

On seeing and manipulating molecules

Adam Marblestone, PhD

July 2020

Talk at Oxford Future of Humanity Institute

Dynamic range of physical addressability

$x, y, z \sim \text{nanometers}$

$X, Y, Z \sim \text{centimeters}$

$c \sim 4^{20} \gg 23000$

image vs. construct

Summary

Image:

- Using expansion microscopy and in-situ optical sequencing of DNA, we are on path to “*arbitrary resolution, infinite color microscopy*” for bio
- Sequencing neuron-indexing RNA barcodes this way should allow *full mammalian brain connectomes* for ~\$30M

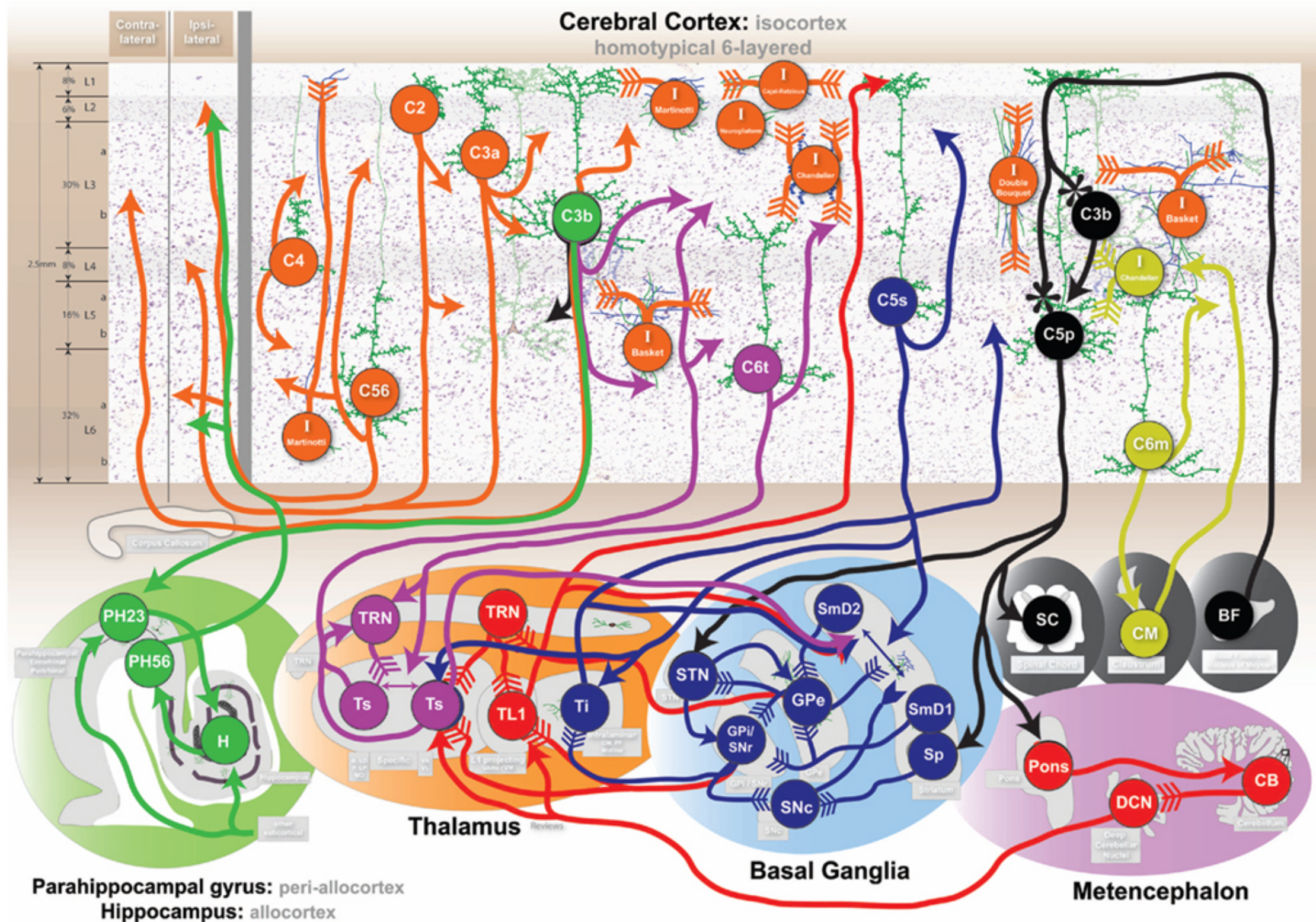
Construct:

