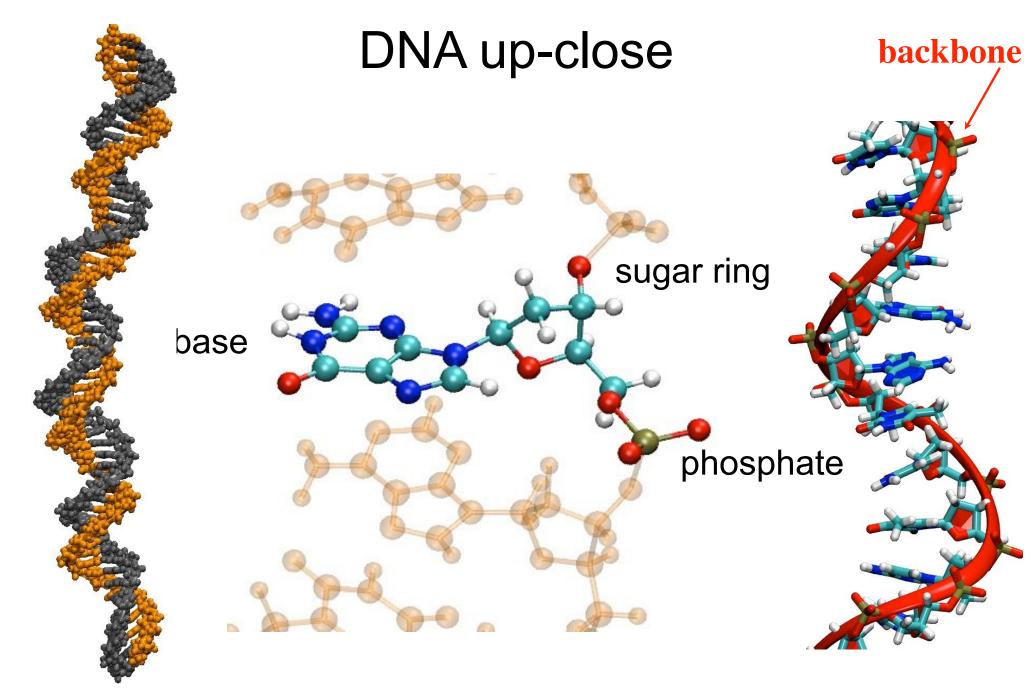
### DNA nanotechnology

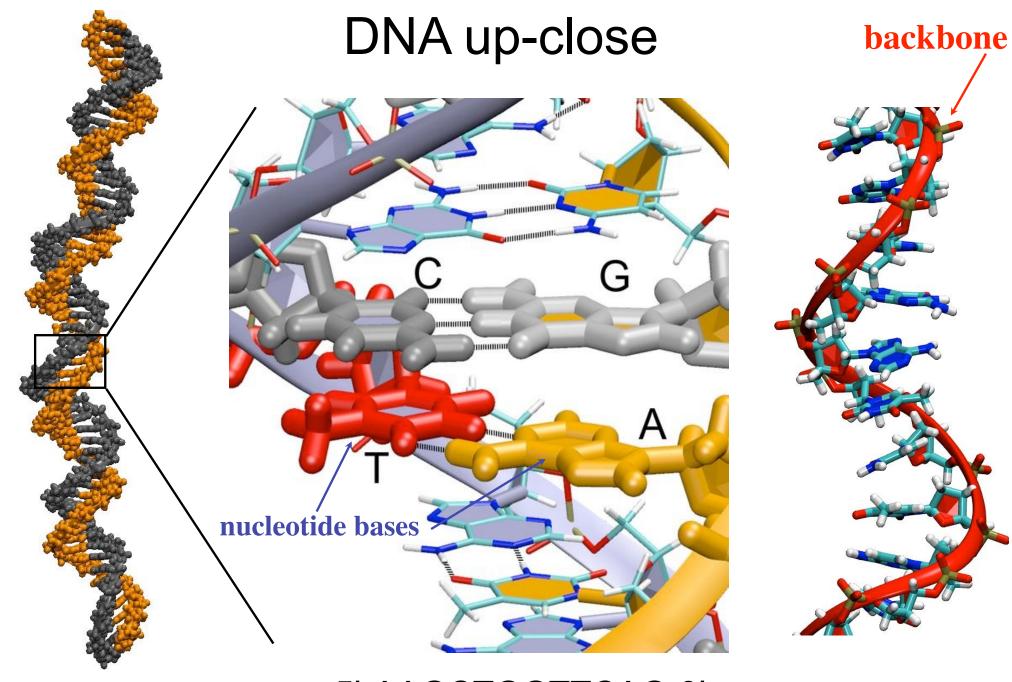
Aleksei Aksimentiev Department of Physics, UIUC



Double stranded DNA

5'-AAGCTGGTTCAG-3'

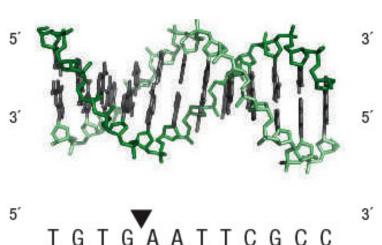
Single stranded DNA

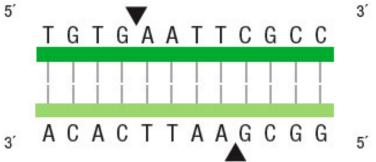


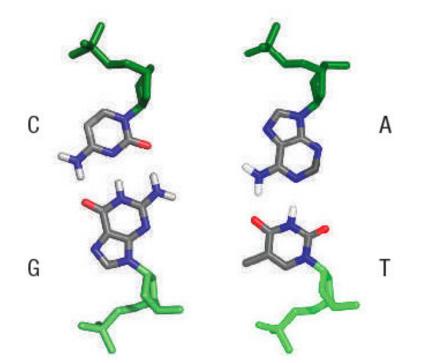
Double stranded DNA

5'-AAGCTGGTTCAG-3'

Single stranded DNA

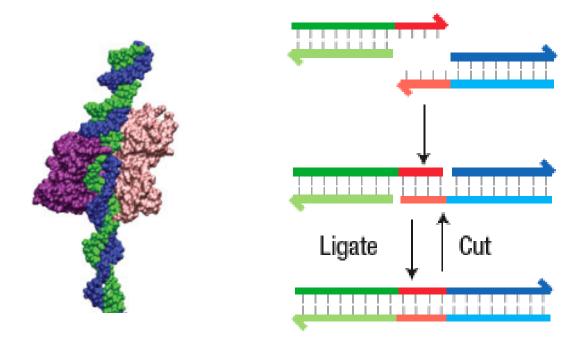






### **DNA** technology

Use restriction enzyme to cut

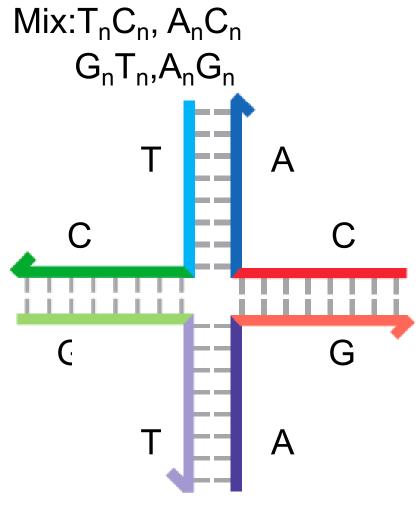


Use ligase to connect

Nature Nanotechnology 2: 275

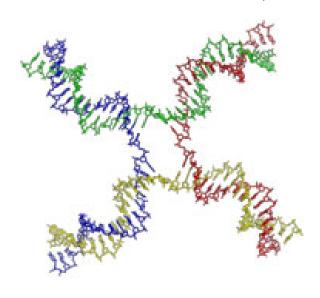
### Self-assembly of DNA structures

Recipe:



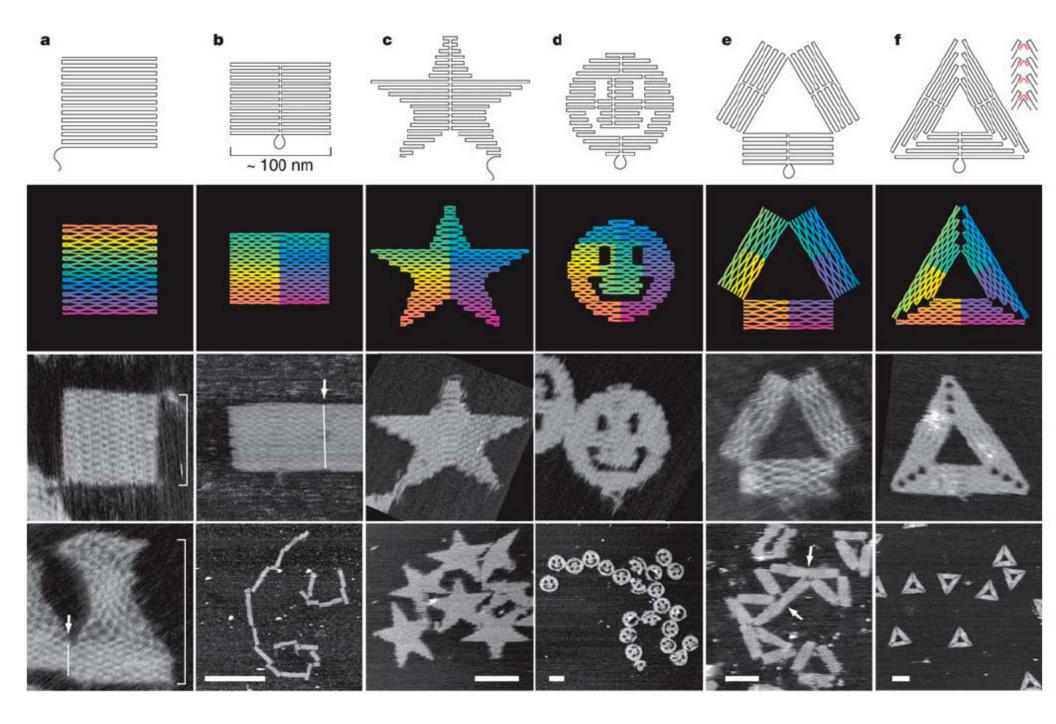
Holliday junction

Persistence length: 50 nm dsDNA 1.5 nm, ssDNA



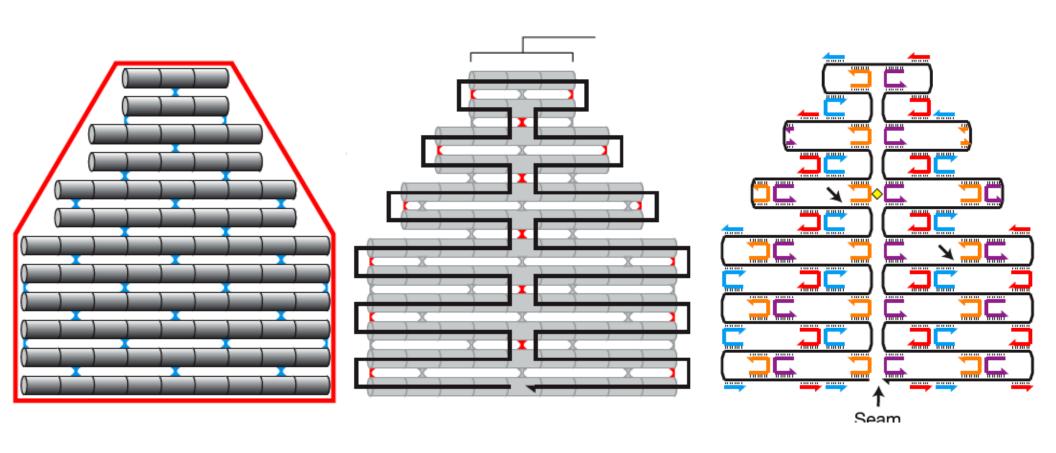
DNA sequence is designed chosen to promote hybritization of complimentary fragments and reduce non-specific association

