

The background of the slide features a complex, multi-colored molecular structure, likely a DNA origami nanostructure. It consists of numerous small spheres (atoms) connected by thin lines (bonds), forming a dense, interconnected network. The colors used include shades of cyan, purple, pink, and red, set against a light blue background.

Molecular Dynamics of DNA origami nanostructures

Christopher Maffeo
PI: Aleksei Aksimentiev

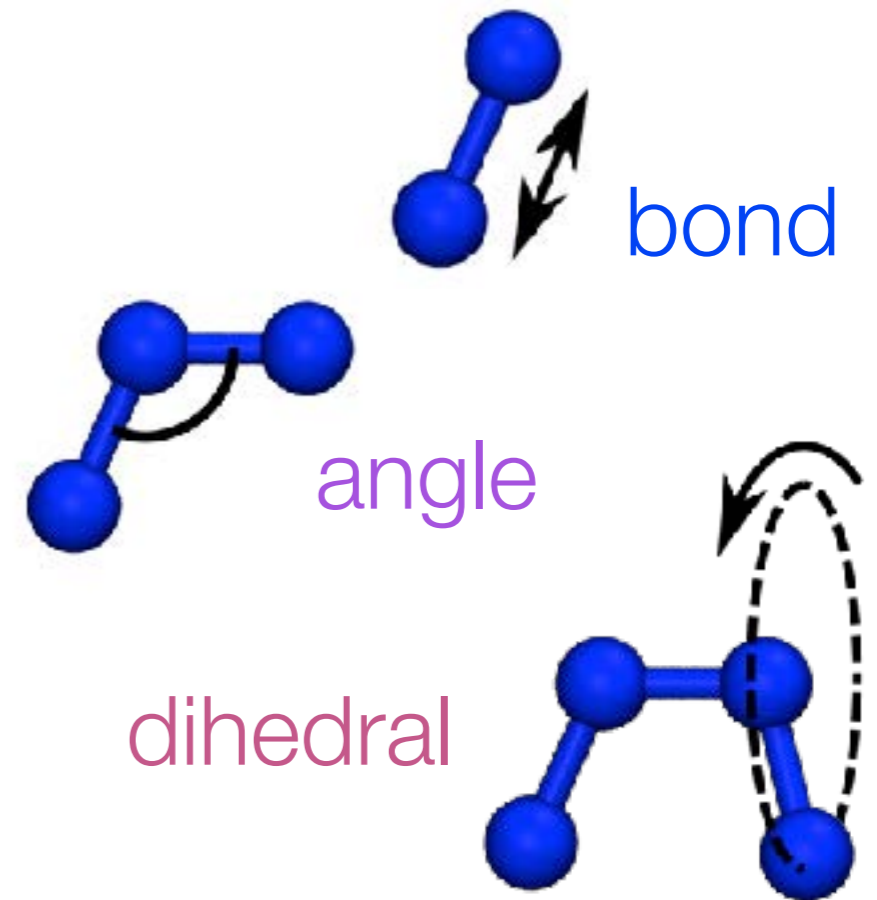
Department of Physics
University of Illinois at Urbana-Champaign

Blue Waters Symposium
June 5, 2018

All-atom Molecular Dynamics (MD)

Atoms modeled as classical point particles
Interactions prescribed by CHARMM36 force field
with CUFIX corrections
Simulations run using NAMD[†] on Blue Waters

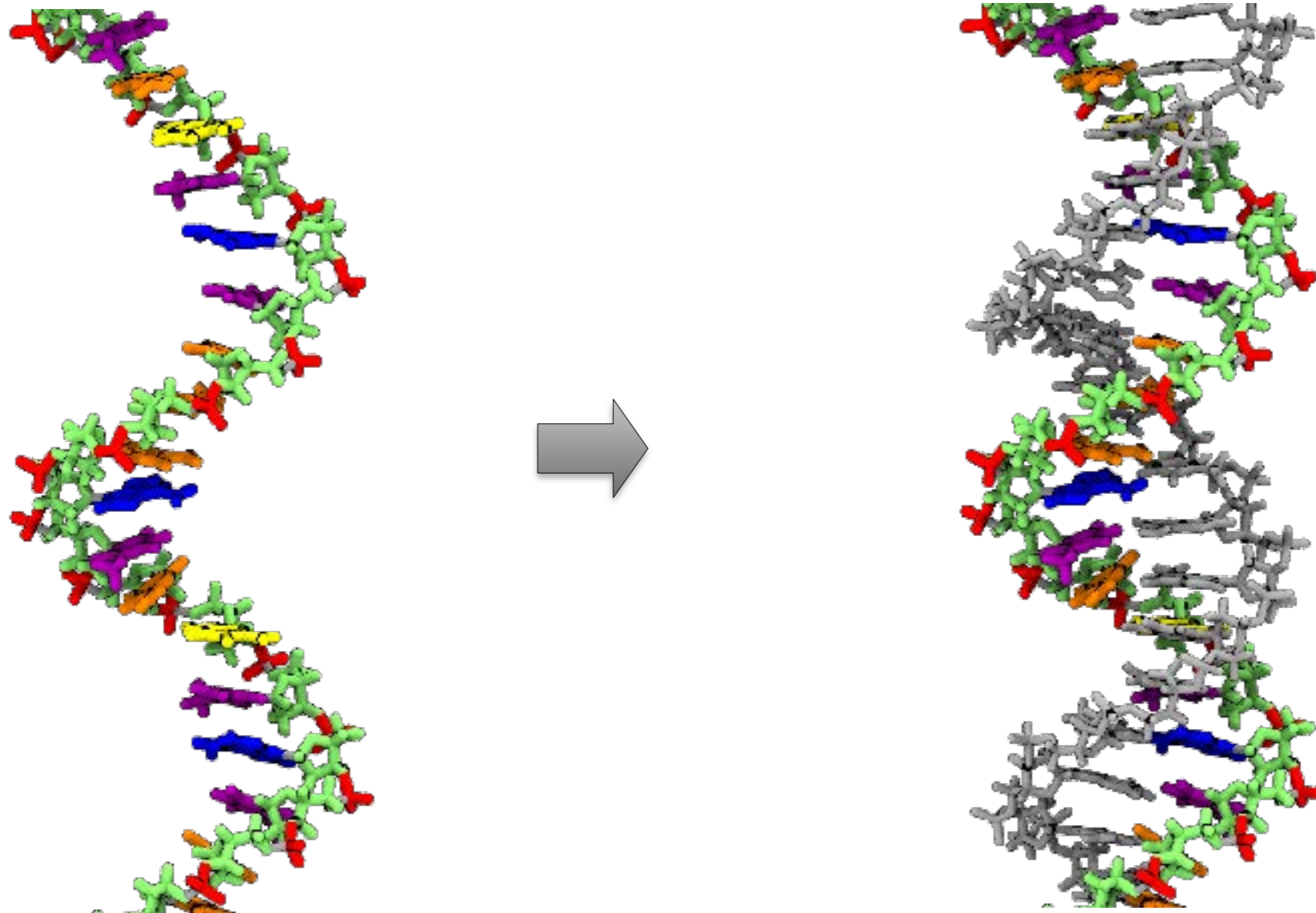
$$U = \sum_{\text{bonded}} \left\{ \begin{aligned} &k(r_{ij} - r_0)^2 \\ &+ k_\theta(\theta - \theta_0)^2 \\ &+ k(1 + \cos(n\psi + \phi)) \end{aligned} \right\} \\ + \sum_{i>j} \left\{ \begin{aligned} &-U_{\min} \left[\left(\frac{R_{\min}}{r_{ij}} \right)^{12} - 2 \left(\frac{R_{\min}}{r_{ij}} \right)^6 \right] \\ &+ \frac{Cq_i q_j}{\epsilon_0 r_{ij}} \end{aligned} \right\}$$



Lennard-Jones
(van der Waals)

electrostatic

Single-stranded DNA hybridizes with sequence specificity



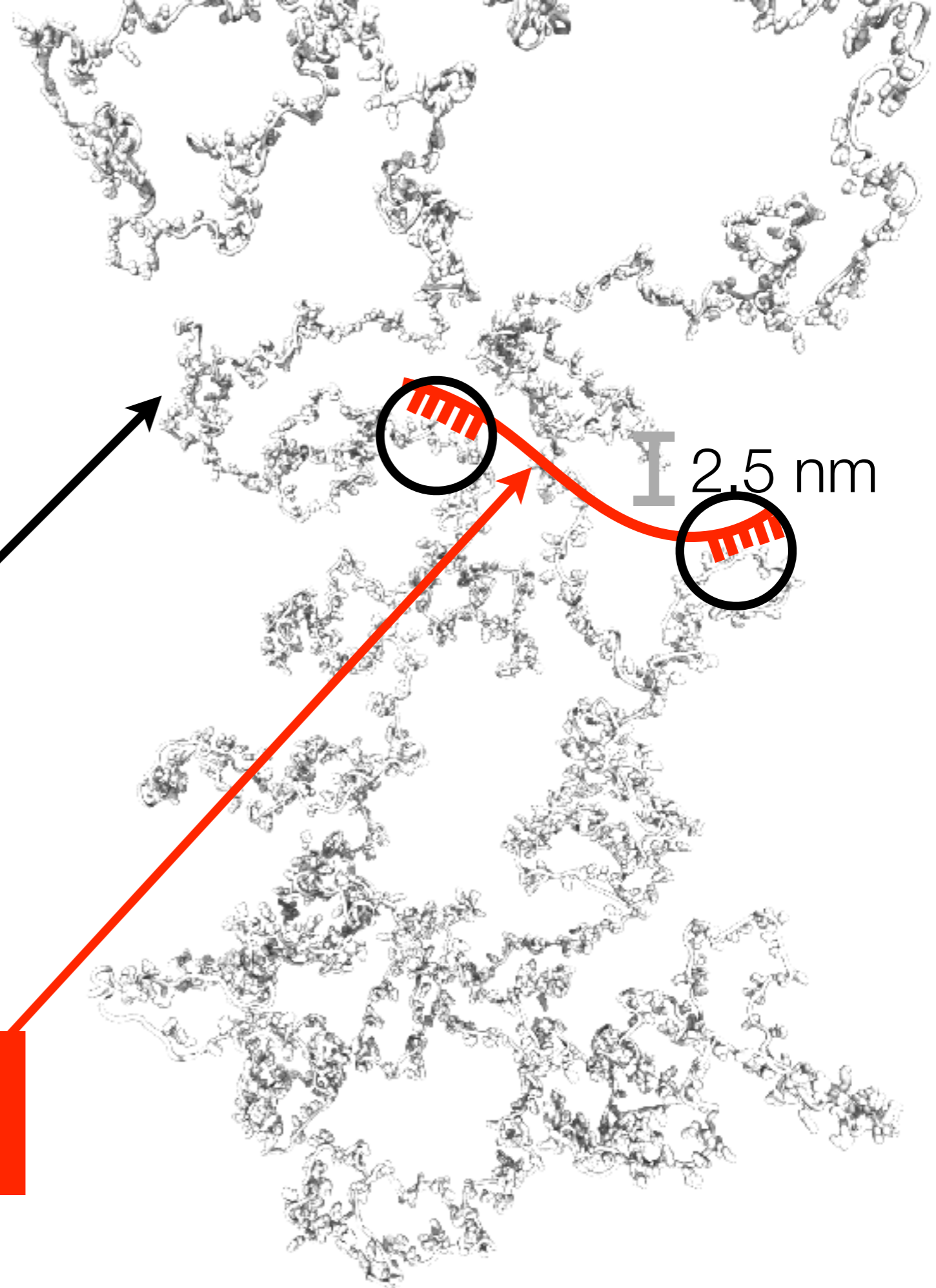
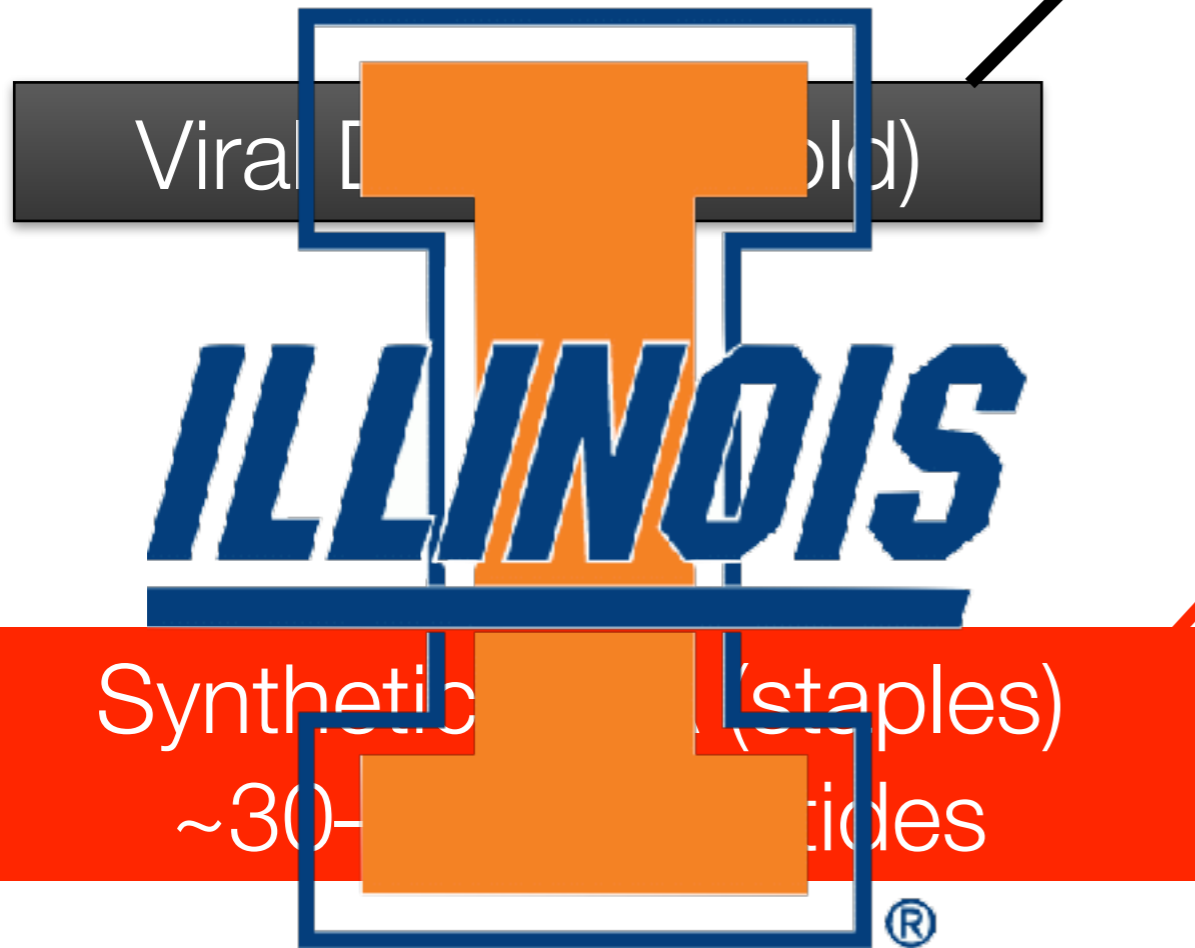
phosphate

sugar

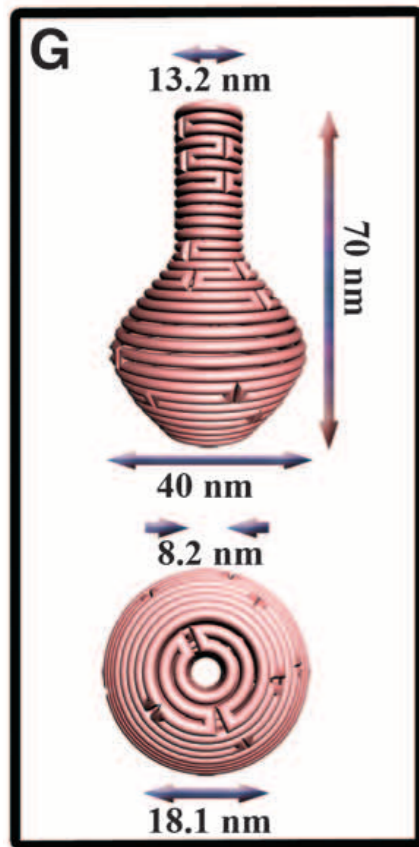
adenine • thymine
guanine • cytosine

DNA origami

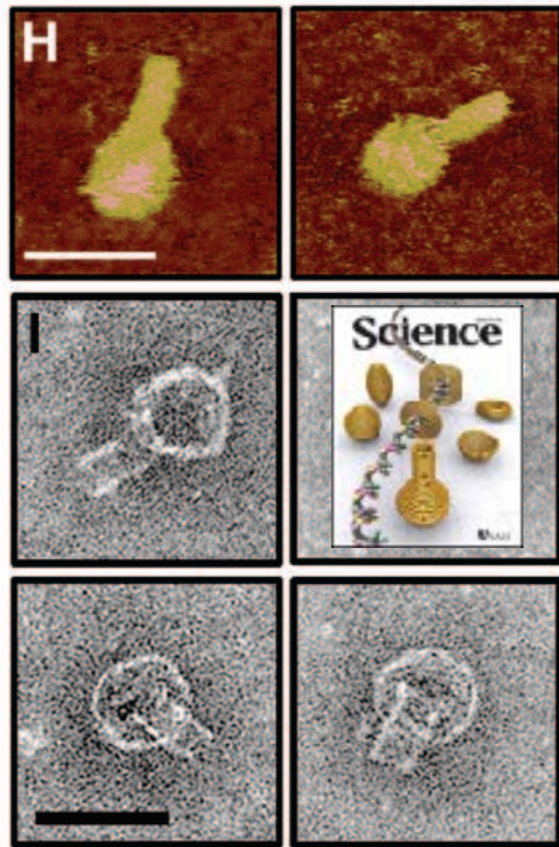
Building a structure with nanoscale precision by **folding** DNA



