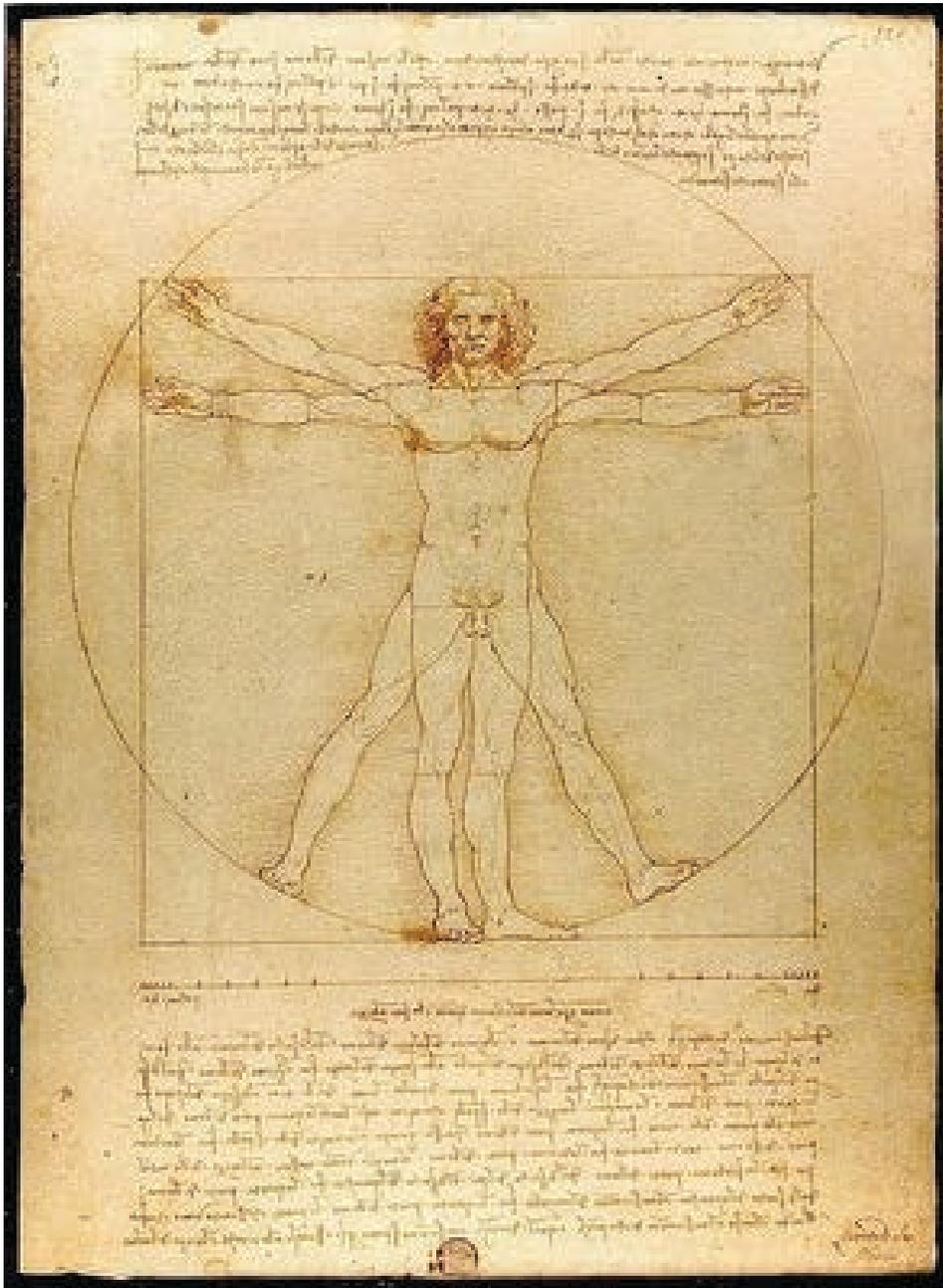


# Close encounters with DNA

Aleksei Aksimentiev  
Department of Physics  
University of Illinois at Urbana-Champaign



# WHAT IS LIFE?

*The Physical Aspect of the  
Living Cell*

BY

ERWIN SCHRÖDINGER

SENIOR PROFESSOR AT THE DUBLIN INSTITUTE FOR  
ADVANCED STUDIES

*Based on Lectures delivered under the auspices of  
the Institute at Trinity College, Dublin,  
in February 1940*



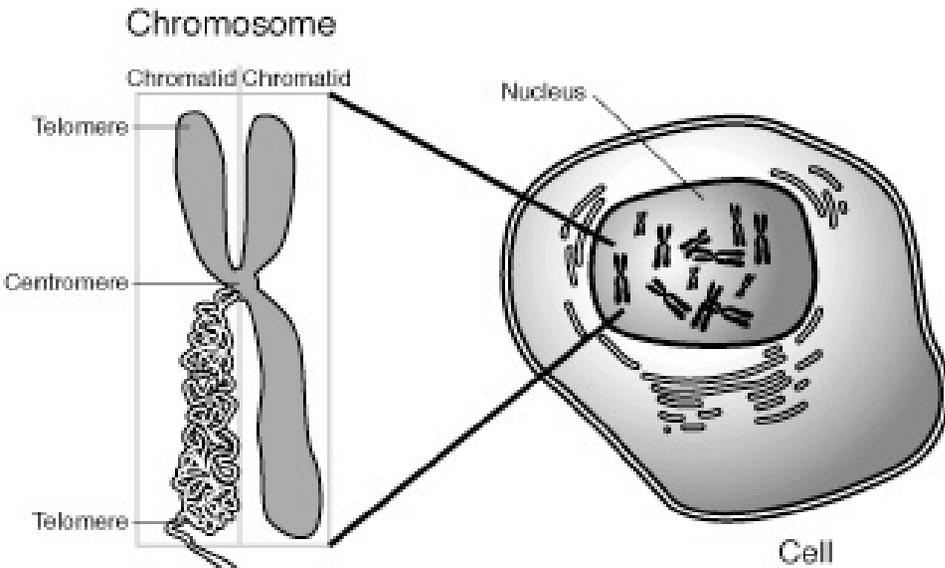
4339

CAMBRIDGE

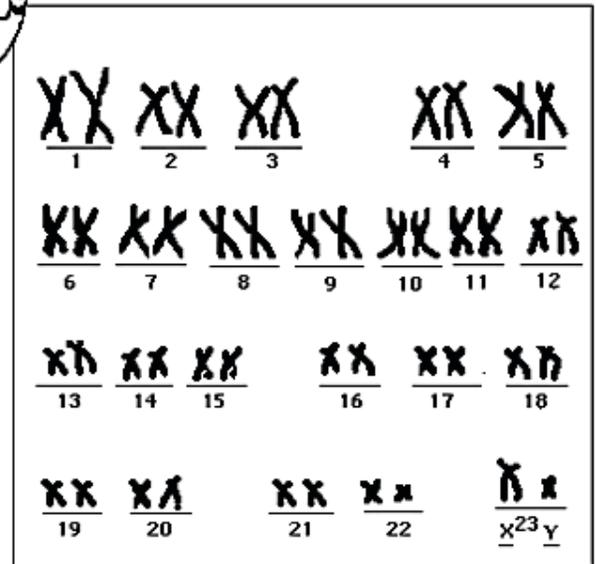
AT THE UNIVERSITY PRESS

1948

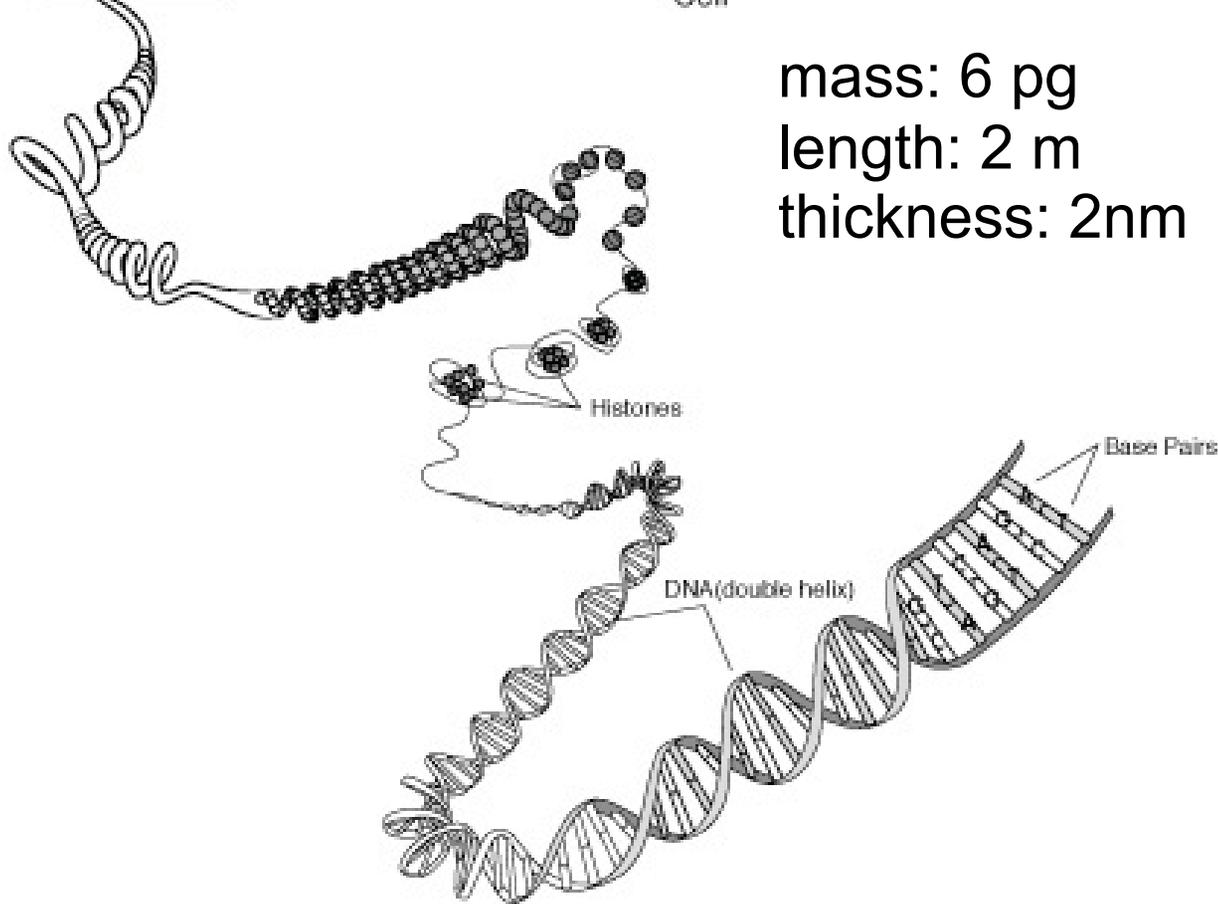
# DNA, the blueprint



HUMAN CHROMOSOMES



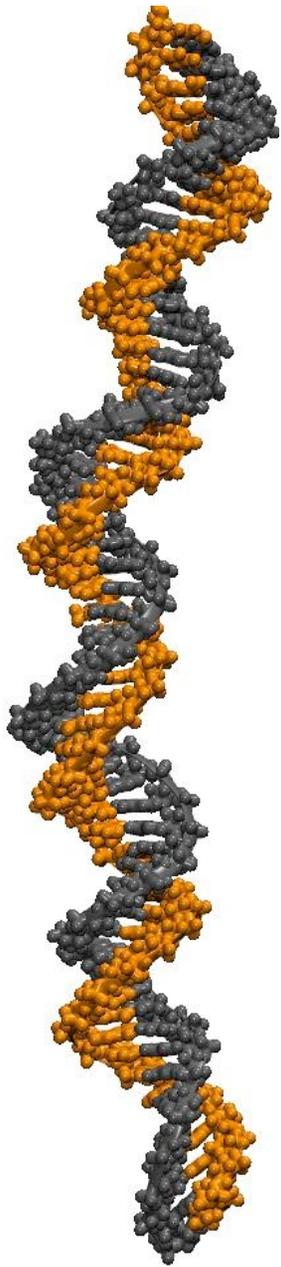
mass: 6 pg  
length: 2 m  
thickness: 2nm



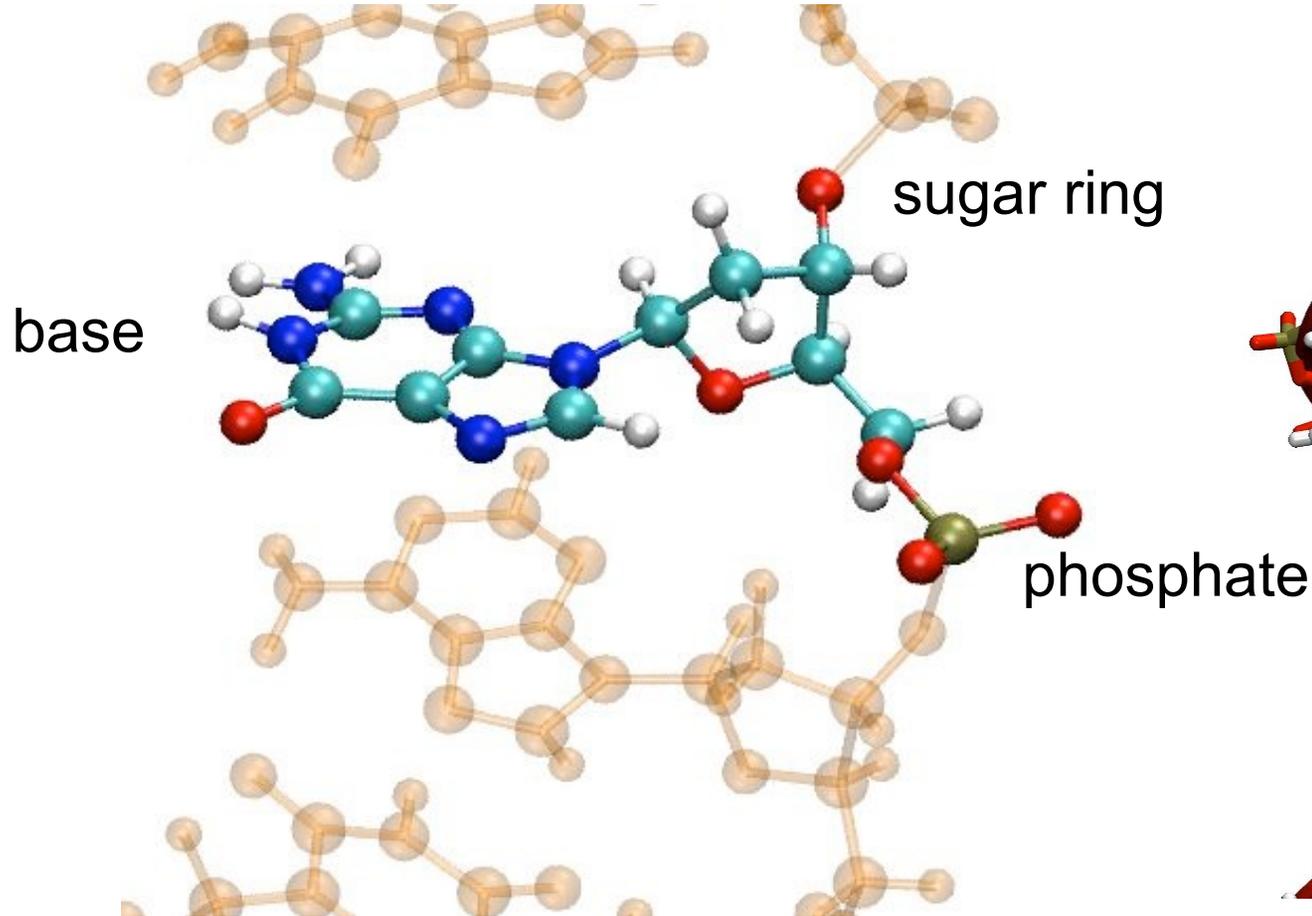
...GTGTGACTCGT  
GGTCCGTAATGTC  
GTTAATGGTGACC  
GTGTGGCCTGATG  
GTTAGTGTGTGA...

# DNA code is written in atoms

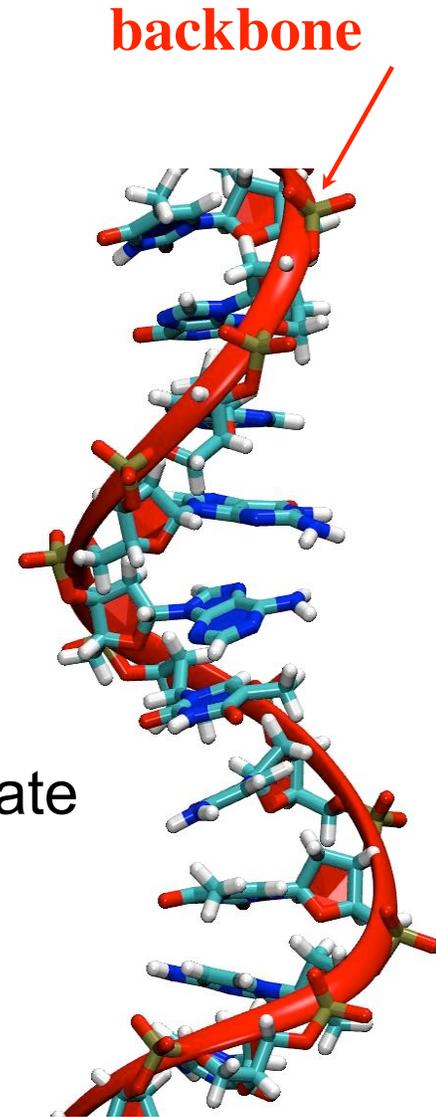
Highly charged: 2 electron charges per 0.32nm



Double stranded DNA  
(persist. length ~50nm)



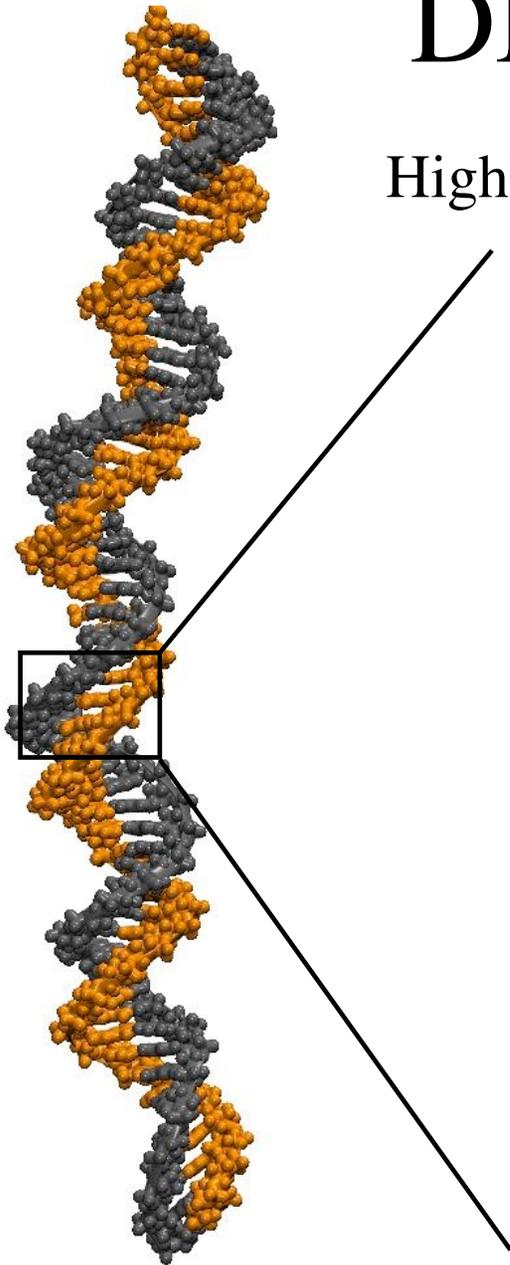
The sequence has direction:  
5'-AAGCTGGTTCAG-3'