- DNA origami allows ~5 nm patterning of diverse materials over ~100 nm length scales by self-assembly, with trivial/facile design
- We should be able to organize DNA origami into larger systems by patterning them on *shrunk* DNA microarrays
- A “*molecular 3D printer*”, made through various steps involving DNA origami, DNA templating of proteins / peptides, and modular protein engineering with fixed backbones and *programmable interfaces*, could be an interesting first step to explore and demo “APM” principles

Part I: image

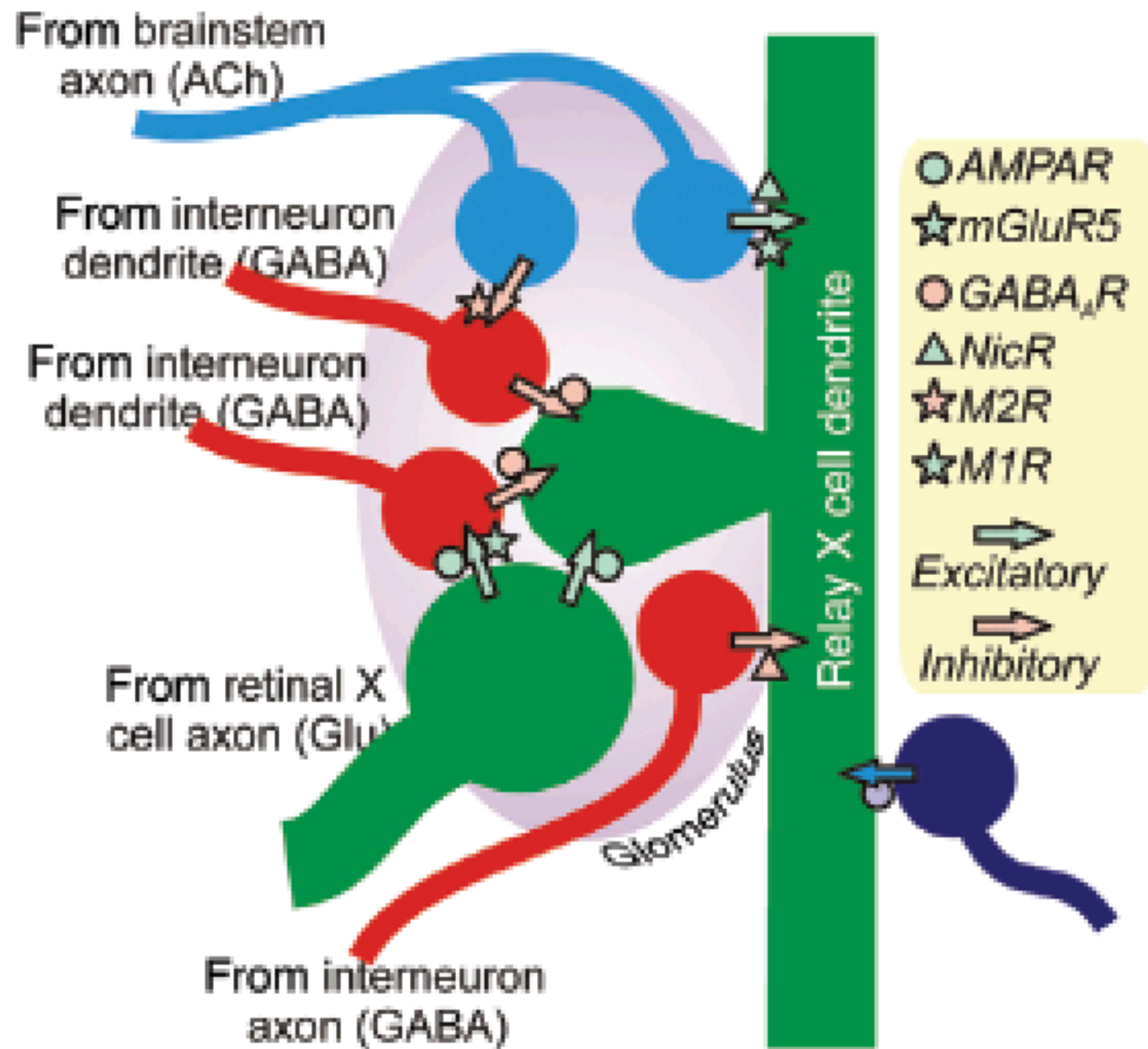
How to scalably map the brain's architecture