### How far we can take this?

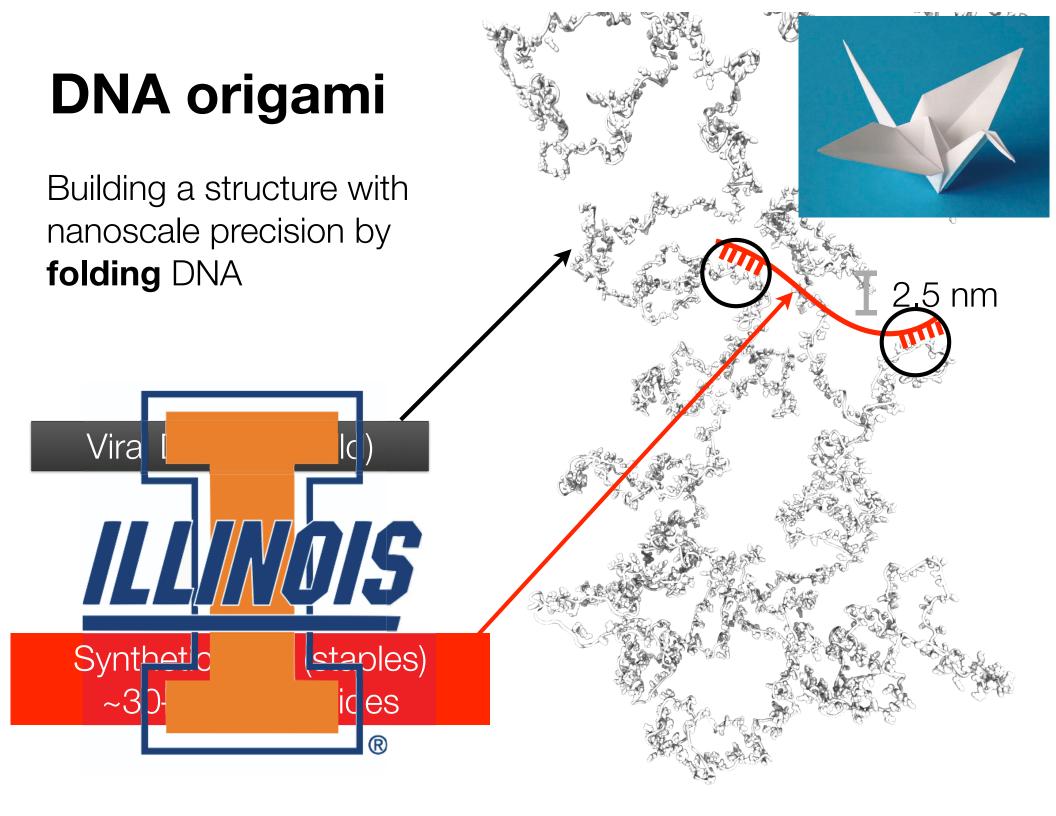


### **DNA** origami

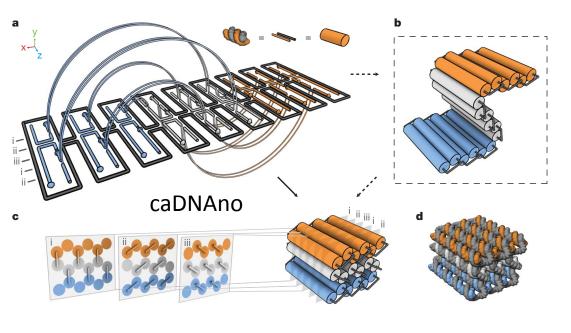
Idea: direct folding of a long single strand of DNA into desired shapes.



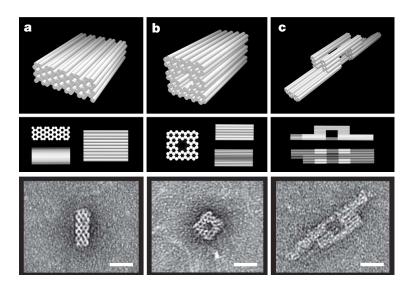
Paul Rothemund (2006), NATURE Vol 440:297



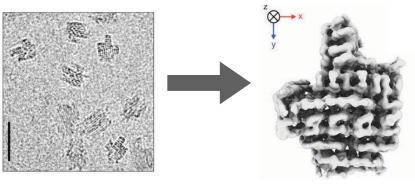
## Design and characterization of DNA nanostructures



Computer-aided design of DNA origami with caDNAno (Shih group, Harvard U.)

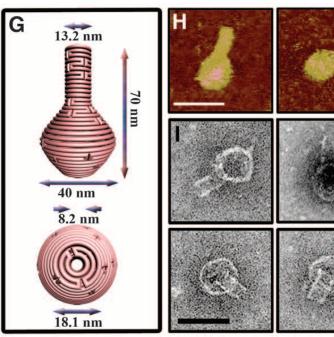


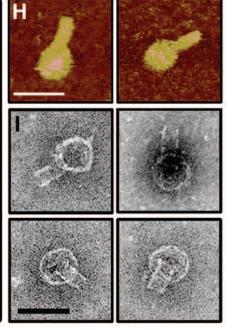
Transmission electron microscopy and/or atomic force microscopy validates the design

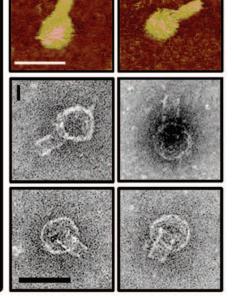


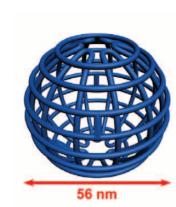
Cryo-EM reconstruction, the only experimentally derived structural model

### DNA origami structures

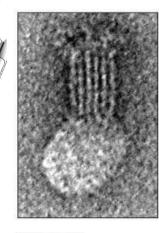






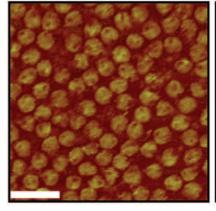


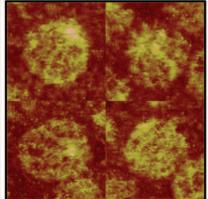




Dietz and coworkers, Science (2012)







Yan and coworkers, Science (2011)

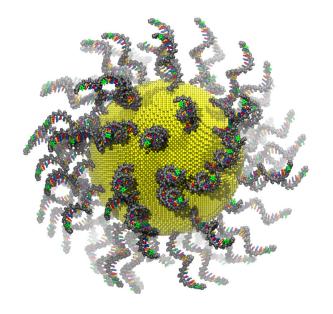
Shih and coworkers, Science (2009)

Yan and coworkers, Science (2013) 12.5 mM MgCl<sub>2</sub> 30 mM MgCl<sub>2</sub>

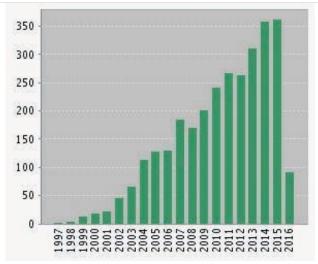
25 nm

### DNA nanotechnology

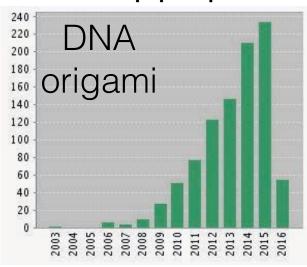
DNA-functionalized nanoparticle:

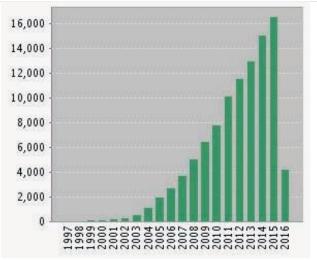


All-atom model build using Functionalization Workbench

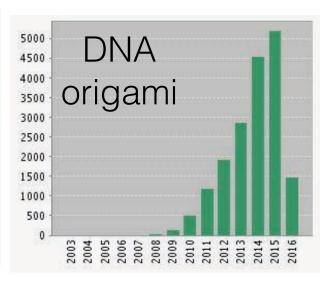


Number of papers published





**Number of citations** 



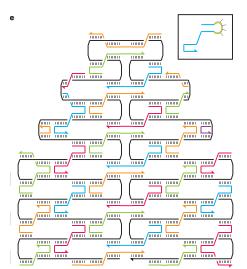
DNA nanotechnology is a rapidly expanding field

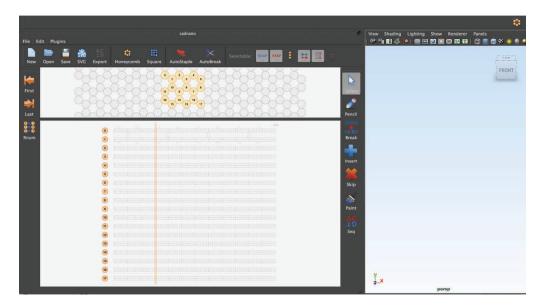
#### caDNAno

- Computer-Aided Design of DNA origami made by Shih group at Harvard.
- Designed as a plugin of Autodesk MAYA.