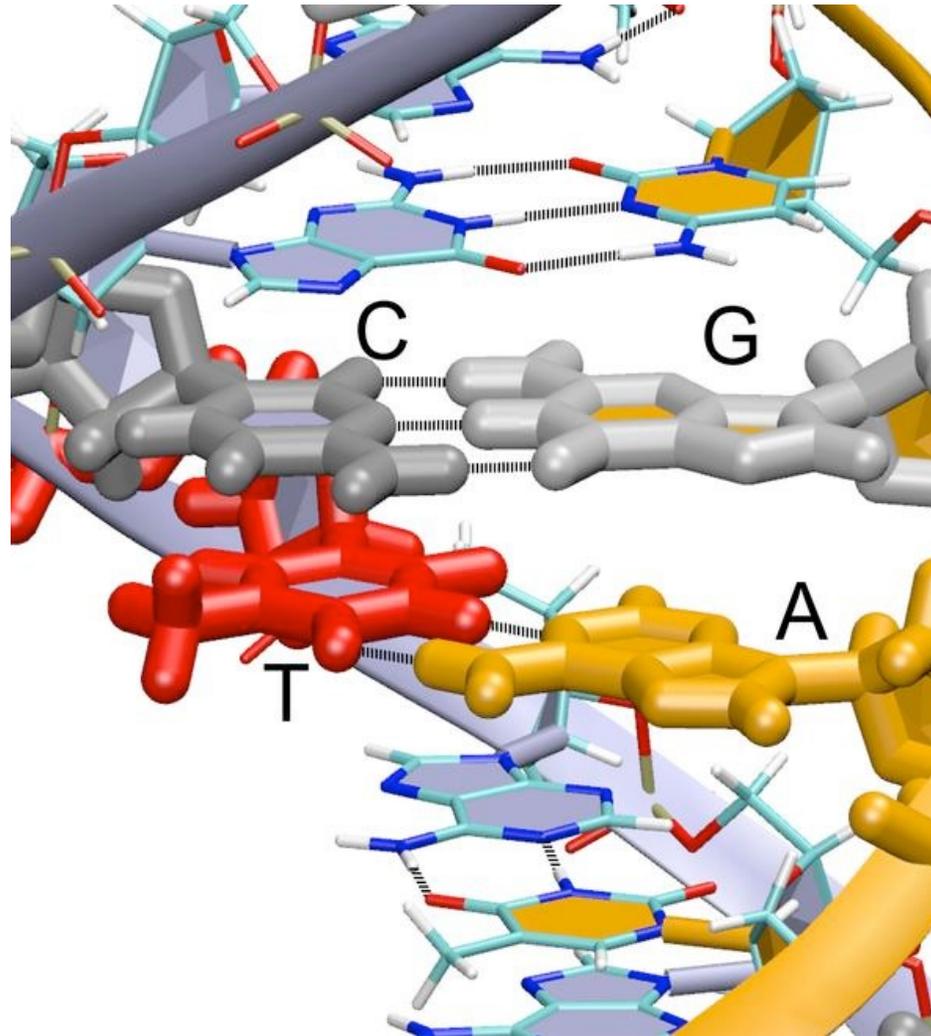
Single stranded DNA  
(persist. length ~1.5nm)

# DNA code is written in atoms

Highly charged: 2 electron charges per 0.32nm

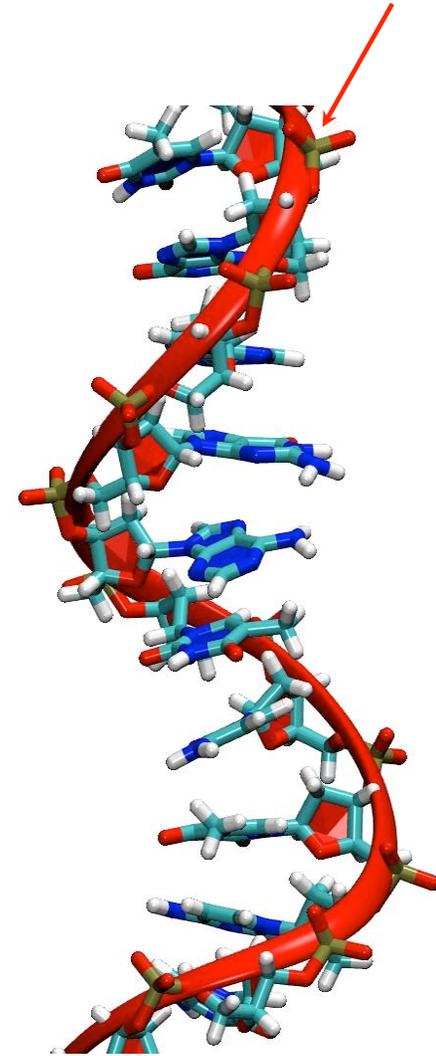


Double stranded DNA  
(persist. length ~50nm)



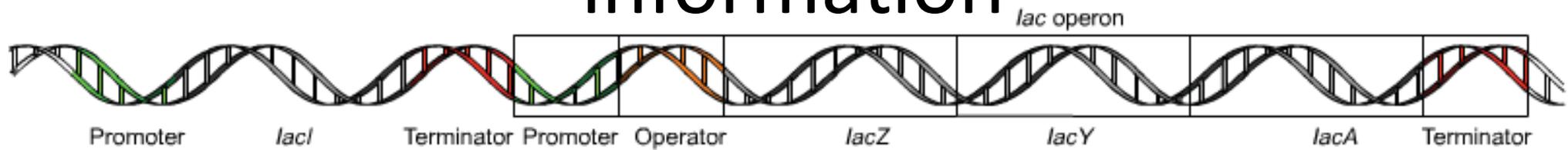
The sequence has direction:  
5'-AAGCTGGTTCAG-3'

**backbone**



Single stranded DNA  
(persist. length ~1.5nm)

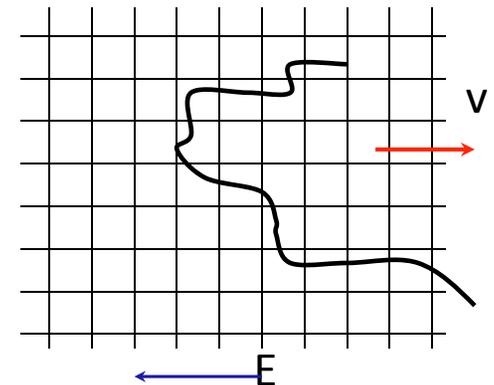
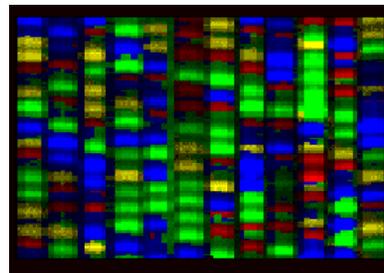
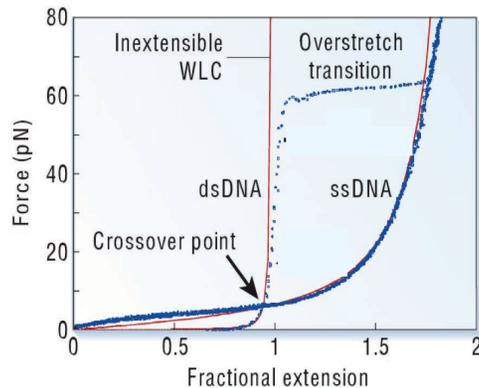
# The sequence contains biological information



Central dogma of molecular biology



# The physical properties enable functionality

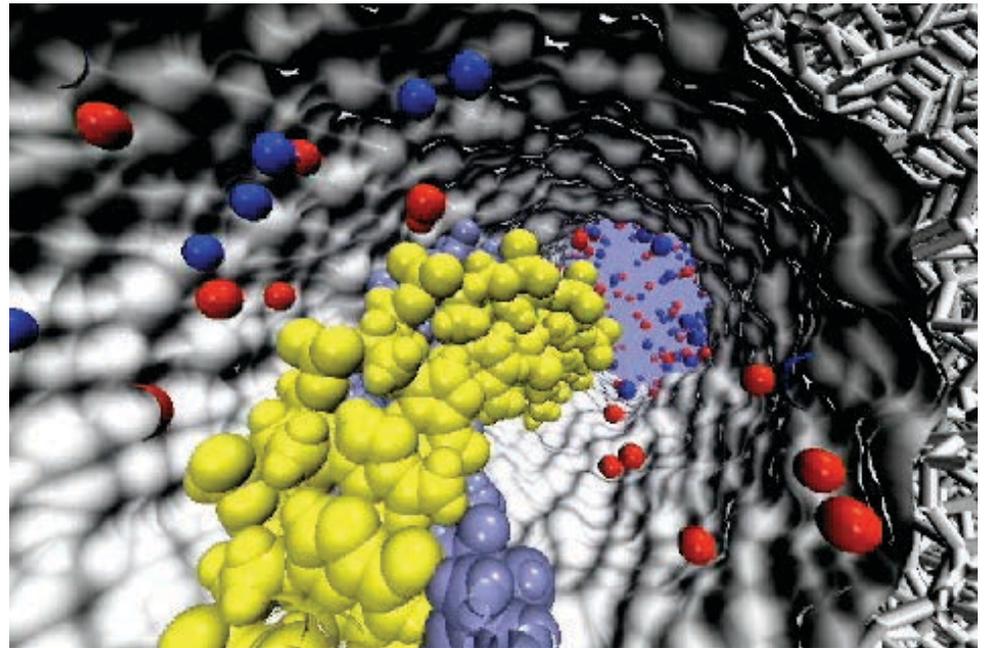


# Molecular dynamics simulations, a computational (force) microscope

Massive parallel computer  
Blue Waters, ~200,000



Atoms move according to  
classical mechanics ( $F=ma$ )



Time scale:  $\sim 0.1-100 \mu\text{s}$

Length scale: 10K - 100M  
atoms or  $(< 50 \text{ nm})^3$

Interaction between atoms is  
defined by molecular force field

# Journal of Physics

## Condensed Matter

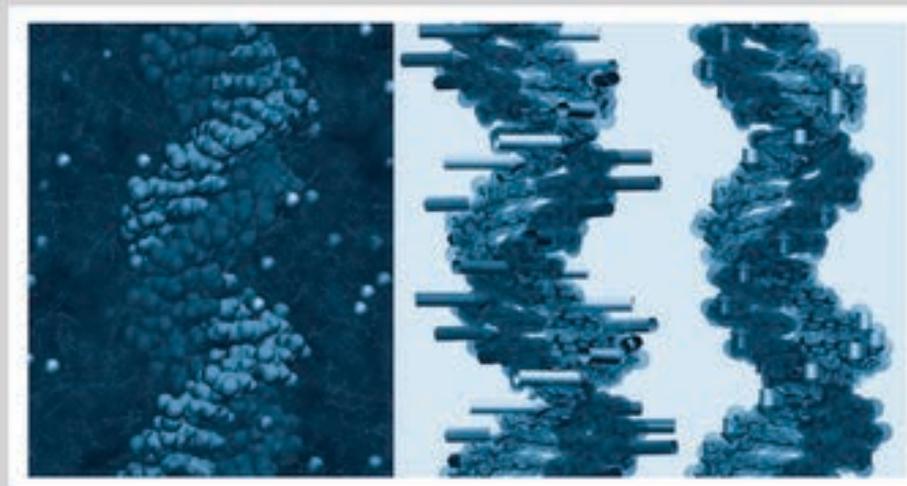
*Journal of Physics: Condensed Matter* 26: 413101 (2014)

Volume 26 Number 41 15 October 2014

### Topical review

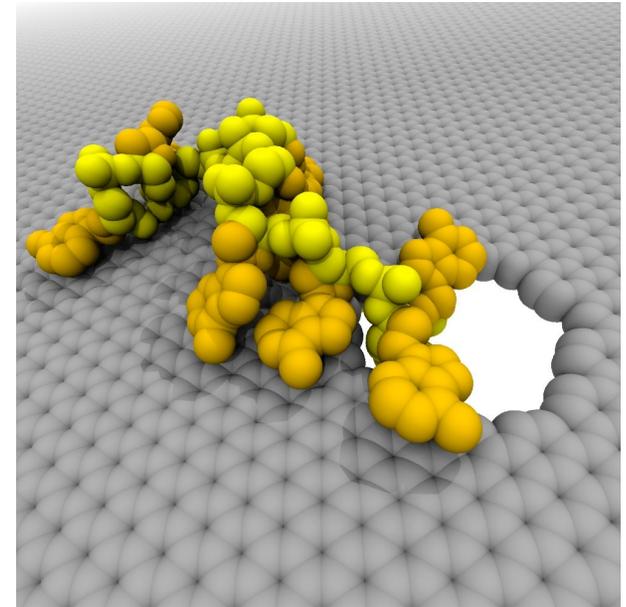
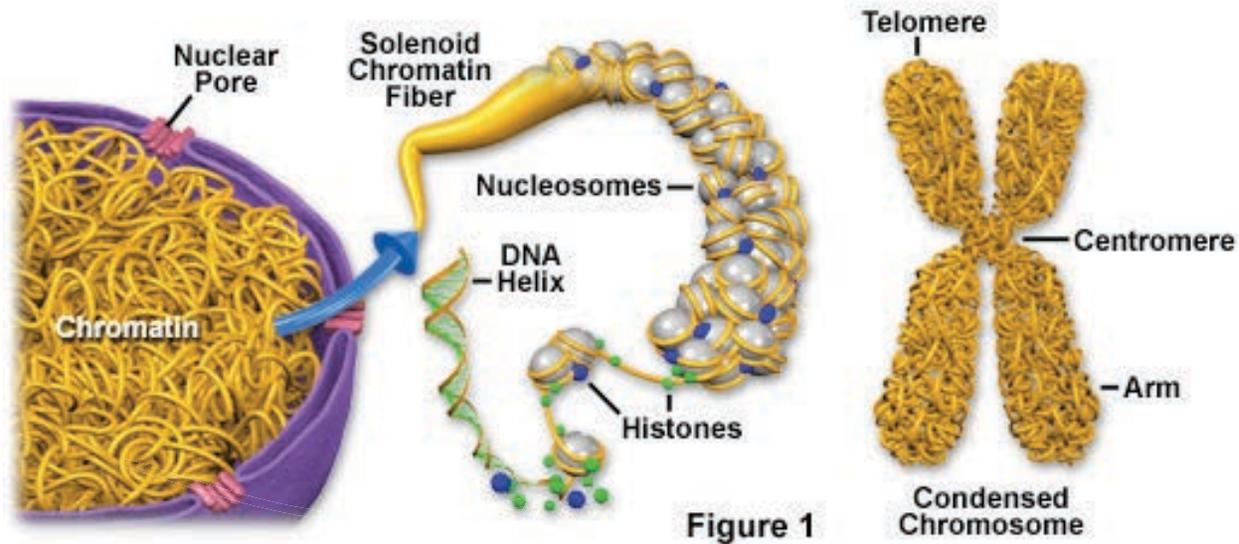
#### Close encounters with DNA

*C Maffeo, J Yoo, J Comer, D B Wells, B Luan and A Aksimentiev*



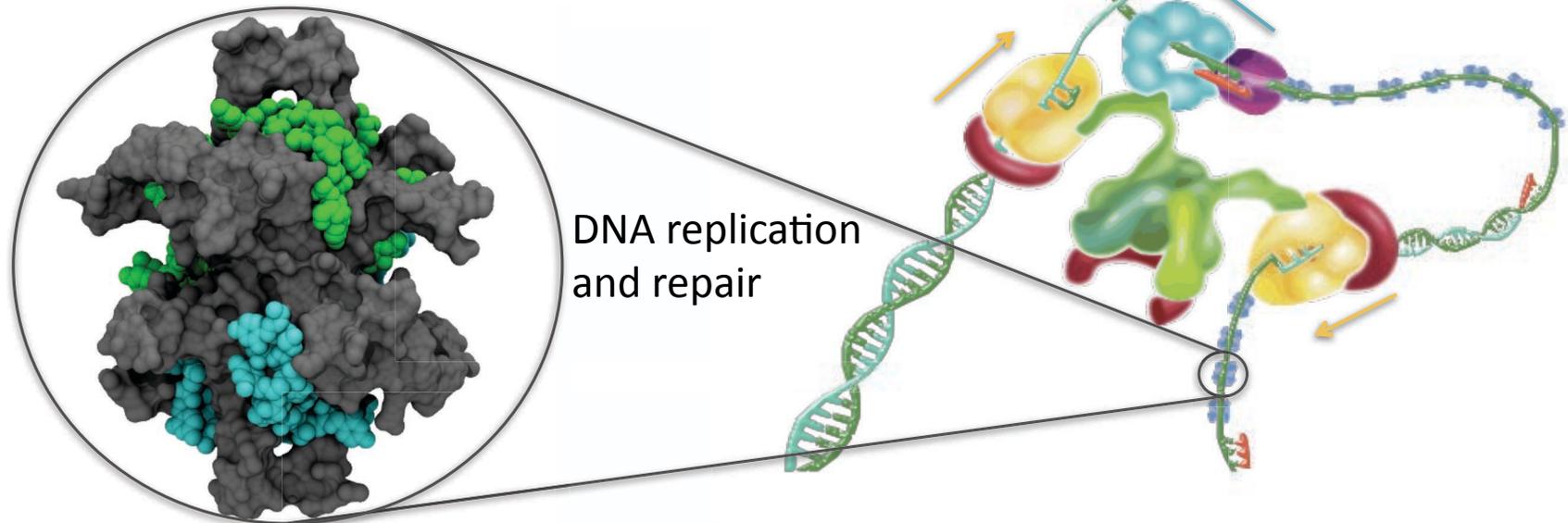
# DNA systems

Chromatin and Condensed Chromosome Structure

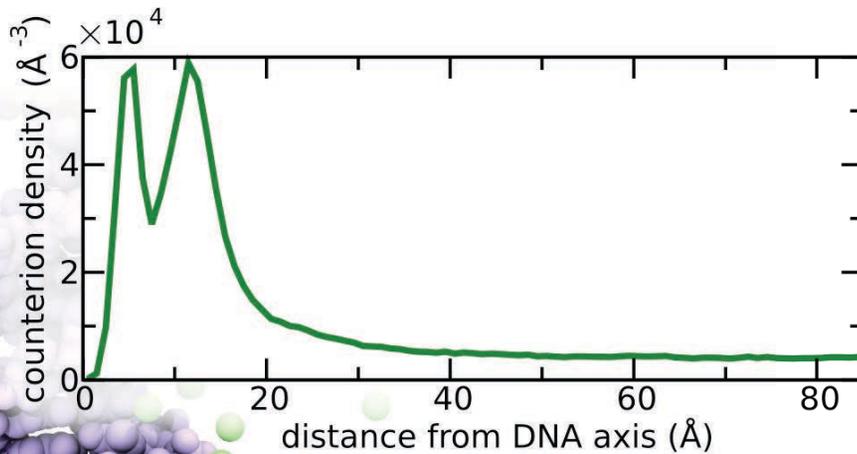
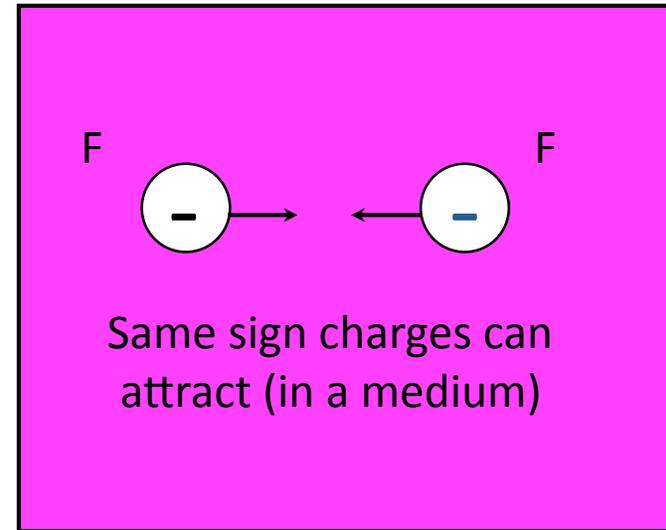
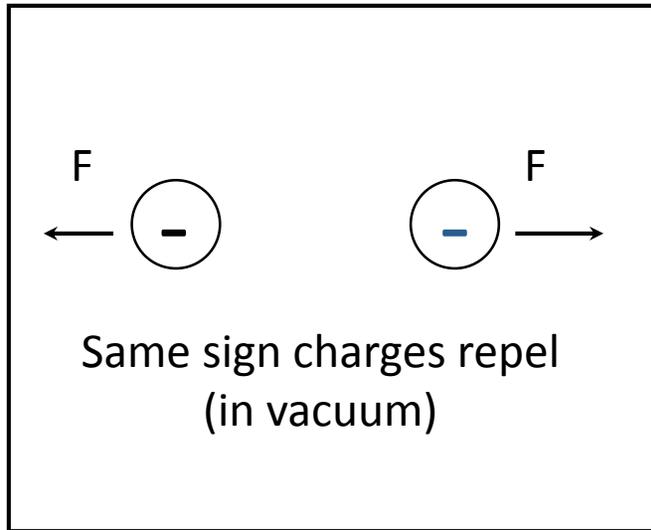