Key circuits span the entire brain (cm)

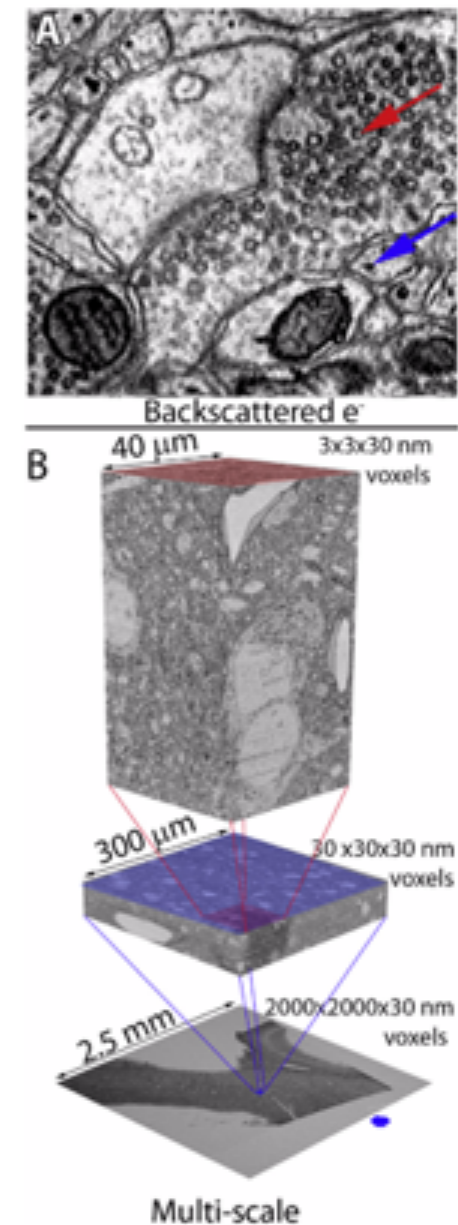
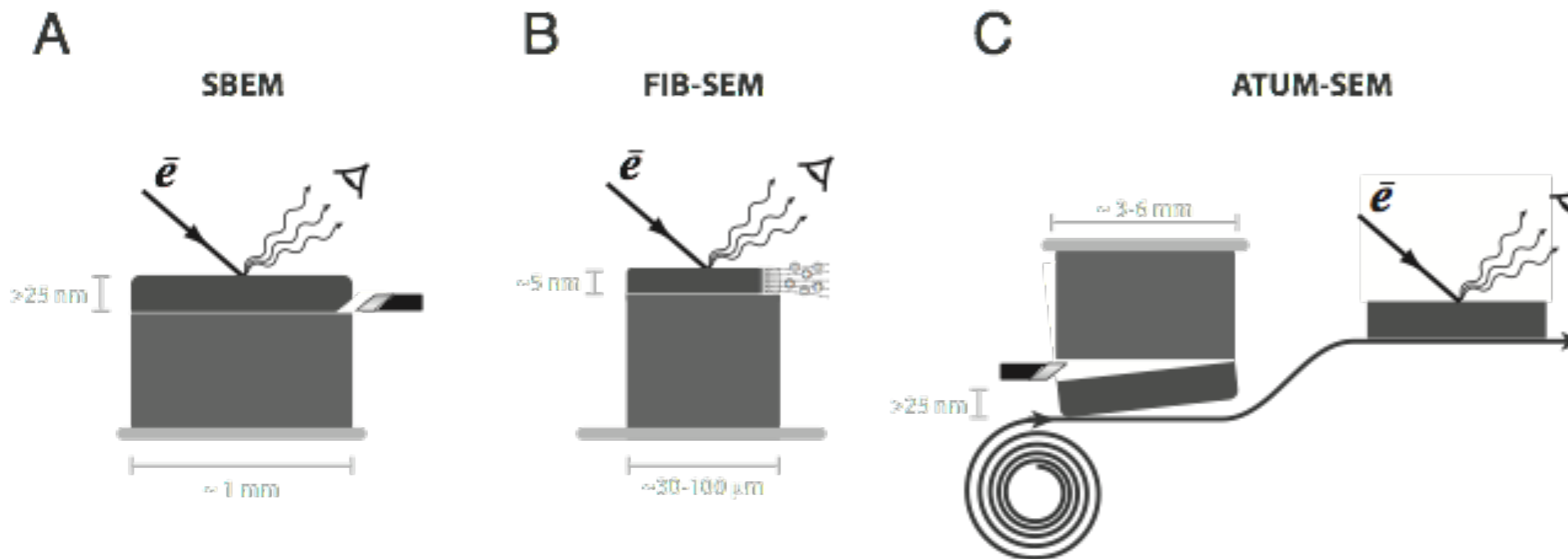