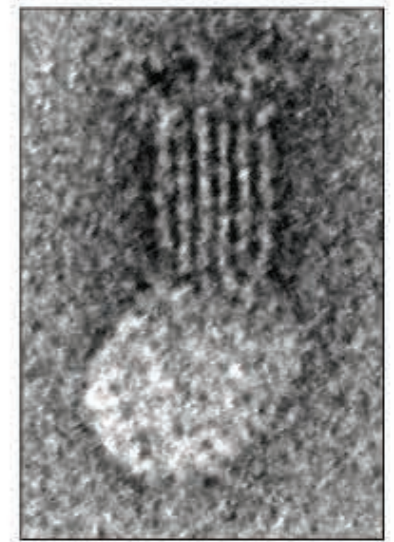
DNA origami structures



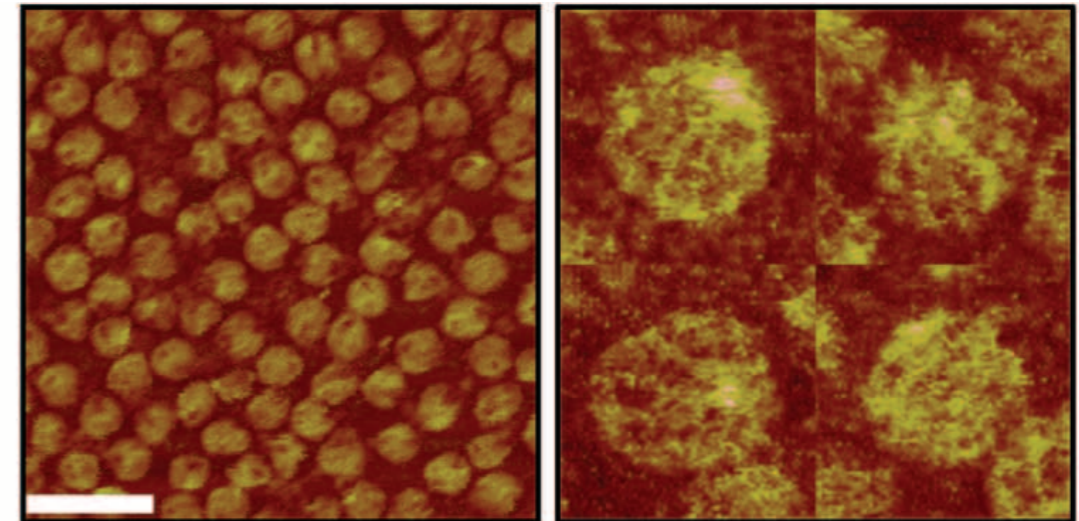
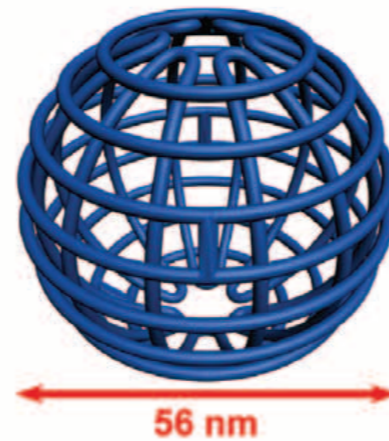
Yan and coworkers, Science (2011)



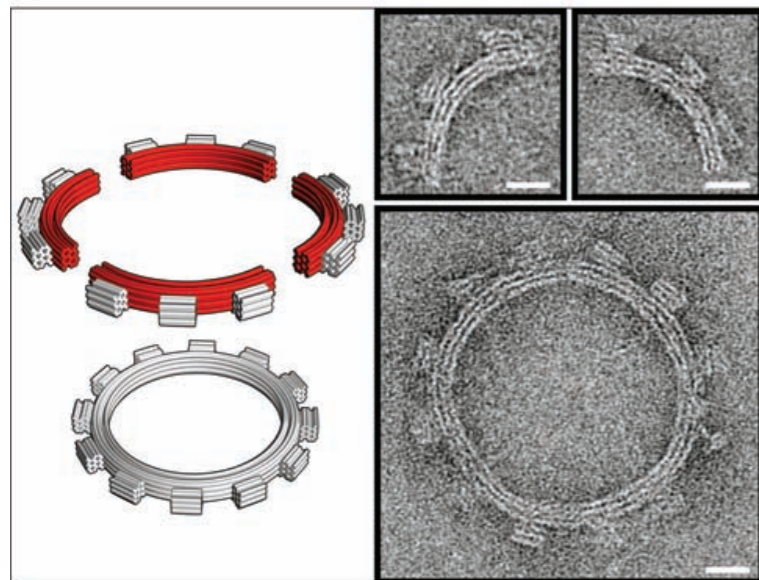
Dietz and coworkers, Science (2012)



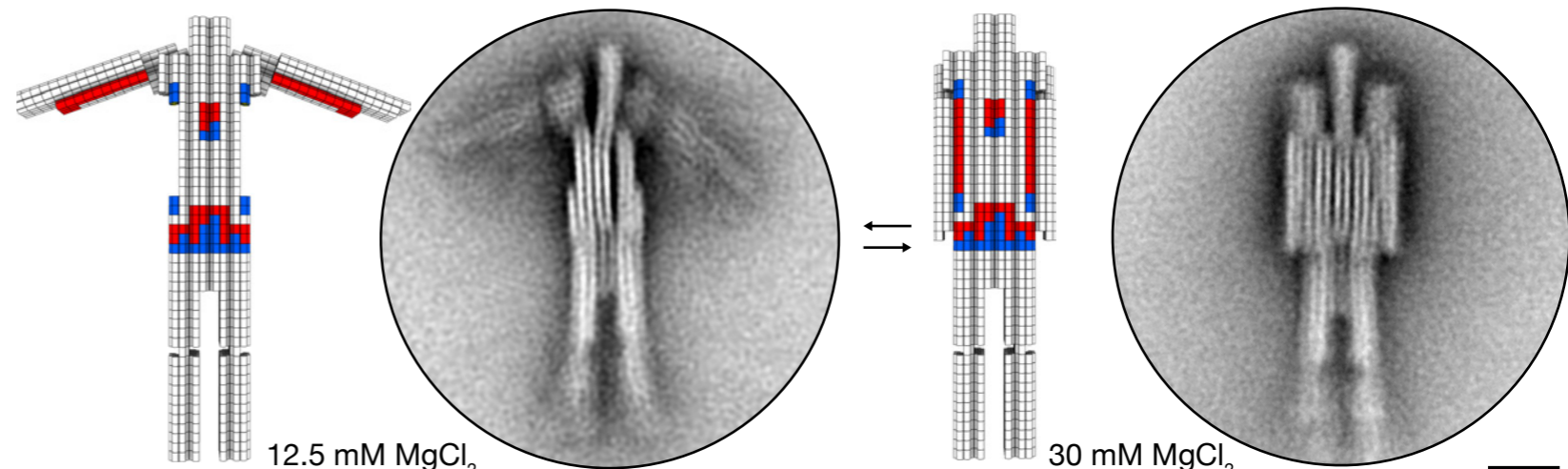
25nm



Yan and coworkers, Science (2013)

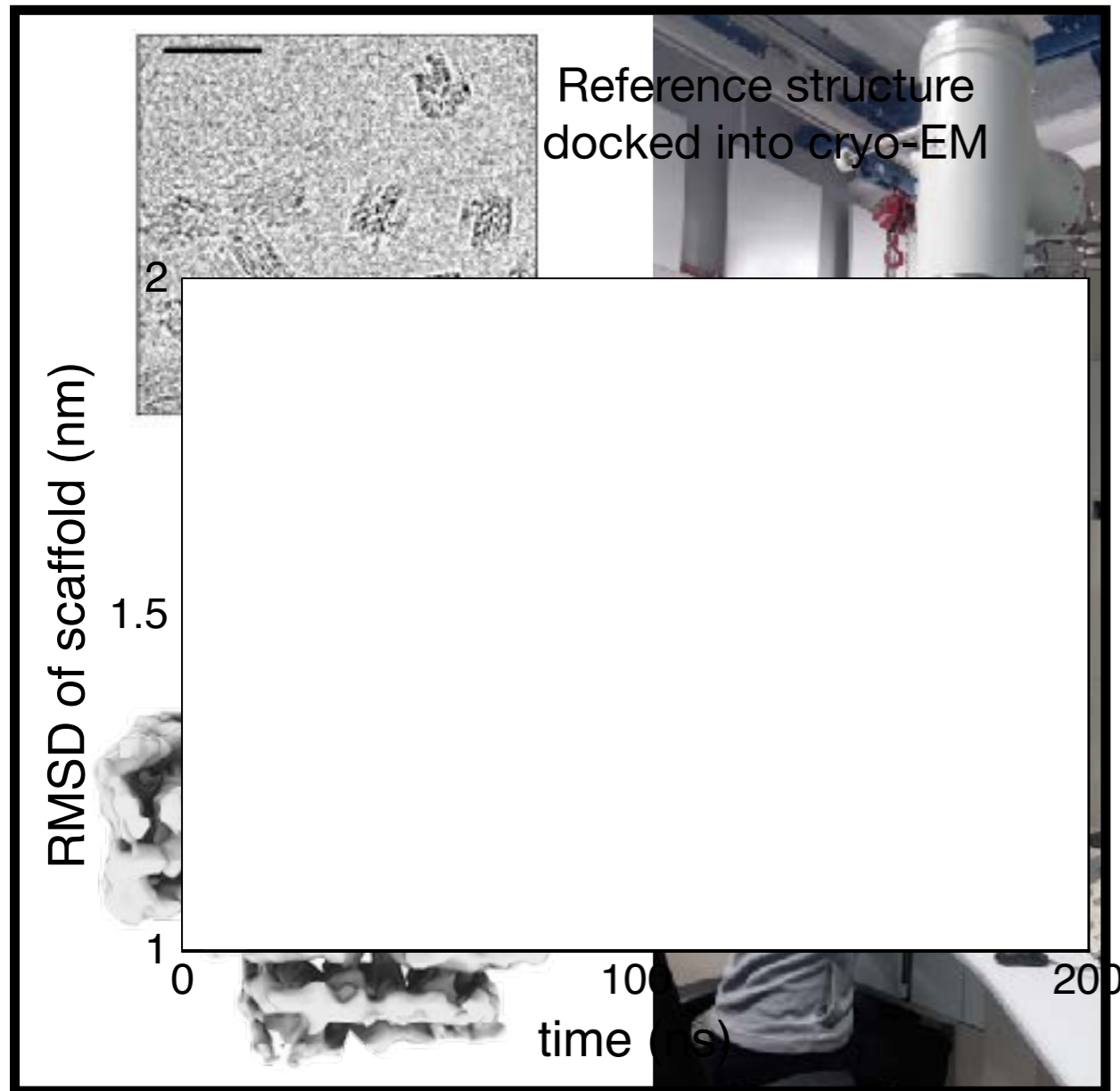


Shih and coworkers, Science (2009)

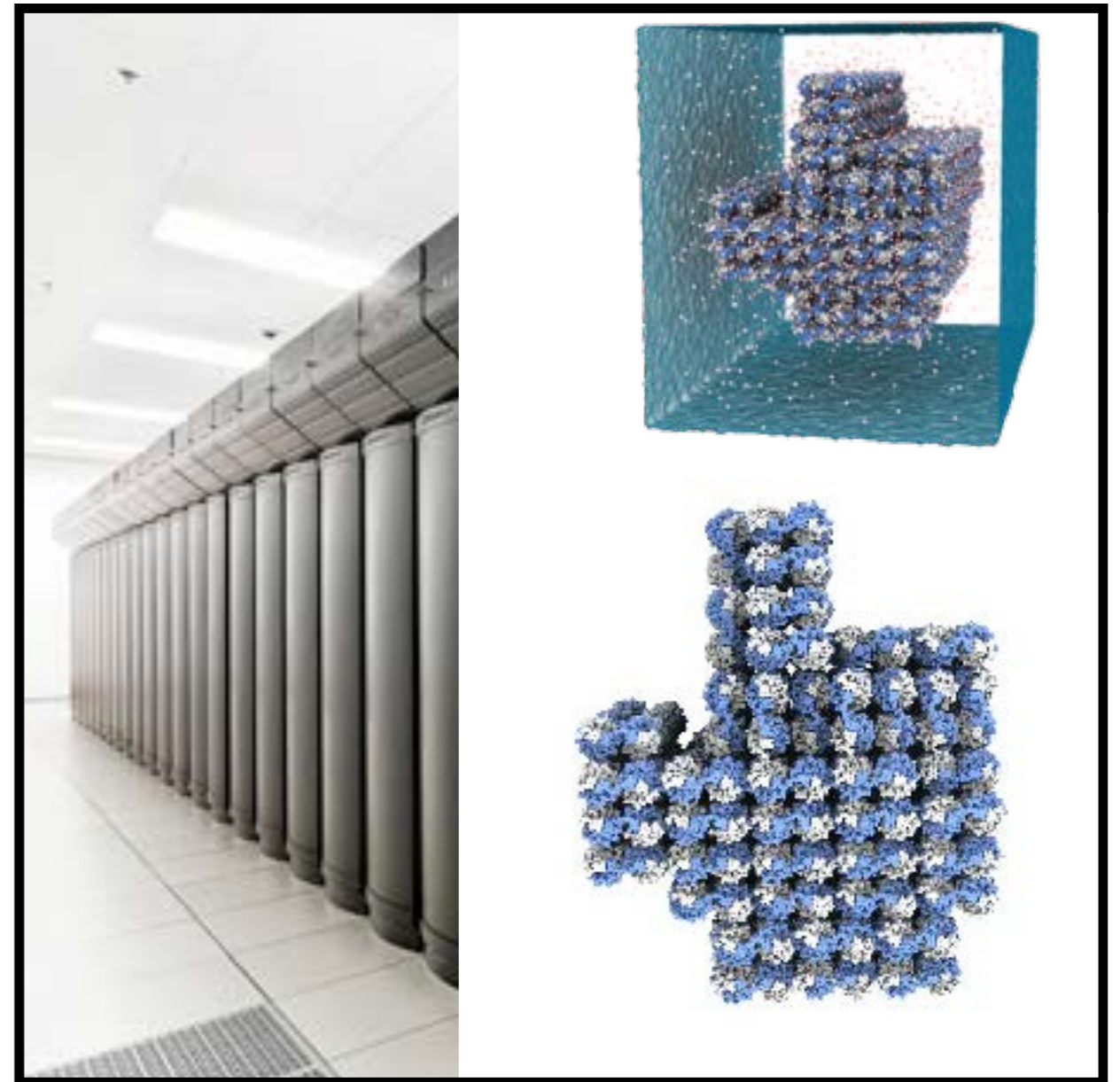


Dietz and coworkers, Science (2015)

Cryo-electron microscopy and all-atom simulation for DNA origami structure prediction