<http://micro.magnet.fsu.edu/cells/nucleus/chromatin.html>

Graphene nanopore sequencing

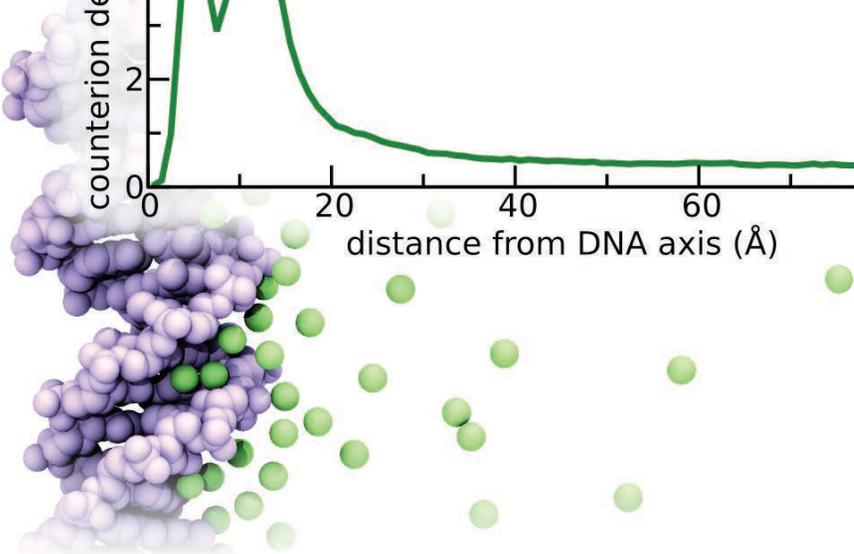


# Interesting physical properties



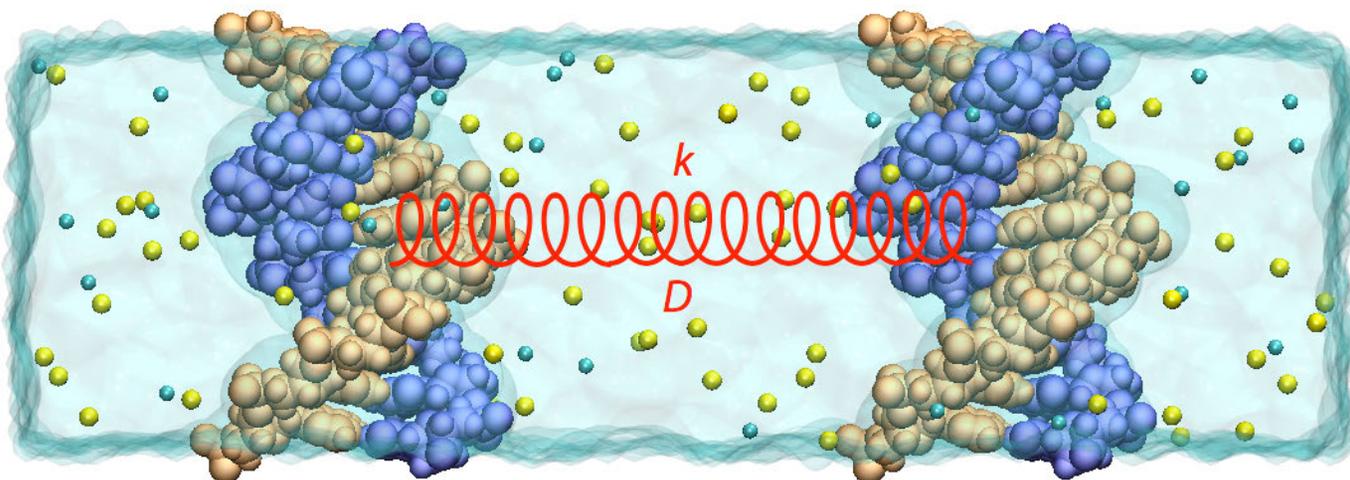
Effective attraction between DNA is observed when counterions have charge  $\geq 2e$

DNA lives in water and is surrounded by counterions

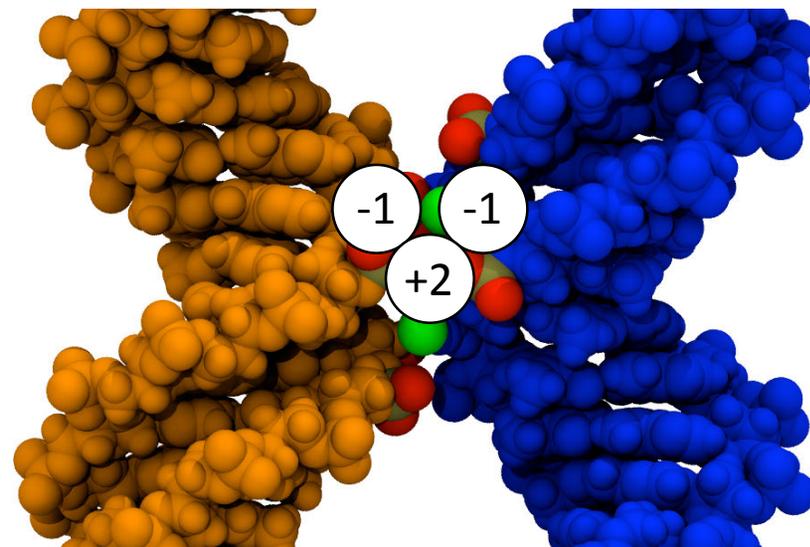
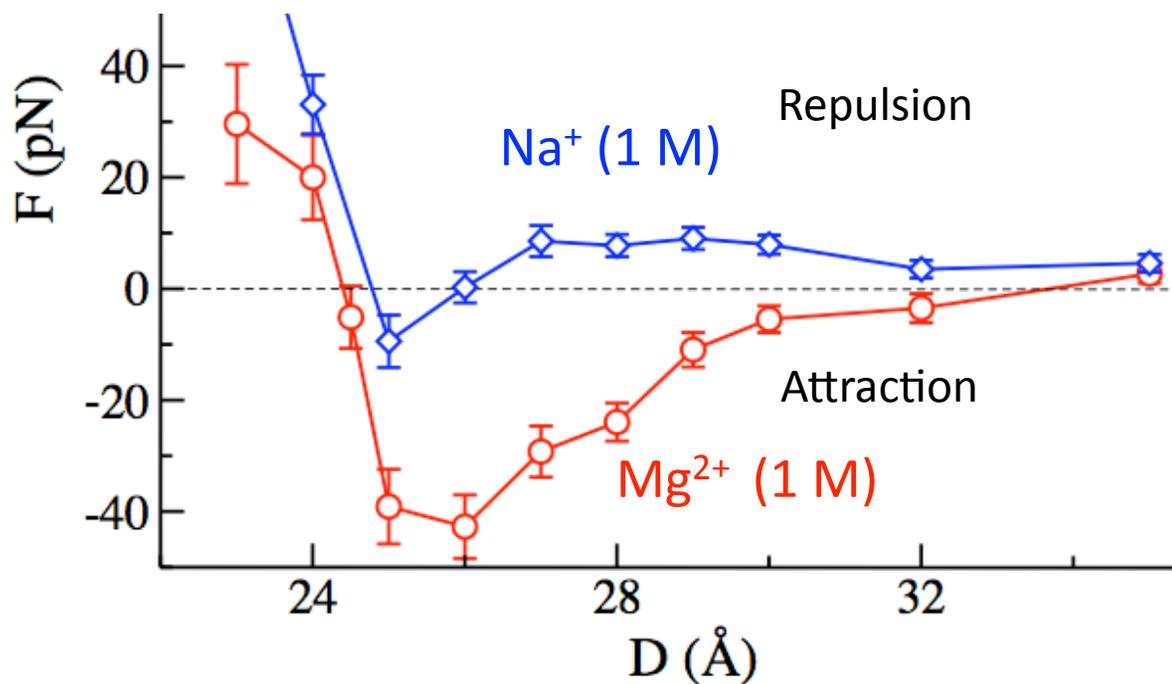


# Direct MD simulation of DNA-DNA force

*J. Am. Chem. Soc.* 130, 15754 (2008)

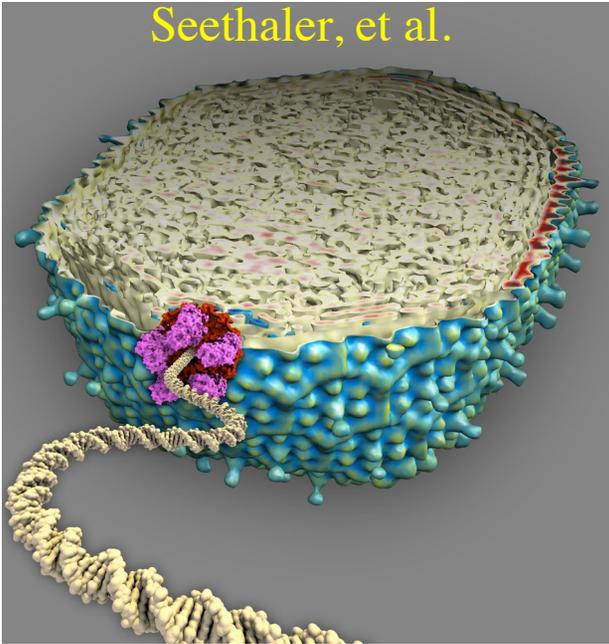


A virtual spring measures the effective force



# MD simulation of dense DNA arrays

Seethaler, et al.



## What we control

DNA density (or harmonic constraint radius)

$[\text{Na}^+]_{\text{buf}} \sim 200 \text{ mM}$

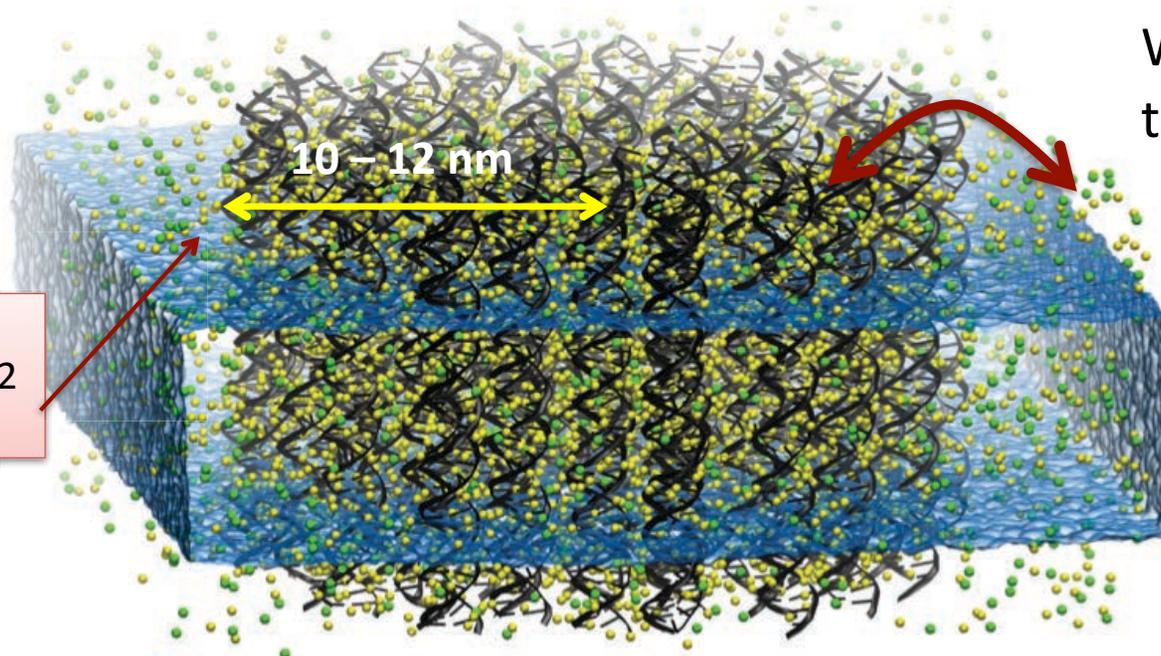
$[\text{Mg}^{2+}]_{\text{buf}} \sim 0 \text{ or } 20 \text{ mM}$

## What we measure

Pressure as a function of [ion] & [DNA]

DNA / ion distribution:

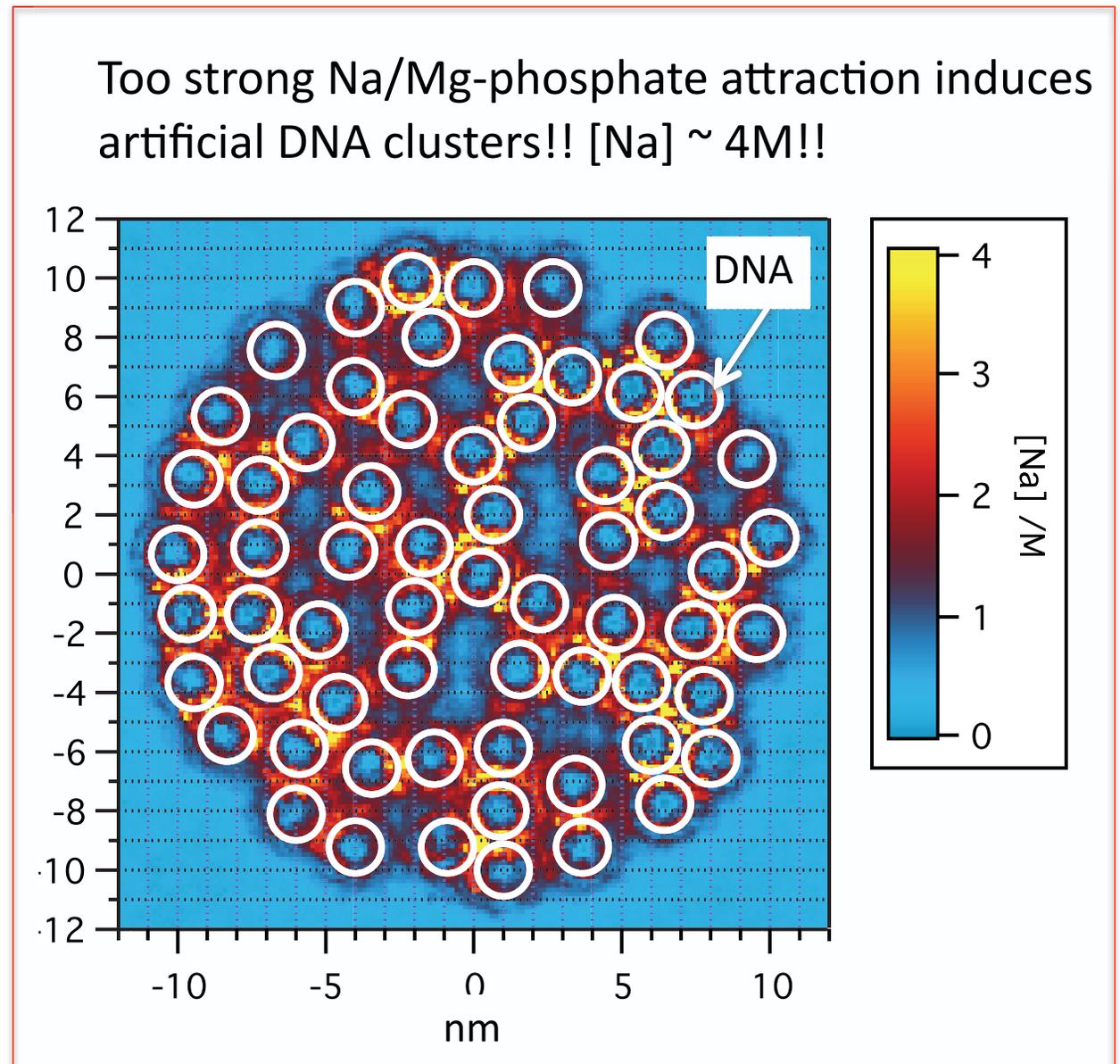
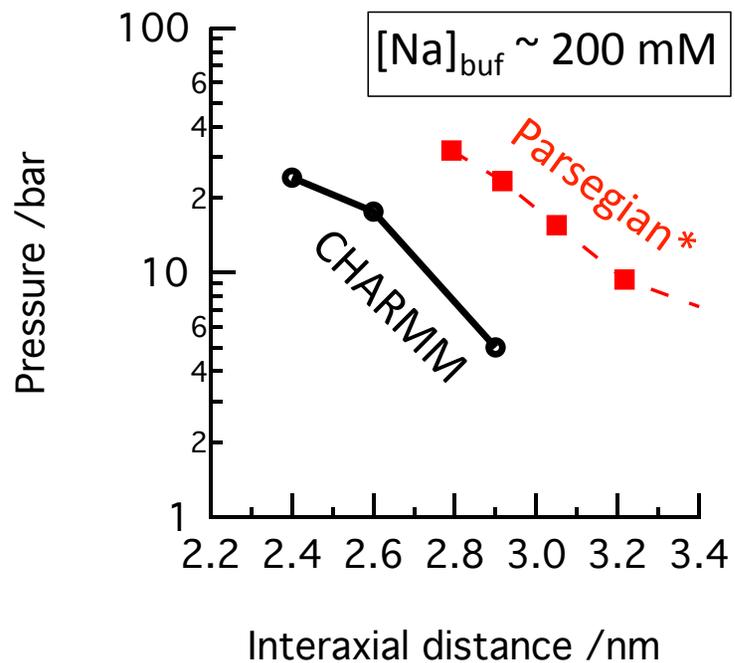
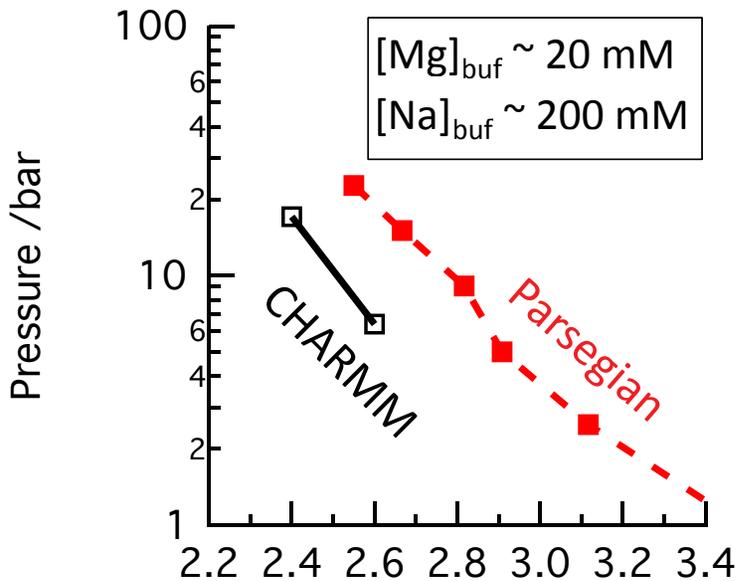
DNA / ion diffusion inside the array