Cognitive consilience: primate non-primary neuroanatomical circuits underlying cognition

...yet are also organized at micron and nm scale



Structural brain mapping today



Current practice: widely believed that electron microscopy (EM) is the **only** viable method for cellular-resolution connectomics

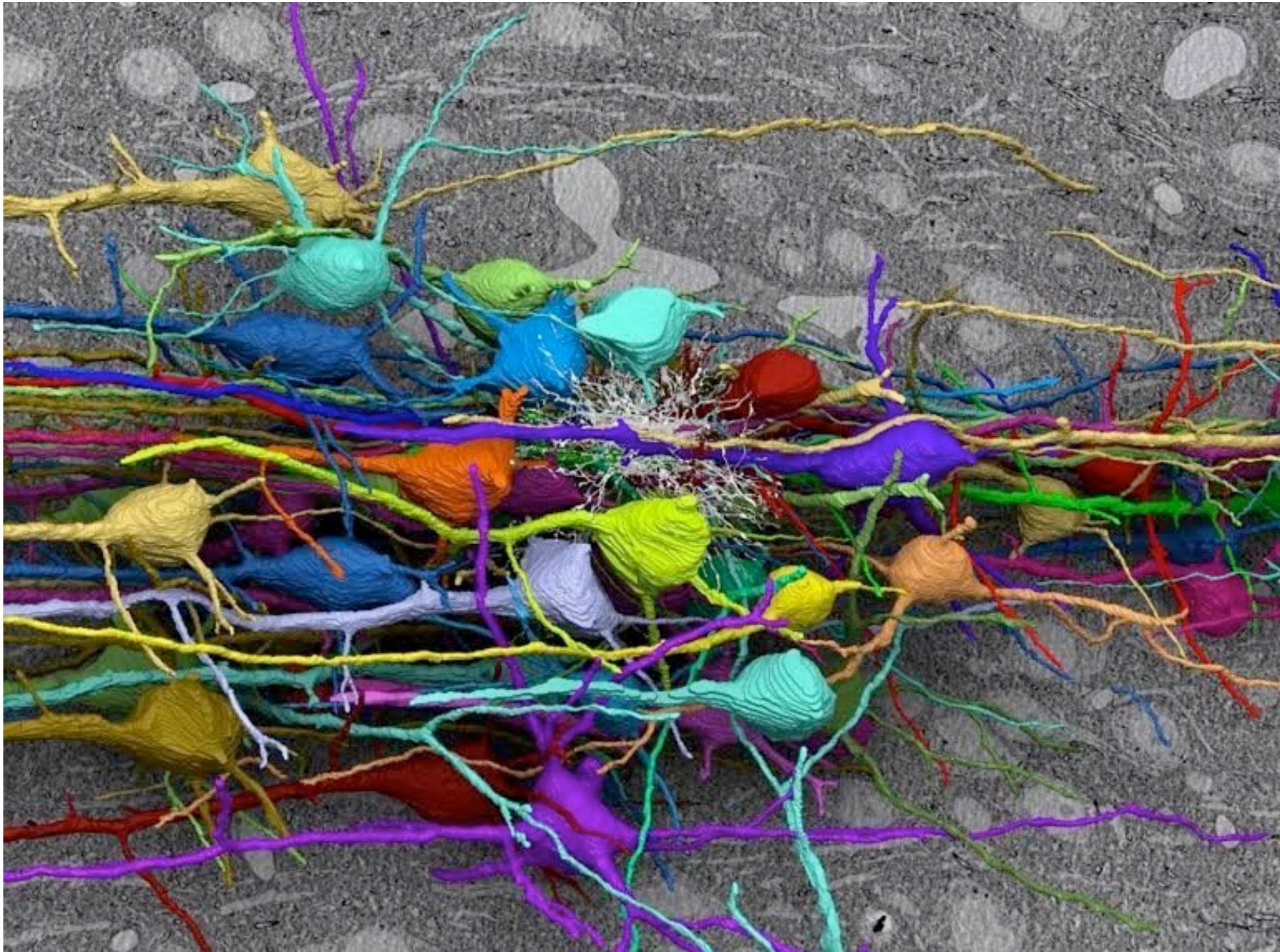