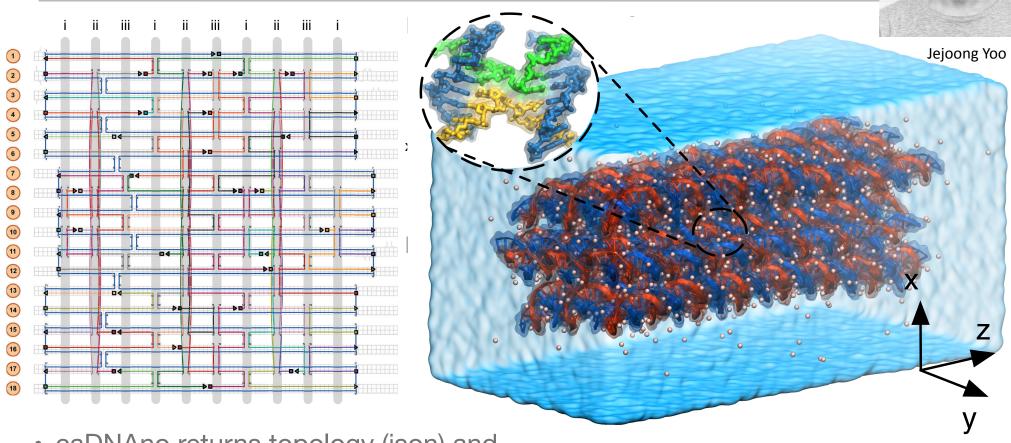
• Limited to a design of antiparallel DNA helices in a honeycomb or square

lattice.



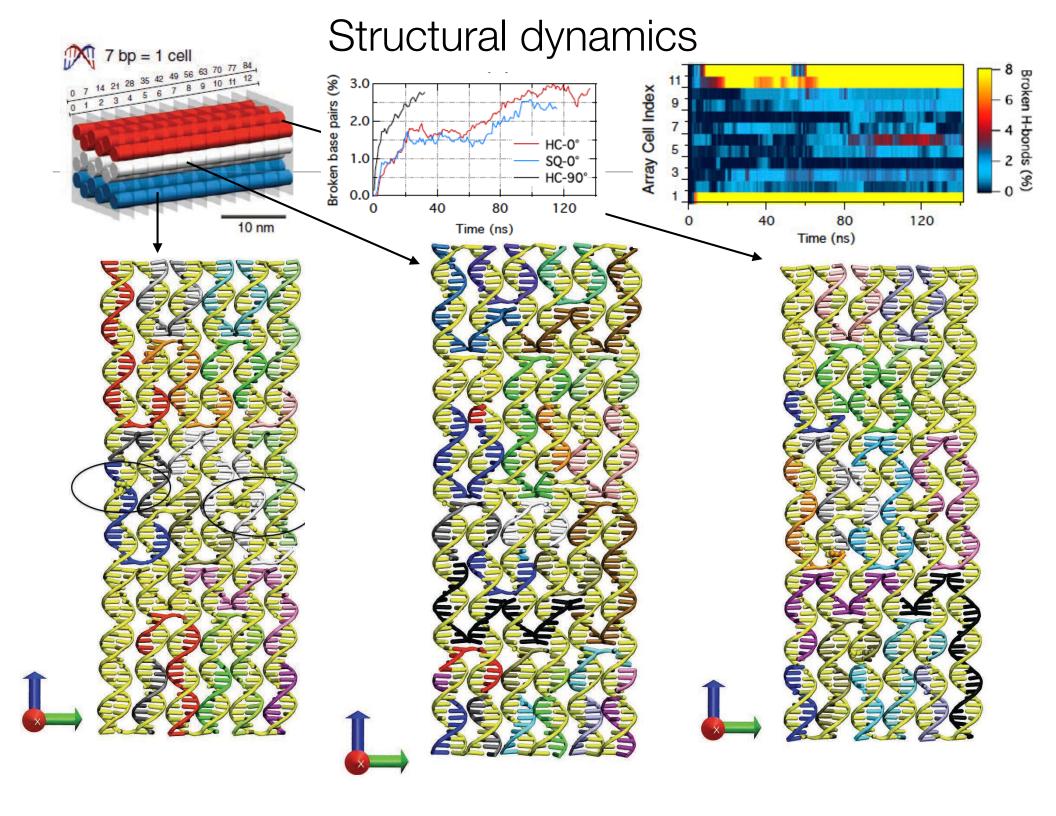


#### From caDNAno to all-atom

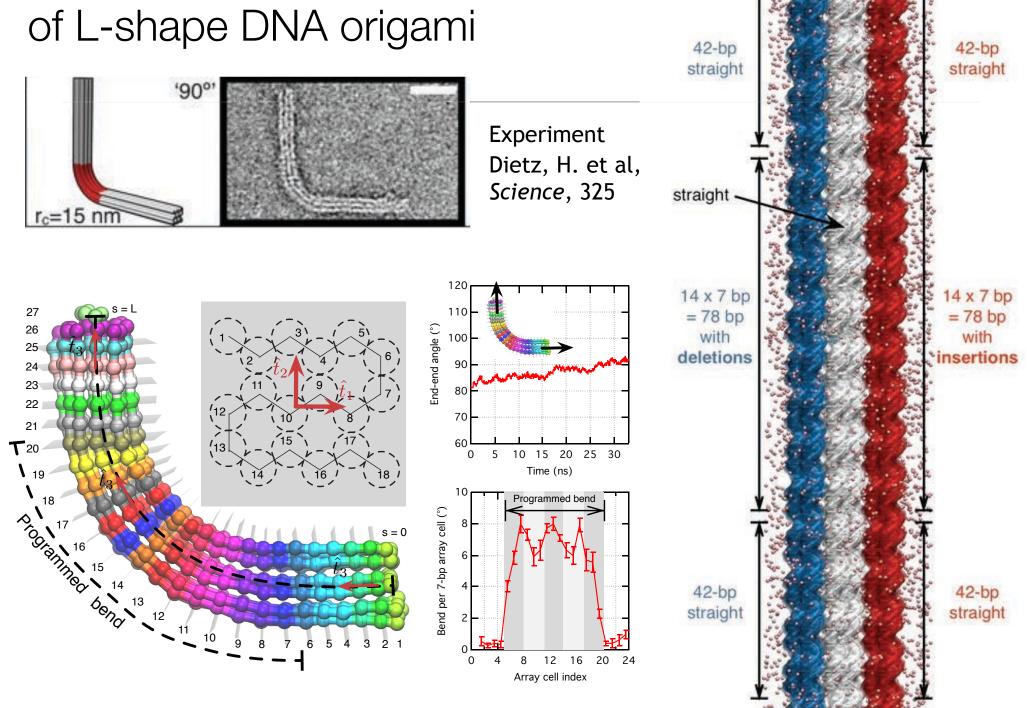


- caDNAno returns topology (json) and sequence (csv) information.
- cadnano2pdb.pl combines json and csv files into a PDB file.

- \* CHARMM36 force field
- ★ Explicit water
- \*  $[MgCl_2] \sim 10 \text{ mM}$
- \* NAMD
- \* 1 to 3M atoms
- \* 500 to 1,000 CPUs



## All-atom MD simulation

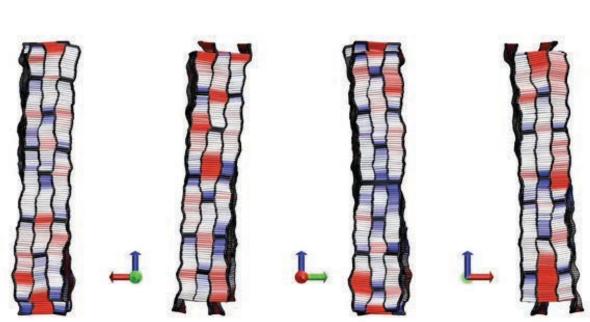


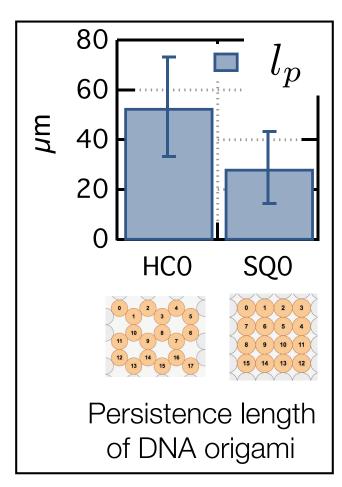
### Structural fluctuations reveal local mechanical properties

20 🕏

MD trajectories allow us to compute natural bending and torsion as well as persistence length

- Inter-DNA distance in color map
- Chicken wire frame represents center line of helices & junction

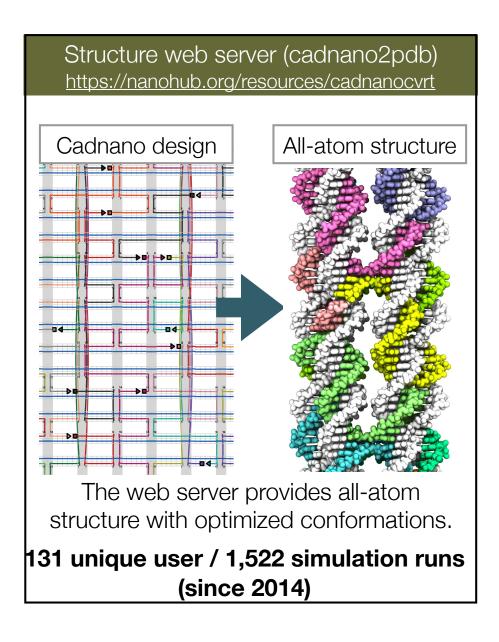




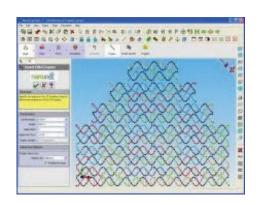
Our simulations predict higher rigidity for honeycomb-lattice design.

