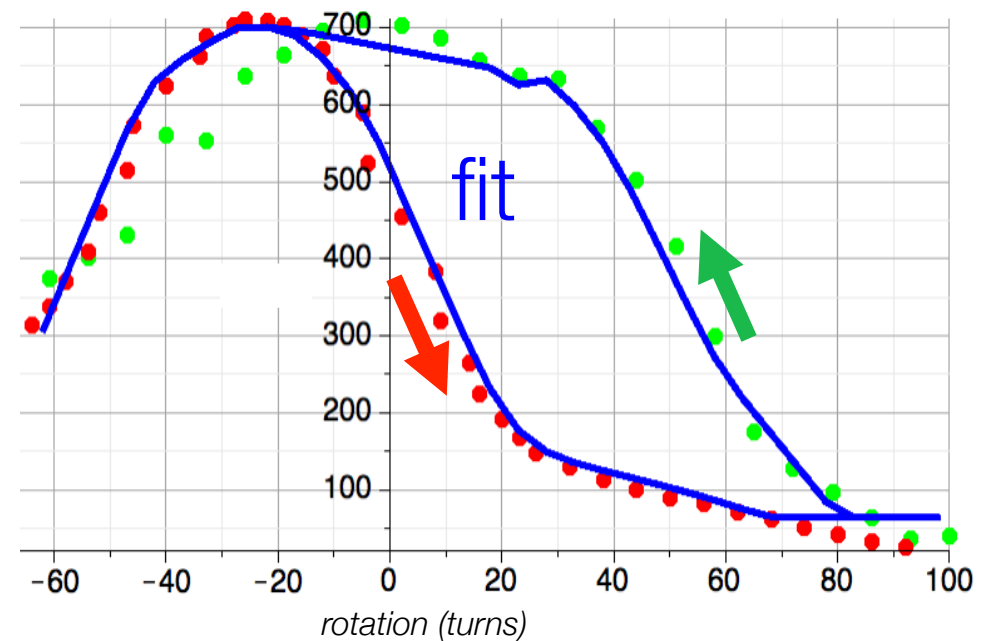
right
 $\Delta Lk \sim +1$

STATISTICAL MECHANICS AND THE FIT

eq. nég. \leftrightarrow ouv. \leftrightarrow pos. \leftrightarrow 4ème état
 \mathbf{k}_1
 \mathbf{k}_{-1}