Problems:

- Manual human segmentation, taking minutes per cubic *micron* (Kasthuri, 2015)
- Does not provide molecular information

$x, y, z < 10 \text{ nm}$

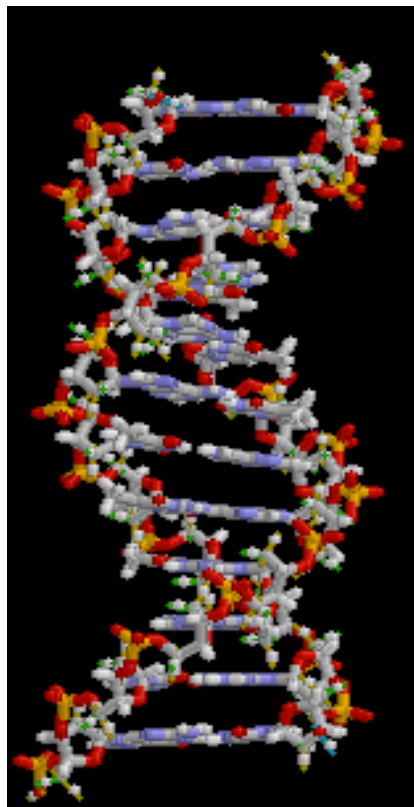
$X, Y, Z < 1 \text{ mm}$

$c \sim 1$



Scalable brain mapping: unique ID's for structure

4^N possible DNA sequences of length N “letters”