Yoo and AA, *PNAS* 110:20099 (2013)

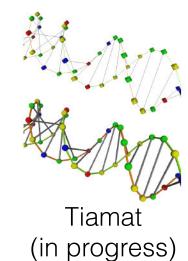
### DNA structure converters



Further developments requested by experimentalists:



Nanoengineer (done)



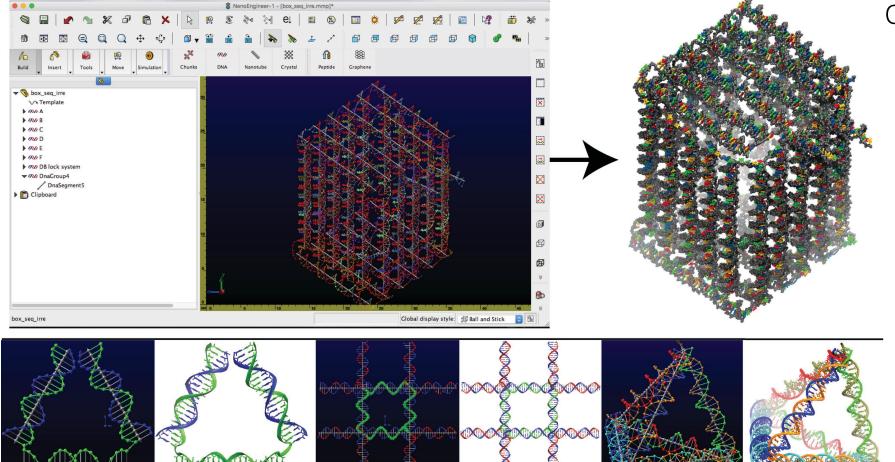
vHelix (planned)



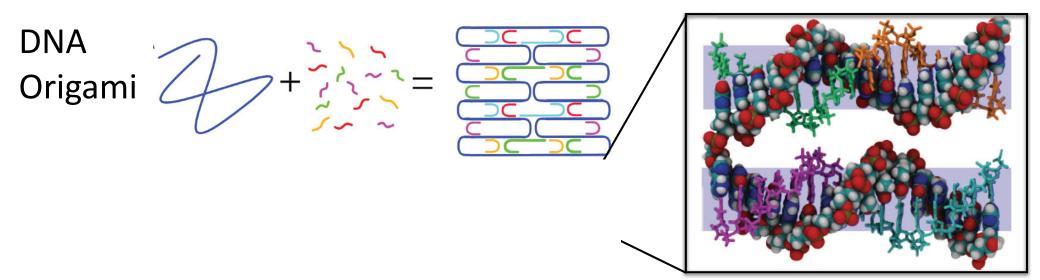


#### All-atom PDB





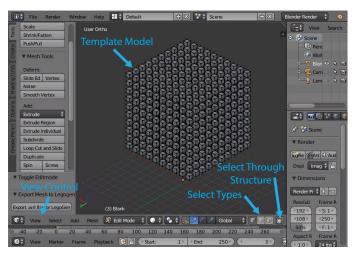
### Tiled DNA nanostructures







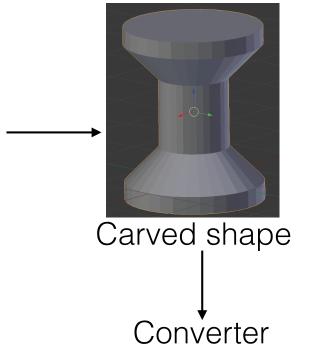
### LegoGen workflow @ nanoHub.org

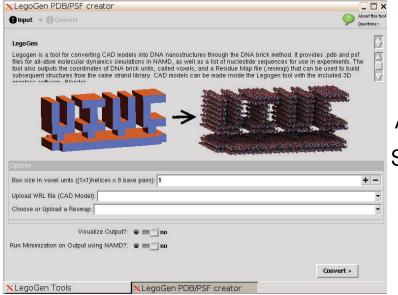


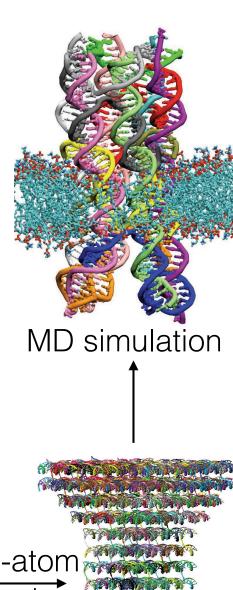
Blender (@nanoHub)

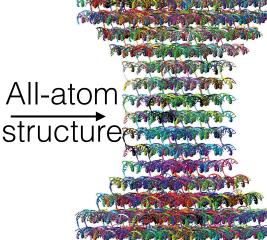


Experimental realization

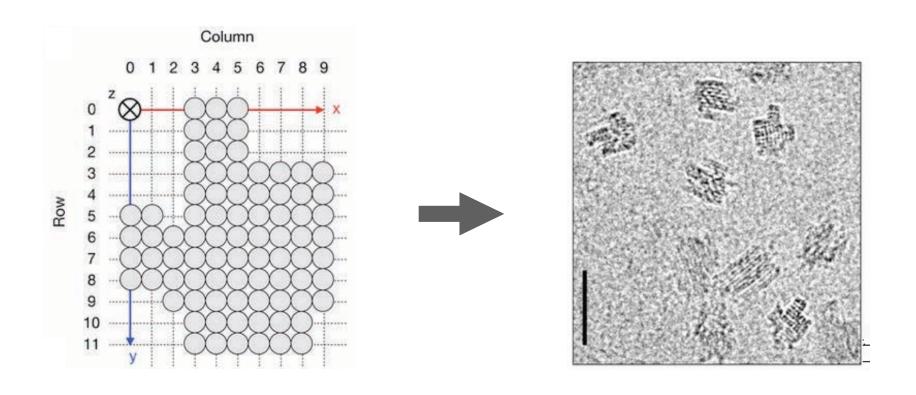






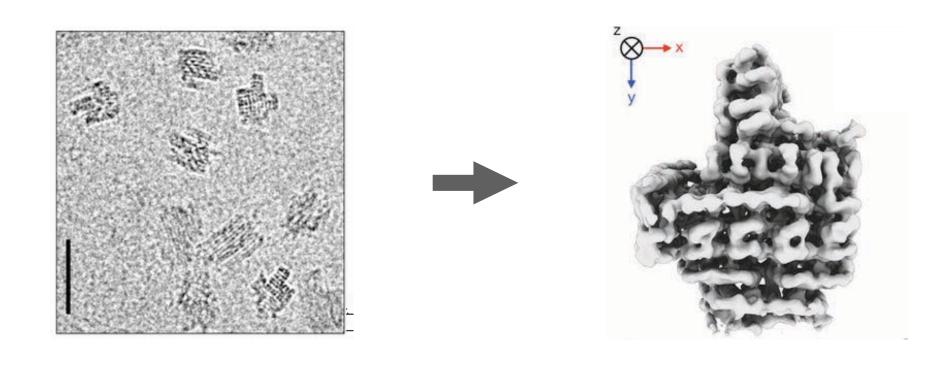


## Cryo-EM reconstruction versus all-atom simulation



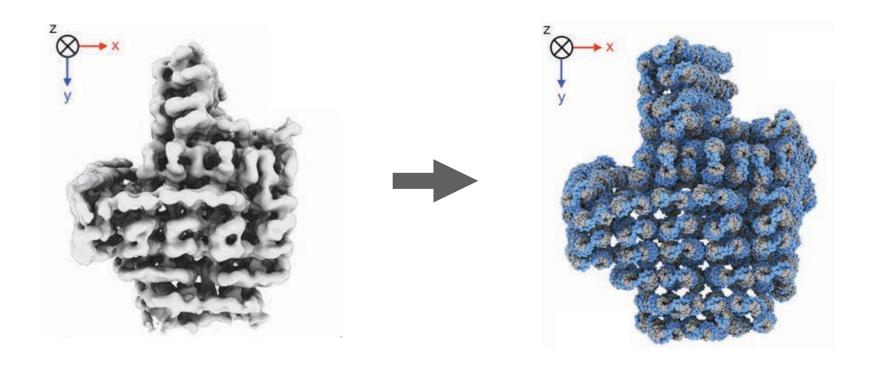
Bai et al, PNAS 109:20012 (2012)

## Cryo-EM reconstruction versus all-atom simulation



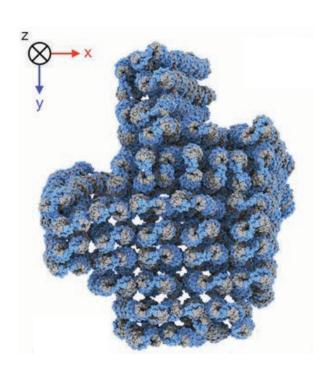
Bai et al, PNAS 109:20012 (2012)

## Cryo-EM reconstruction versus all-atom simulation

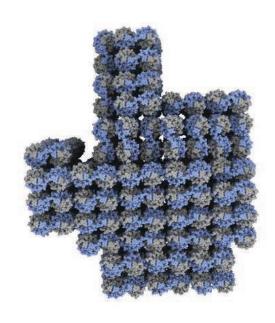


Bai et al, PNAS 109:20012 (2012)

## MD simulation of the cryo-EM object starting from a caDNAno design



Bai et al, PNAS 109:20012 (2012)

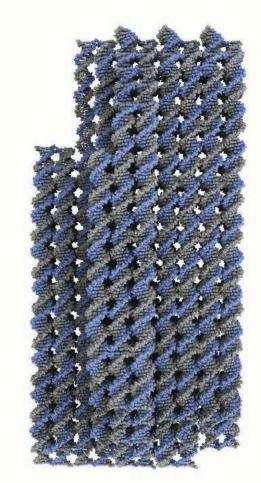


7M atom solvated model 130 ns MD trajectory

## MD simulation of the cryo-EM object starting from a caDNAno design

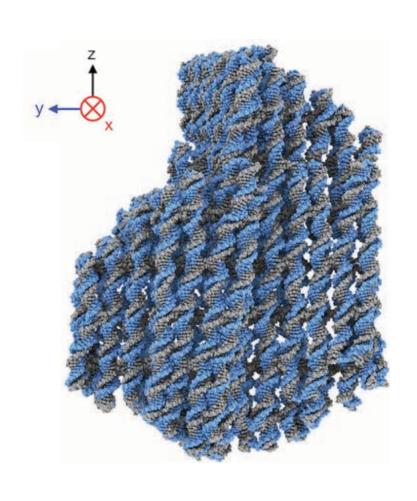


Bai et al, PNAS 109:20012 (2012)