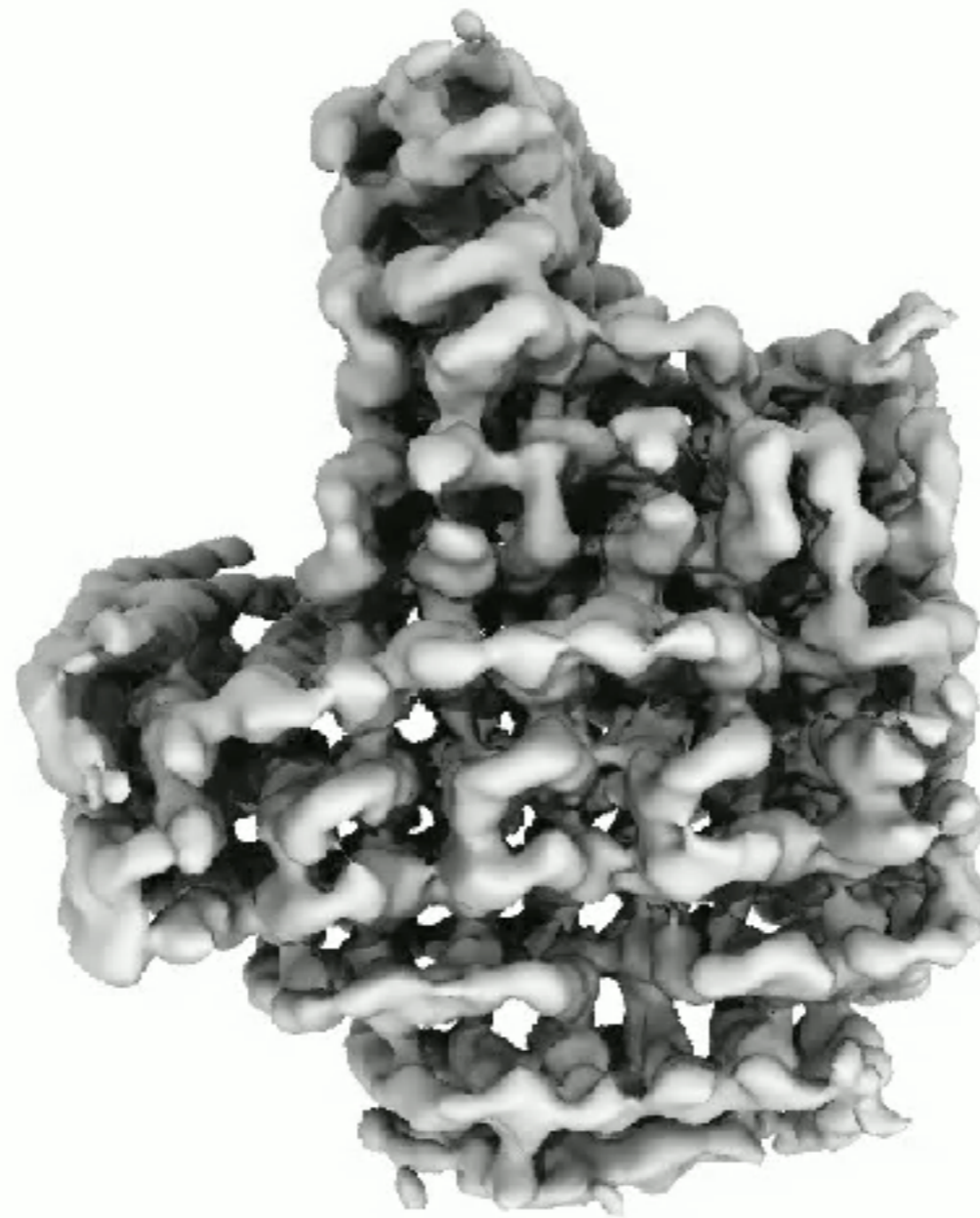


PNAS 109:20012



Nucleic Acids Research 44:3013

Comparison between simulation and experiment

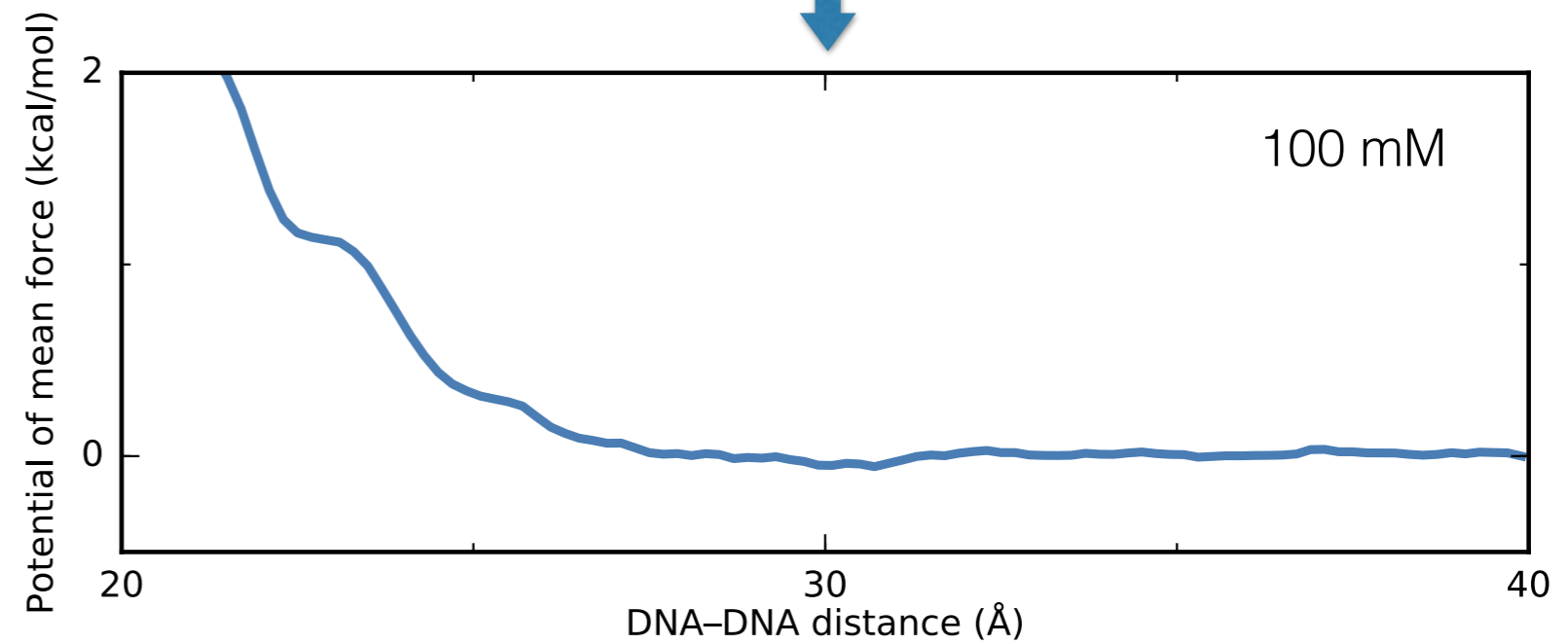
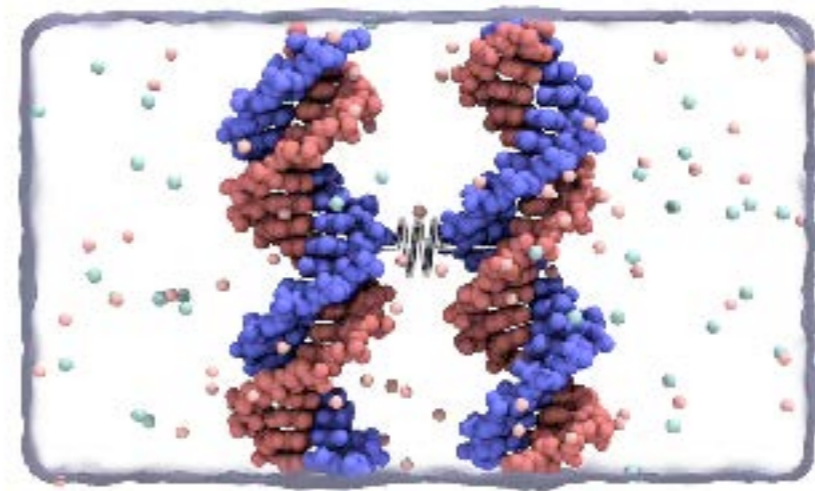
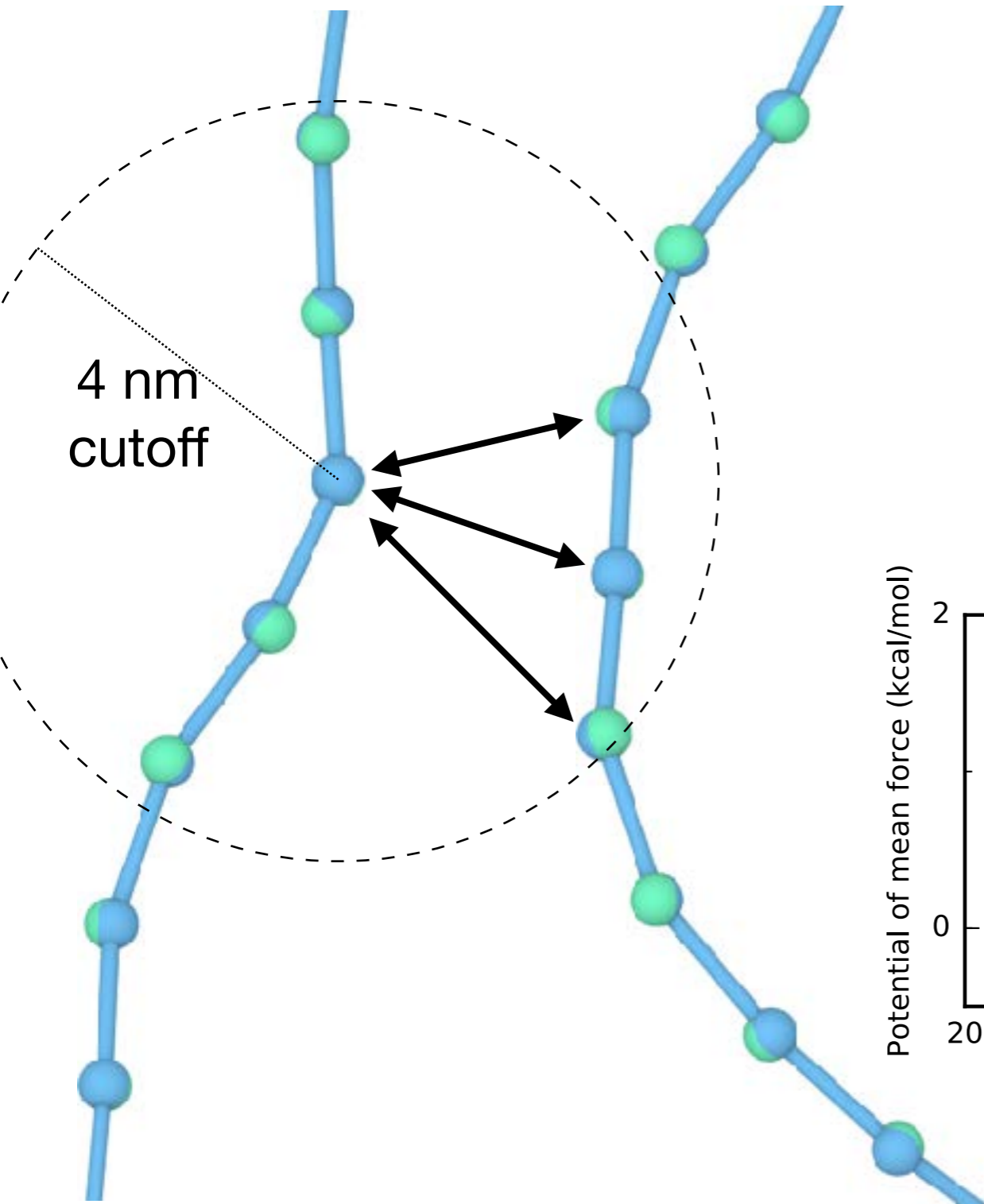


EM density

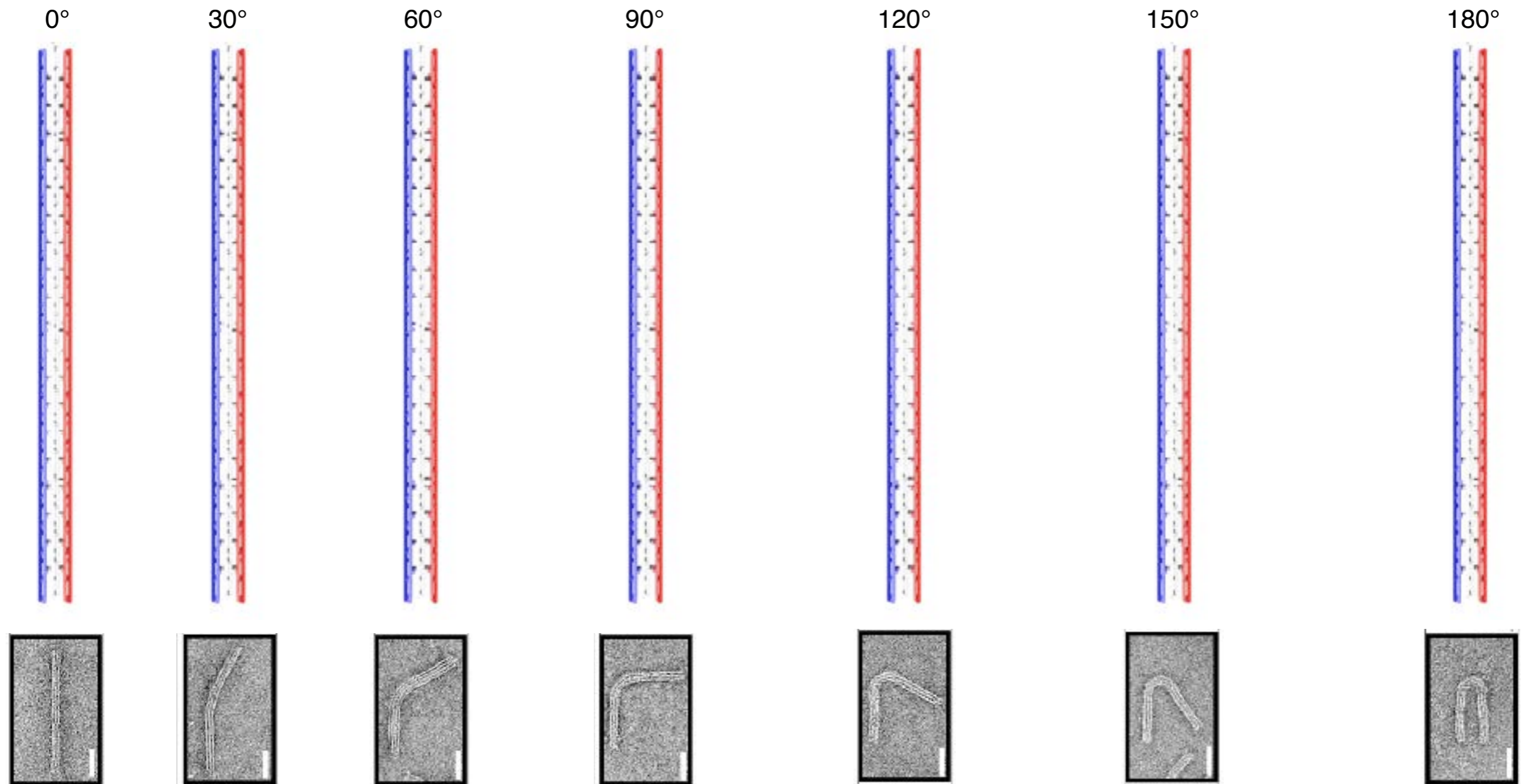
psuedo-atomic model

simulation

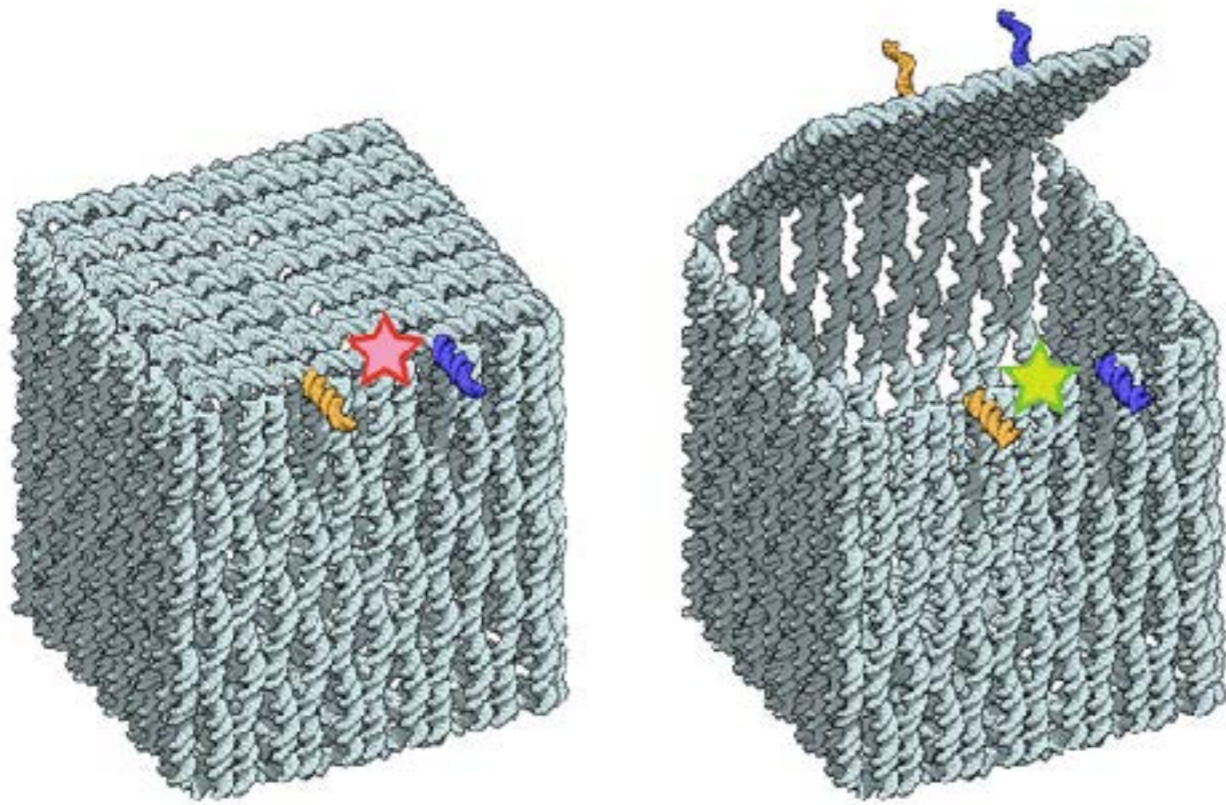
Interactions in a simple coarse-grained DNA model



