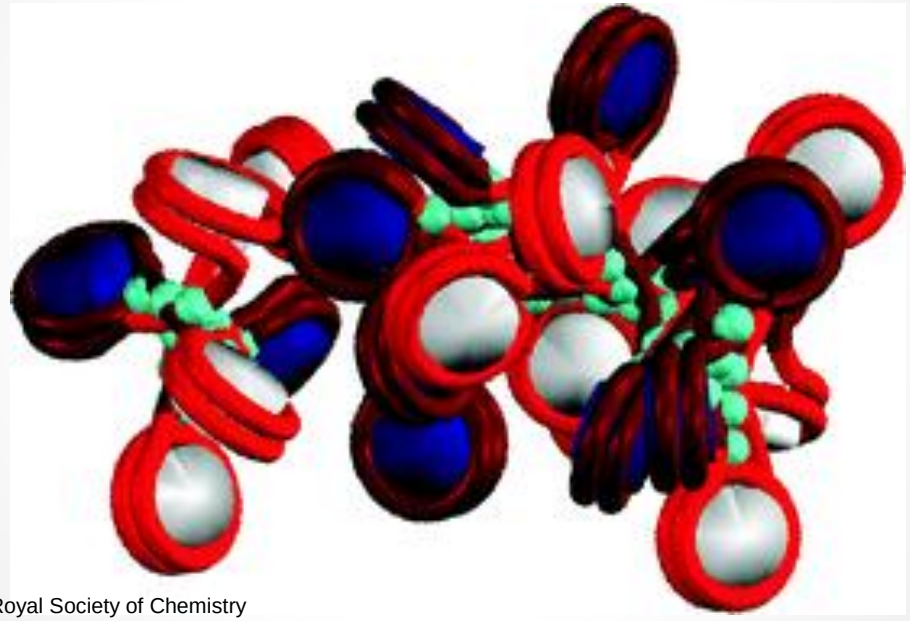
Chromatin Folding



Royal Society of Chemistry

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