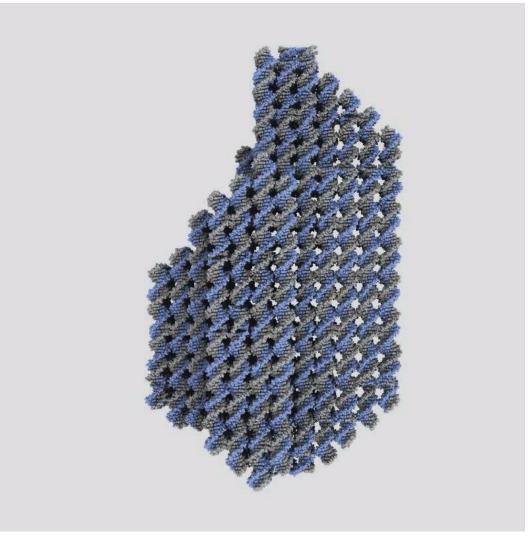


7M atom solvated model 130 ns MD trajectory

## MD simulation of the cryo-EM object starting from a caDNAno design



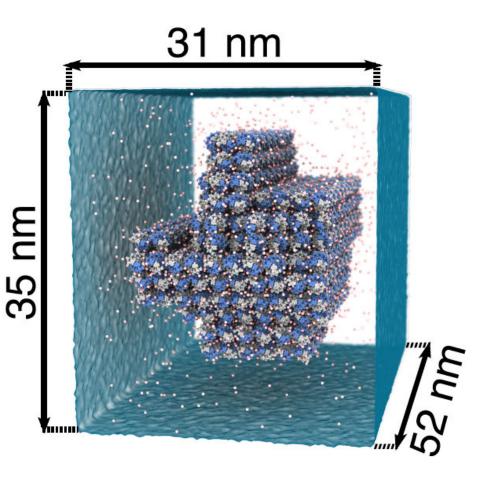
Bai et al, PNAS 109:20012 (2012)



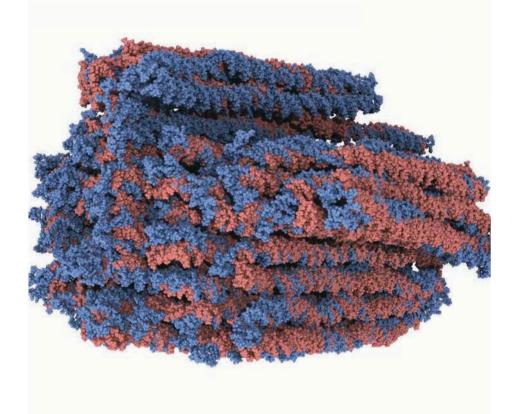
7M atom solvated model 130 ns MD trajectory

### Direct comparison with cryo-EM reconstuction

Simulation on Blue Waters (UIUC)



<u>Time scale</u>: 200 ns / Size ~7,000,000 atoms

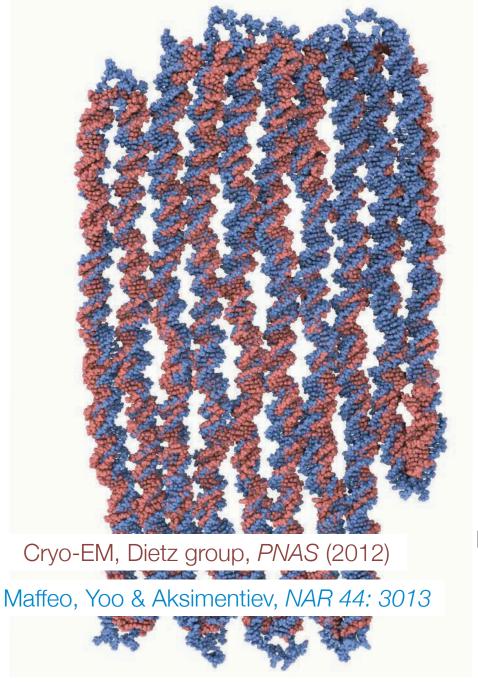


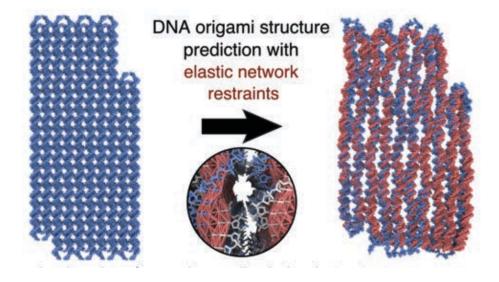
Maffeo, Yoo & Aksimentiev, NAR 44: 3013

Cryo-EM, Dietz group, PNAS (2012)

http://bionano.physics.illinois.edu/origami-structure

### De novo prediction of DNA origami structure





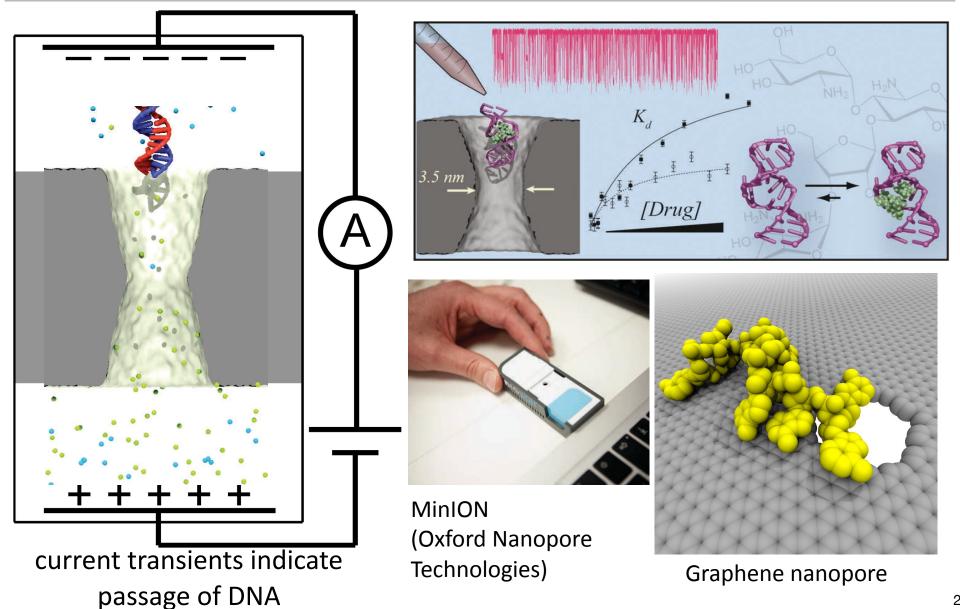
Modest computational cost (10 hours single workstation)

Server implementation has been requested by experimentalists

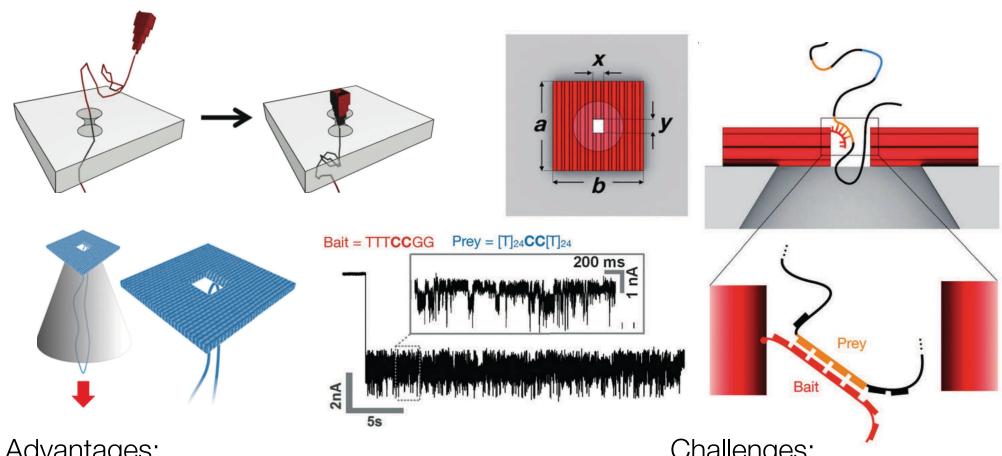
nanoHub implementation pending

http://bionano.physics.illinois.edu/origami-structure

## Nanopores for DNA and protein sequencing and drug design



#### The hybrid DNA origami/solid-state nanopore



#### Advantages:

- subnanometer control over pore geometry
- -functionalization with auxiliary components

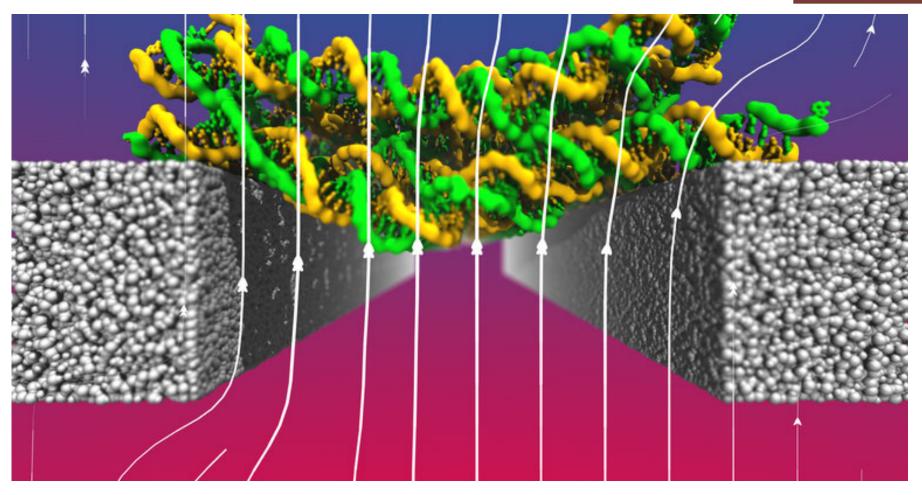
Nicholas A. W. Bell et al. Nano Lett. 2012 12 (1), 512-517 Hernández-Ainsa, S. et al. Nano Lett. 2014, 14, 1270-1274. Wei, R. et al. Angew. Chem., Int. Ed. 2012, 51, 4864-4867.