Coarse-grained model captures programmed curvature



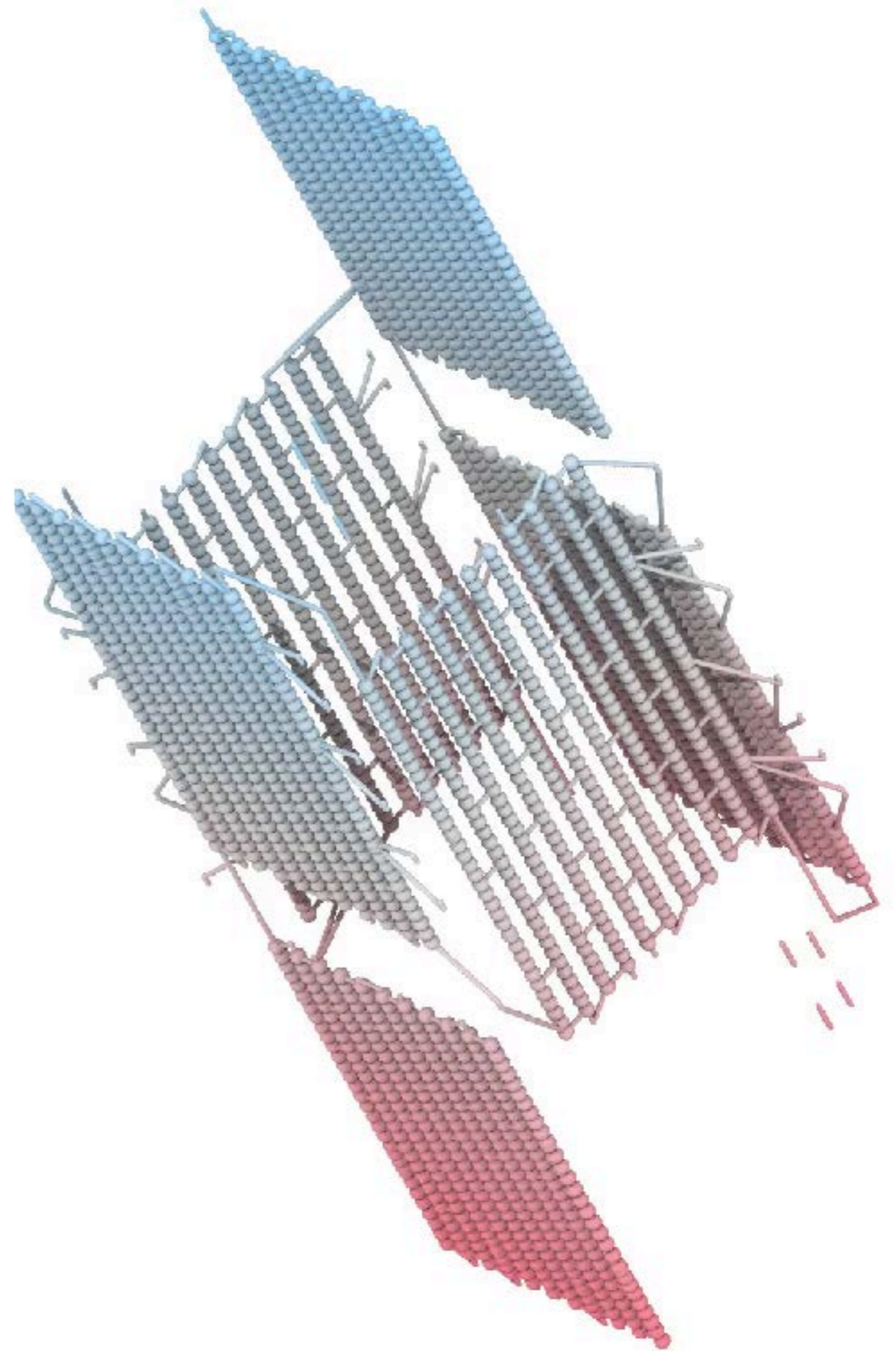
Adaptive resolution simulation of DNA origami systems



Andersen et al., Nature 2009



Birkedal Group

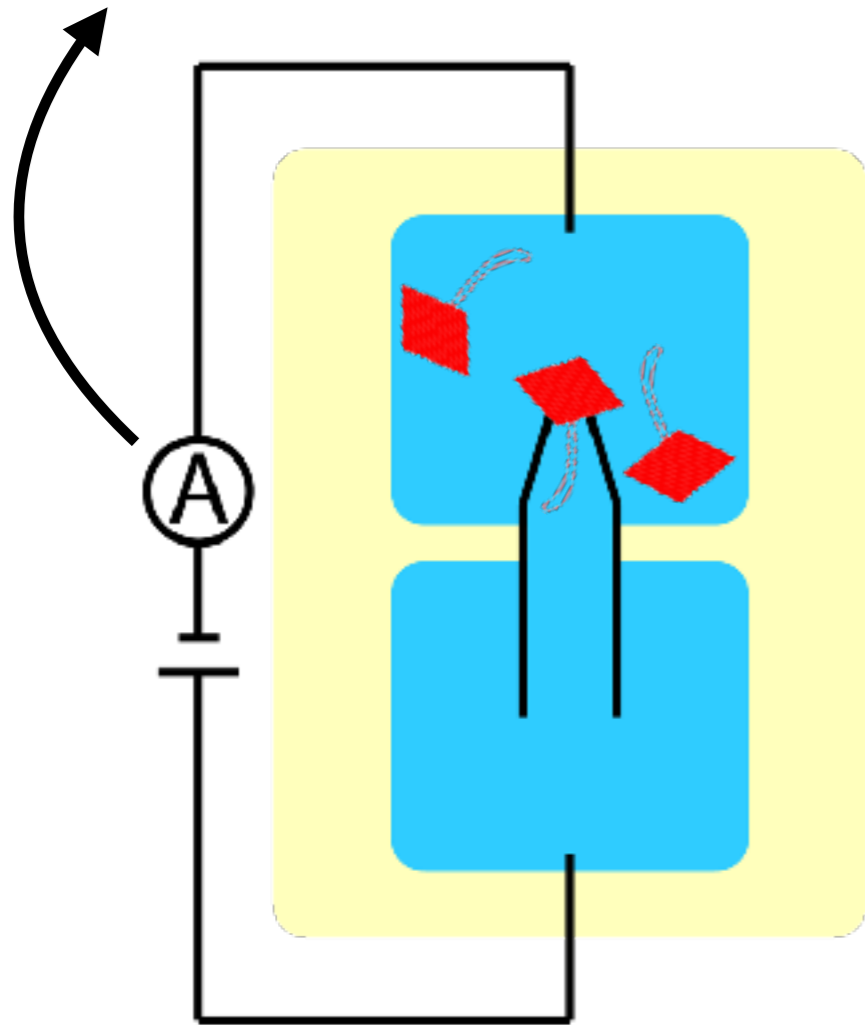
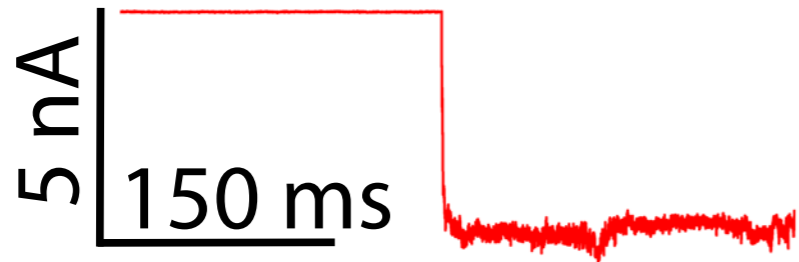




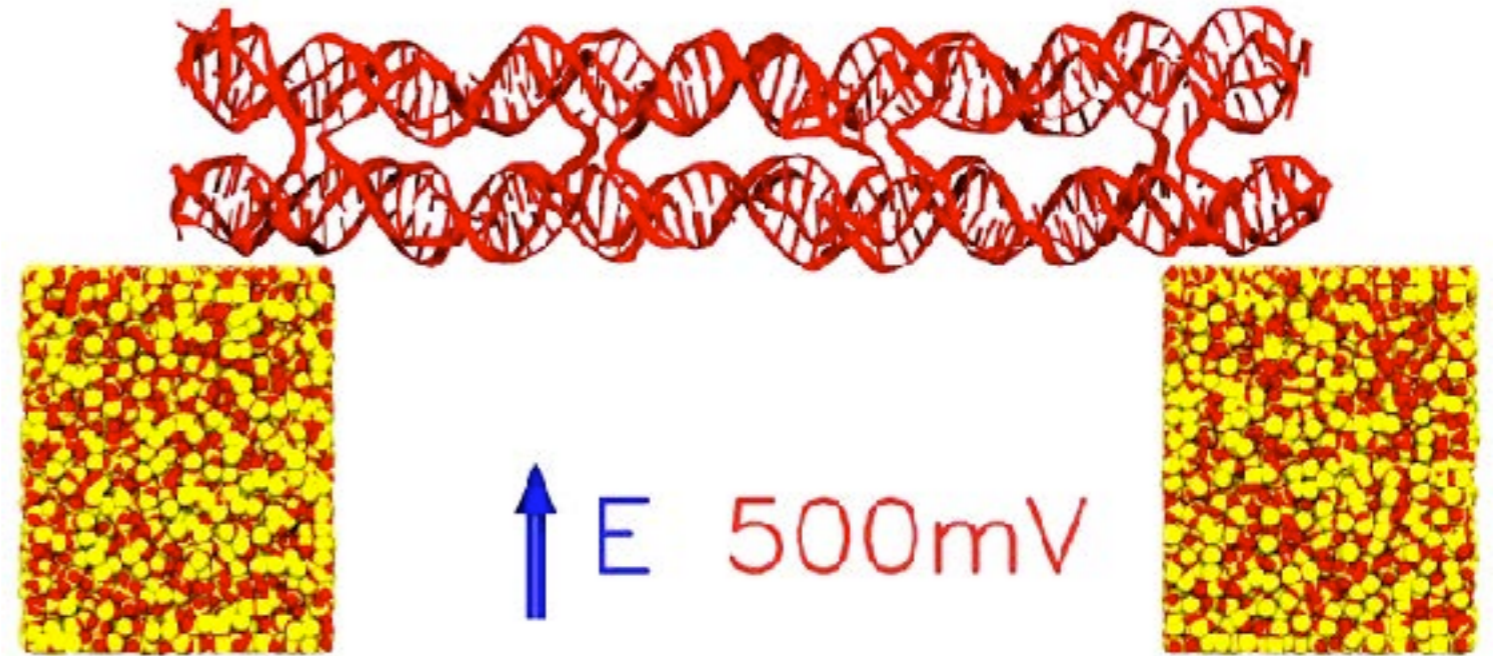
Keyser Group

DNA-based Voltage sensing

Experimental setup

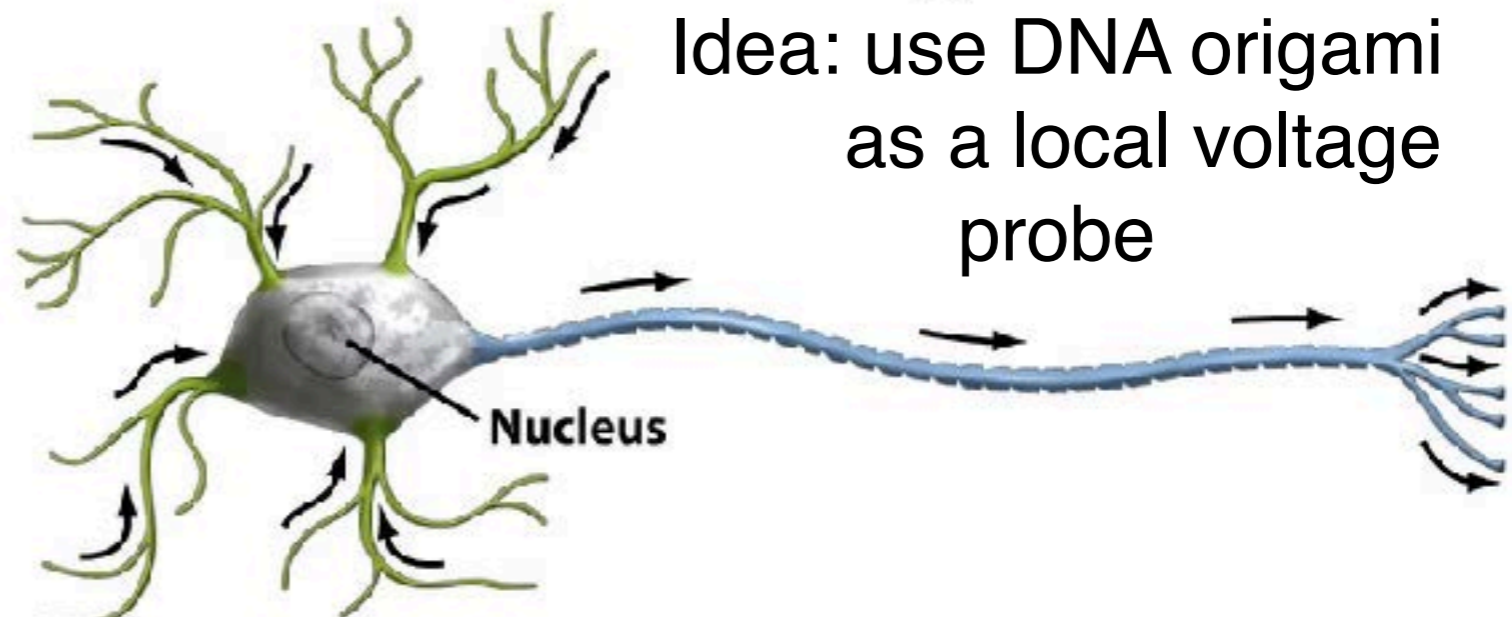


All-atom MD simulation



ACS Nano 9:1420-1433 (2015)