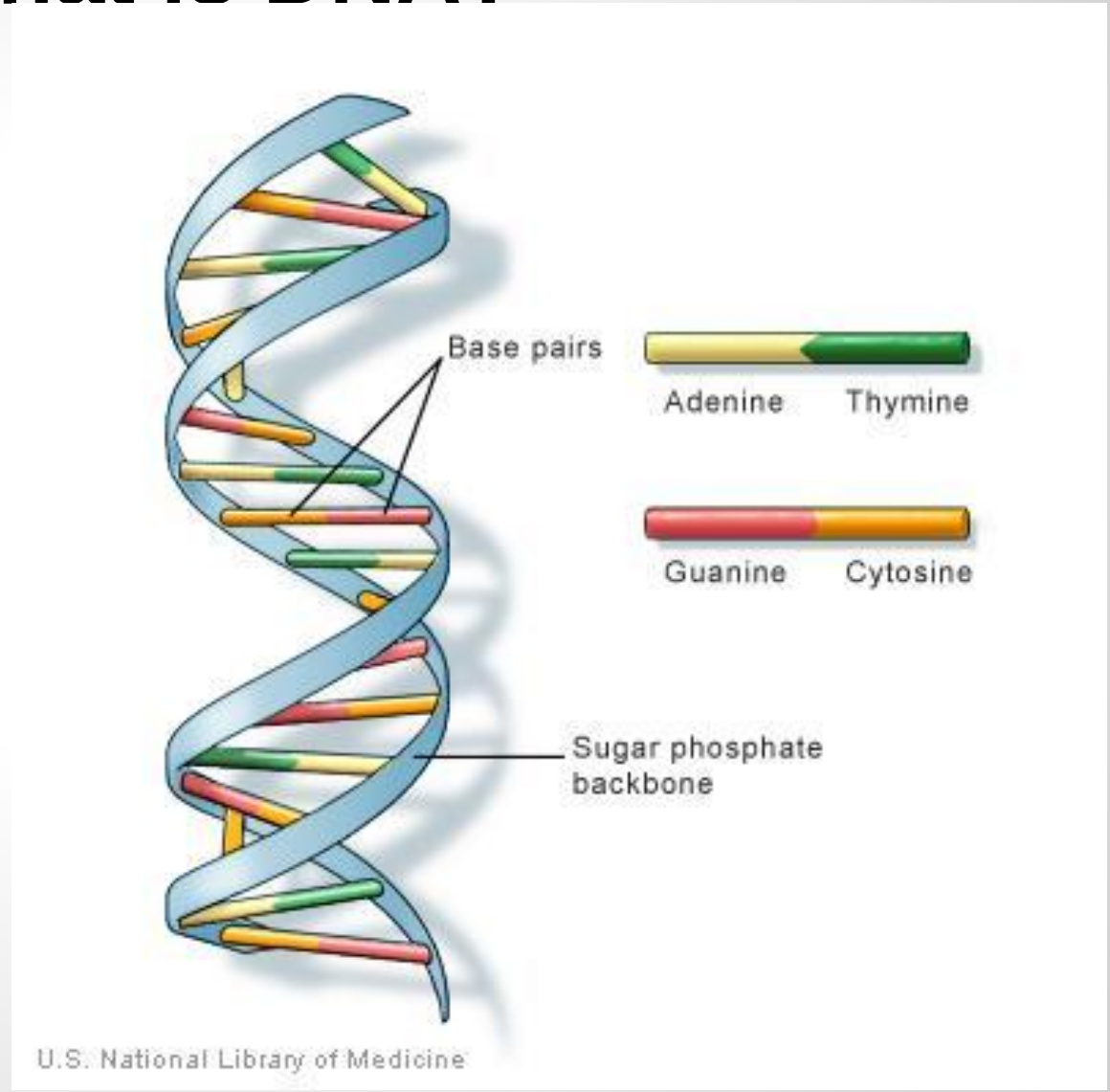
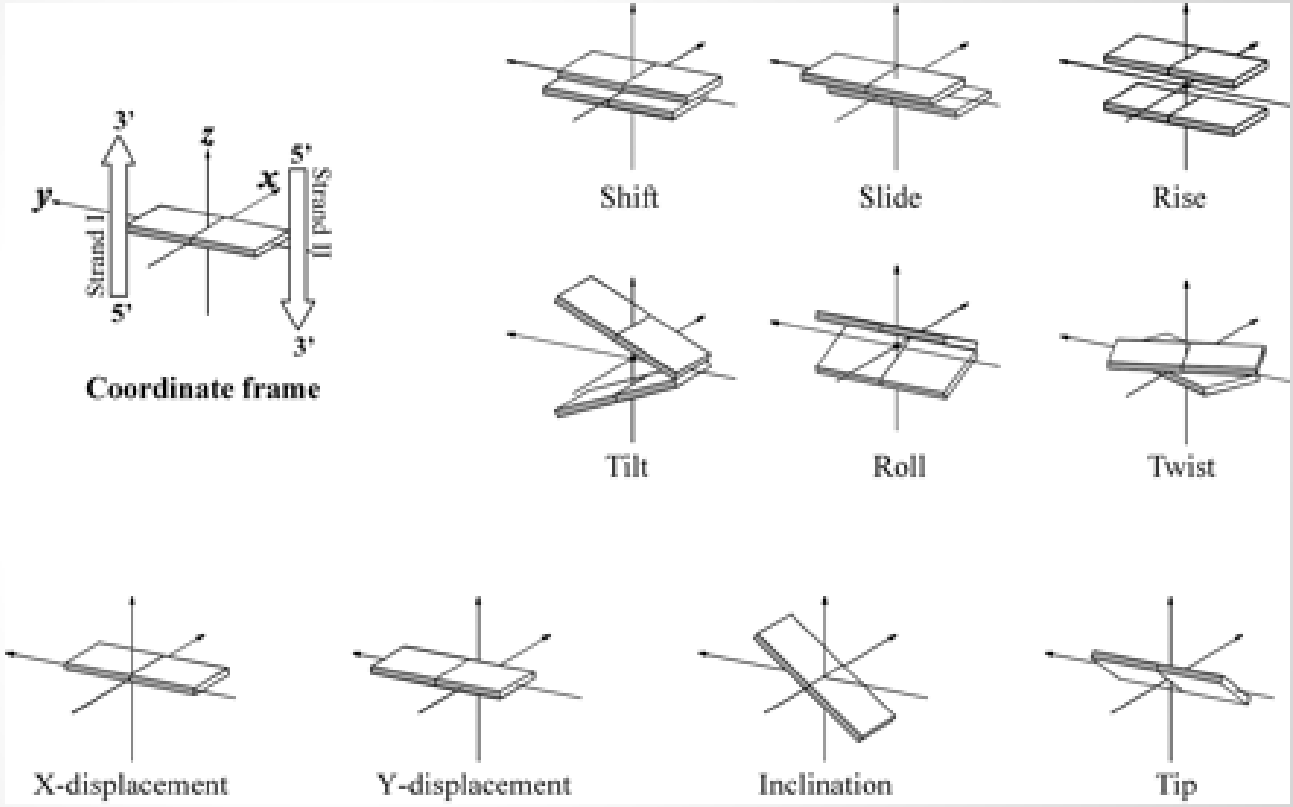
What is DNA?