#### Challenges:

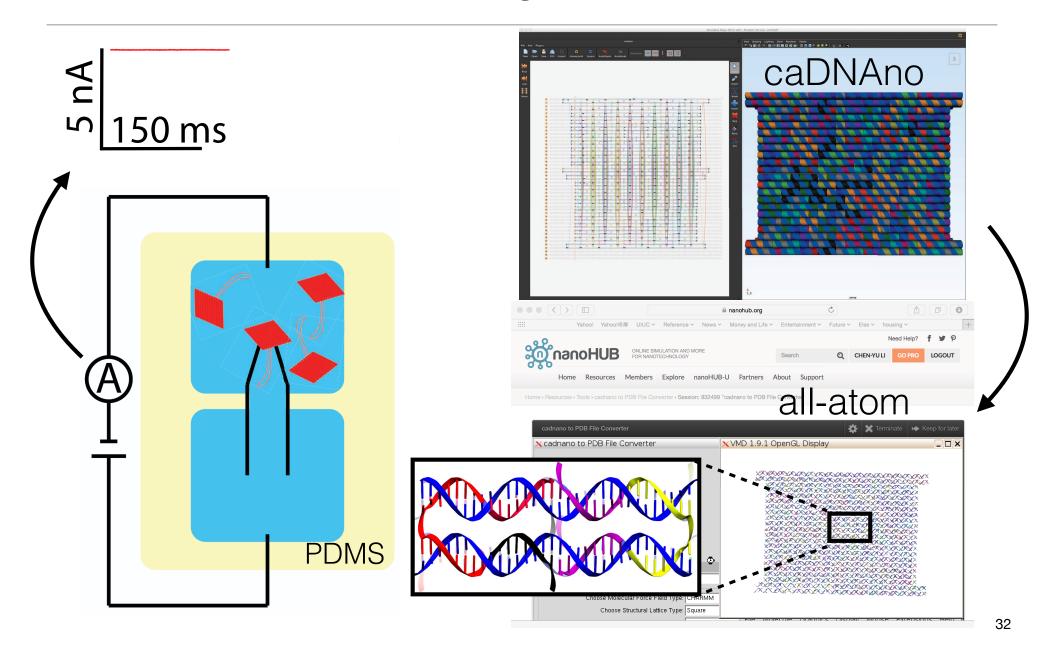
- -leakage current
- -structural integrity

#### Ionic conductivity and structural deformation of DNA origami **nanoplate**

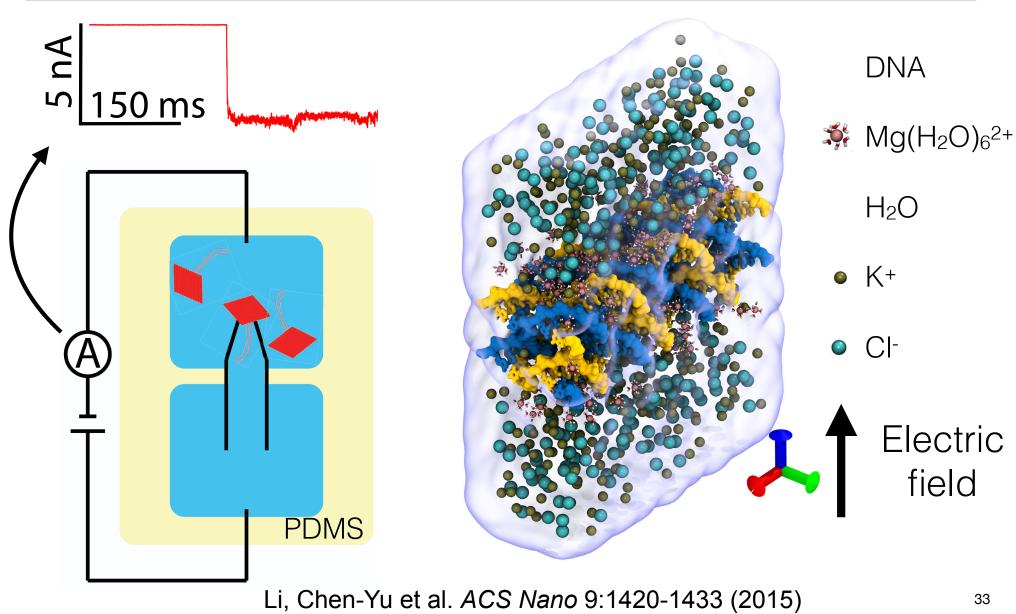




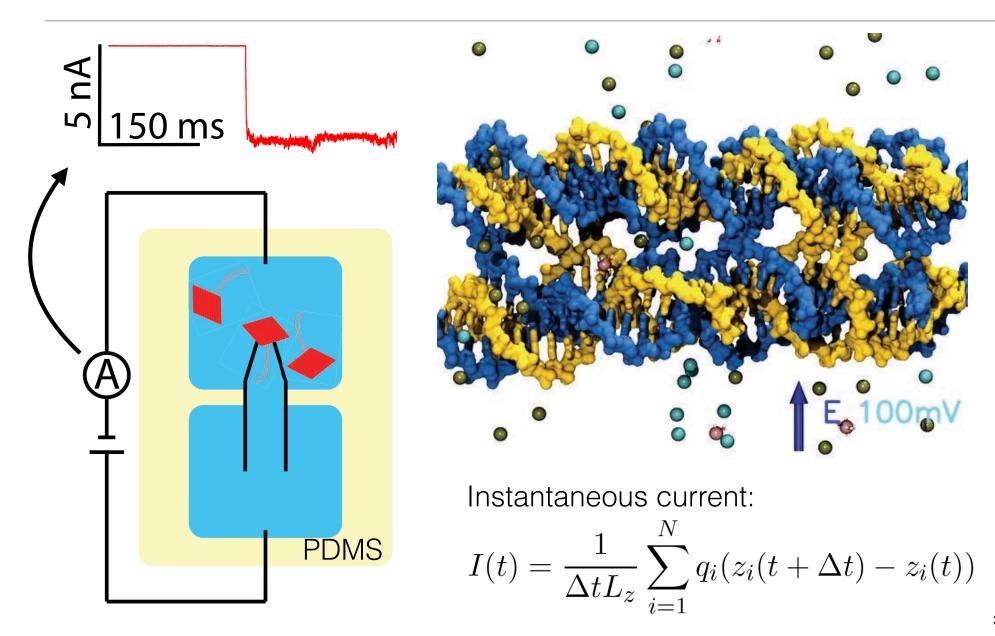
#### MD simulation of DNA origami conductivity



#### MD simulation of DNA origami conductivity

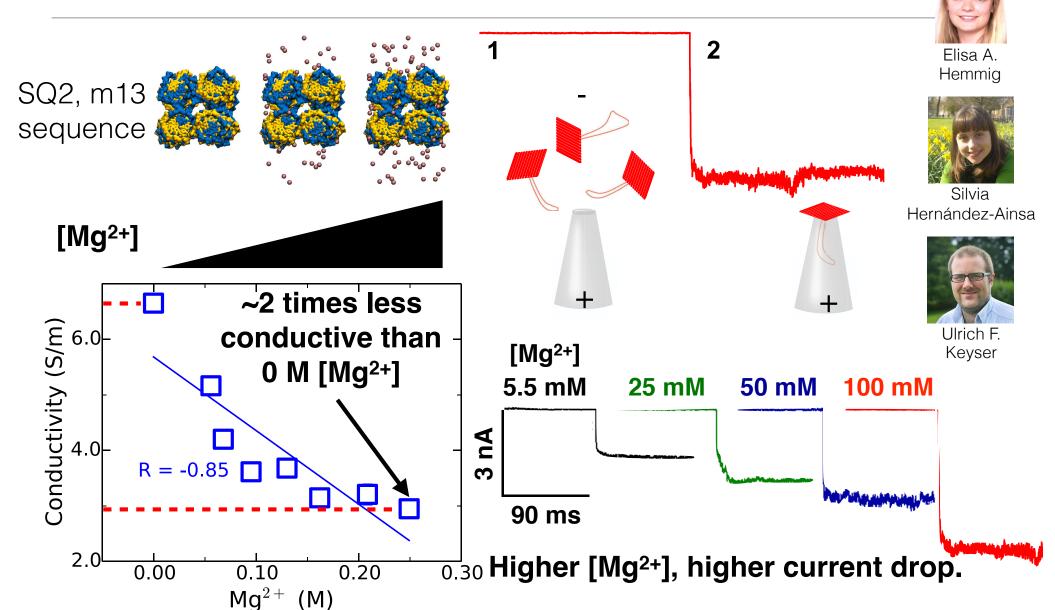


#### MD simulation of DNA origami conductivity



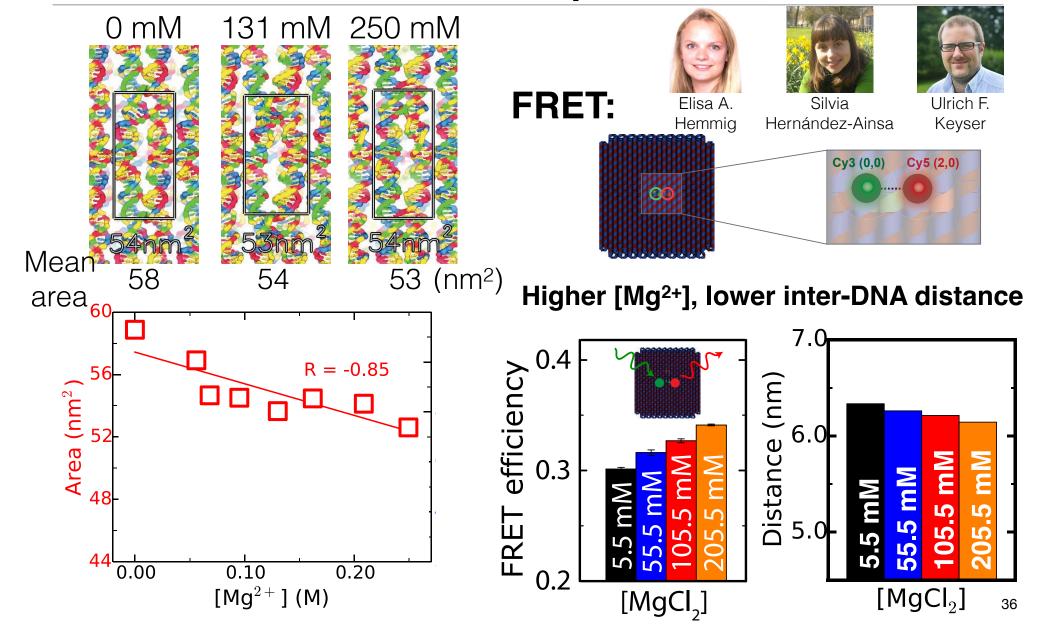
Effect of Mg<sup>2+</sup>

Higher [Mg<sup>2+</sup>] makes DNA origami less conductive.