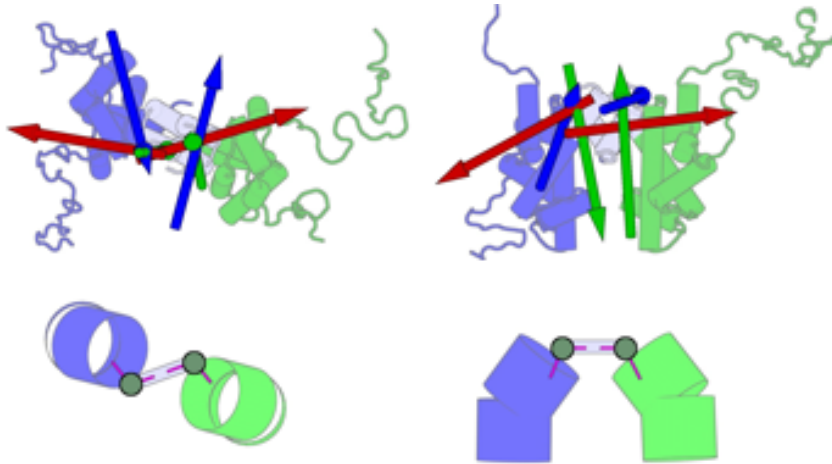


a torque-induced transition

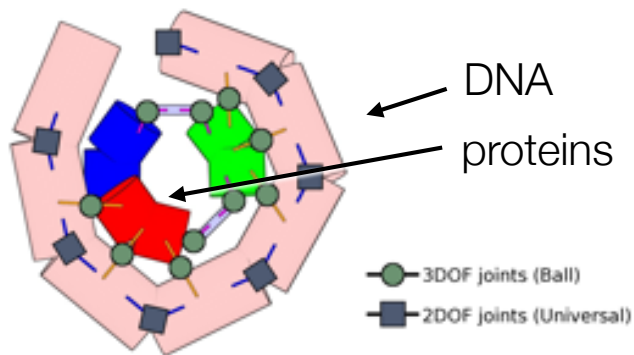


RIGID BODY DYNAMICS + SKELETAL ANIMATION

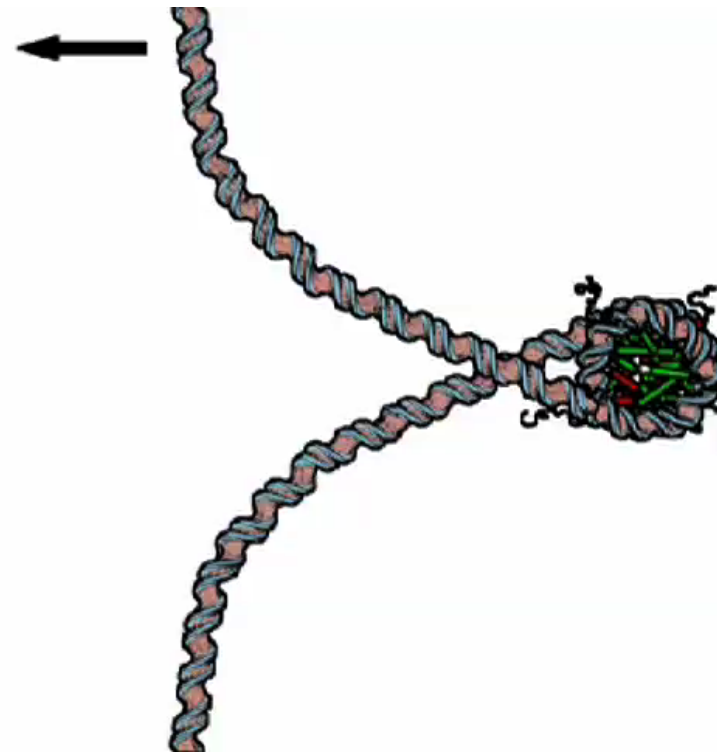
1. normal modes analysis



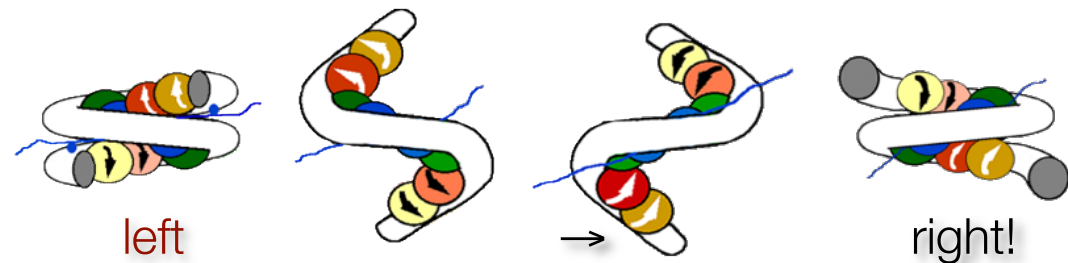
2. nucleosome structuration



3. Brownian dynamics at constant torque

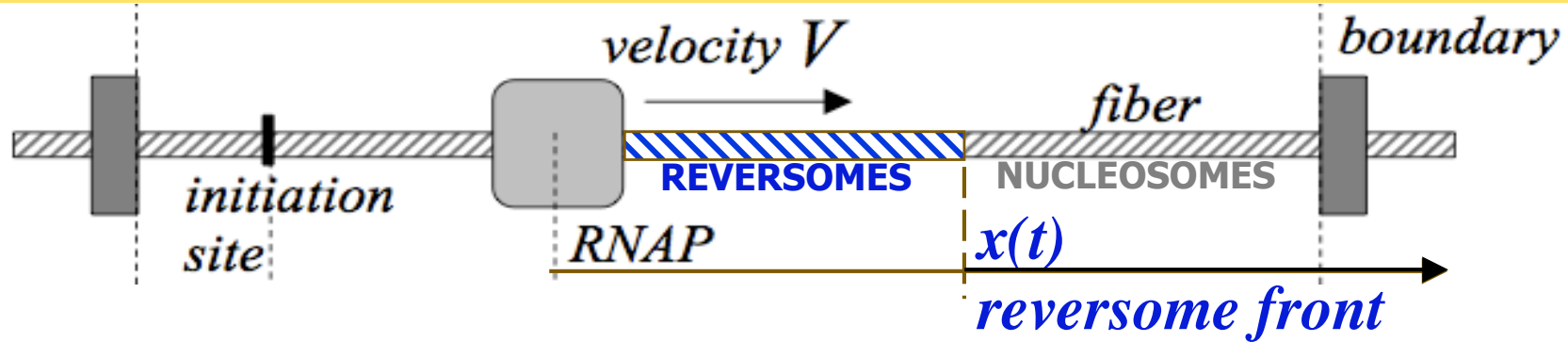


result: chiral transition:



Animation by Hua Wong

REVERSONE FRONT SPEED



linking number conservation:

$$\left(\frac{\omega_0 t}{2\pi} \right) = \left[\Lambda \Delta Lk + \frac{\tau}{2\pi} \right] \cdot x(t)$$

RNA pol
rotation

reversome fiber
internal twist
(ΔLk nucl to rev)

reversome
fiber torsion
(\ll)

Λ linear density

Γ applied torque

L_p twist pers. length

$\tau = \frac{\Gamma}{L_p k_B T}$ fiber torsion

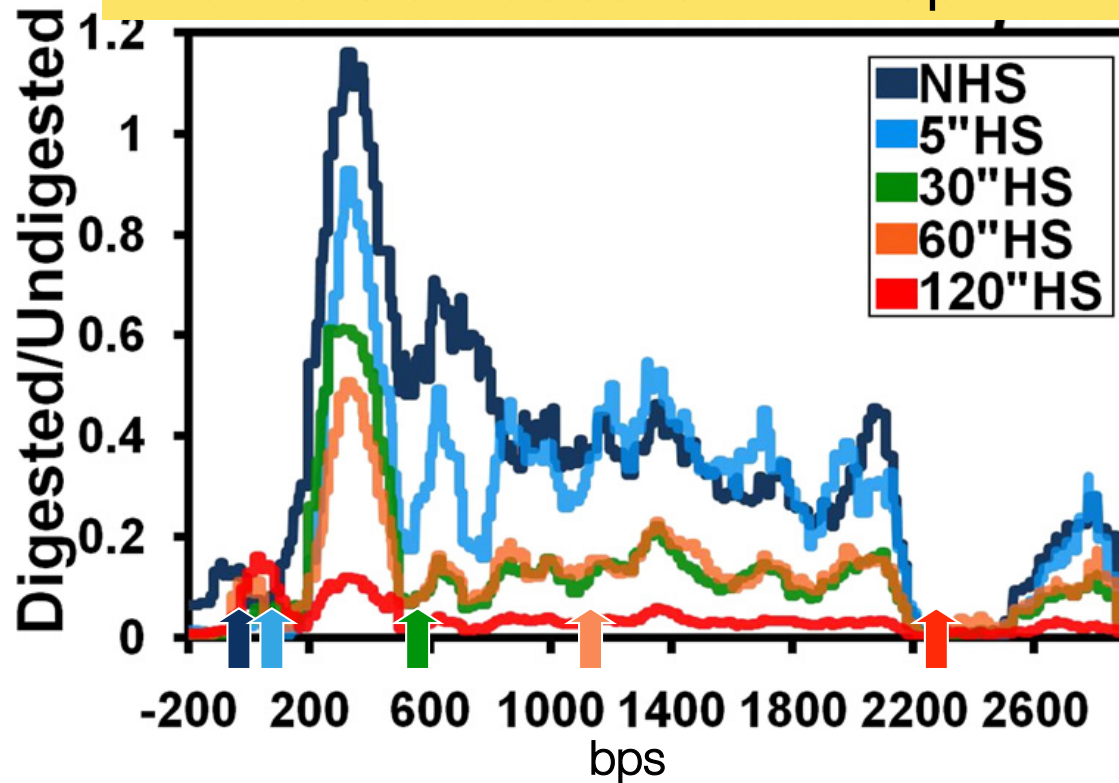
τ_c critical torsion

reversome front progression:

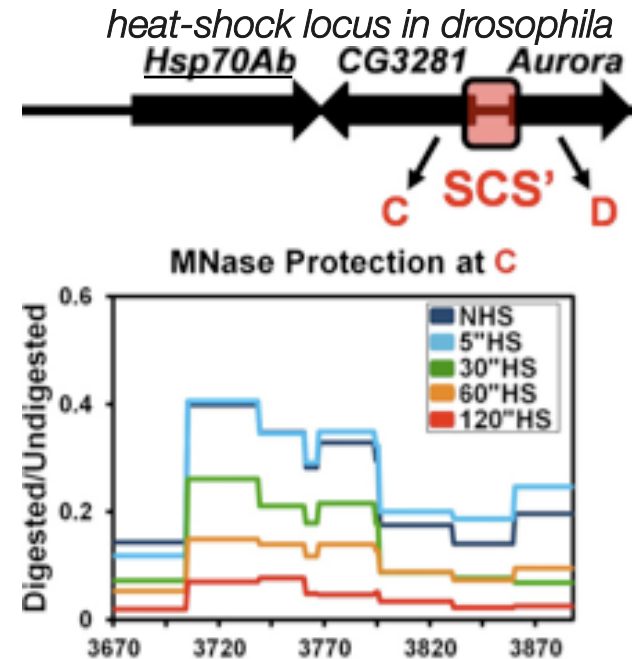
$$x(t) = v t + c, \quad v = \frac{\omega_0}{2\pi \Lambda \Delta Lk + \tau_c} \simeq \frac{\omega_0 / 2\pi}{\Lambda \Delta Lk} \rightarrow \boxed{V = 1 \text{ nucl./s}} \\ = 200 \text{ bps/s}$$