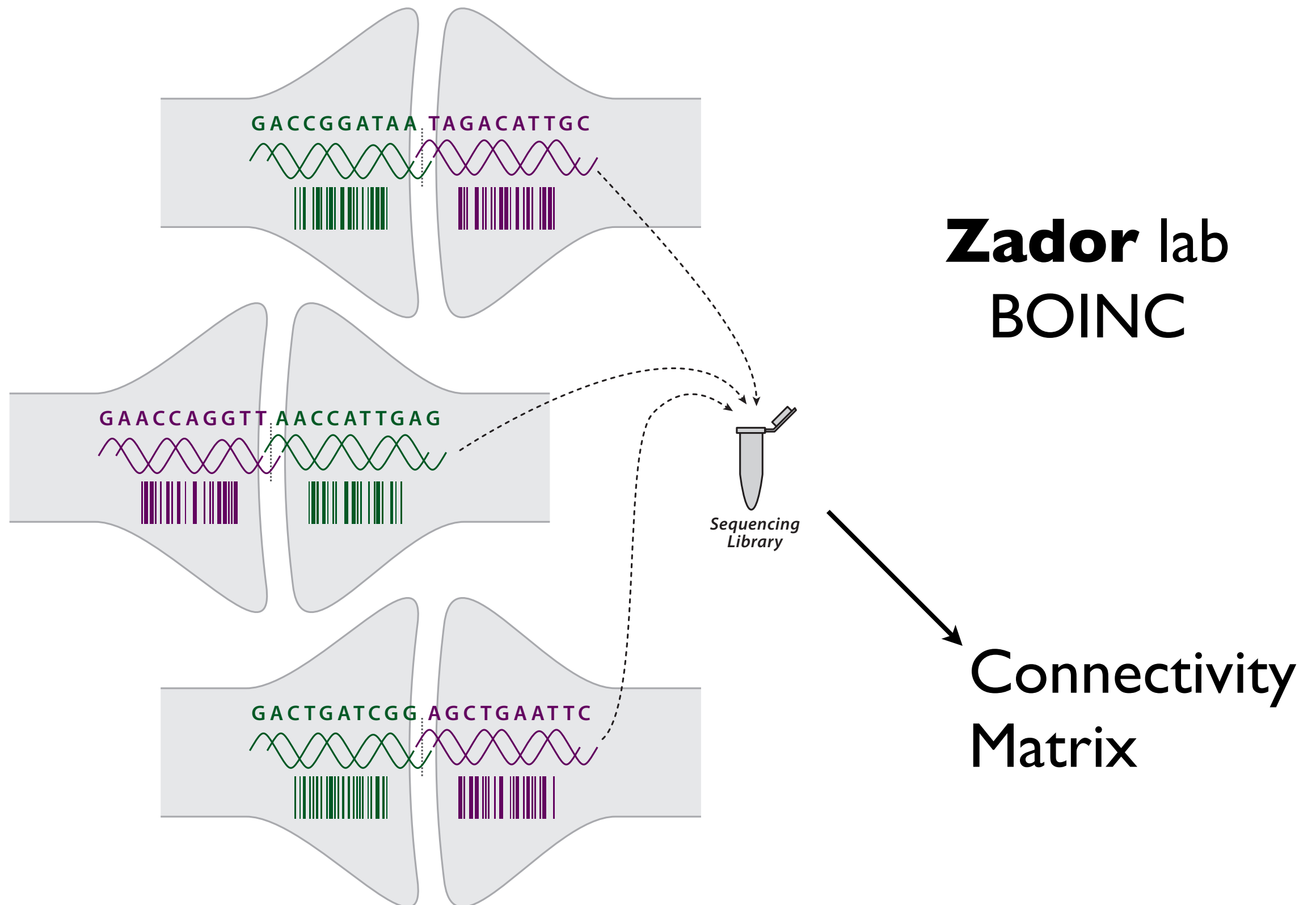
=
01010010101010010101
0101010101001010110111
0010110101010111010011



Zador, Cepko, Tabin, Walsh, Church et al:

can give every neuron a uniquely-identifiable DNA “barcode”