### Mechanism of Mg<sup>2+</sup>

# Mg<sup>2+</sup> makes DNA origami more compact, by screening the DNA-DNA repulsion.

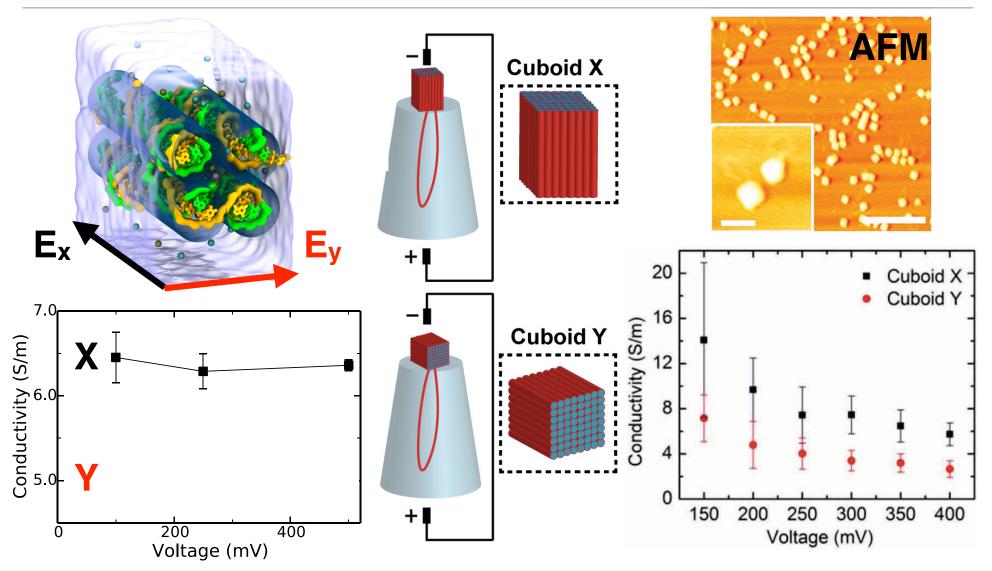






Jinglin Kong

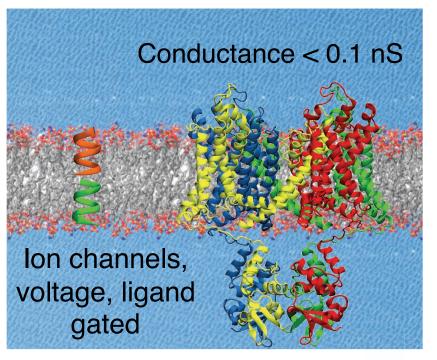
Ulrich F. Keyser

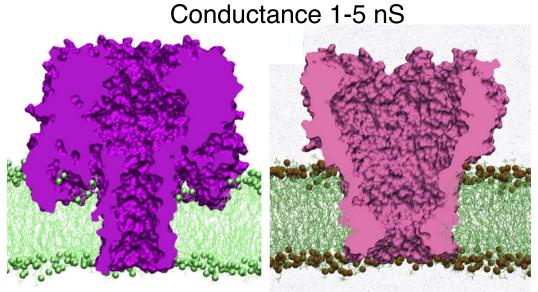


Anisotropic conductivity

Li, Chen-Yu et al. ACS Nano 9:1420-1433 (2015)