PETESH-LIS EXPERIMENT

a wave of nucleosome disruption



(Petesh and Lis, Cell 2008)



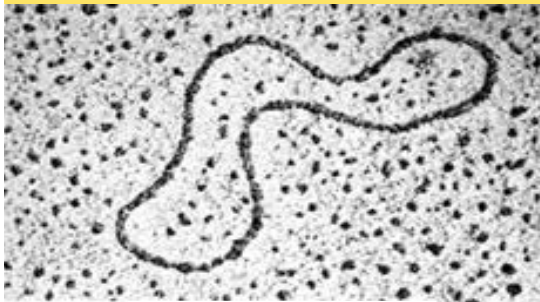
30'' : all the loop
and only the loop

reversome-wave
interpretation:

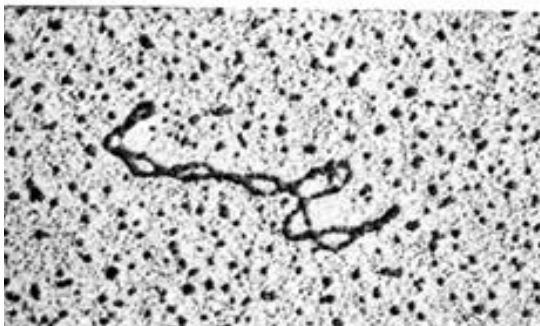
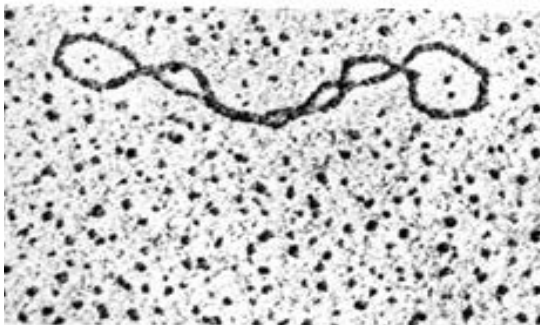
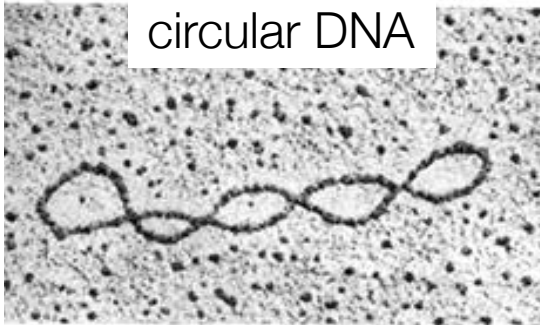
- ➡ RNA pol at start
- ➡ 100 bps elongation → 10 turns, 5 rev., 1000 bps
- ➡ 600 bps elongation → 60 turns, 30 rev., 6000 bps
- ➡ 1200 bps elongation → 120 turns, 60 rev., 12000 bps
- ➡ ...

(Zlatanova and Victor, HFSP J 2009)

TOPOLOGY OF DNA



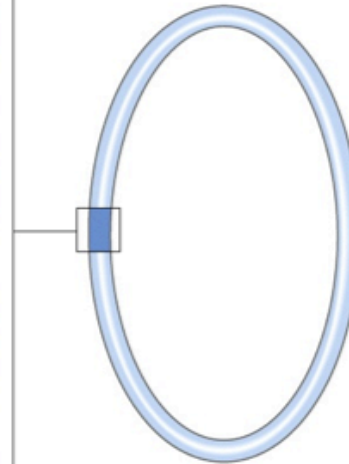
circular DNA



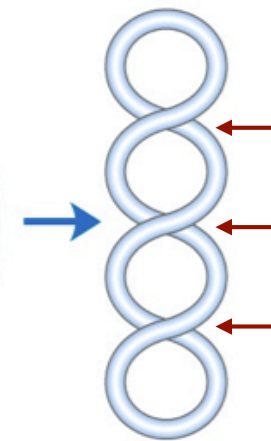
DNA double
helix (coil)
Axis



single (closed) curve
linking number Lk



DNA
supercoil



$Lk = -3$