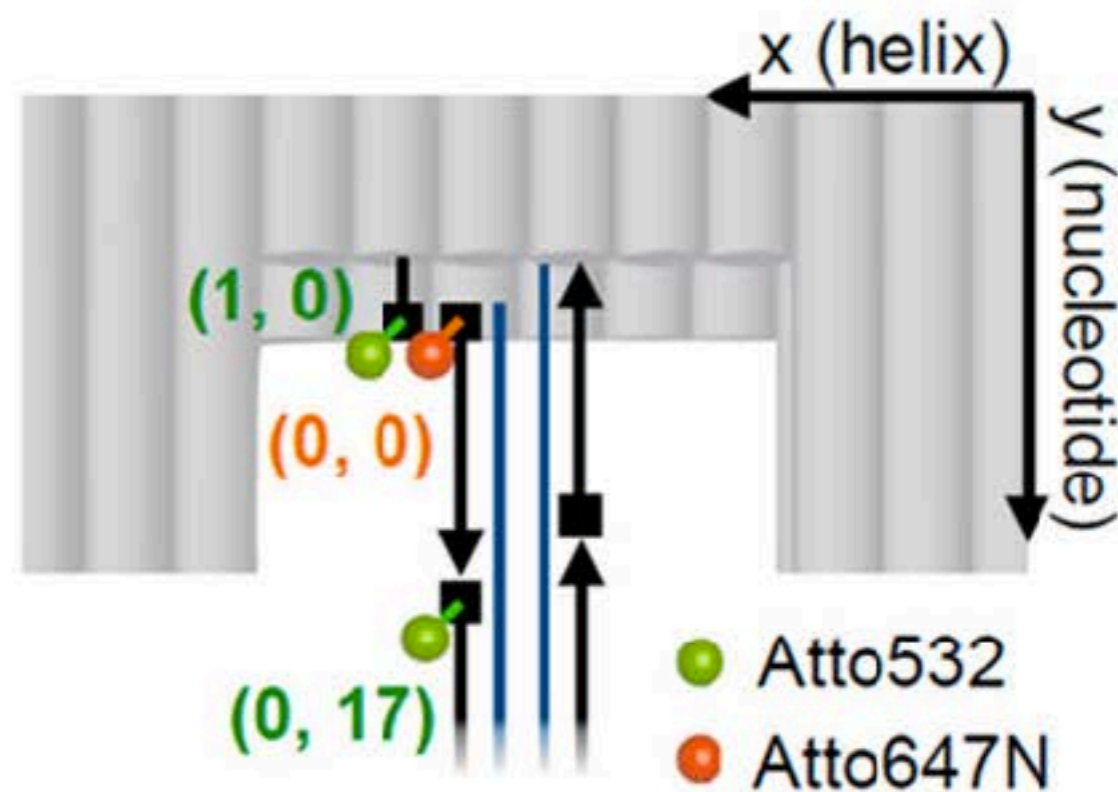
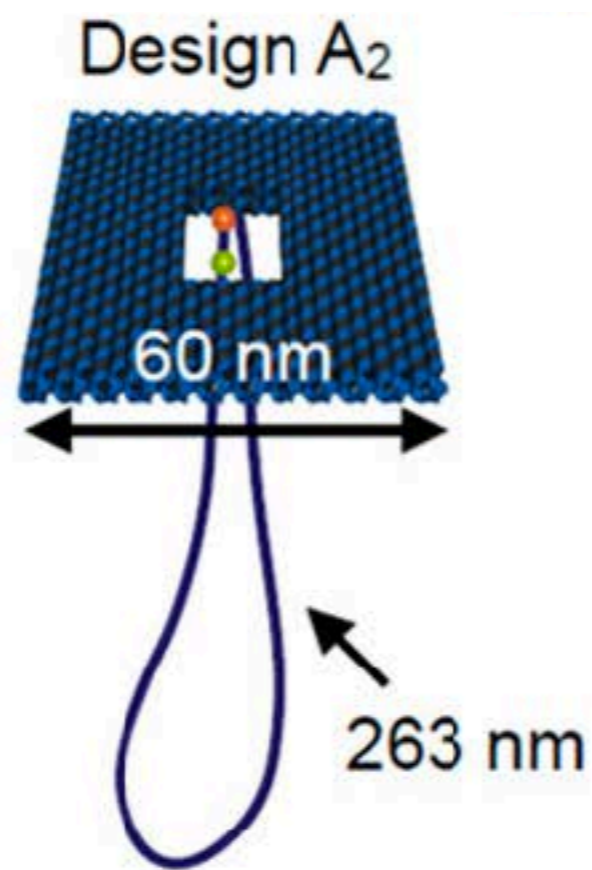
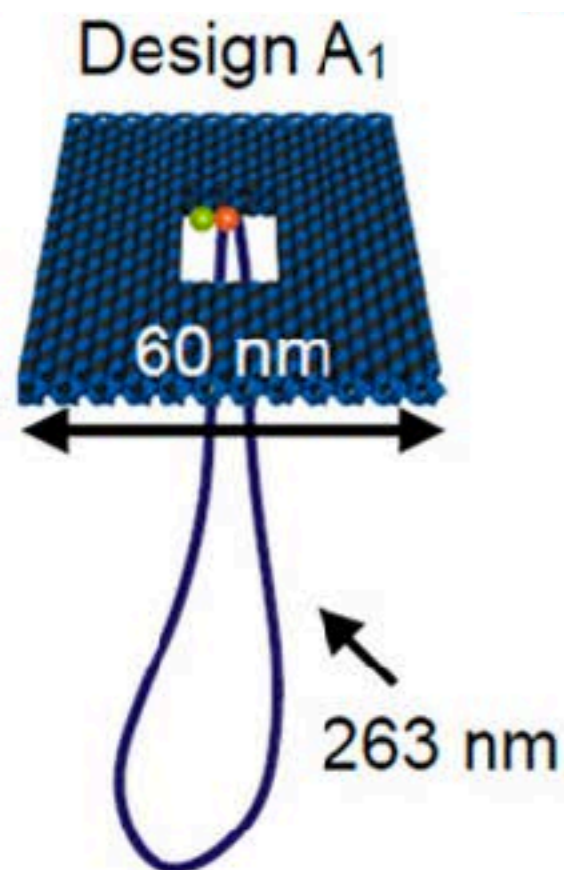
Idea: use DNA origami as a local voltage probe



Design of a nanoscale voltage sensor



Keyser and Tinnefeld Groups



Coarse-grained simulations of a FRET plate capture

~5 bp/bead CG model

40 μ s simulations

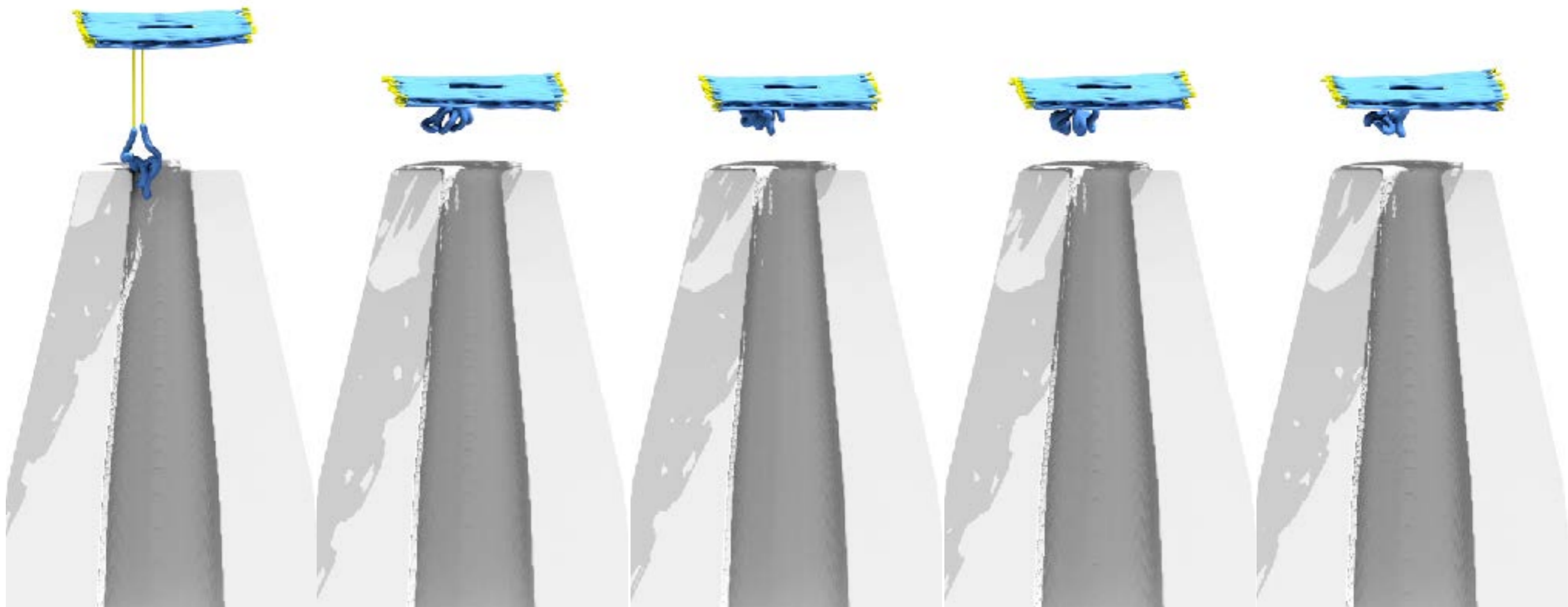
100 mV

200 mV

300 mV

400 mV

600 mV



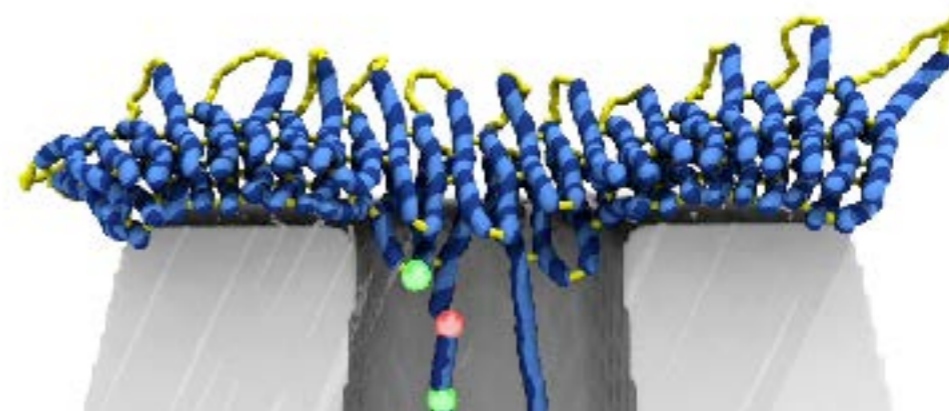
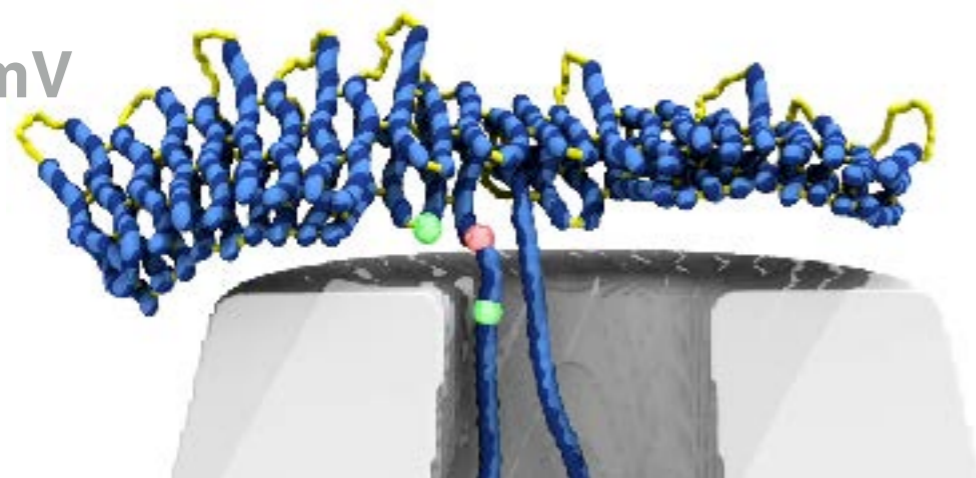
CG simulation of FRET efficiency

2 beads/bp CG model

1 μ s simulations

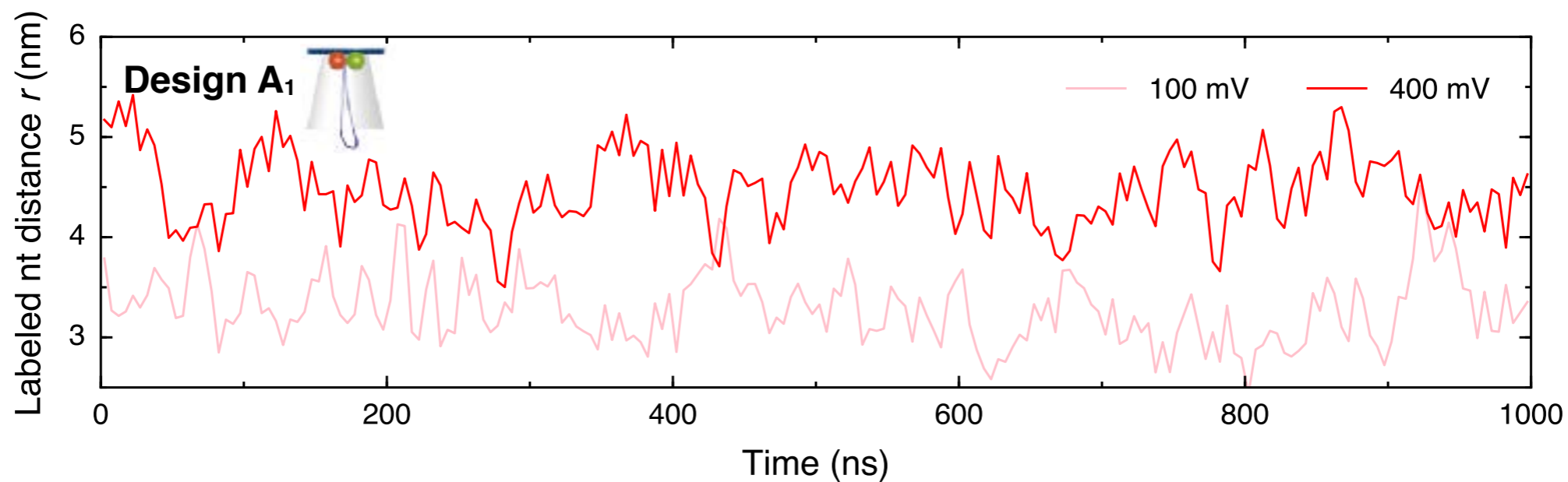
100 mV

400 mV



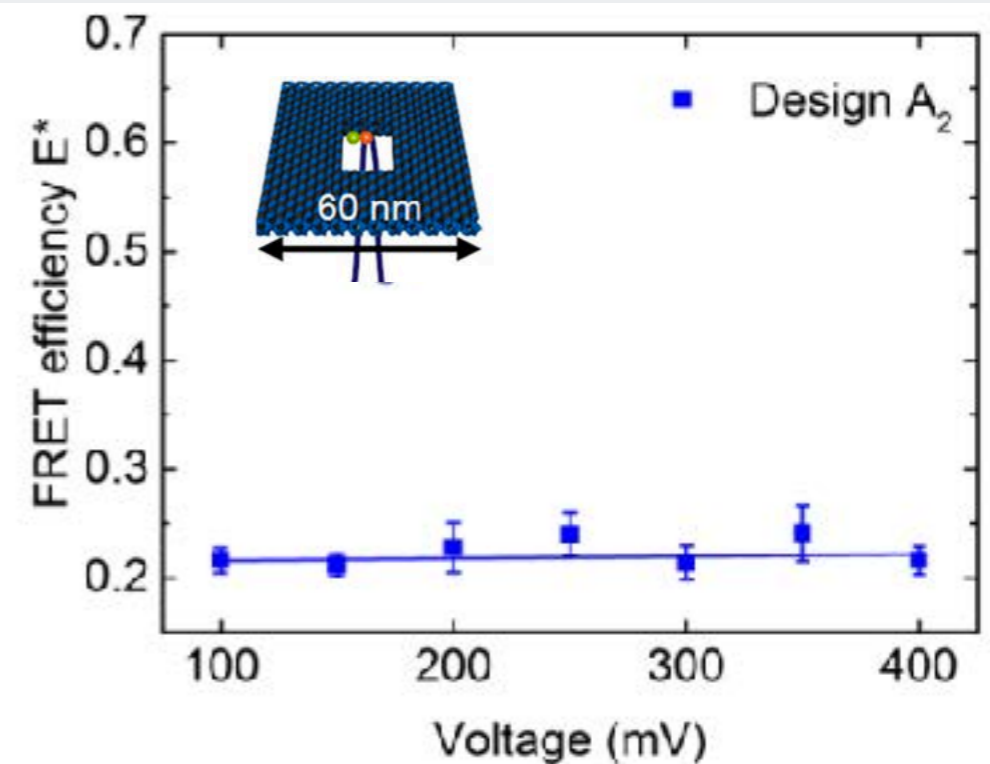
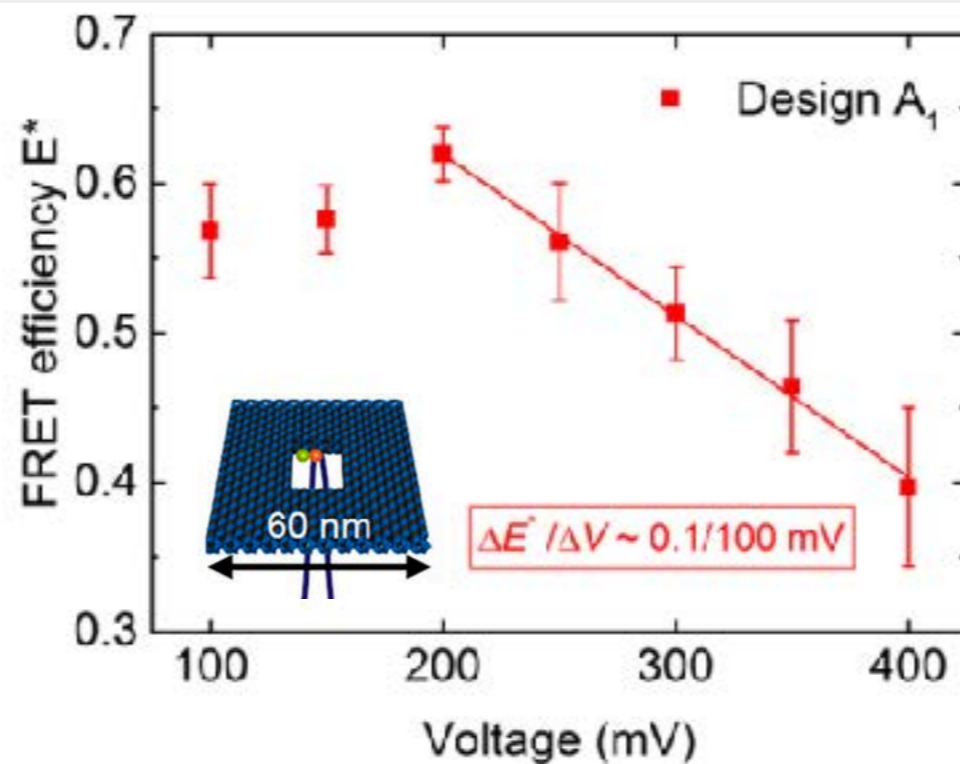
200 mV