Water / salt free to move

Cylindrical harmonic constraint (radius of 10 - 12 nm) only against DNA

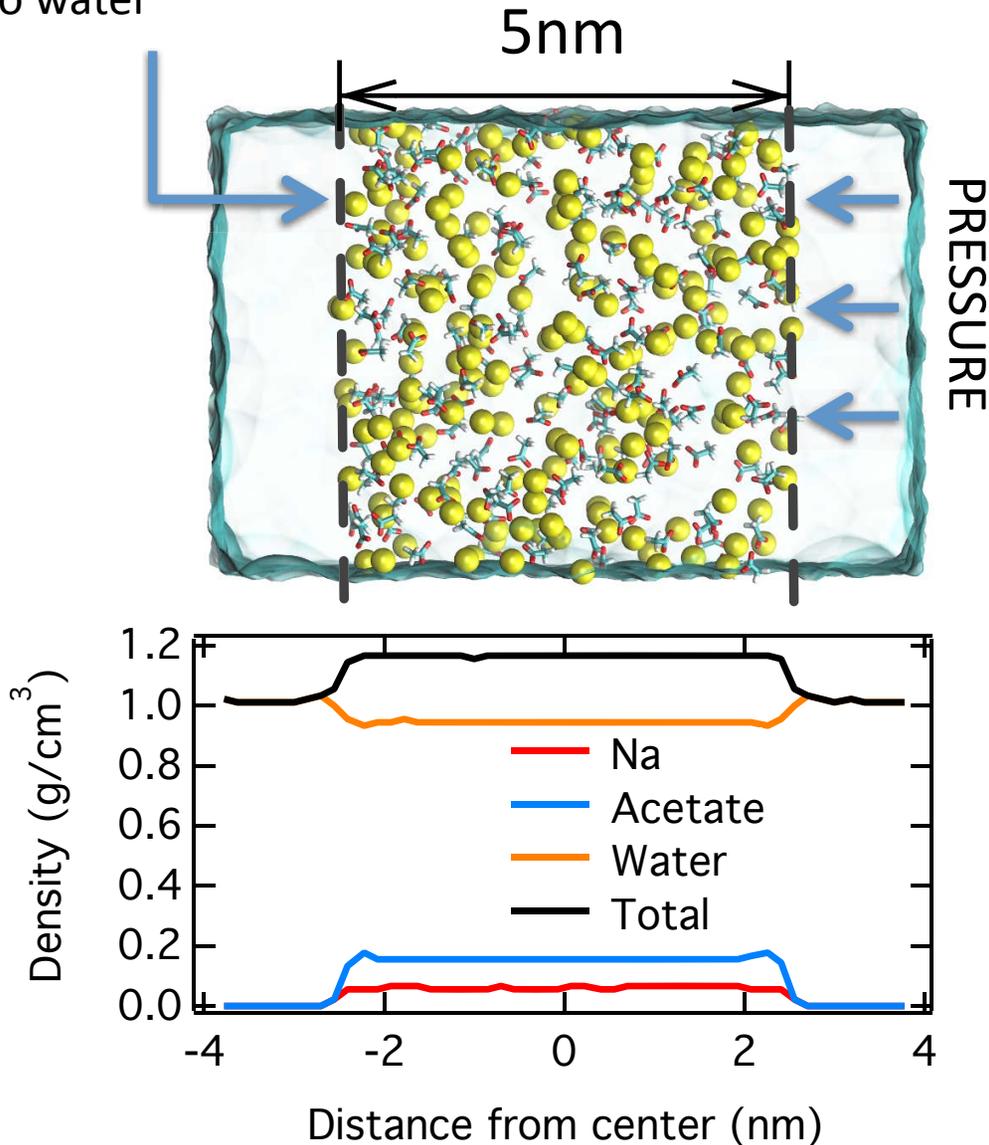
# The standard MD force field fails to predict internal pressure of a DNA array



\* Rau, D. C.; Lee, B.; Parsegian, PNAS (1984)

# Recalibrate ion-DNA parameters using osmotic pressure data

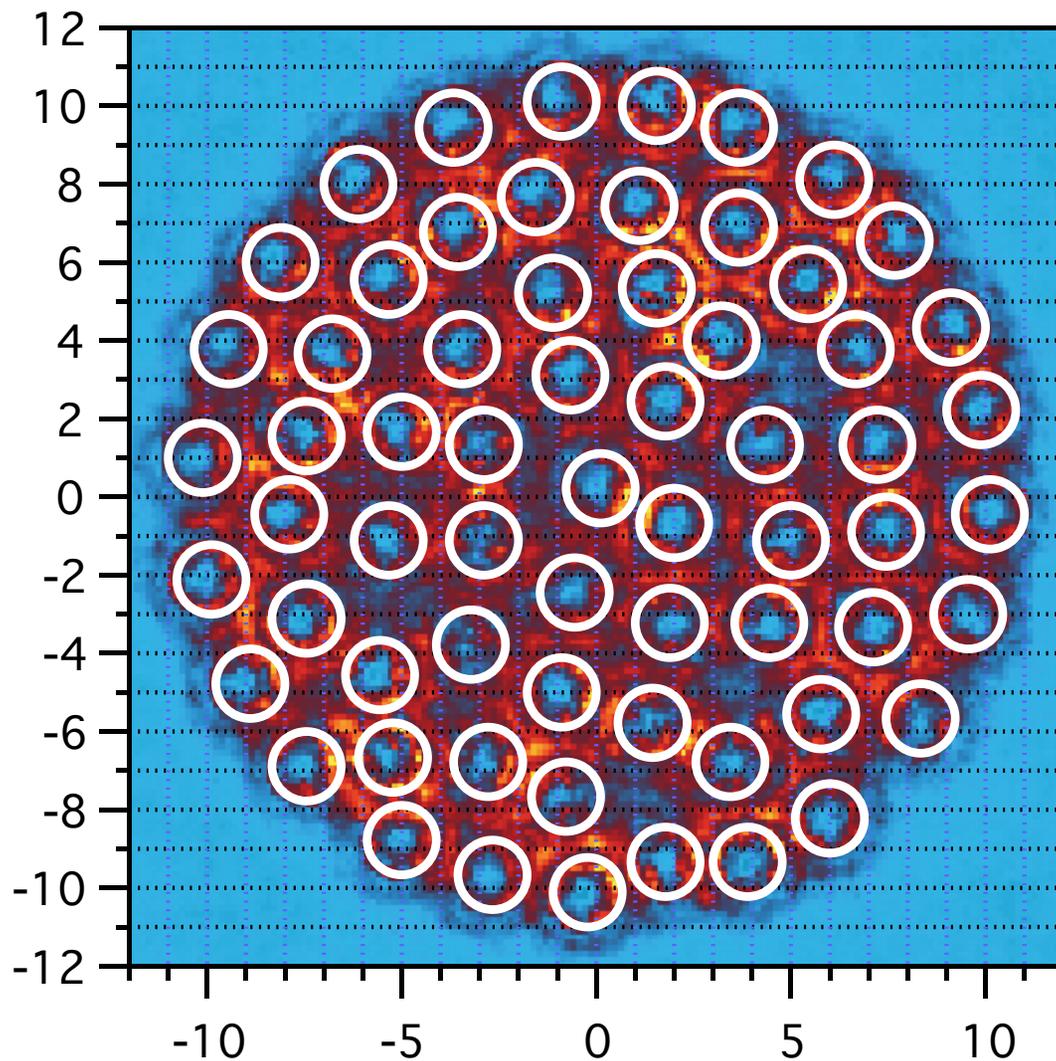
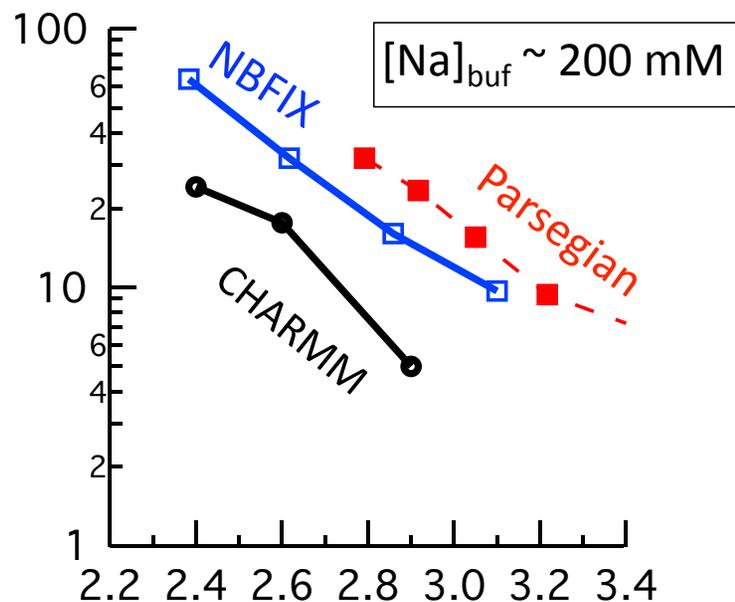
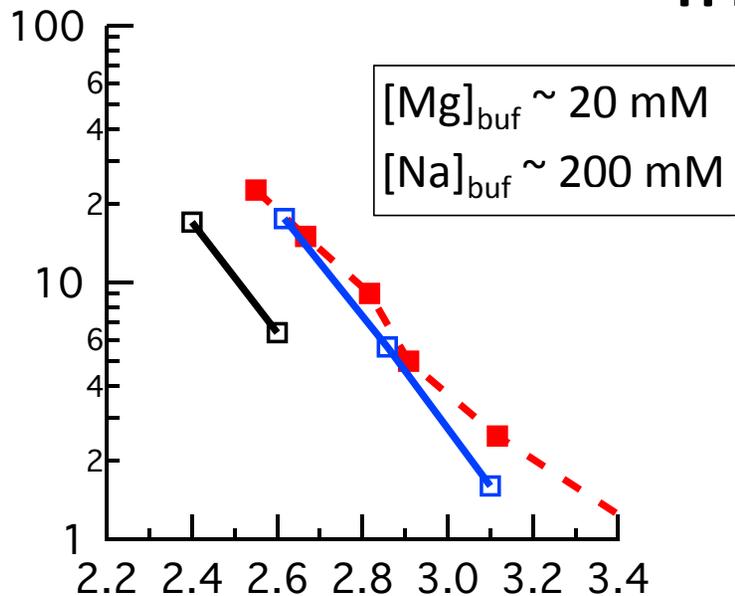
permeable only  
to water



- Osmotic pressure is directly related to ion-pair formation:  $\pi = \phi cRT$
- Pros: modify only ion-DNA phosphate interaction, without altering ion-water interaction.
- Cons: nothing.

\* Luo & Roux, JPCL (2009)

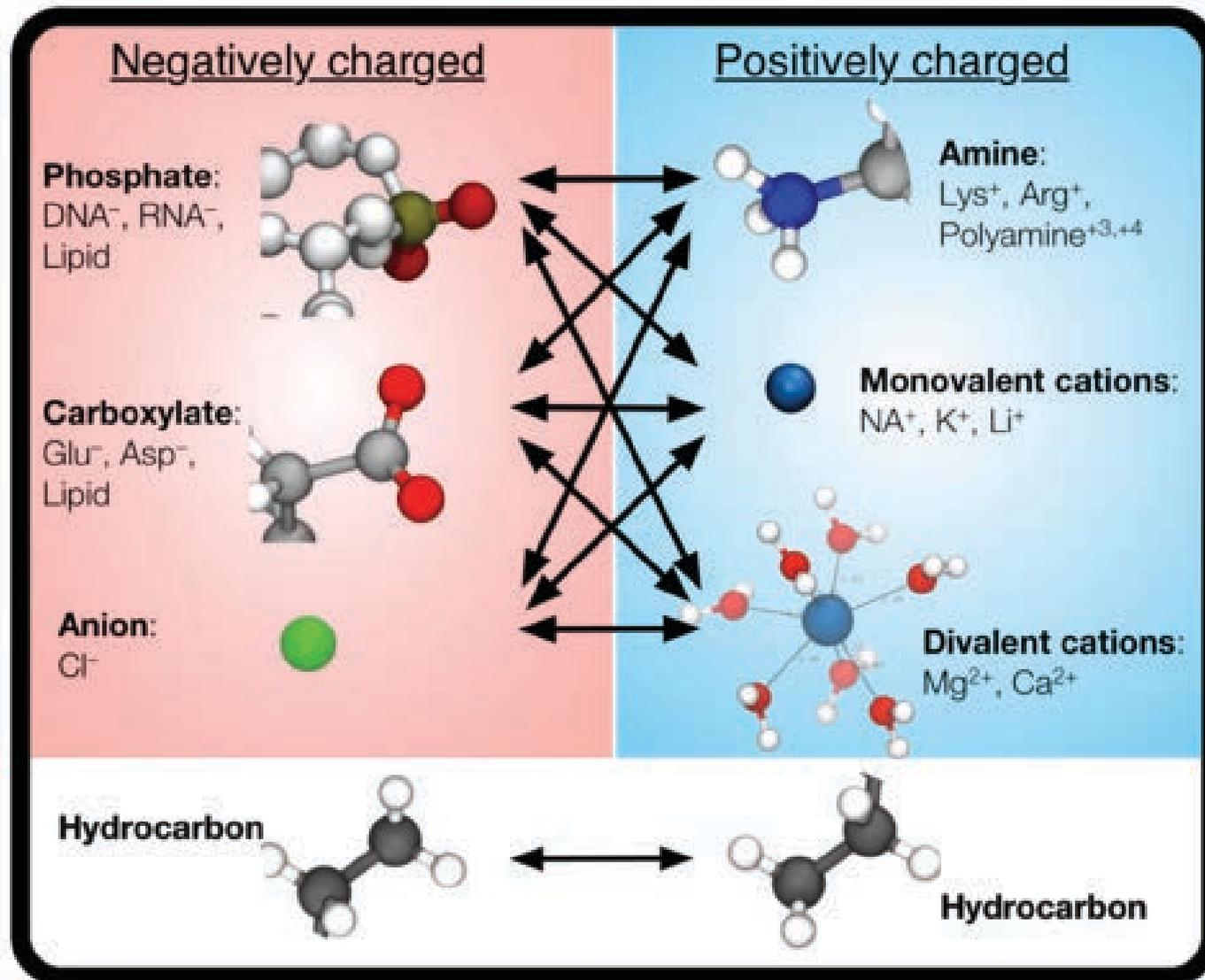
# Improved parametrization of ion-DNA interactions



*J. Phys. Chem. Lett.* 3:45 (2012)

Interaxial distance /nm

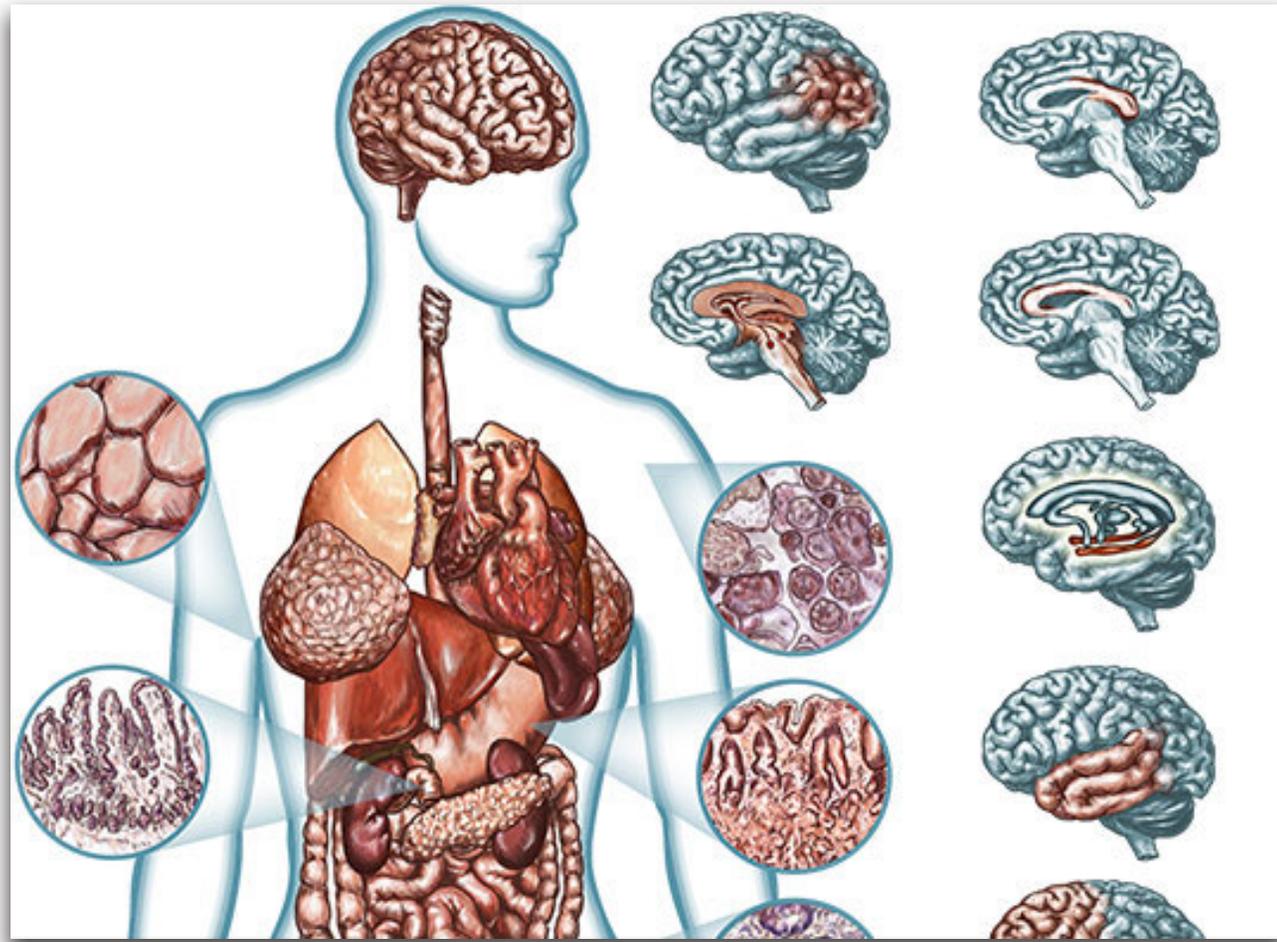
# CUFIX: Accurate parameterization of non-bonded interactions



<http://bionano.physics.illinois.edu/CUFIX>

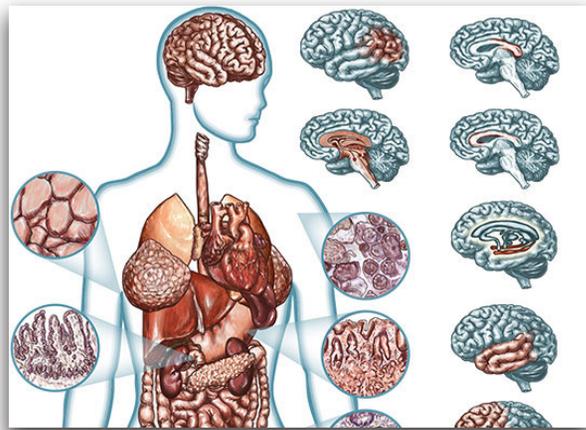
# Cells with identical genome can have different functions

---



- All our cells contain identical genome sequence that defines ~20,000 genes.
- Depending on the cell type, different sets of genes are turned on.