- Carrier genetic information
- Located in cell nucleus
- 2 m long fit into nucleus of diameter 10 microns
- Same DNA in every cell of our body
- Double-Helical structure 10 base pair (repeat)
- Backbone (sugar-phosphate)
- Base Pairs
  - Adenine (A)
  - Thymine (T)
  - Guanine (G)
  - Cytosine (C)



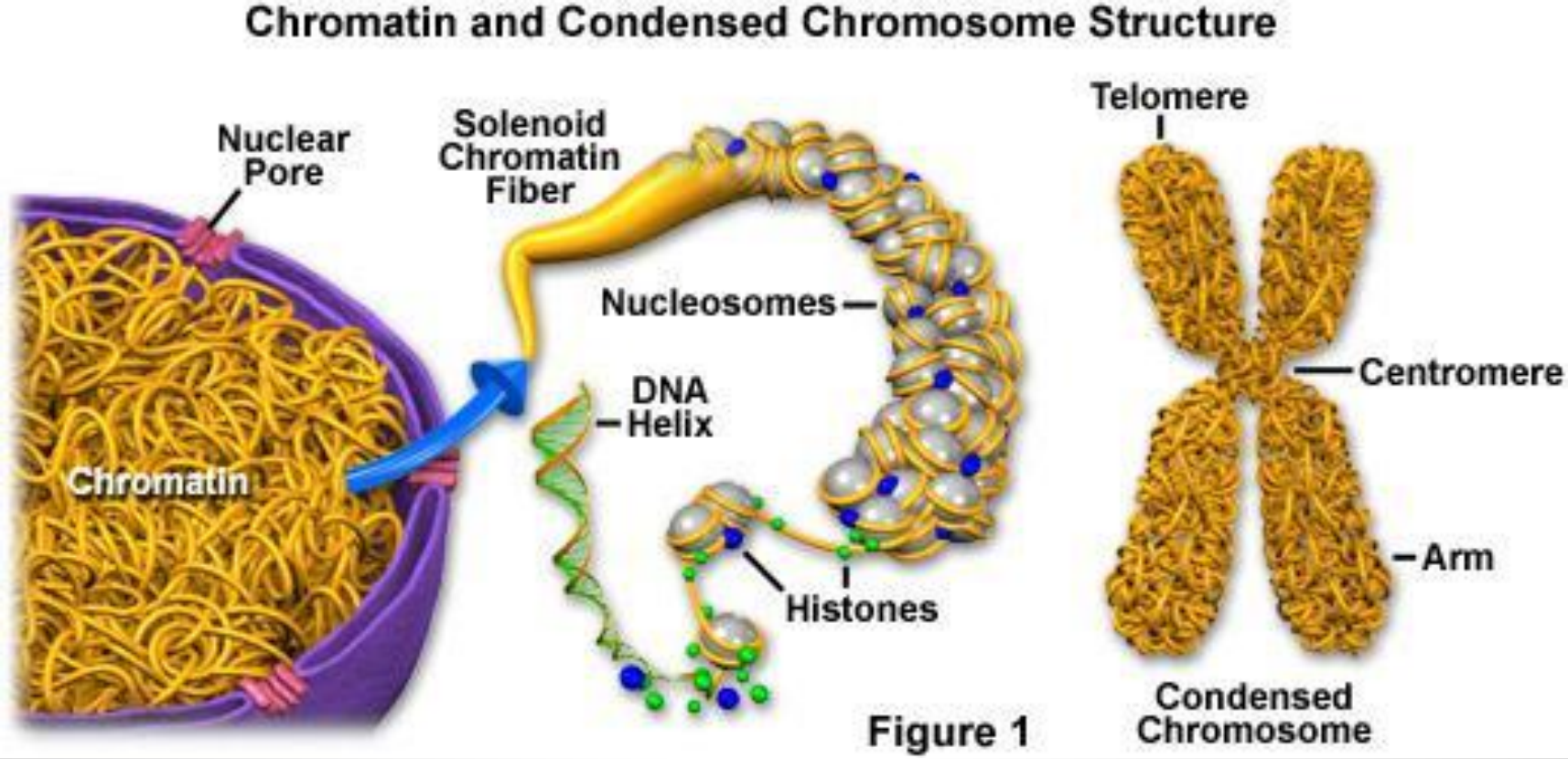
Base Pair Geometry

- Base pairs modeled as rigid bodies
- Double helix is described by the relative orientations of successive base pairs
- 6 types of coordinates to describe base pair conformation; 3 angles and the 3 components of translation



Nucleic Acids Research. Oxford University Press. 2013.
http://nar.oxfordjournals.org/content/31/12/2975/F1.expansion