300 mV

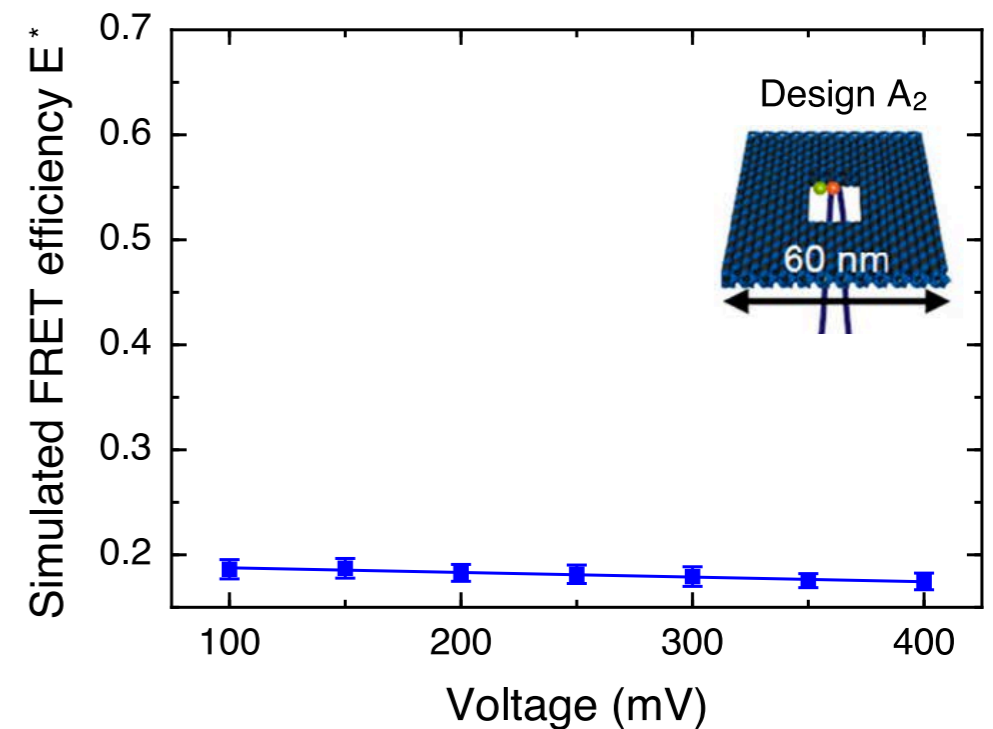
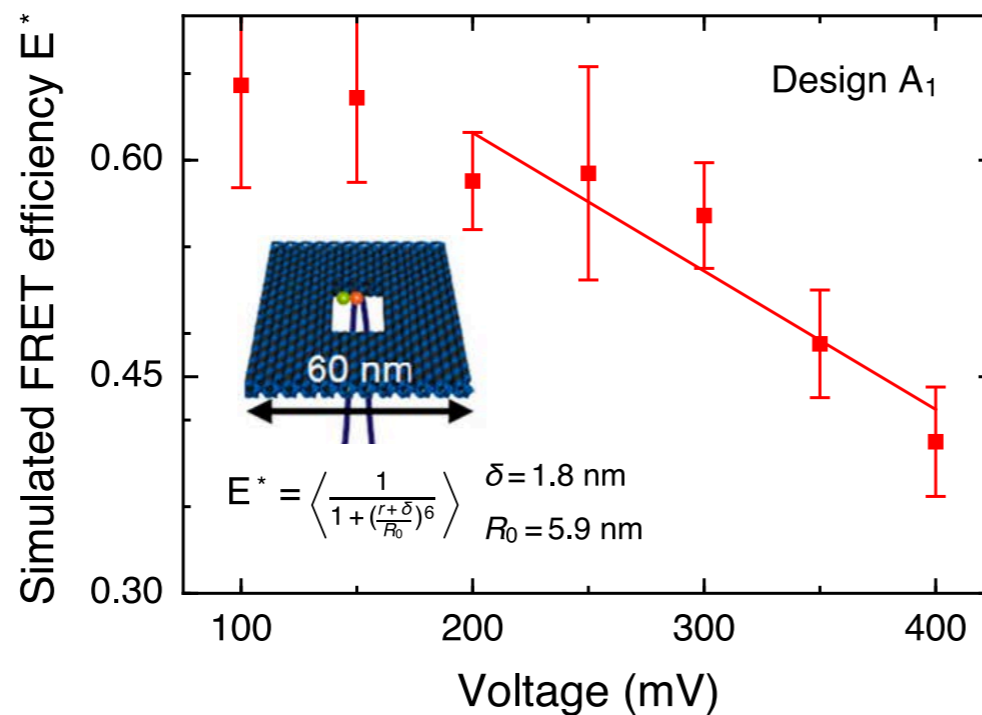


Voltage sensing with DNA origami

Experiment:



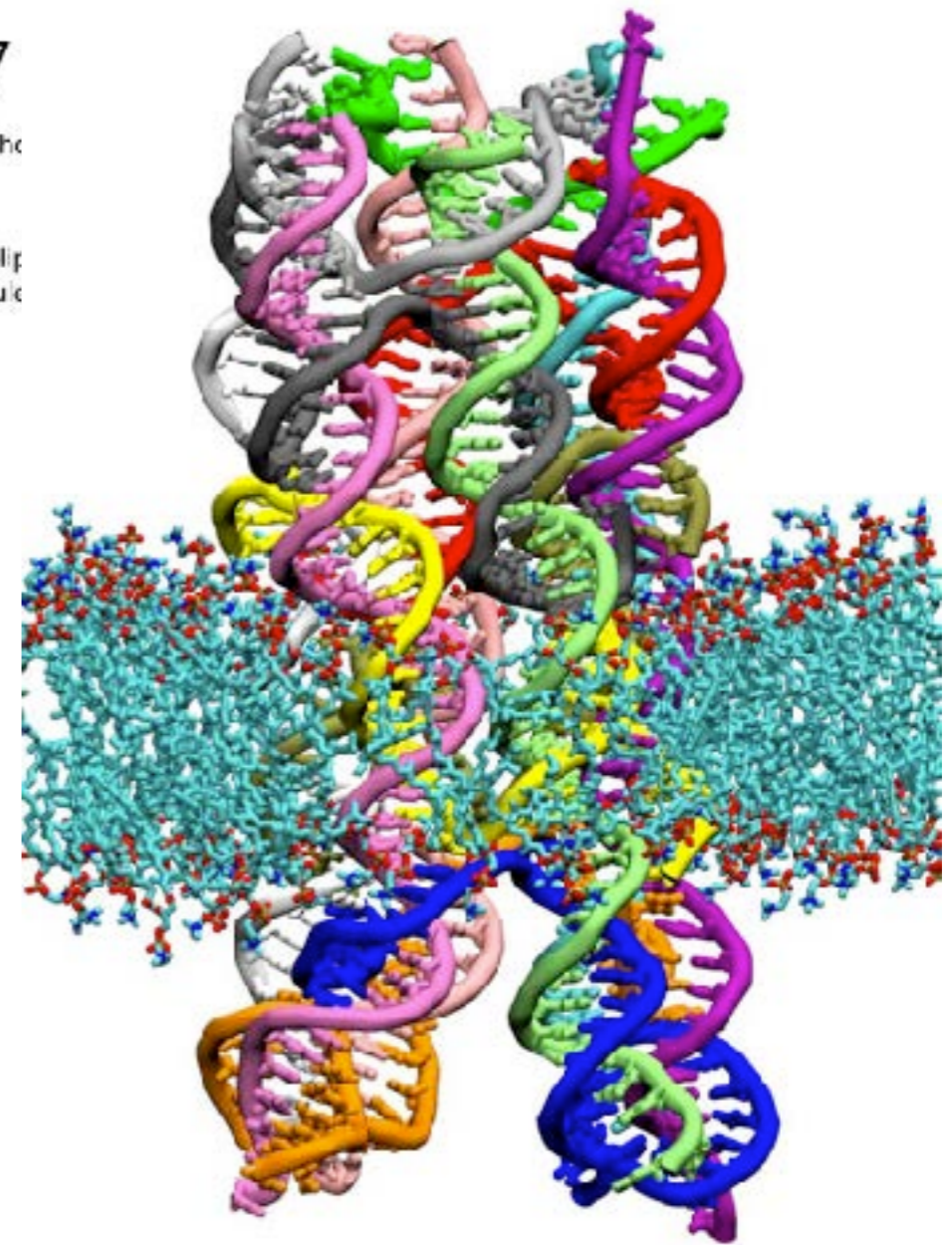
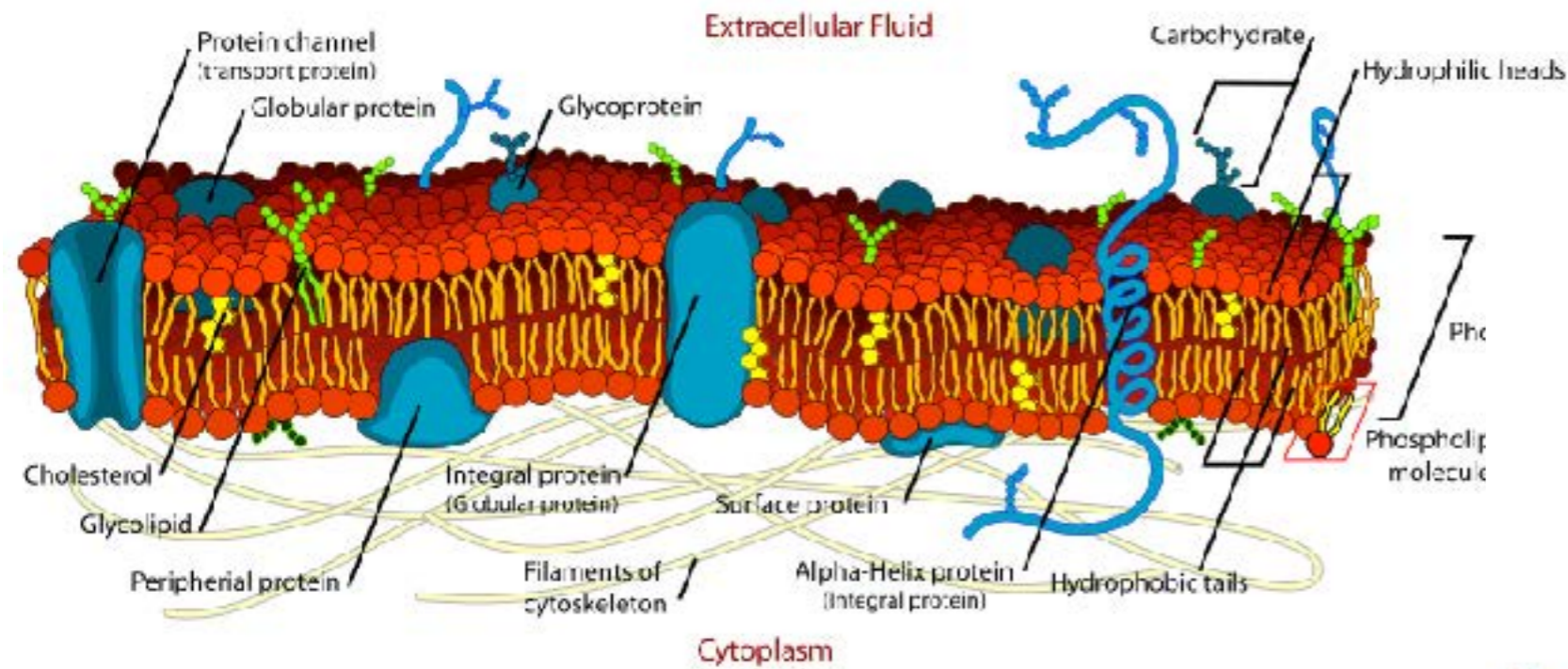
Simulation:



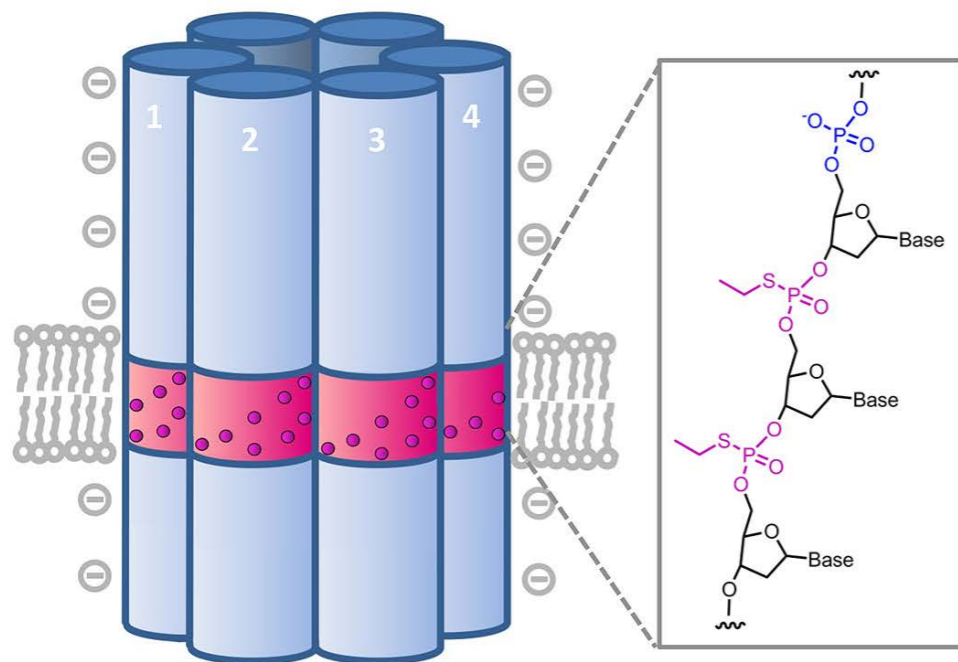
DNA Ion Channels



Jejoong Yoo



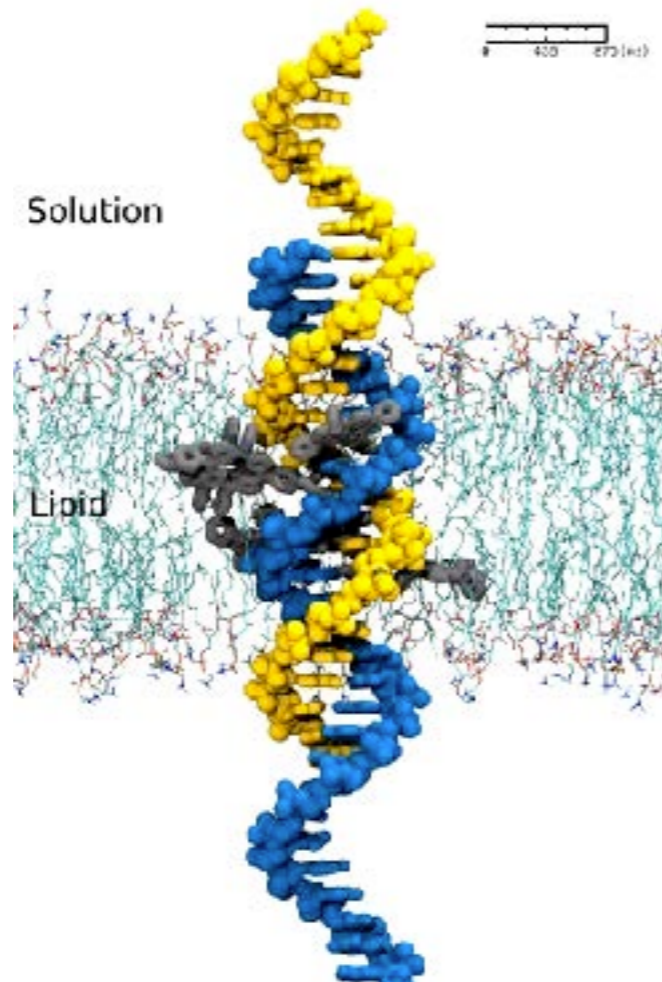
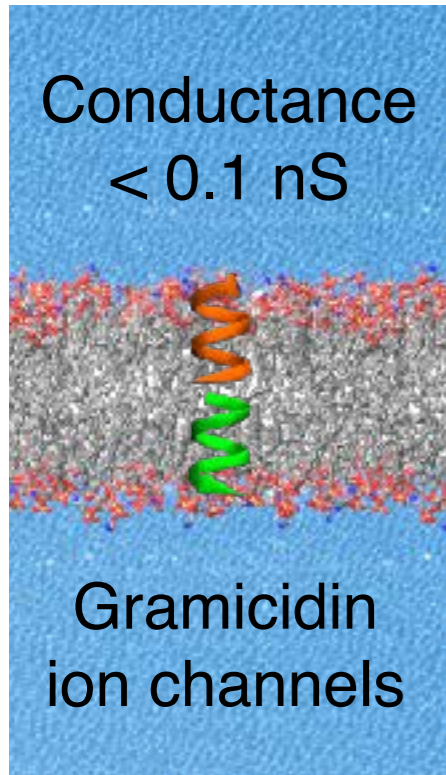
Nano Letters, 13: 2351



Porins, 1 nS conductance

Yoo & Aksimentiev, *JPCCL* 6, 4680 (2015)