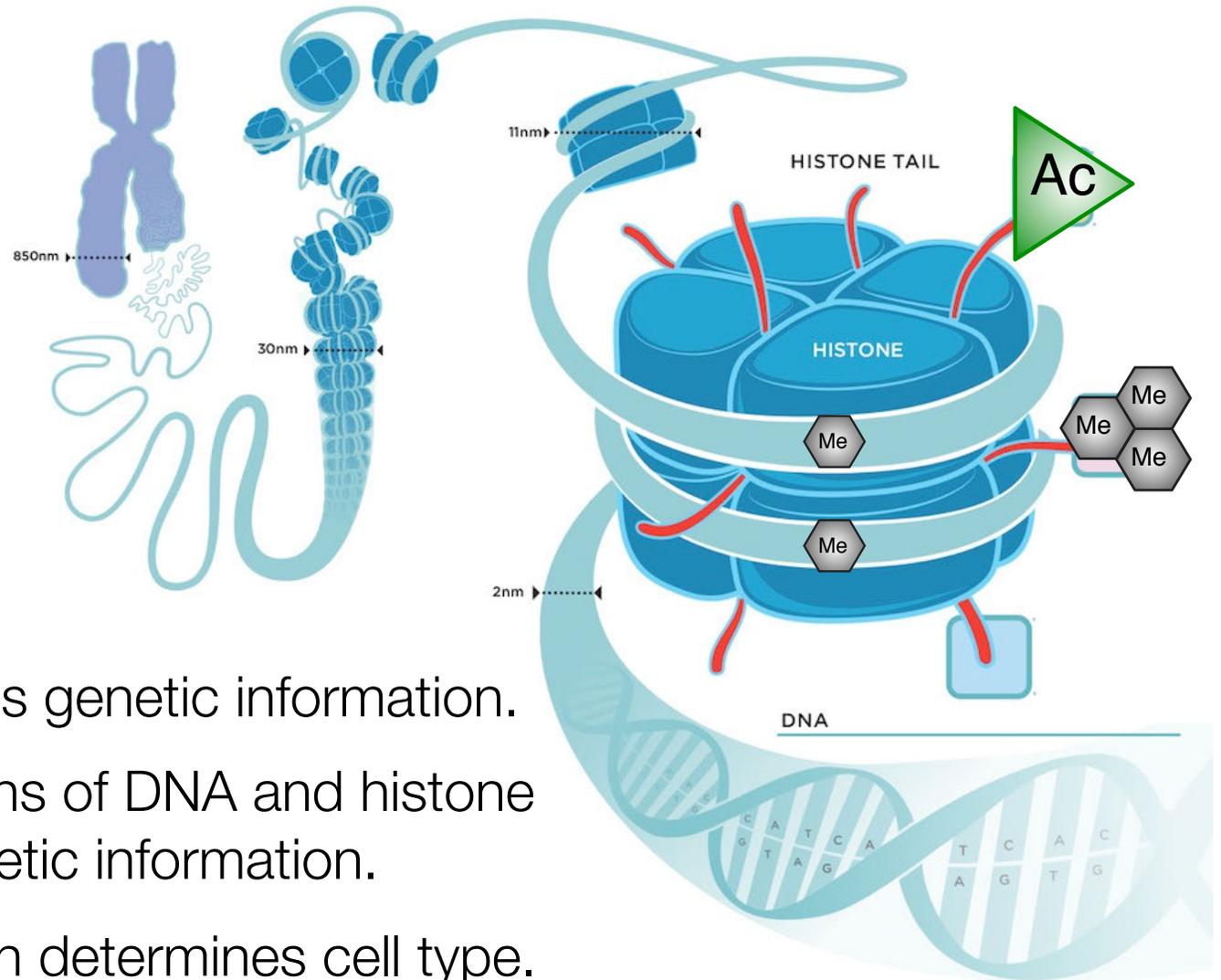
# Beyond DNA sequence: Epigenetic regulation



CHROMOSOME

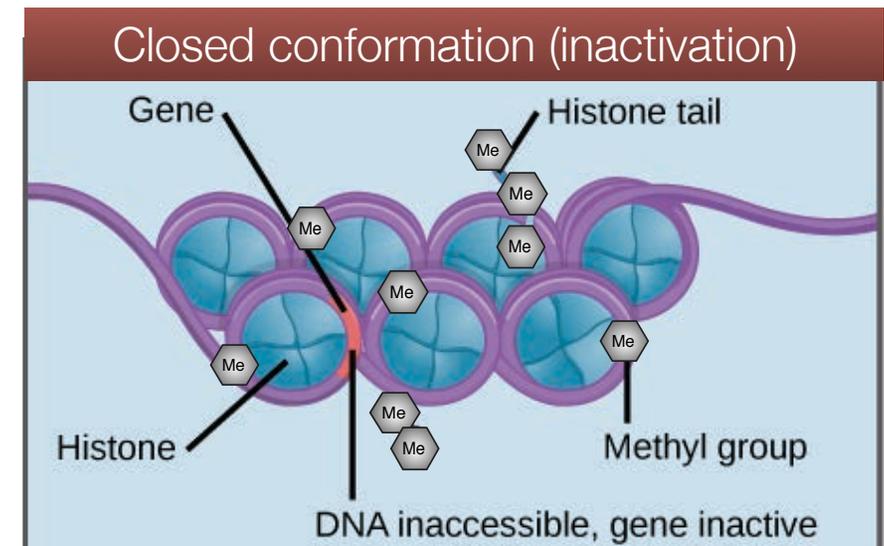
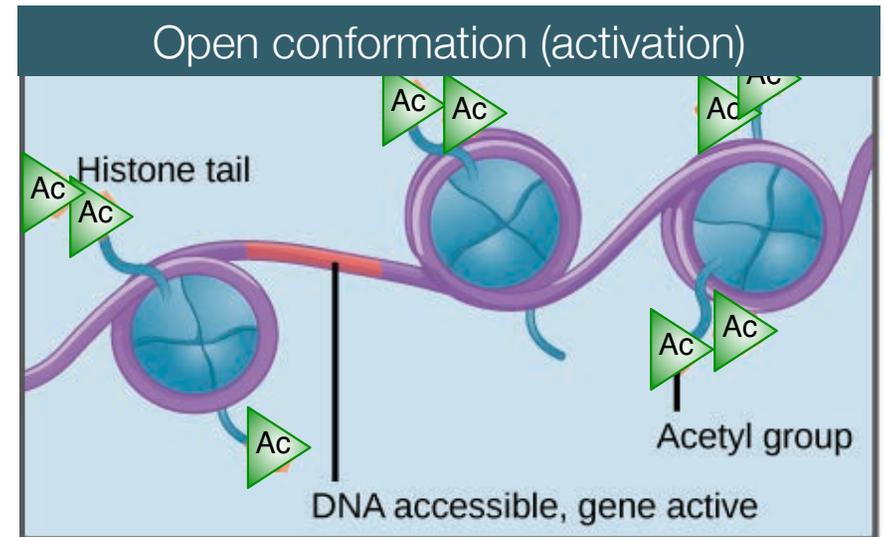
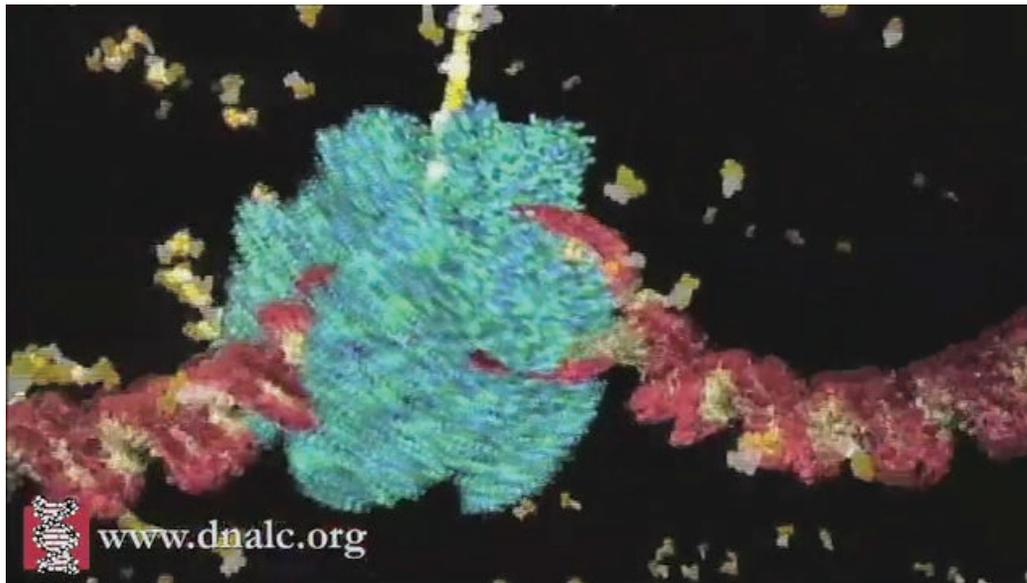
CHROMATIN FIBRE

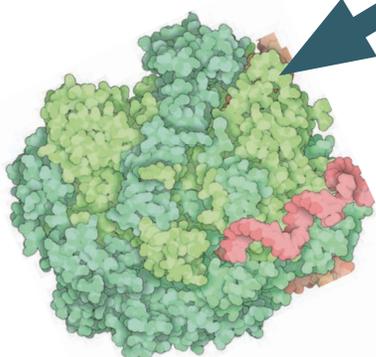
NUCLEOSOME



- DNA sequence carries genetic information.
- Chemical modifications of DNA and histone proteins carry epigenetic information.
- Epigenetic information determines cell type.

# DNA compaction regulates gene transcription

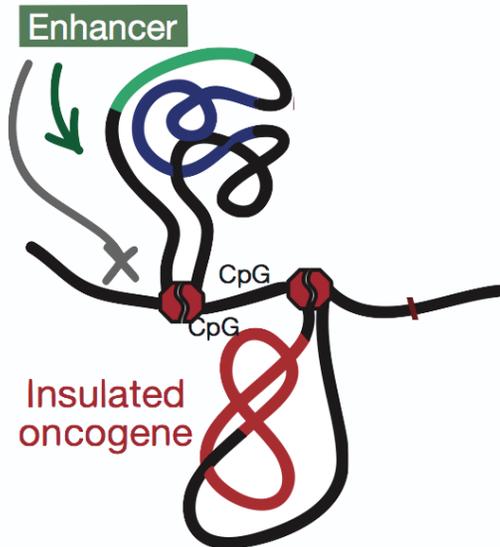


 **RNA polymerase** reads DNA sequence.

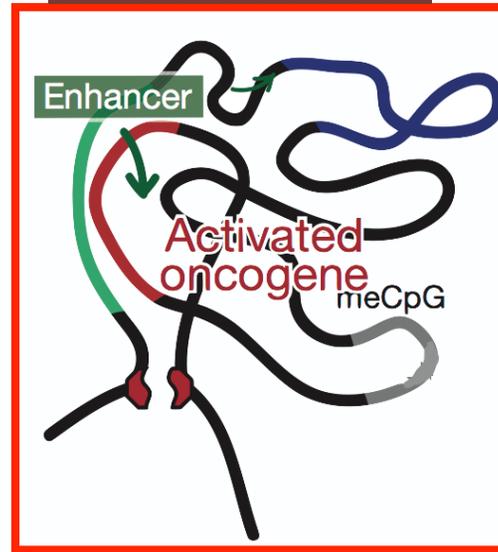
For a given cell, only a subset of ~20,000 genes is accessible to RNA polymerase.

# DNA organization in chromosome is a key to understanding development and disease

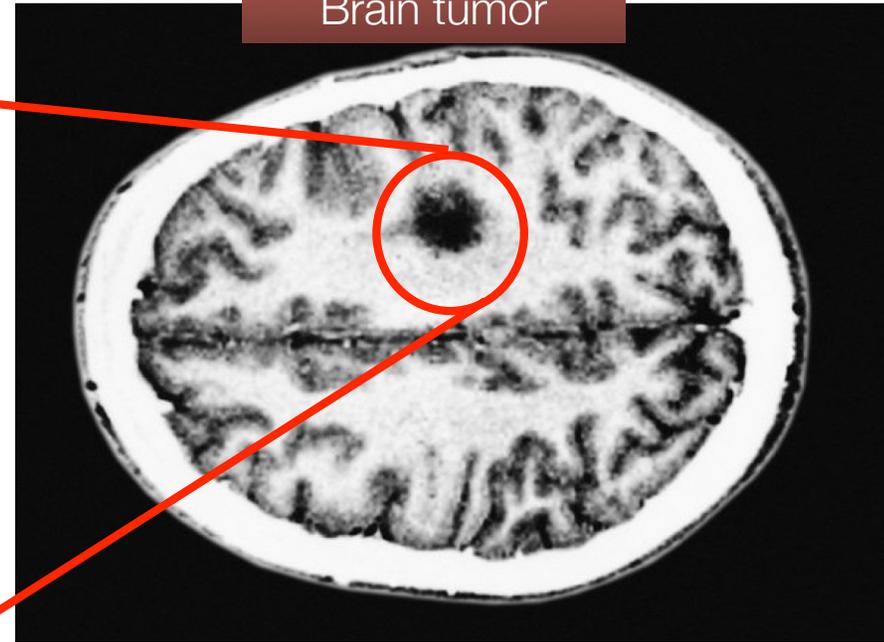
Inactive oncogene  
in normal neurons



Active oncogene  
in brain tumors



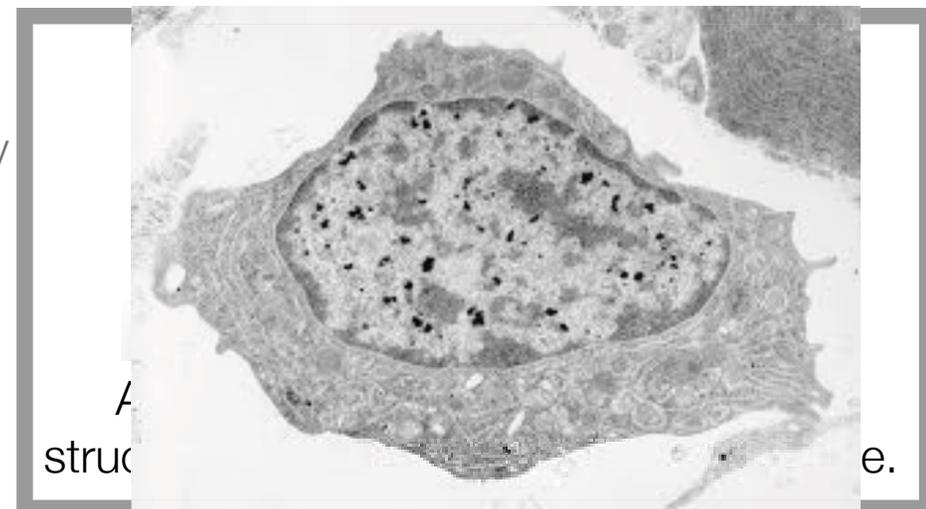
Brain tumor



Bernstein and coworkers, *Nature* (2015)

Highlight in New York Times on Dec 23, 2015

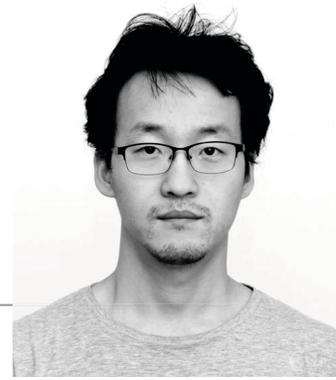
- 3D organization of chromatin changes dynamically depending on **developmental** & **aging** stages.
- **Cancer** cells also have their own chromatin organization.



**DNA senses the  
sequence of neighbors**



# DNA telepathy (?!)



Jejoong Yoo

Your sequence  
I sense...

The homology  
I sense in  
you...