Chromatin

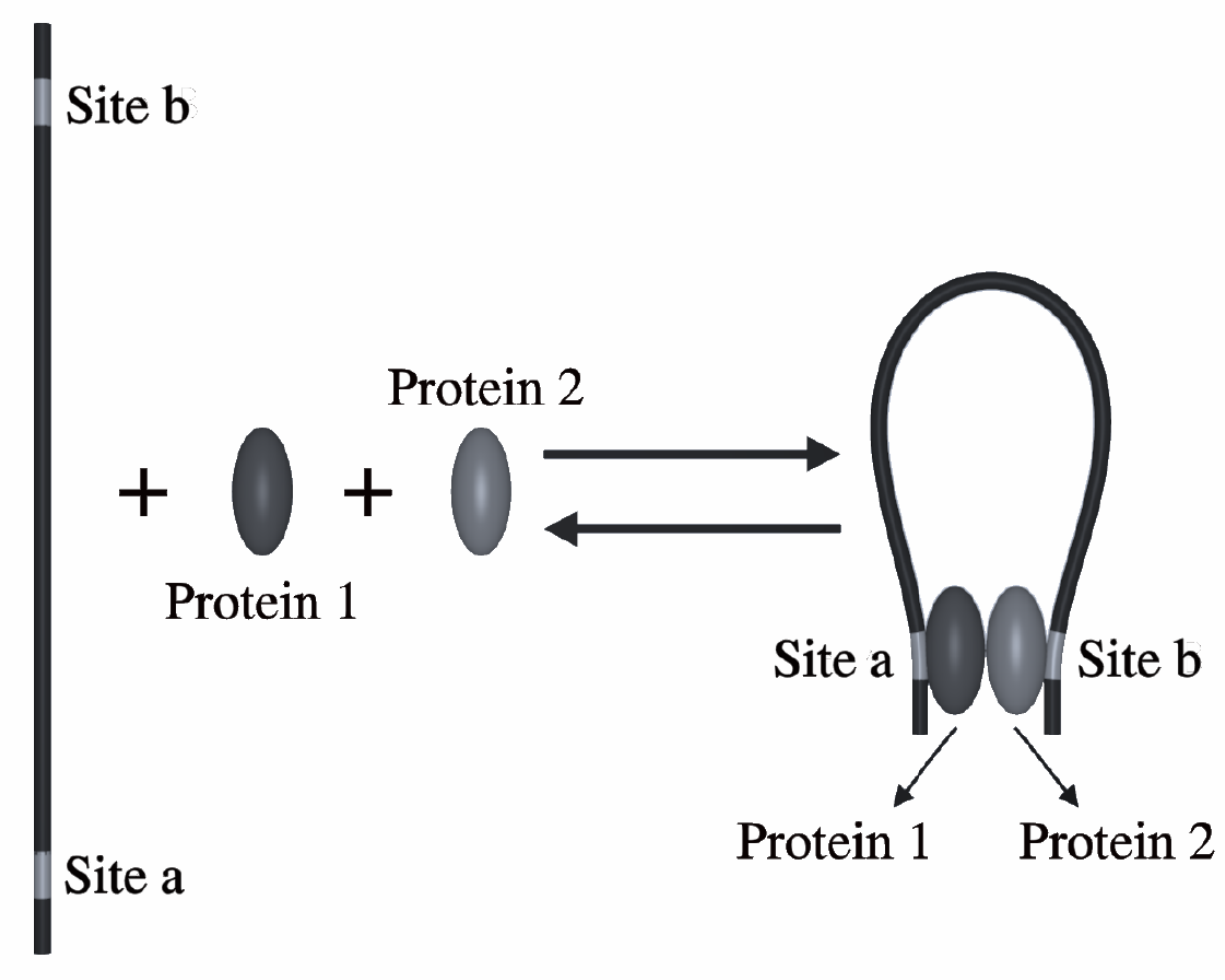


Davidson, Michael and The Florida State University. Chromatin and Chromosomes. 10 May 2005. <http://micro.magnet.fsu.edu/cells/nucleus/chromatin.html >

- Chromatin = DNA + histones (and other proteins)
- 8 histones make an octamer core
- DNA wraps around the octamer core (roughly 150-bp) to form a nucleosome core particle