DNA Ion Channels

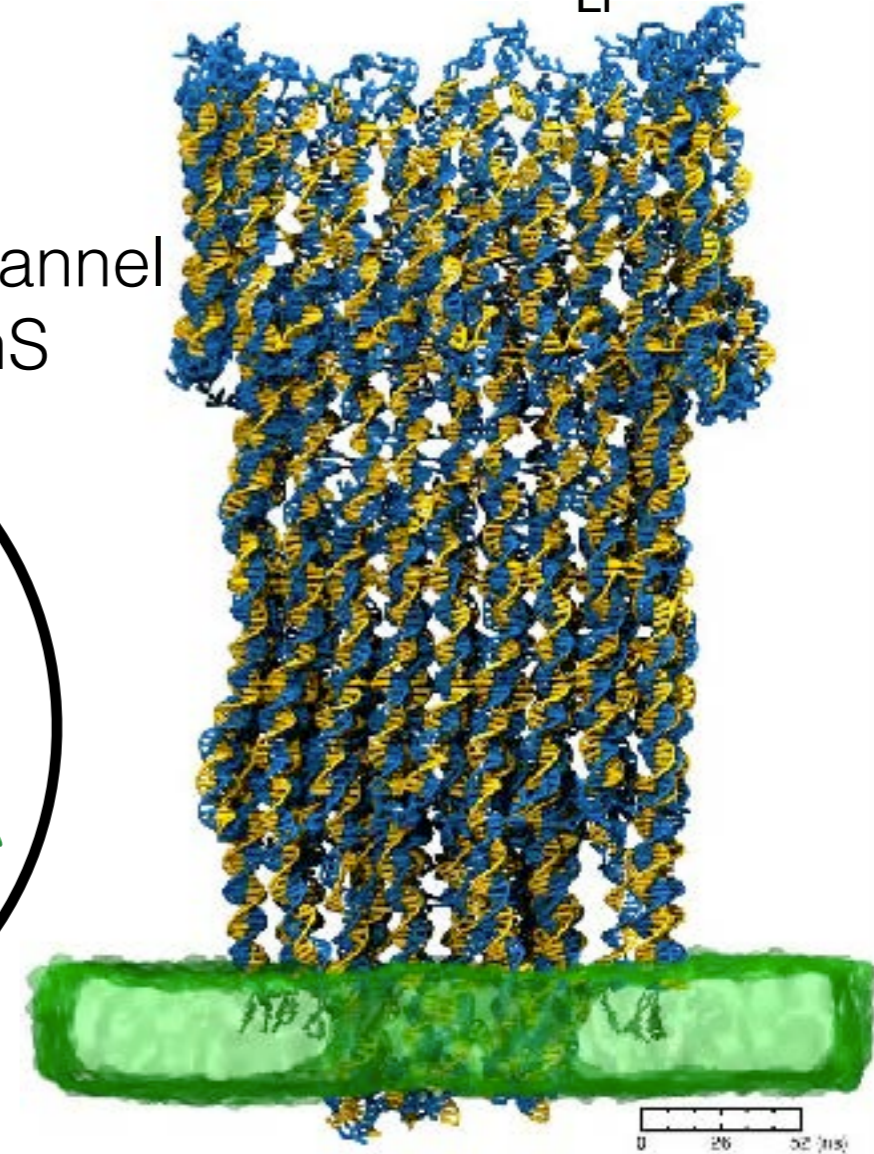
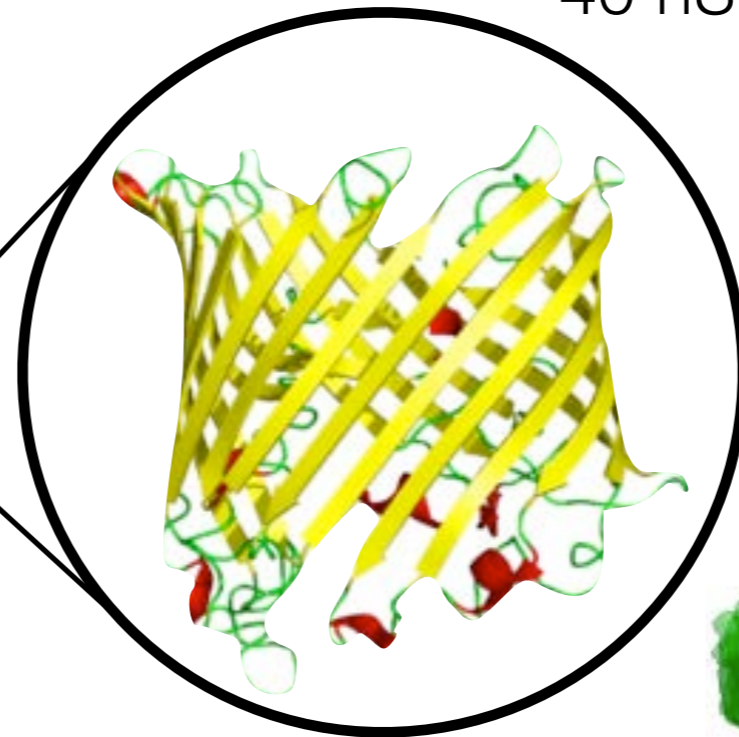
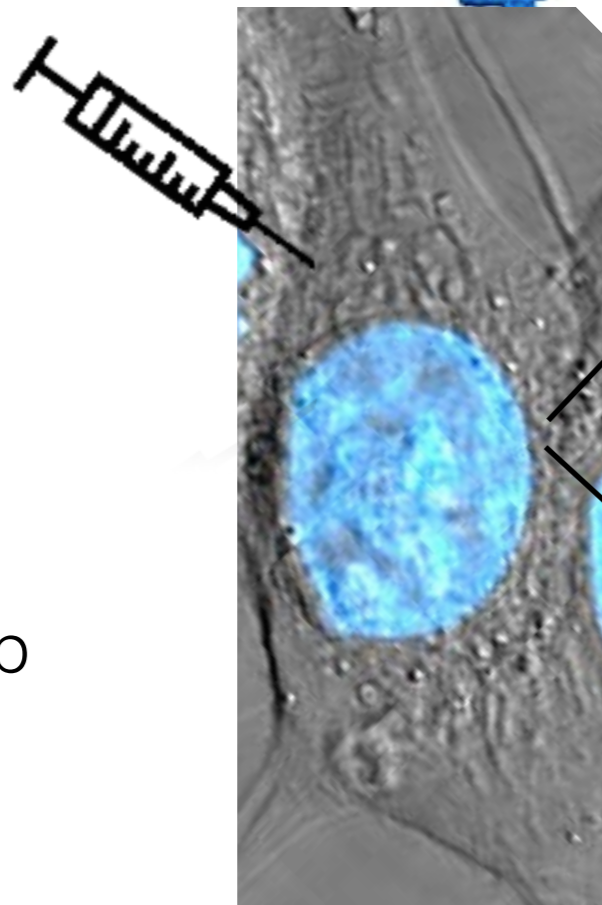


Membrane channel made of
a single DNA duplex (0.1 nS)

Nano Letters 16:4665 (2016)



Porin-like DNA channel
40 nS



ACS Nano 10:8207 (2016)

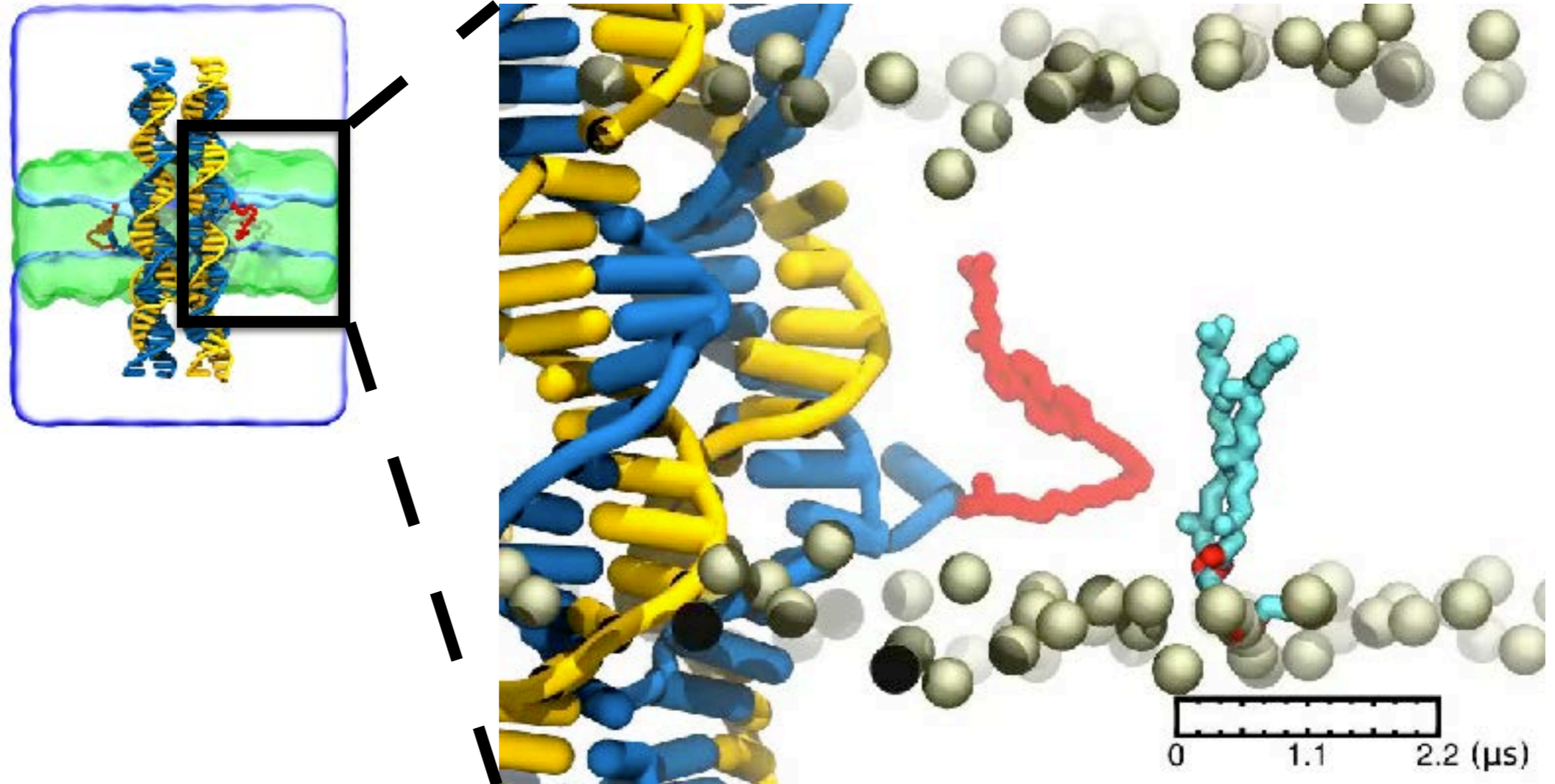


All-atom MD simulation of lipid-DNA interface



Chen Yu Li

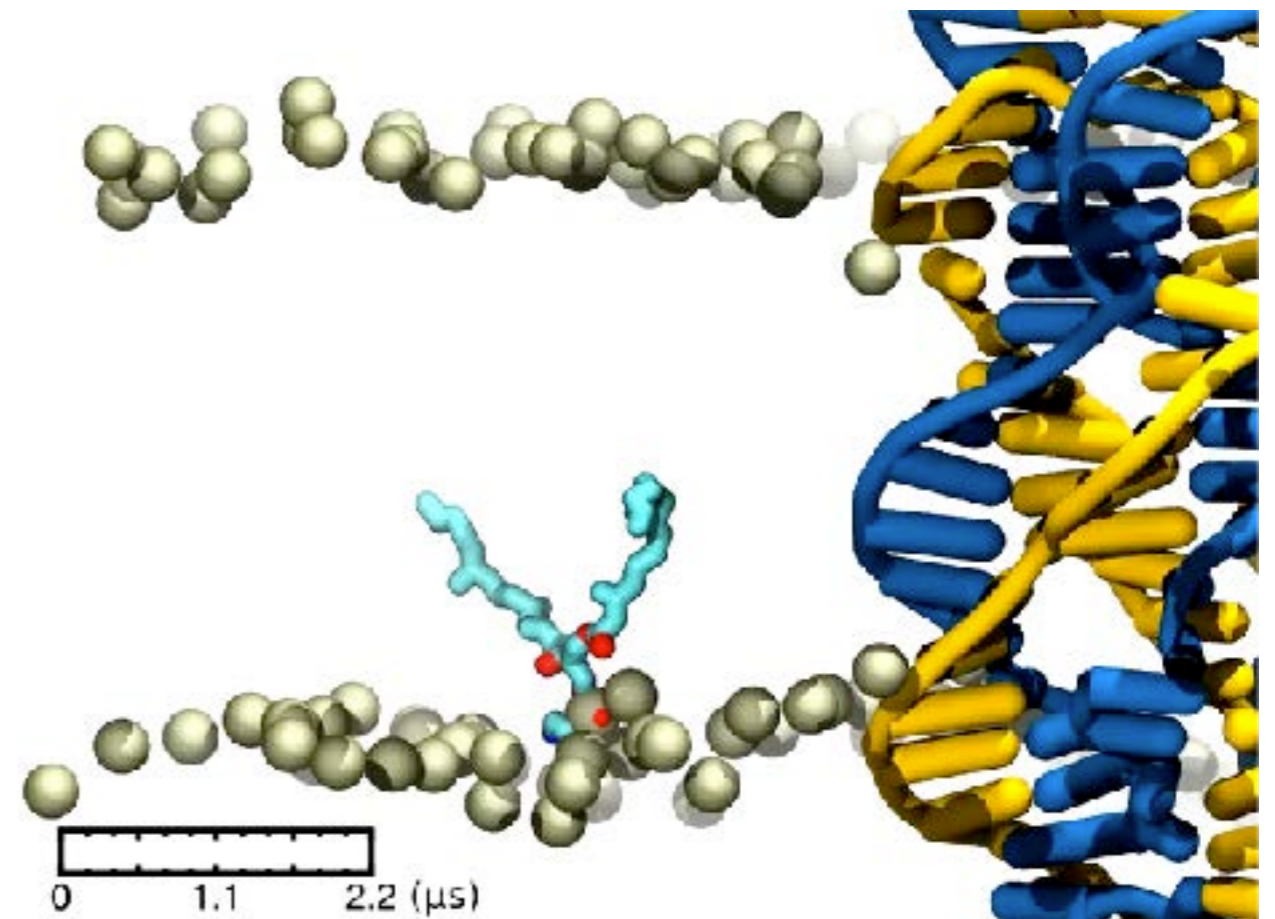
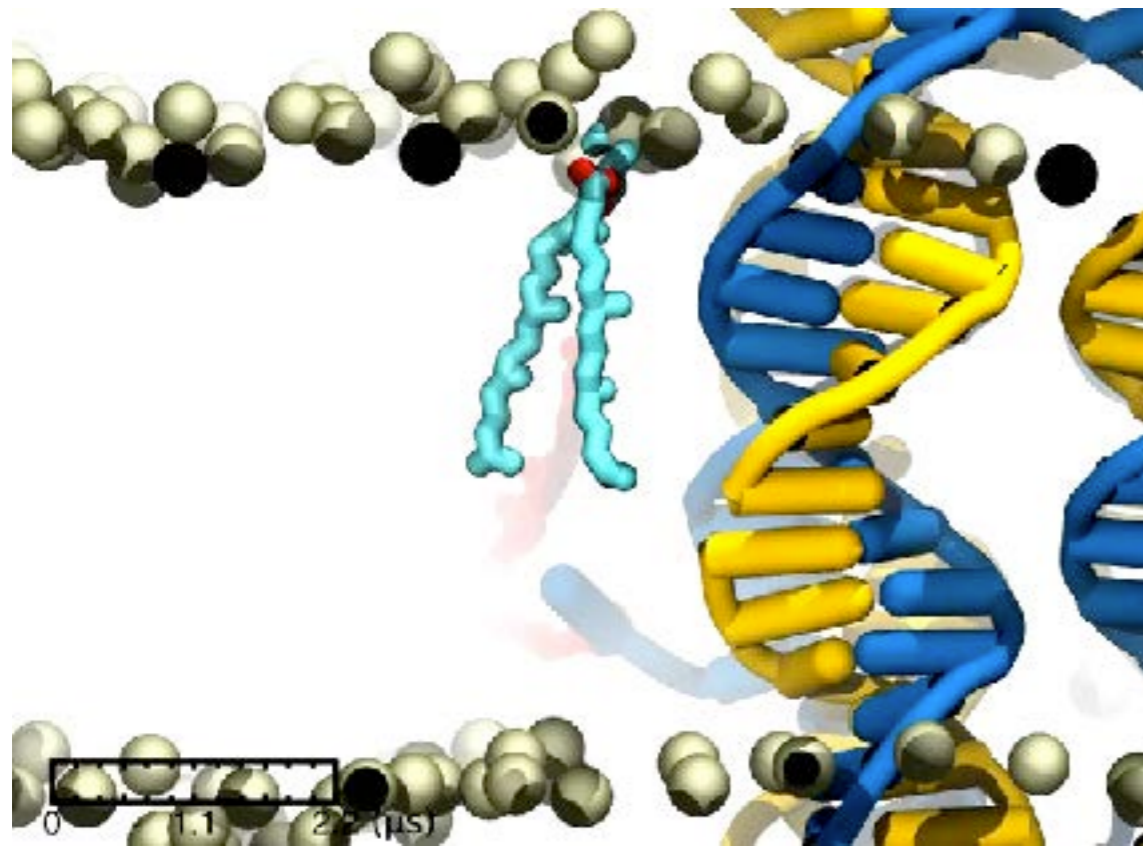
No applied electric field