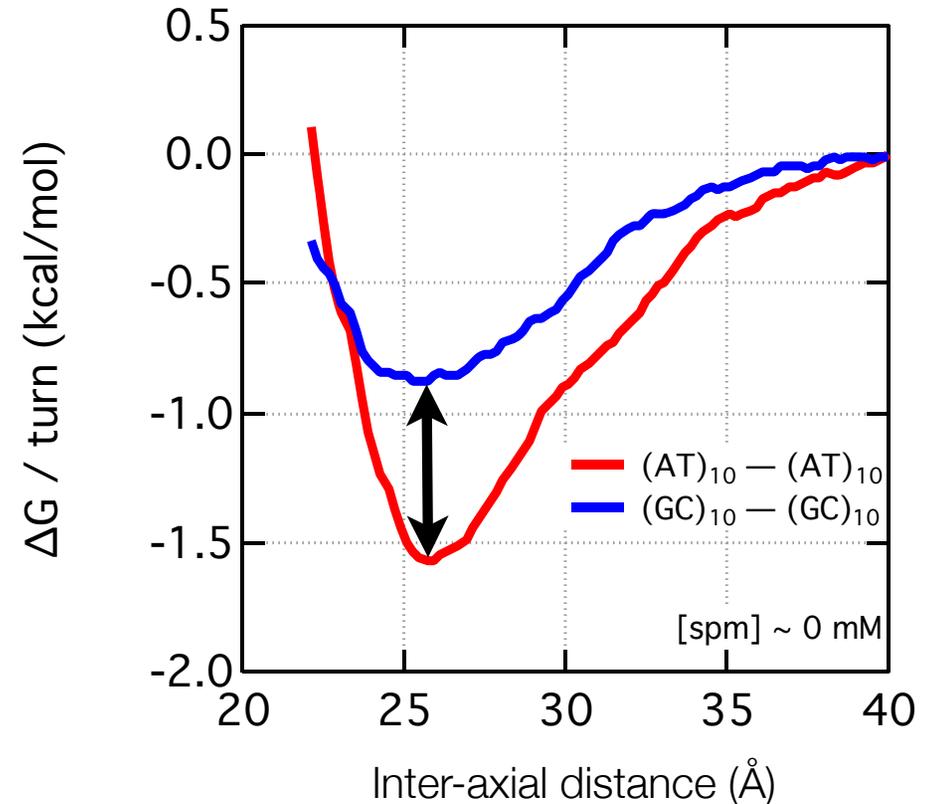
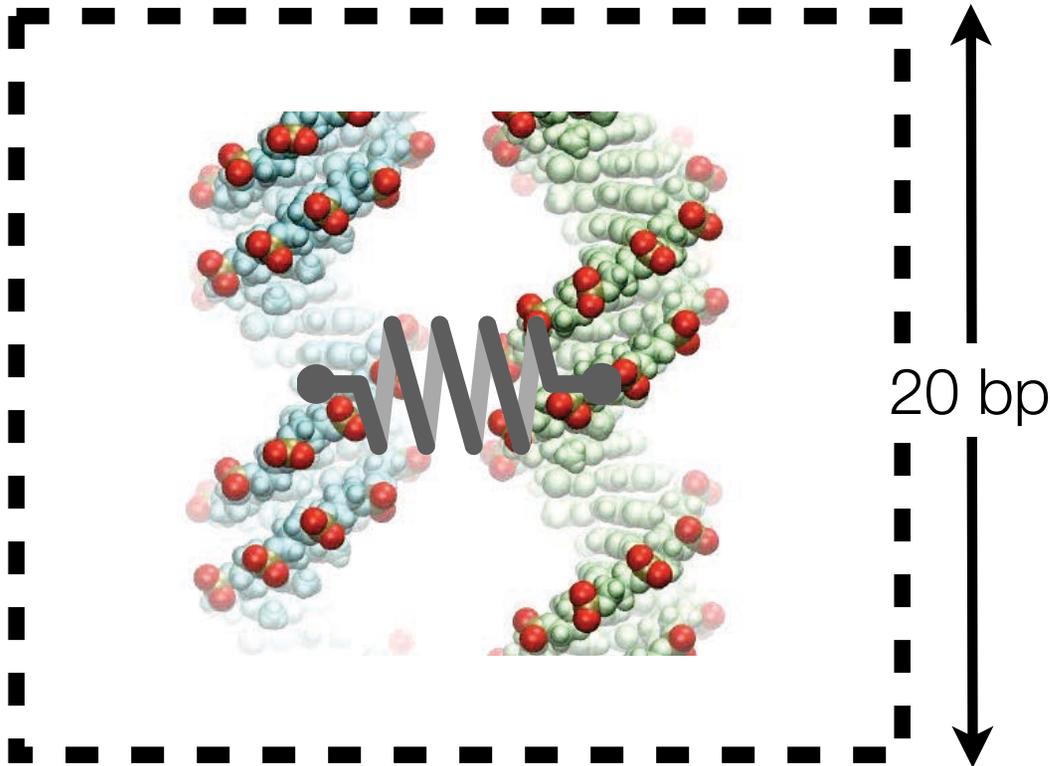
Leikin and Kornyshev

*Journal of Physical Chemistry B* (2008)

DNA can recognize complementary  
sequence without any mediator protein

- **DNA telepathy** means sensing and colocalization of homology sequences
- But, often debated due to lack of evidence.
- We validate this hypothesis.

# Free energy calculations predict **stronger attraction** for DNA molecules having **higher AT contents**



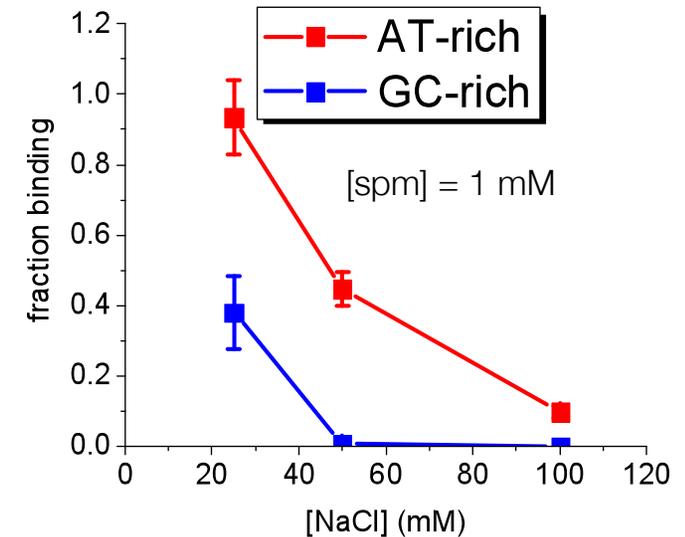
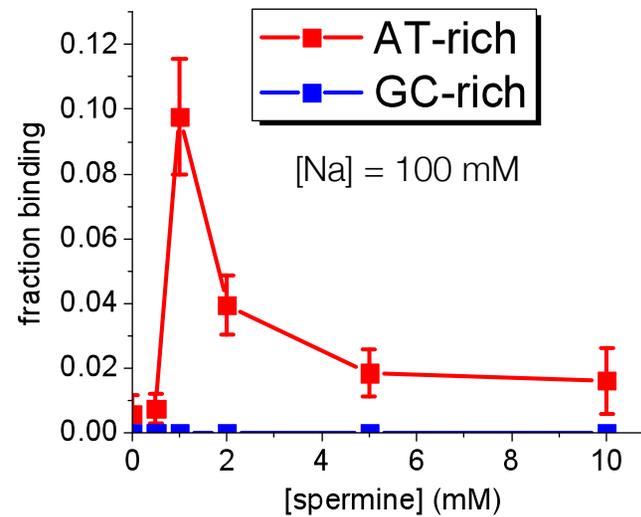
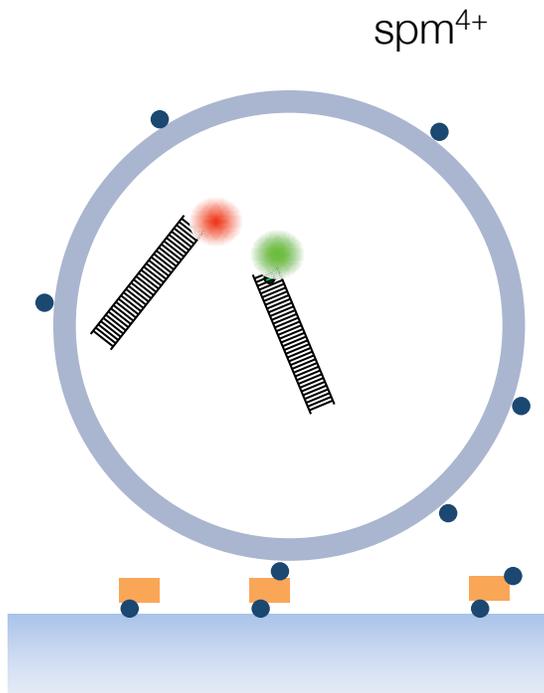
- AMBER99bsc0 force field with custom refinement of amine-phosphate interactions.
- Sub-mM level of spermine; just enough to neutralize DNA.

- Fully atomistic including explicit water.
- Umbrella sampling.

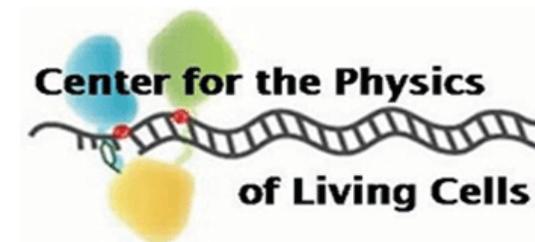
# FRET experiments confirm MD predictions



Hajin Kim (Ha group)

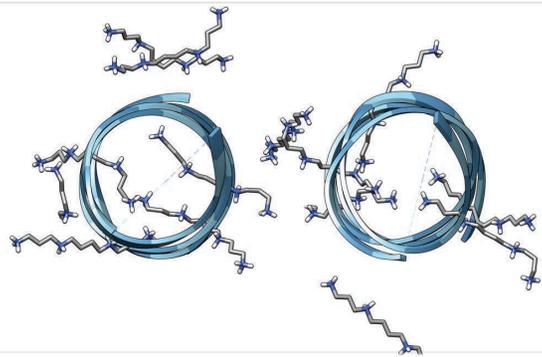


- FRET signal indicates binding of two double stranded DNA

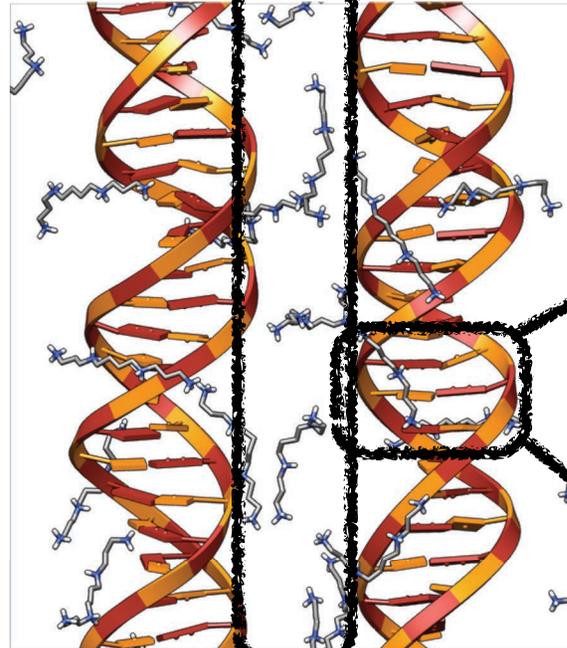
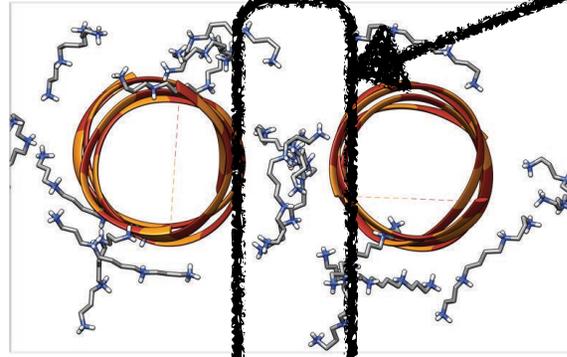


AT-rich segments form **clusters** better because they **share** polyamines with neighbors

**(GC)<sub>10</sub>**    **(GC)<sub>10</sub>**

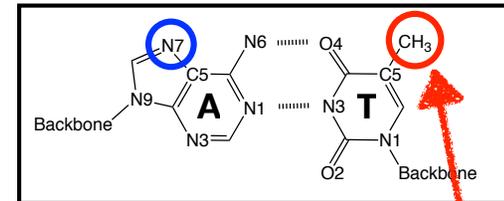
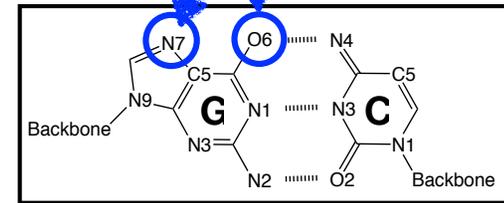


**(AT)<sub>10</sub>**    **(AT)<sub>10</sub>**

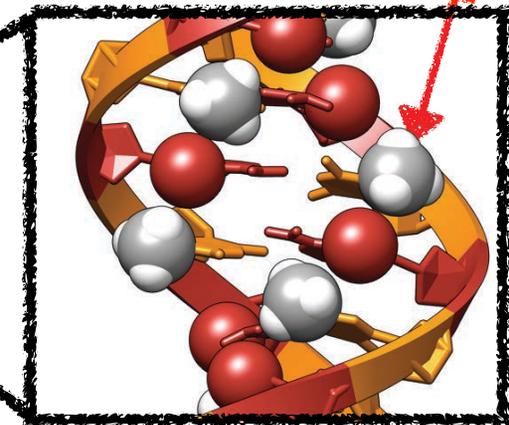


“Bridging” polyamines

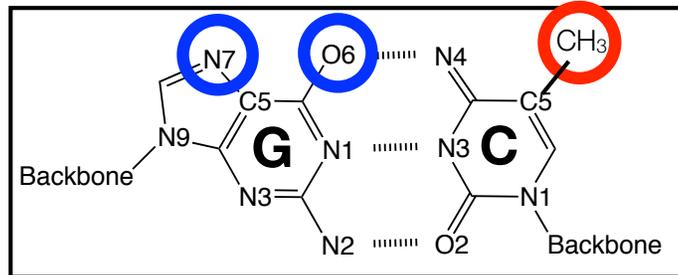
Spermine binding site



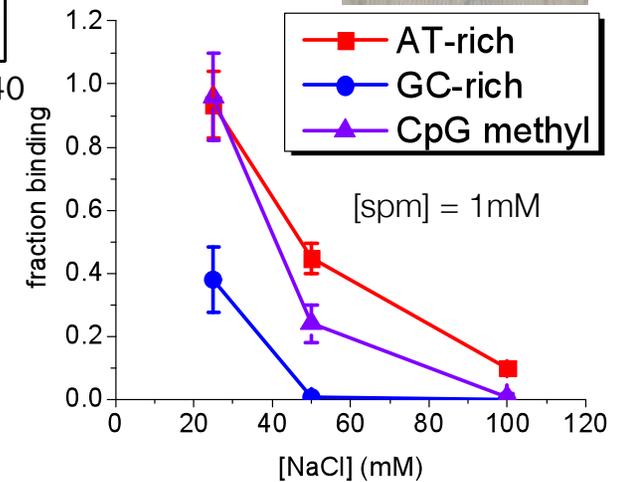
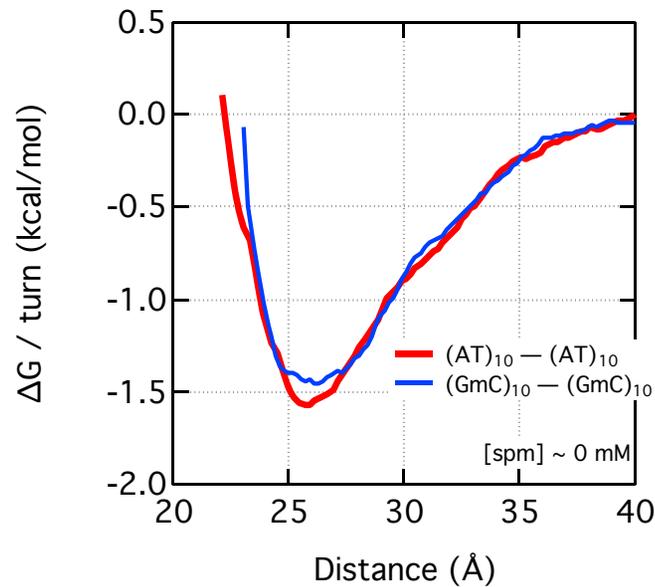
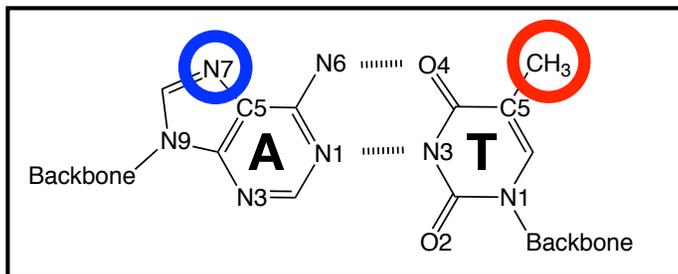
Methyl = Binding blocker



# Methylated CpG is as attractive as AT



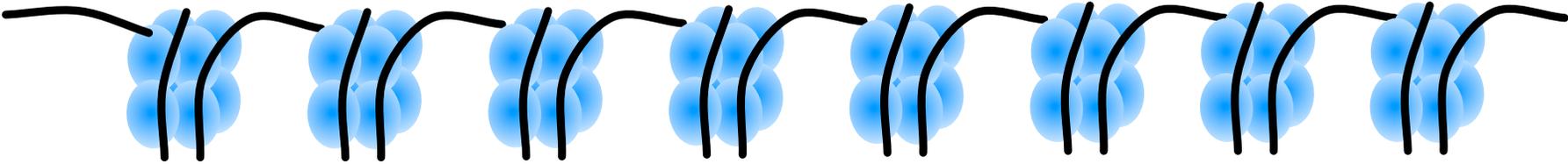
~~⊗~~



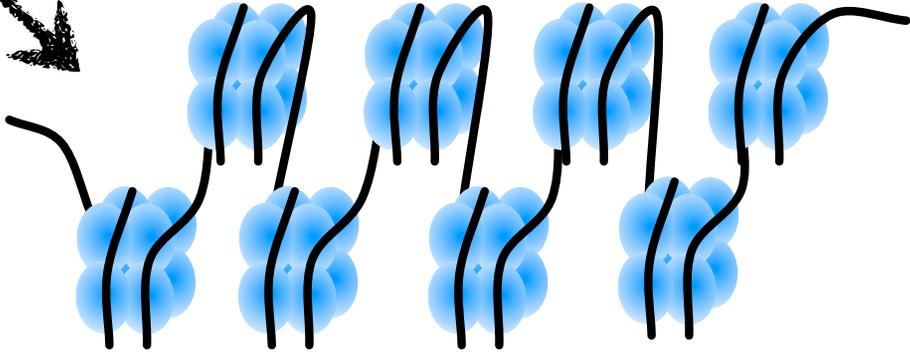
- Possible epigenetic gene inactivation mechanism ?

# Implications to chromatin folding & gene regulations

Gene-rich **GC-rich** domains  
express actively.