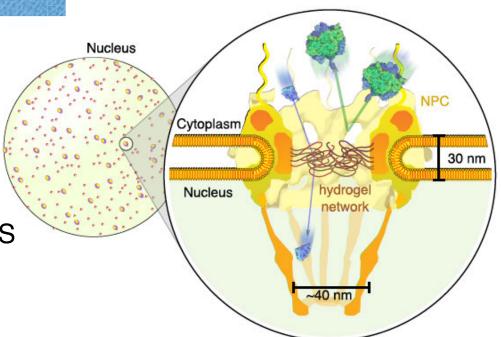
# Membrane channels



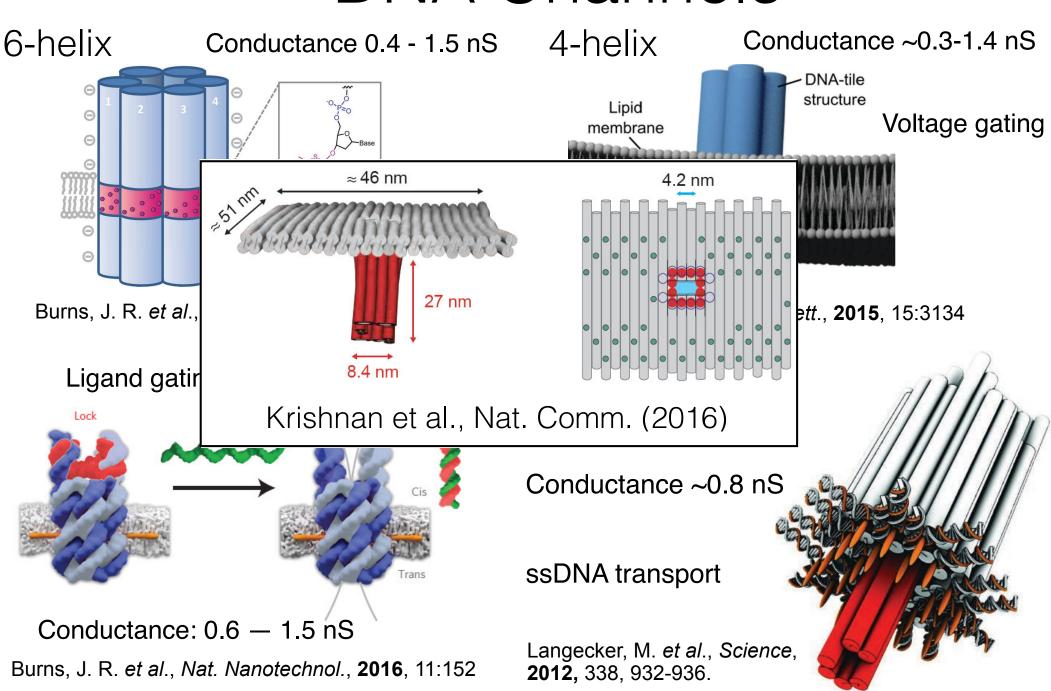


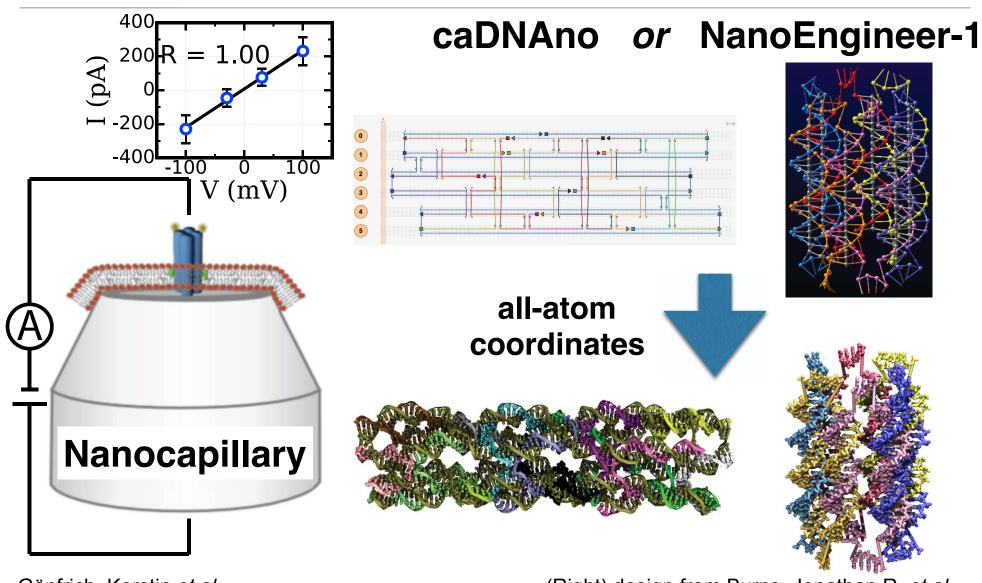
Porins, passive transport

Nuclear pore complex Selective cargo transpor Conductance 10 — 100 nS



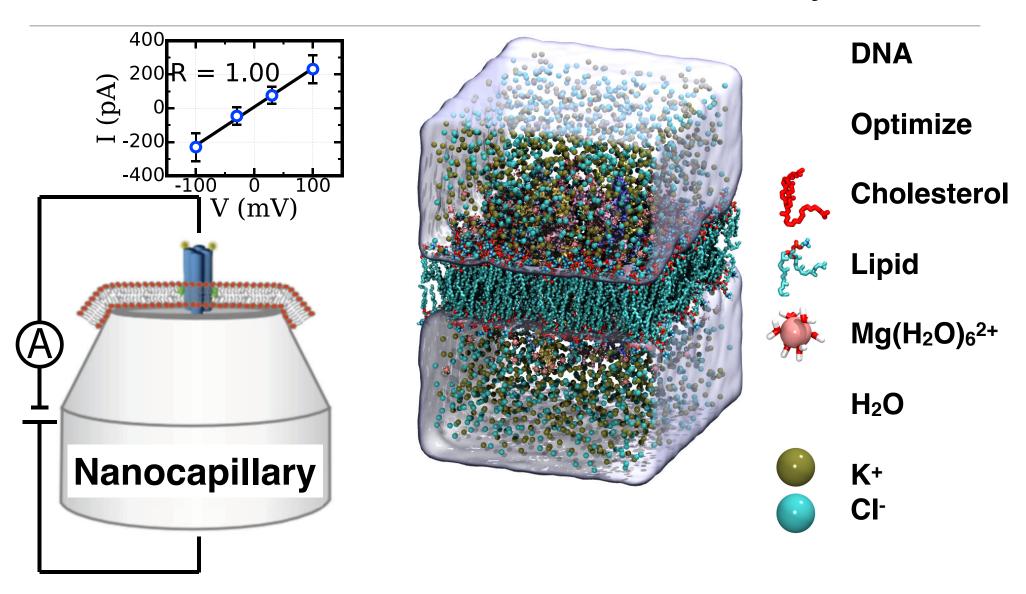
# DNA Channels



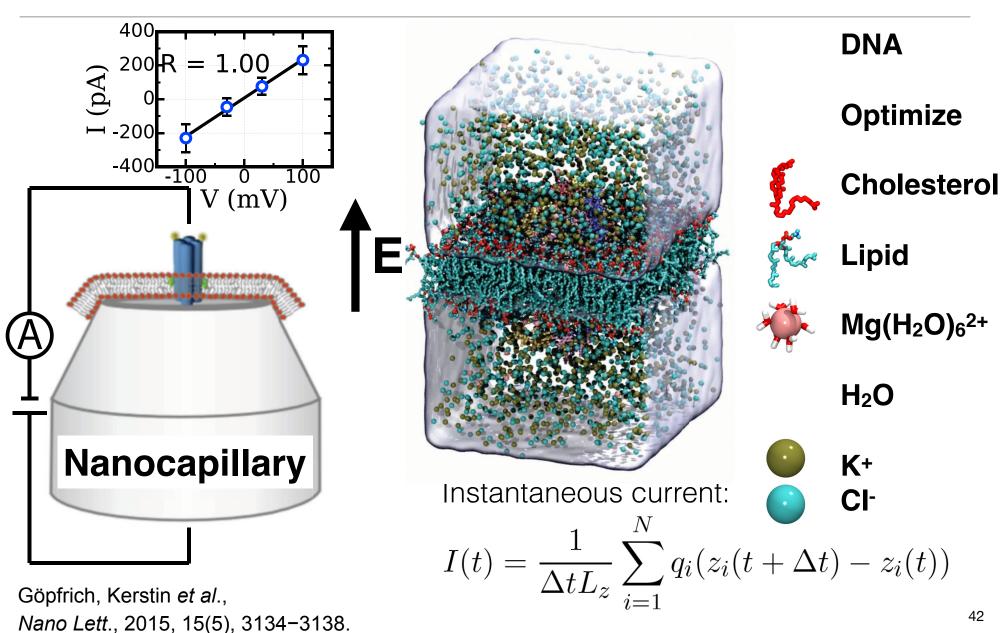


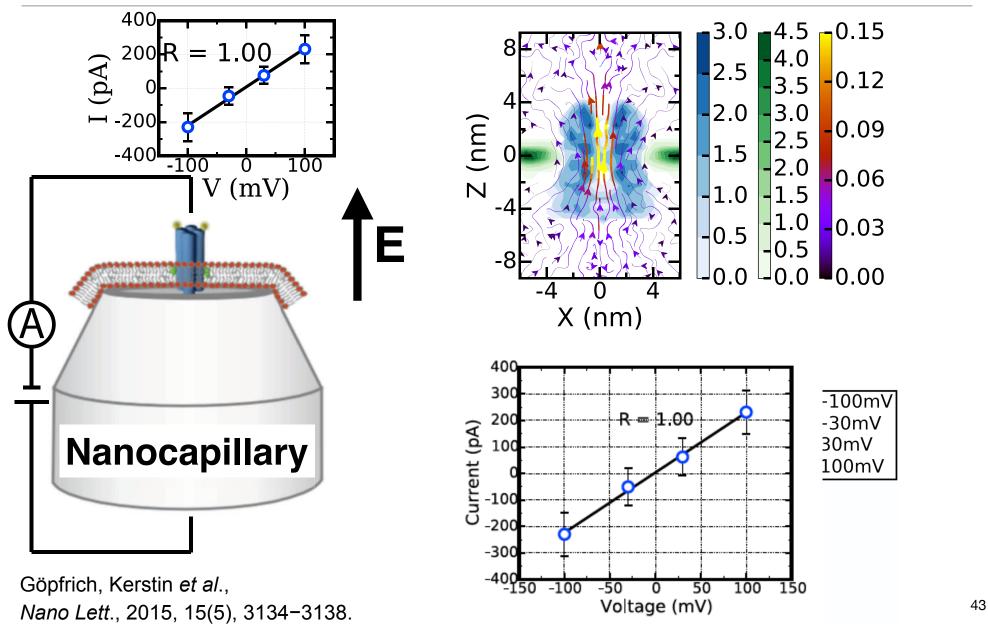
Göpfrich, Kerstin *et al.*, *Nano Lett.*, 2015, 15(5), 3134–3138.

(Right) design from Burns, Jonathan R. *et al.*, *Nat. Nanotechnol.*, 2016, 11, 152–156.



Göpfrich, Kerstin *et al.*, *Nano Lett.*, 2015, 15(5), 3134–3138.

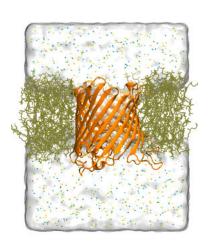




# Does the method work?

### **OprD**

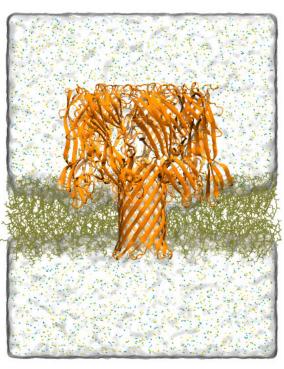
Bias: 80 mV



 $G_{\text{MD}} = < 0.05 \text{ nS}$  $G_{\text{EXP}} = 0.03 \text{nS}$ 

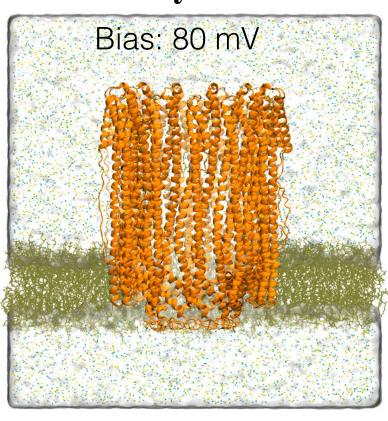
### Alpha-hemolysin

Bias: 100 mV



 $G_{\text{MD}} = 1.1 \text{ nS}$   $G_{\text{EXP}} = 1 \text{ nS}$ 

### ClyA

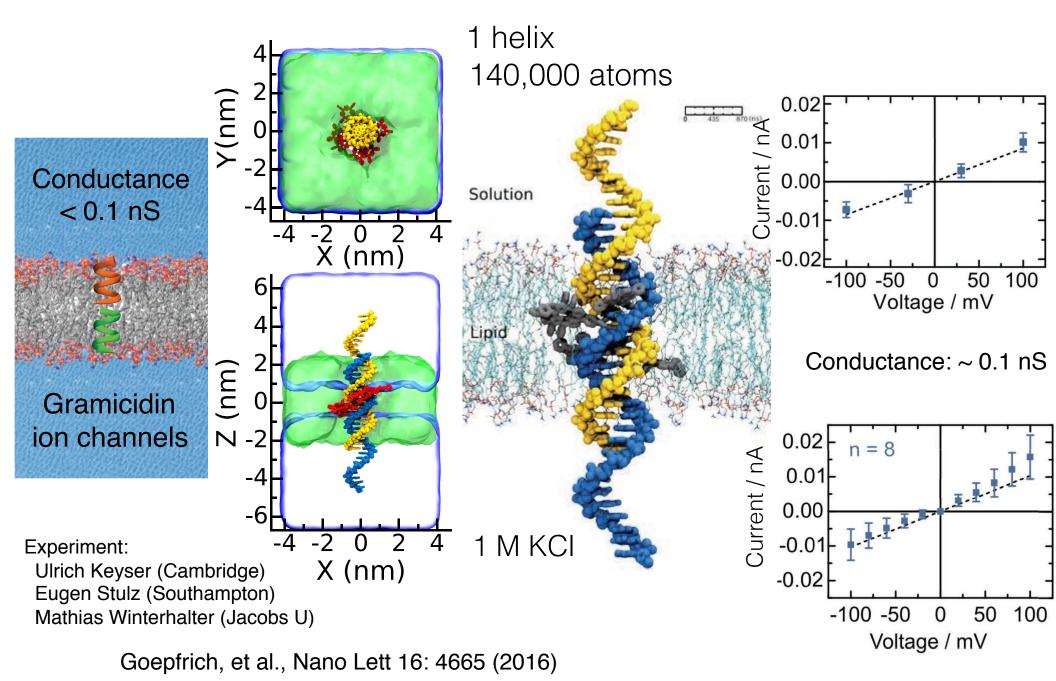


 $G_{\text{MD}}$ = 7.5 nS  $G_{\text{EXP}}$ = 11 nS

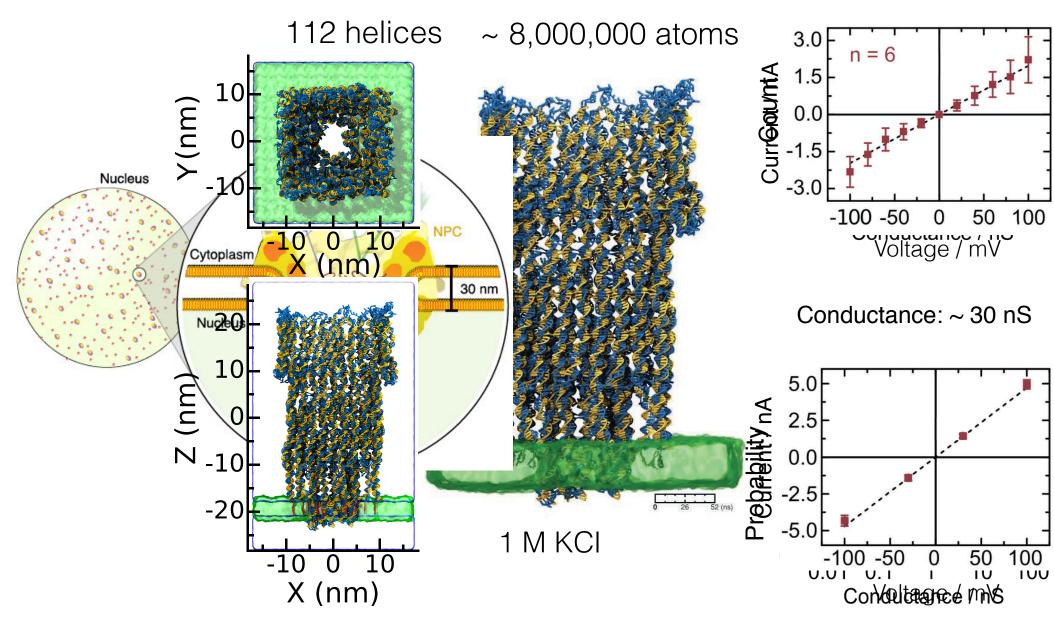
Biophysical Journal 88:3745 (2005)

# The DNA channels

# Small conductance DNA channel

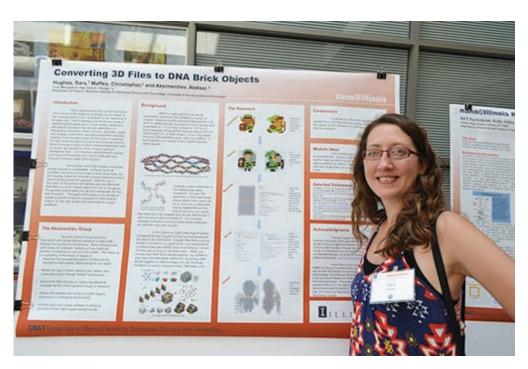


# Large conductance DNA channel



Goepfrich, et al., ACS Nano 10.1021/acsnano.6b03759 (2016)

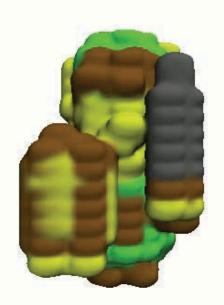
# Opportunities in Education and Outreach



Sara Huges, high school teacher from Chicago (summer 2015)

Developed a lesson "Extending Molecular Geometry:

Nanotechnology"



Web implementation enable exploration

Ongoing projects with local high school (Uni High, Urbana)







http://bionano.physics.illinois.edu/dna-nanotechnology