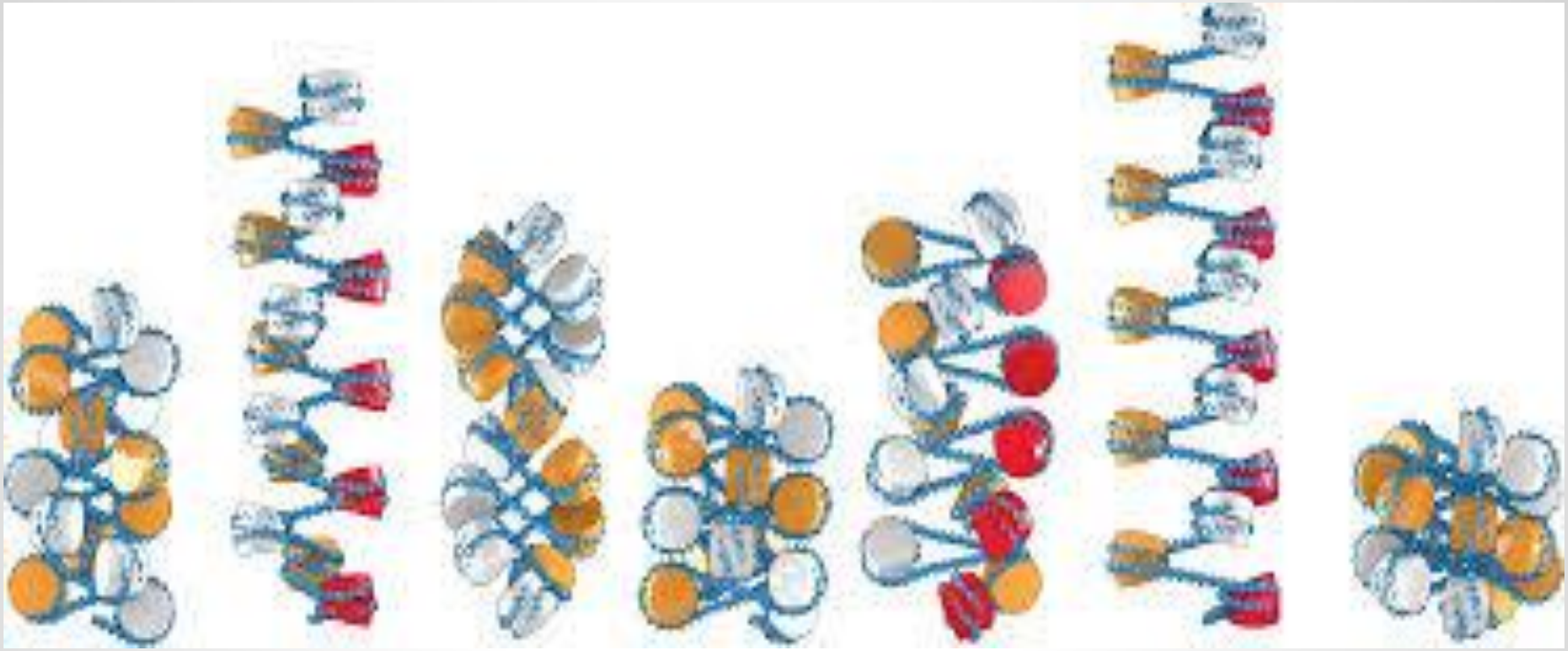
Long-Distance Communication

- Gene expression entails looping frequently
- Proteins 1 and 2 which bind at sites a and b must come in contact for biological processing
- Proteins mediate the looping of DNA



How chromatin architecture affect and/or control looping?

Chromatin Architecture and Nucleosome Positioning

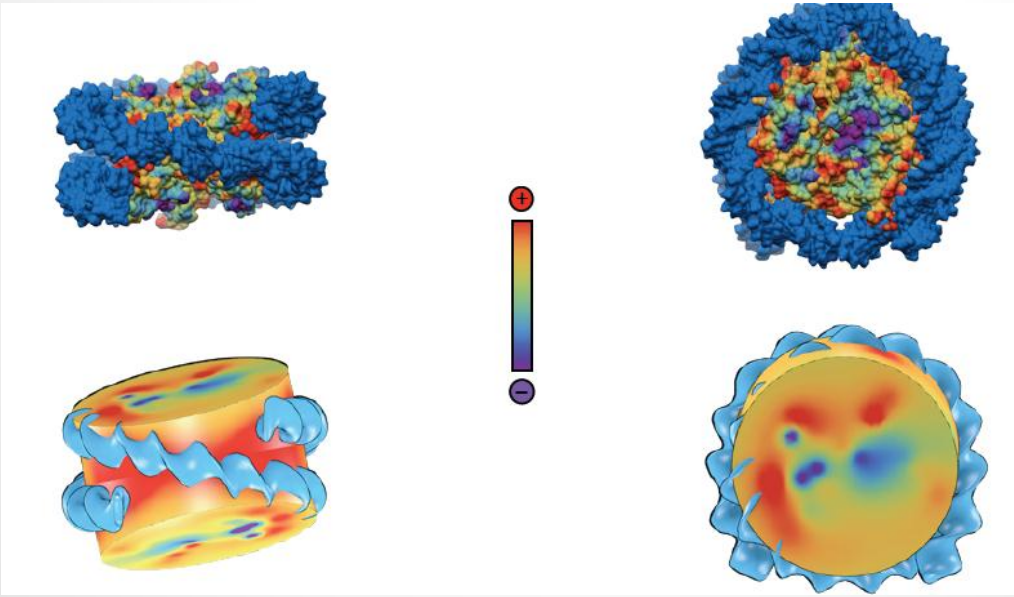


25bp 30bp 32bp 35bp 37bp 40bp 45bp

- The spacing of nucleosomes (the number of free base pairs) controls the chromatin architecture
- Ex) 35 bp more compact and 40bp more spread out in the chromatin

Chromatin Stiffness and Nucleosome Interaction

- Interactions between nucleosome and DNA underlie chromatin stiffness
- DNA negatively charged
- Nucleosomes have positive and negative charges



- Long-range communication related to DNA stiffness

PROBLEM

- Quantity interactions between nucleosomes on chromatin
- Study the effect of nucleosome positioning on those interactions
- Extract effective potentials for nucleosome interactions (covariance analysis)
- Design coarse-grained models of chromosomes based on effective potentials