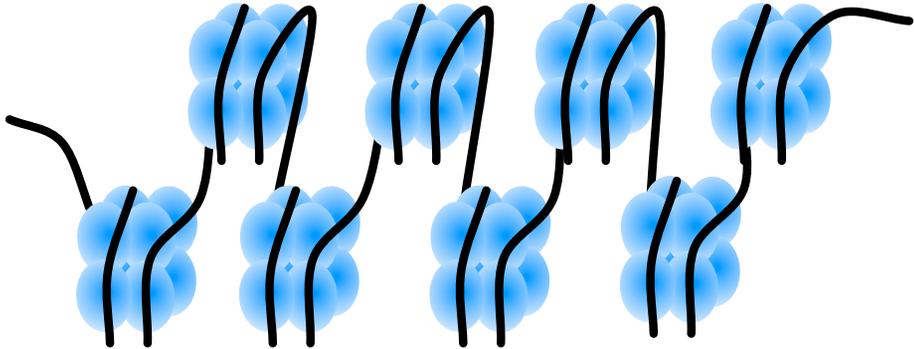


Methylation  
Demethylation

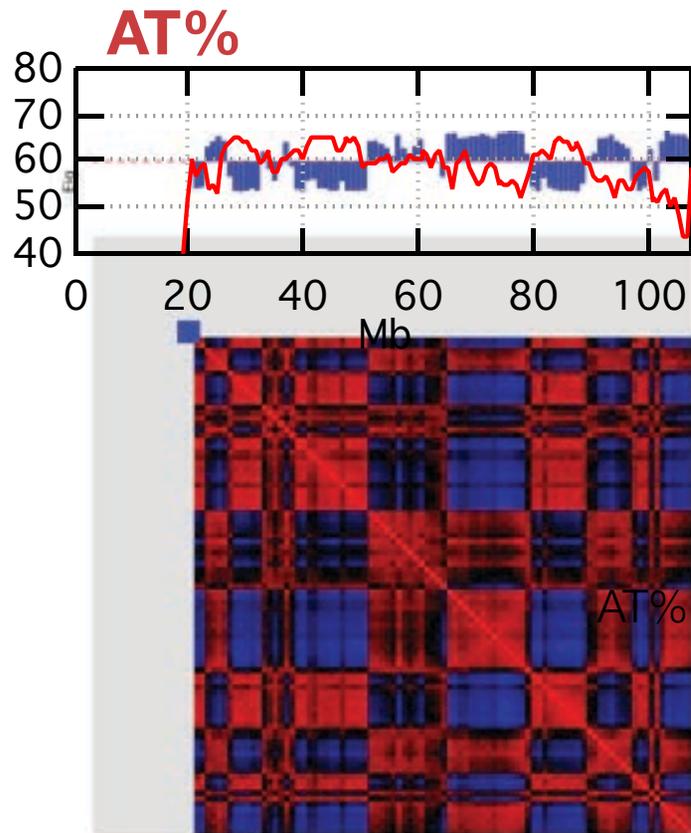


**Methylation** turns off GC-rich domains by compaction.

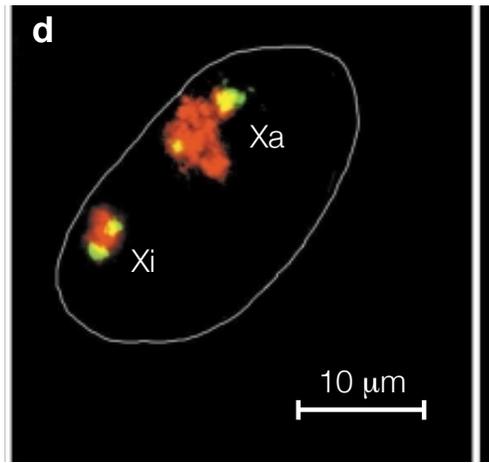
Gene-poor **AT-rich** domains are  
condensed permanently.



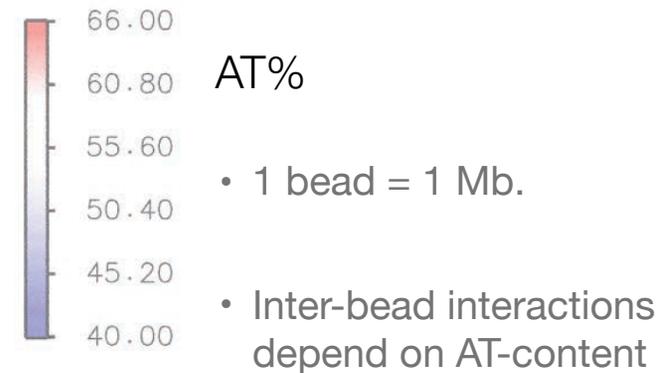
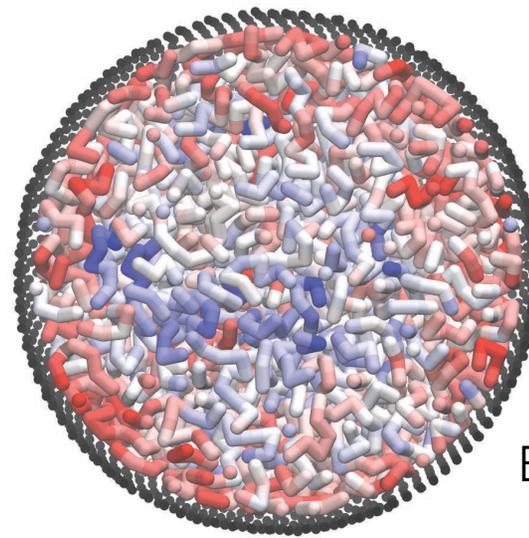
# Implications to chromatin folding & gene regulations



chromosome 14



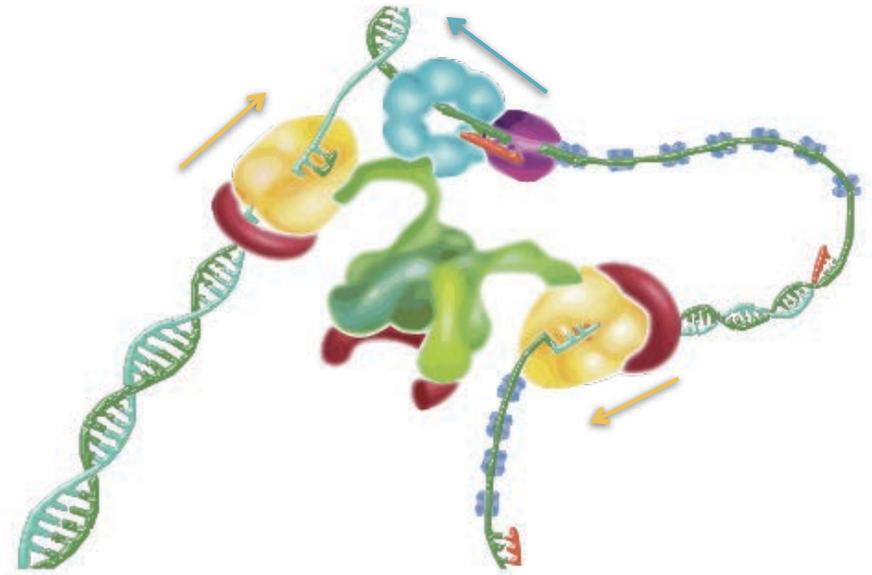
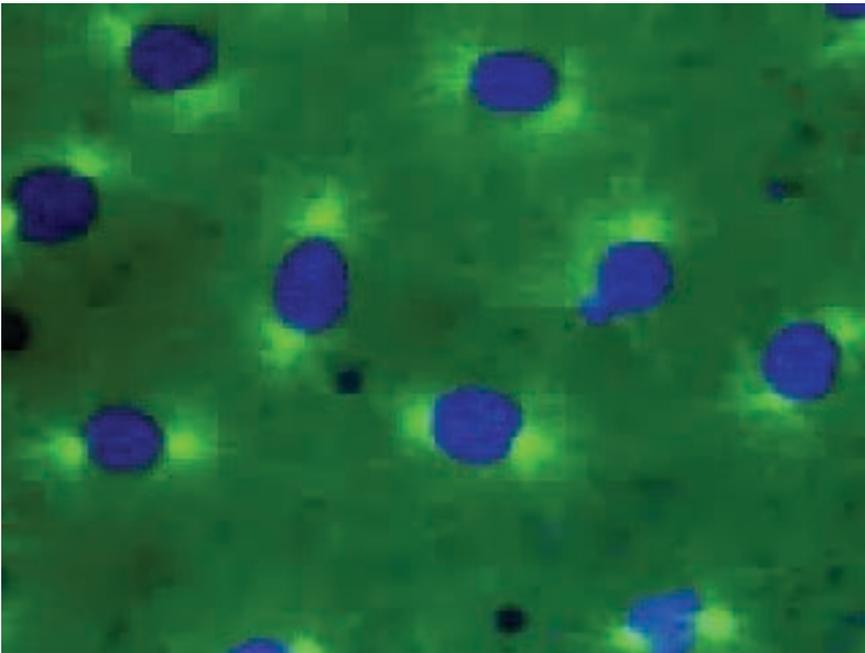
Highly methylated inactive X (Xi) chromosome is more compact than active X (Xa).



Brownian dynamics simulations of chromatin folding in nucleus

# Mitosis and DNA replication

- Mitosis requires replication of a genome
- DNA replication occurs at a replication fork (replisome)
- Can be highly processive: 2900 bases/min (eukaryotes)
- 1000 bases/s in *E. coli*



*Adapted from Mol. Cell 23:155*

Enzymes common to all replisomes:

Helicase

Primase

Polymerase

Ligase (not depicted)

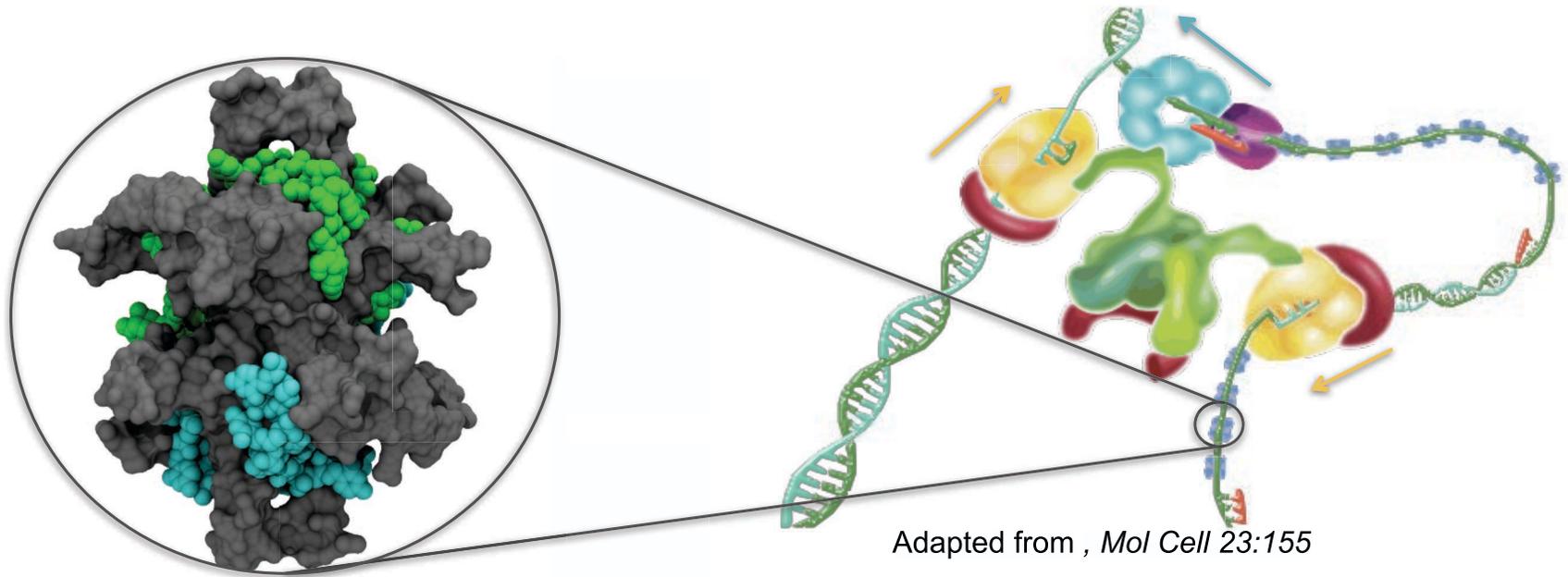
Sliding clamp and clamp loader

ssb

# SSB protects single-stranded DNA

Prevents formation of secondary structure, enzymatic digestion, chemical modification

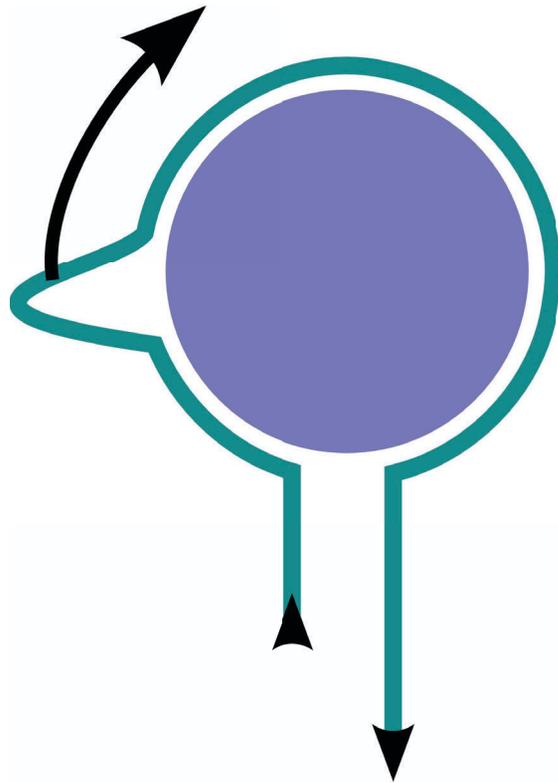
Single-stranded DNA binding protein (SSB) can bind 35 or 65 nucleotides of ssDNA (SSB<sub>35</sub> and SSB<sub>65</sub>) with high affinity



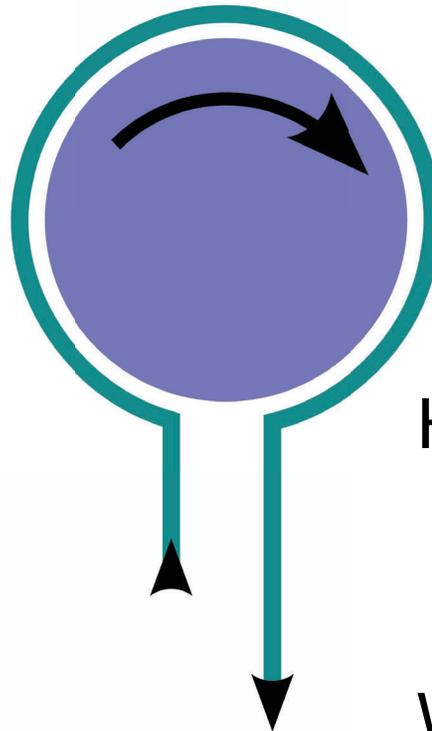
Problem: how is SSB removed when it is no longer needed?

# Diffusion of ssb along DNA

reptation



rolling



What is the microscopic mechanisms of SSB diffusion?

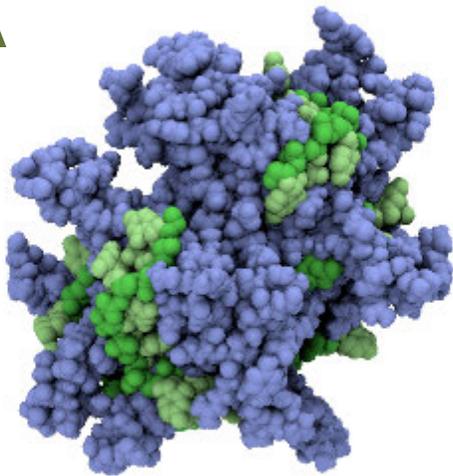
How does dissociation of DNA from SSB occur?

What makes an ssb an ssb?

† Ha group, Nature 461:1092

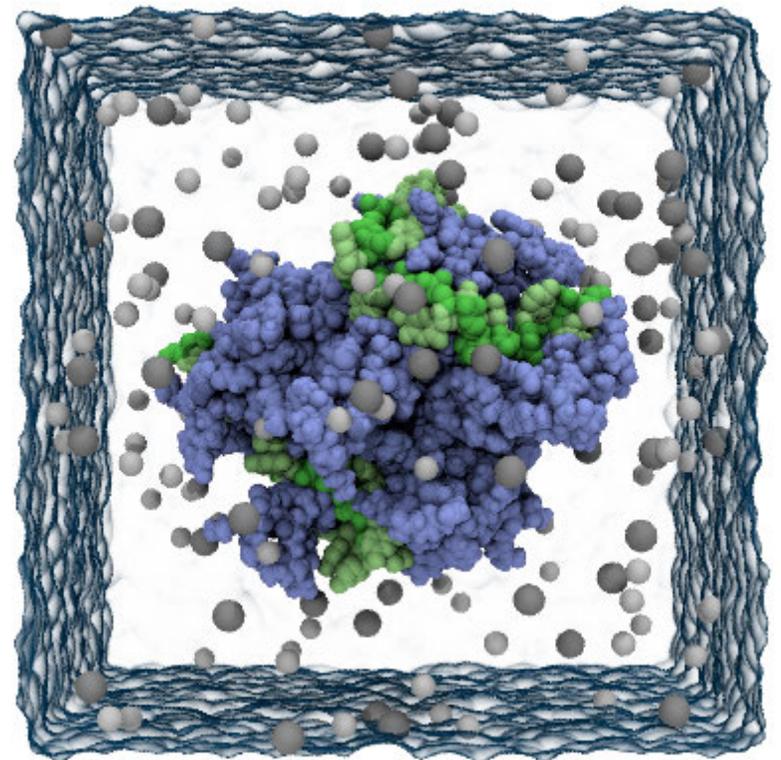
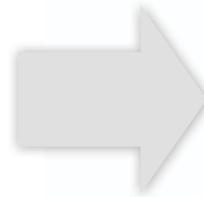
# A model is build from an x-ray crystal structure

SSB  
DNA



PDB:1EYG

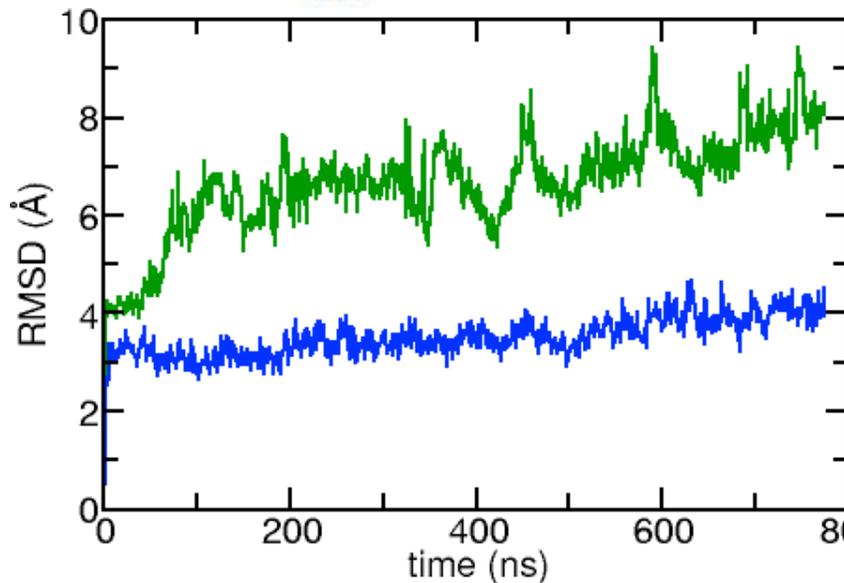
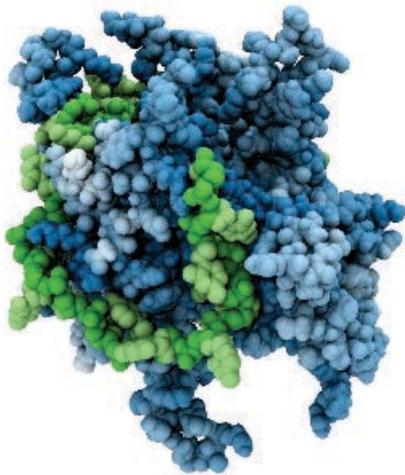
KCl  
water



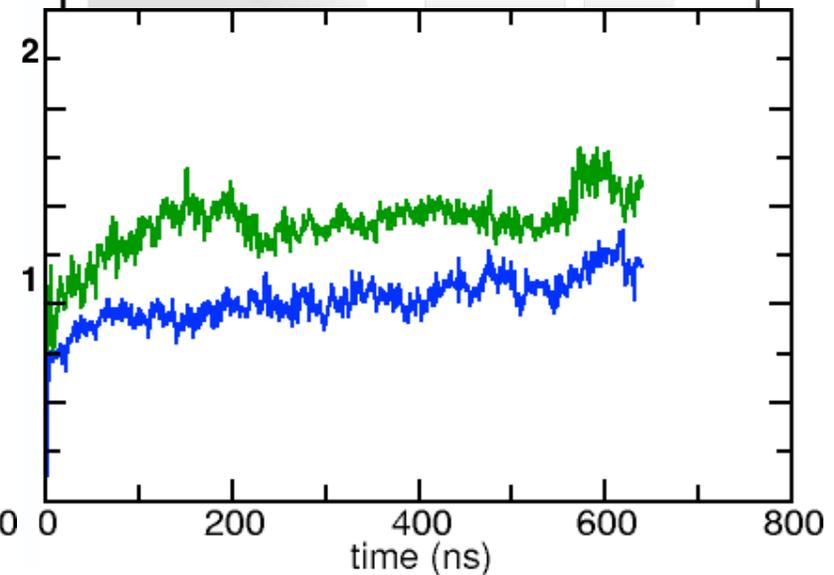
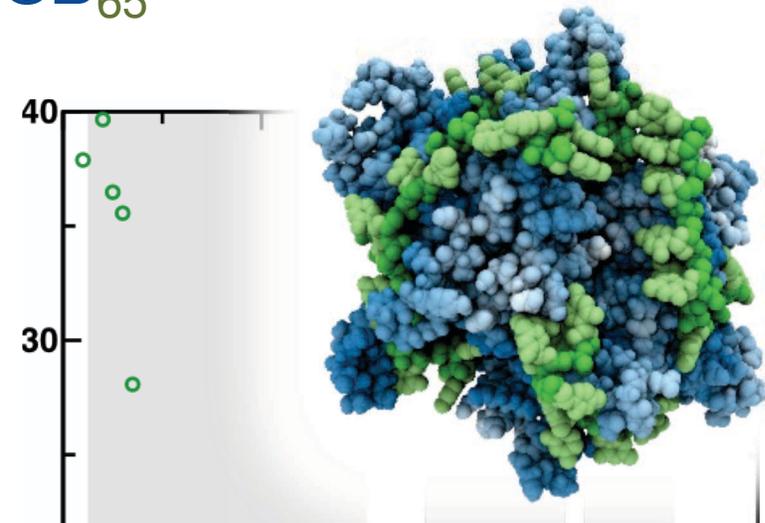
Unresolved DNA was modeled by the crystallographers (Lohman and Waksman groups, Washington U. School of Medicine) and provided to us via Ruobo Zhou of the Ha group.