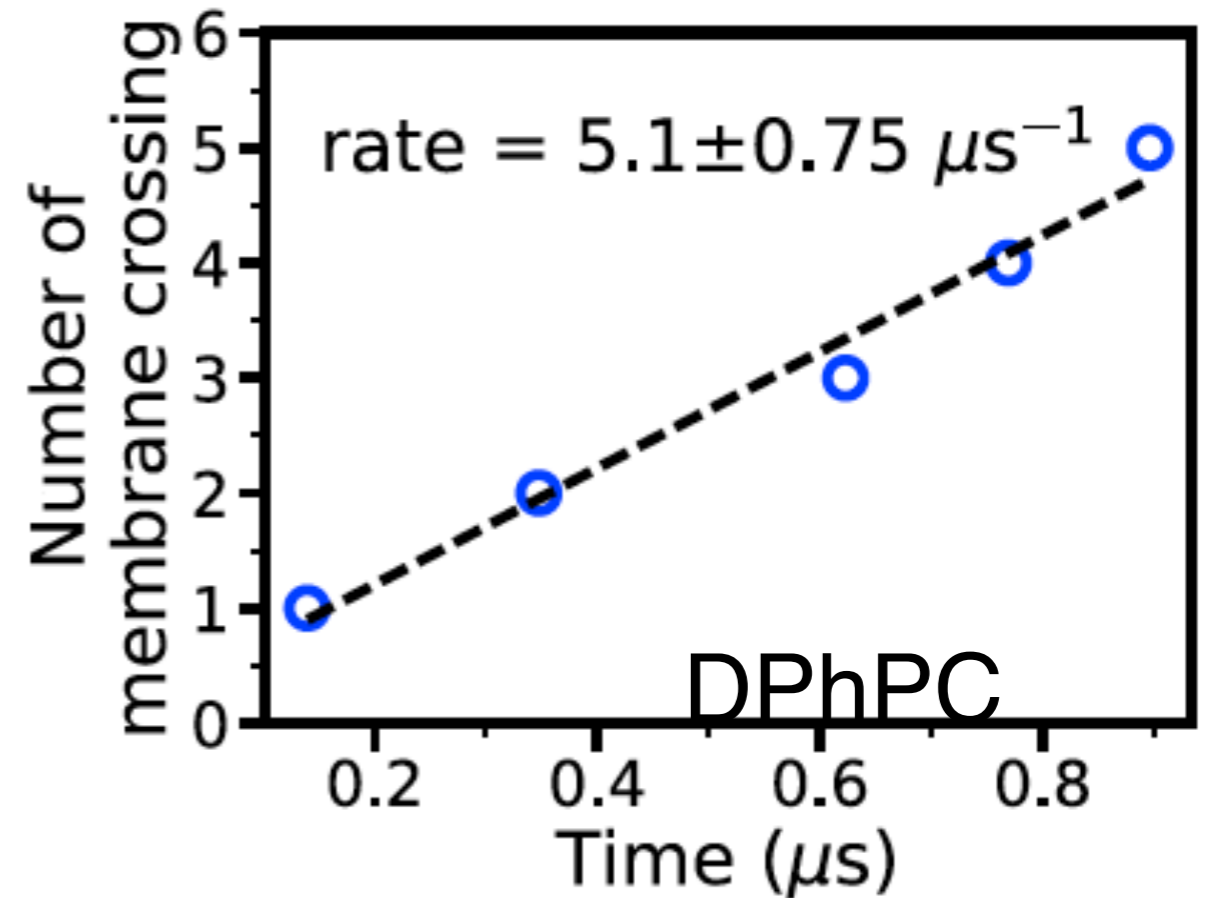
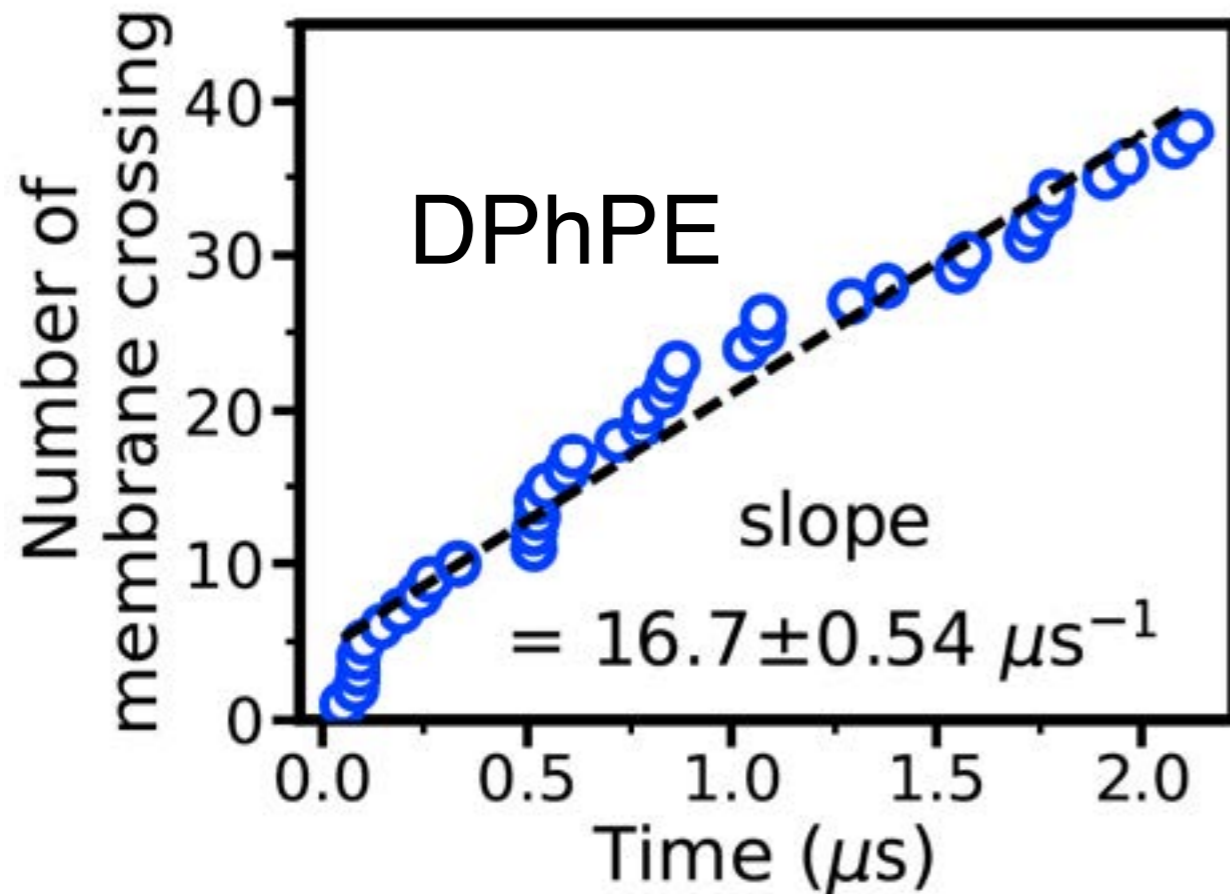
Lipid molecule around the DNA channel can translocate to the other leaflet.

<http://dx.doi.org/10.1101/241166>

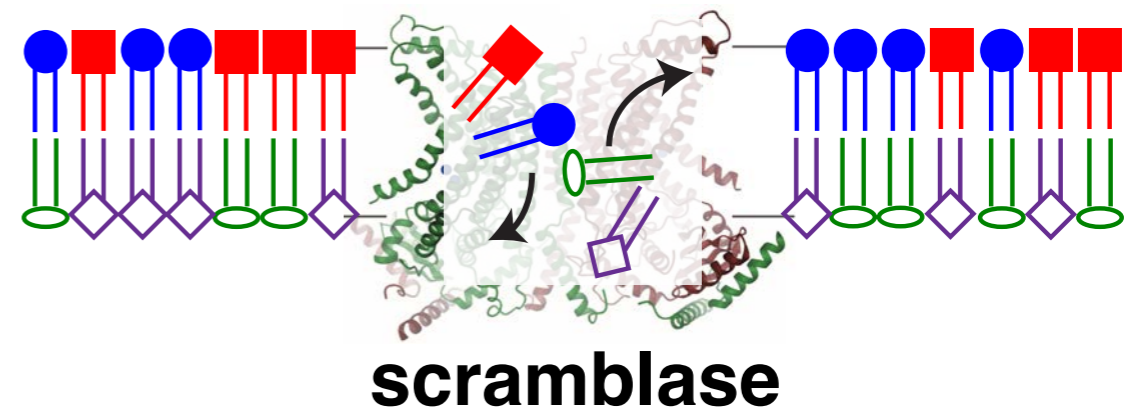
Lipid translocation through toroidal pores is very common and very fast



Lipid translocation through toroidal pores is very common and very fast



3-5 orders of magnitude faster than natural scramblases

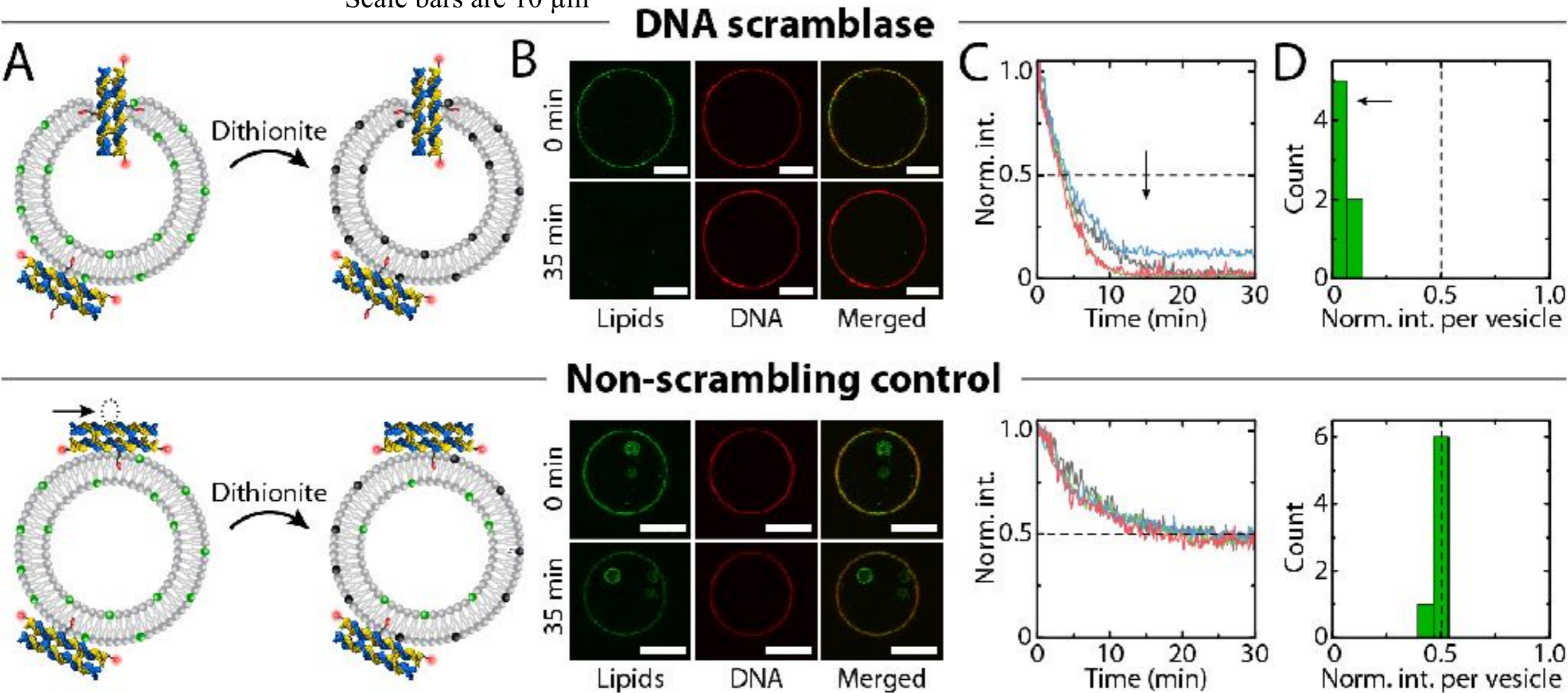


Experimental verification



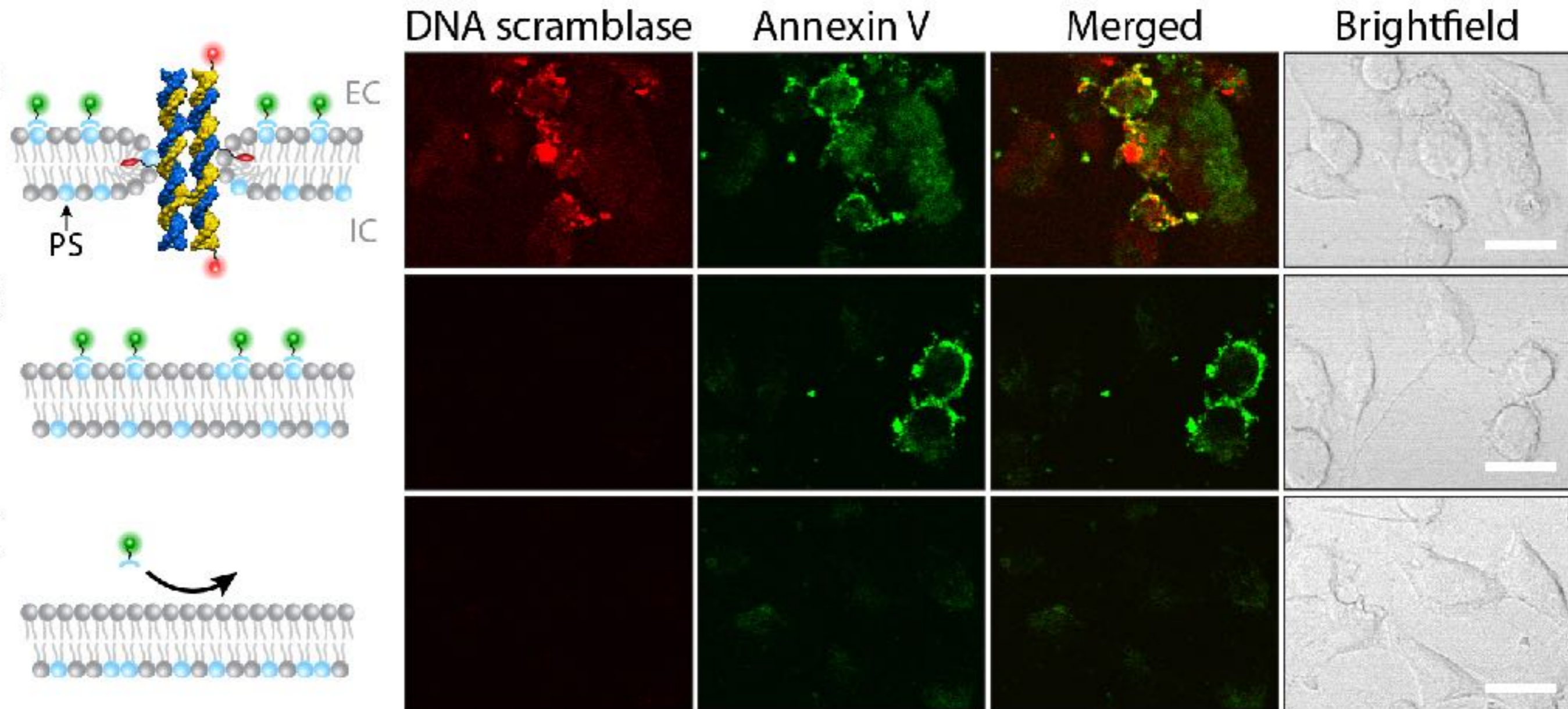
Keyser Group

Scale bars are 10 μm



Works in human cells

Annexin V binds specifically to PS lipids found in inner leaflet of human cells



Breast cancer cells from the cell line MDA-MB-231

Scale bar is 20 μm

Positive control: apoptosis-inducing microbial alkaloid staurosporine

Negative control: DNA folding buffer

<http://dx.doi.org/10.1101/241166>

Acknowledgements



Aksimentiev
Group



Aleksei
Aksimentiev



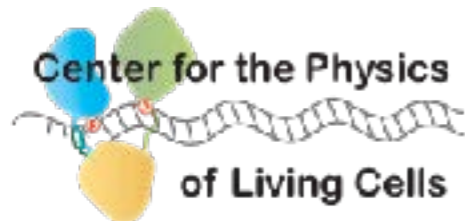
Chen-Yu
Li



Jejoong Yoo



Center for
Macromolecular
Modeling and
Bioinformatics



Victoria Birkedal

Ulrich Keyser

Philip Tinnefeld