# Individual nucleotides are loosely bound to SSB

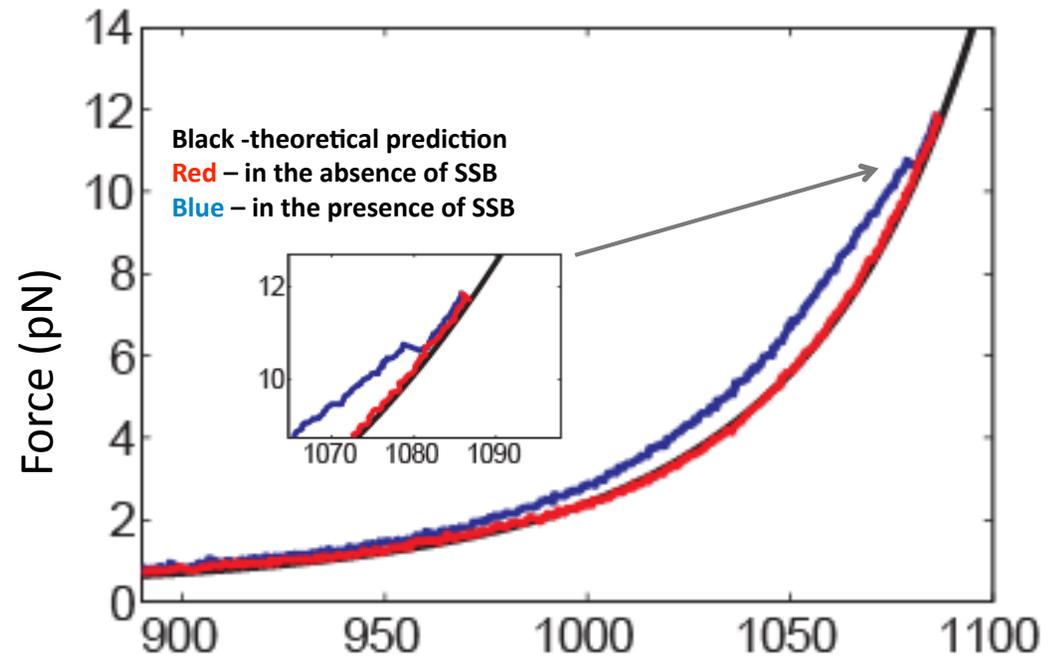
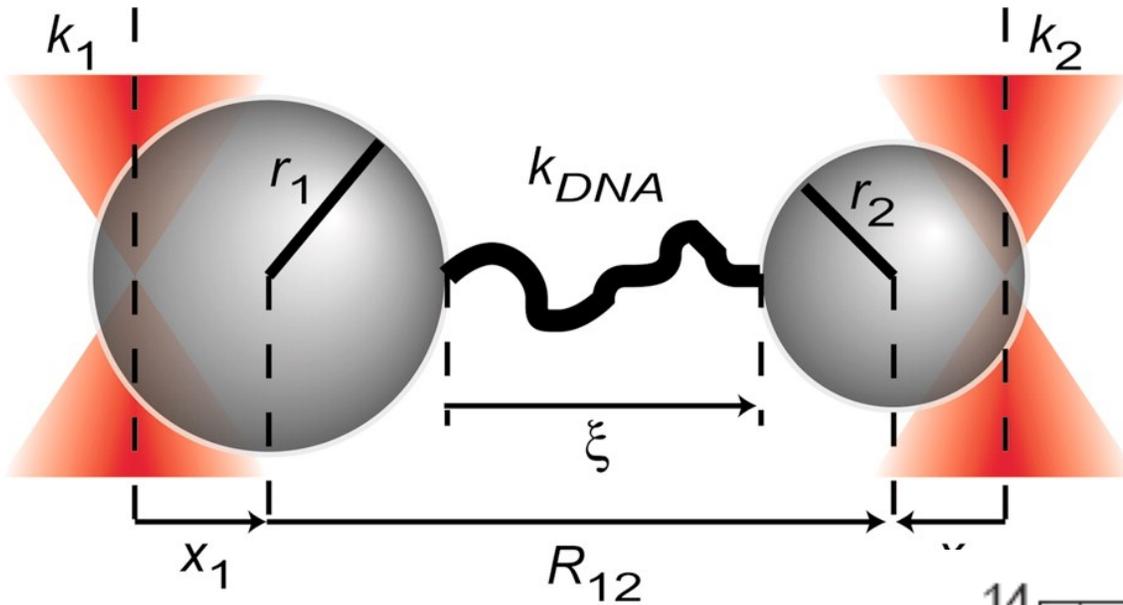
SSB<sub>35</sub>



SSB<sub>65</sub>

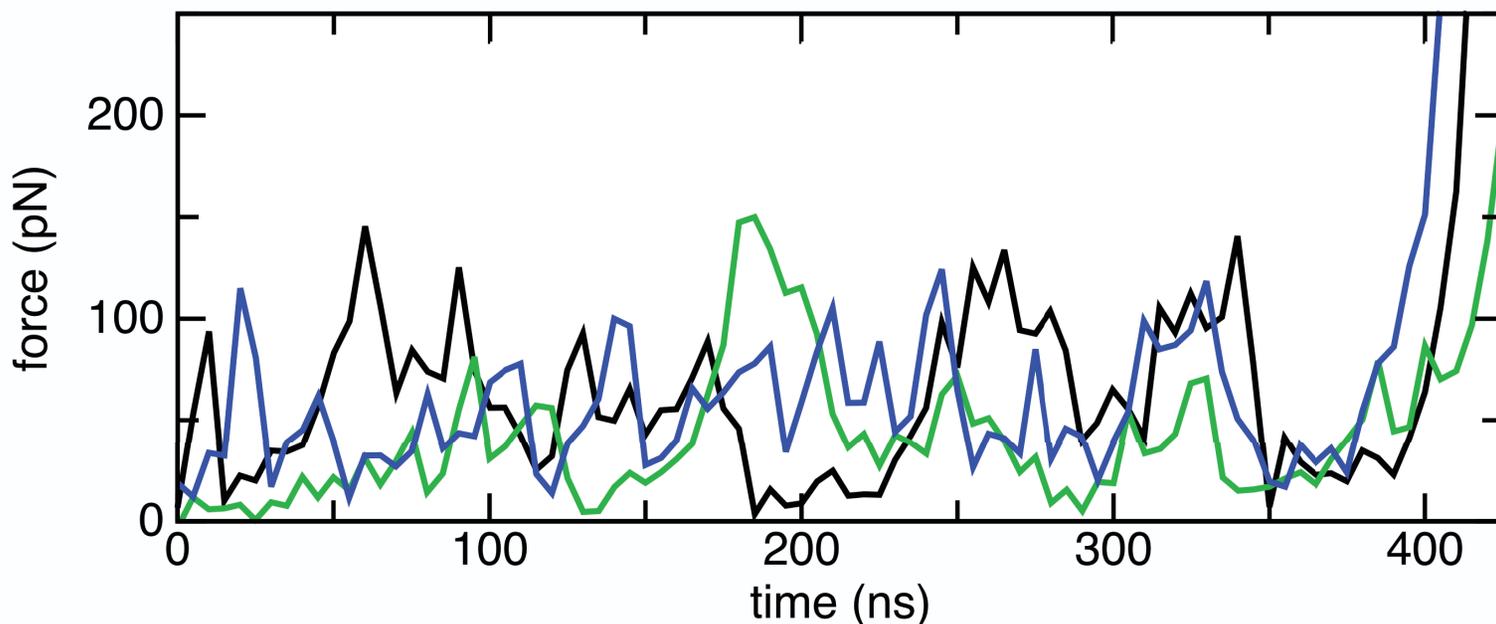
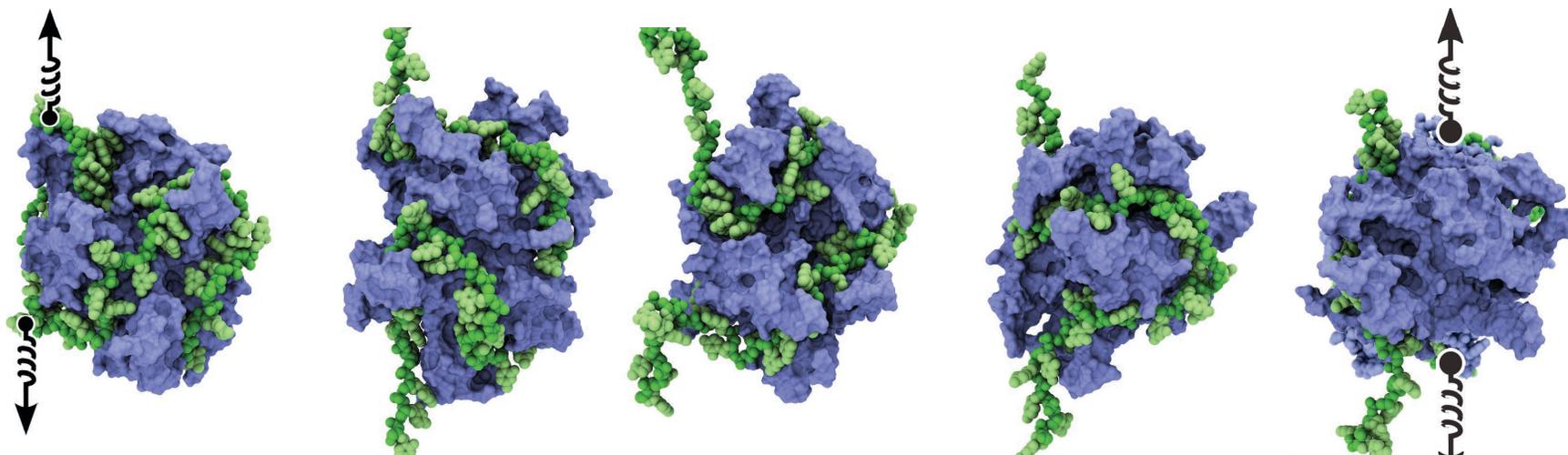


# Mechanics of ssb-DNA (dis)assembly



Chemla group, unpublished

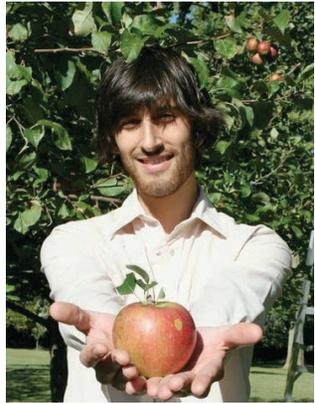
# All-atom simulations cannot quite reach experiment



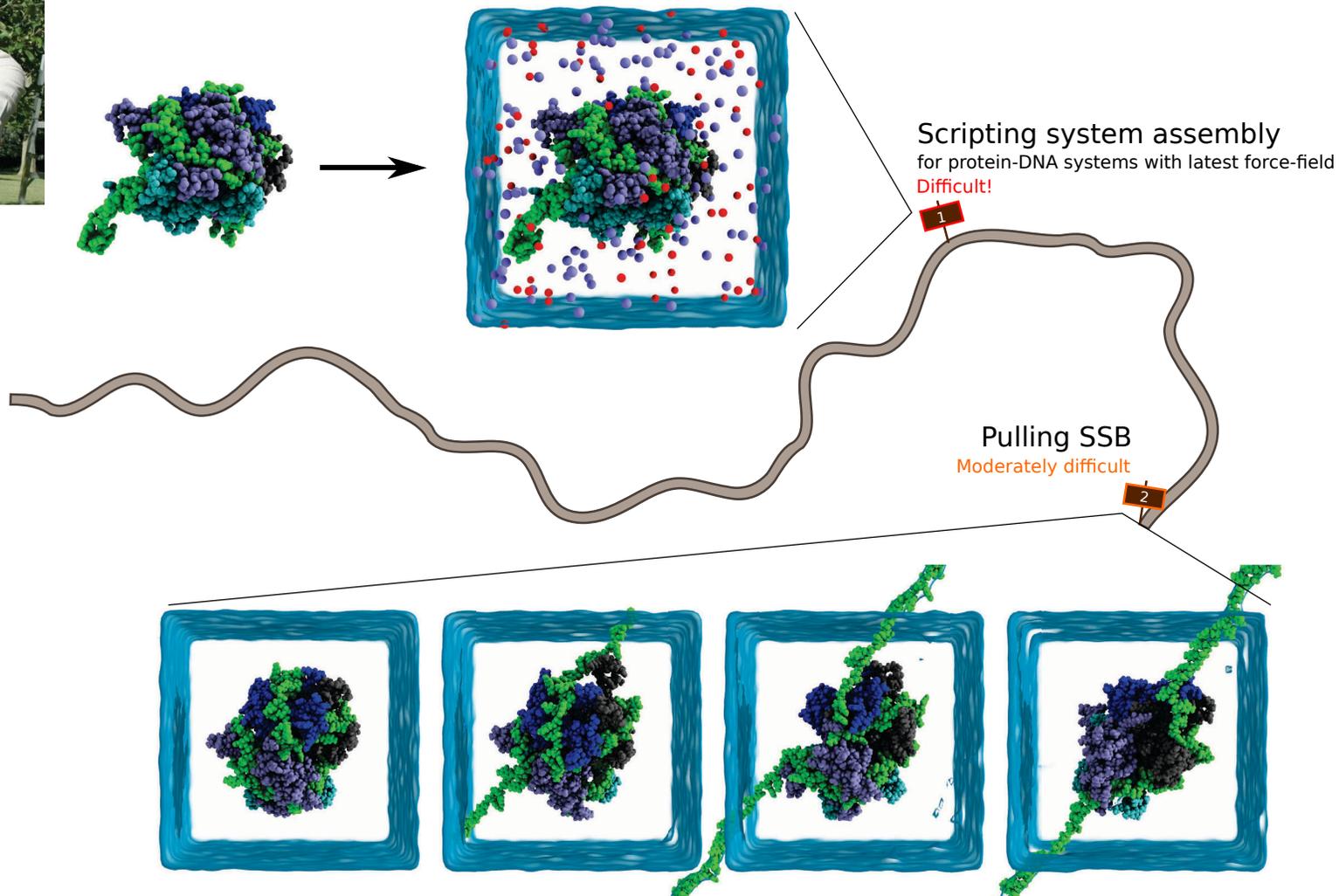
Forces are 1-2 orders of magnitude larger than in experiments

Little hope of observing diffusion-related events

# Atomistic mechanics of single-stranded DNA Binding-Protein



Chris Maffeo



# Journal of Physics

## Condensed Matter

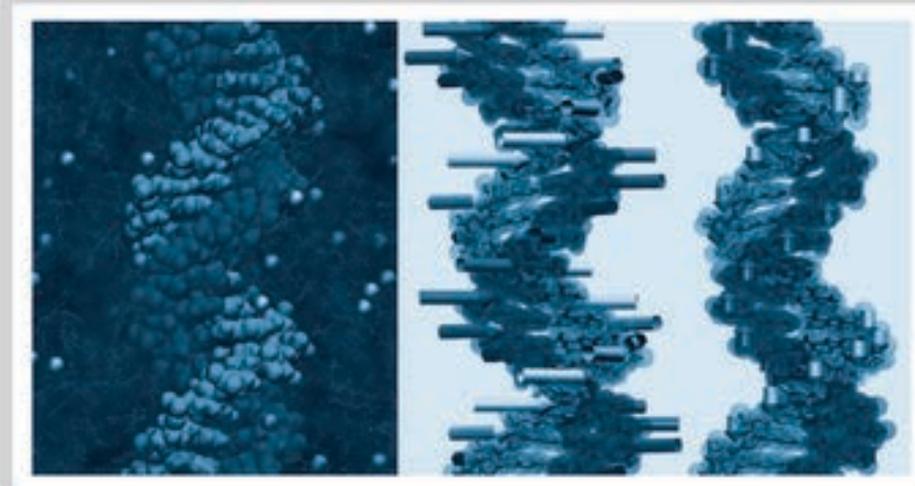
*Journal of Physics: Condensed Matter* 26: 413101 (2014)

Volume 26 Number 41 15 October 2014

### Topical review

#### Close encounters with DNA

*C Maffeo, J Yoo, J Comer, D B Wells, B Luan and A Aksimentiev*



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Shu-Han Chao  
Karl Dekker

Experiment:

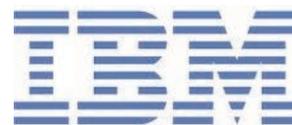
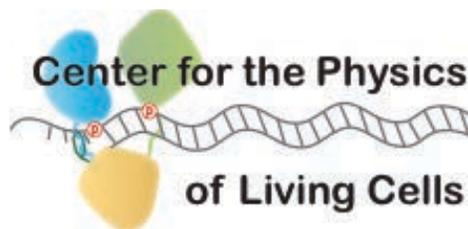
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