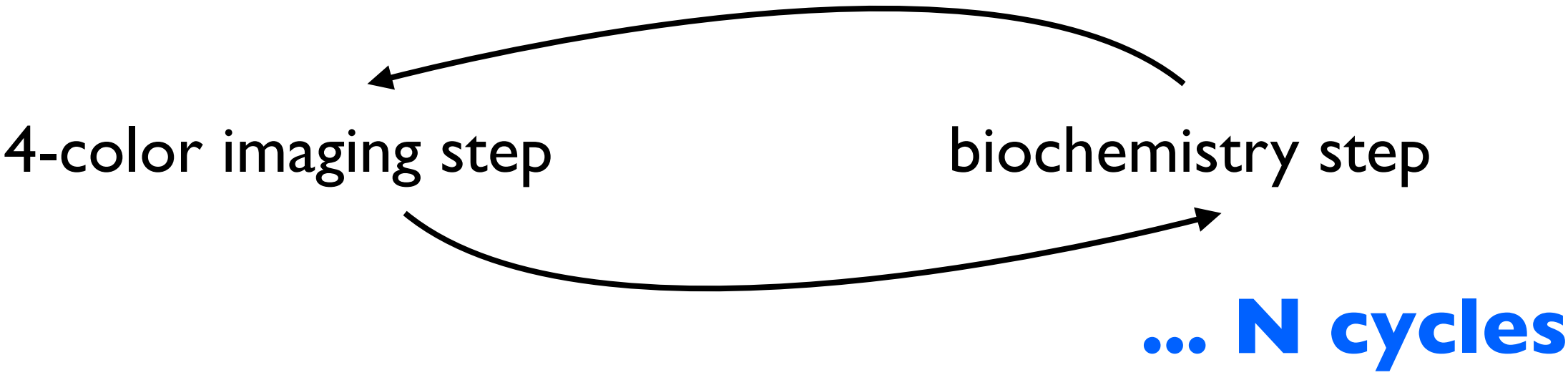
DNA Barcodes via Bulk Sequencing



Scalable brain mapping: unique ID's for structure

digital **4^N color** microscopy

<i># of cycles</i>	<i># of molecules discriminated</i>
1	4
10	4^{10} , about 10^6
30	4^{30} , about 10^{18}



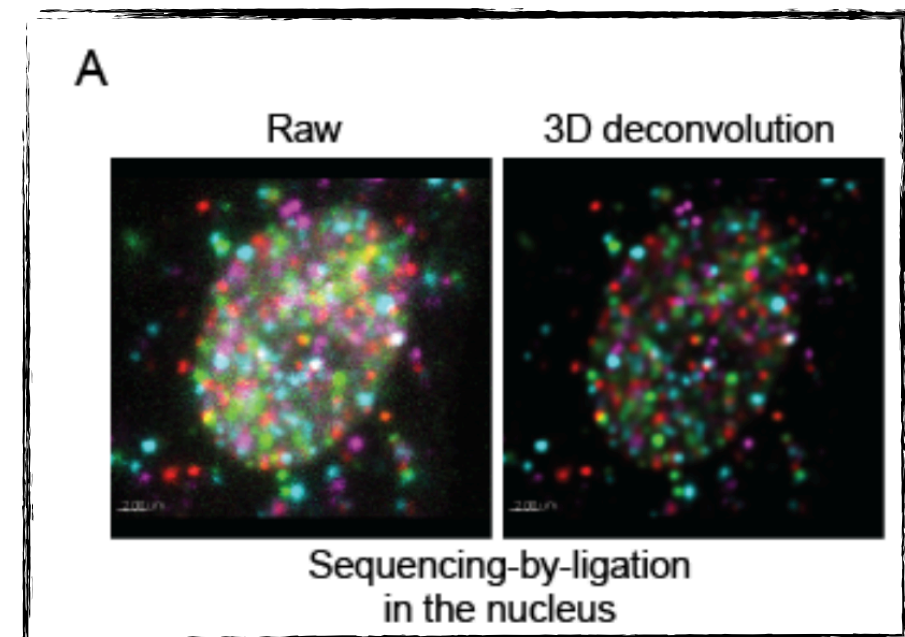
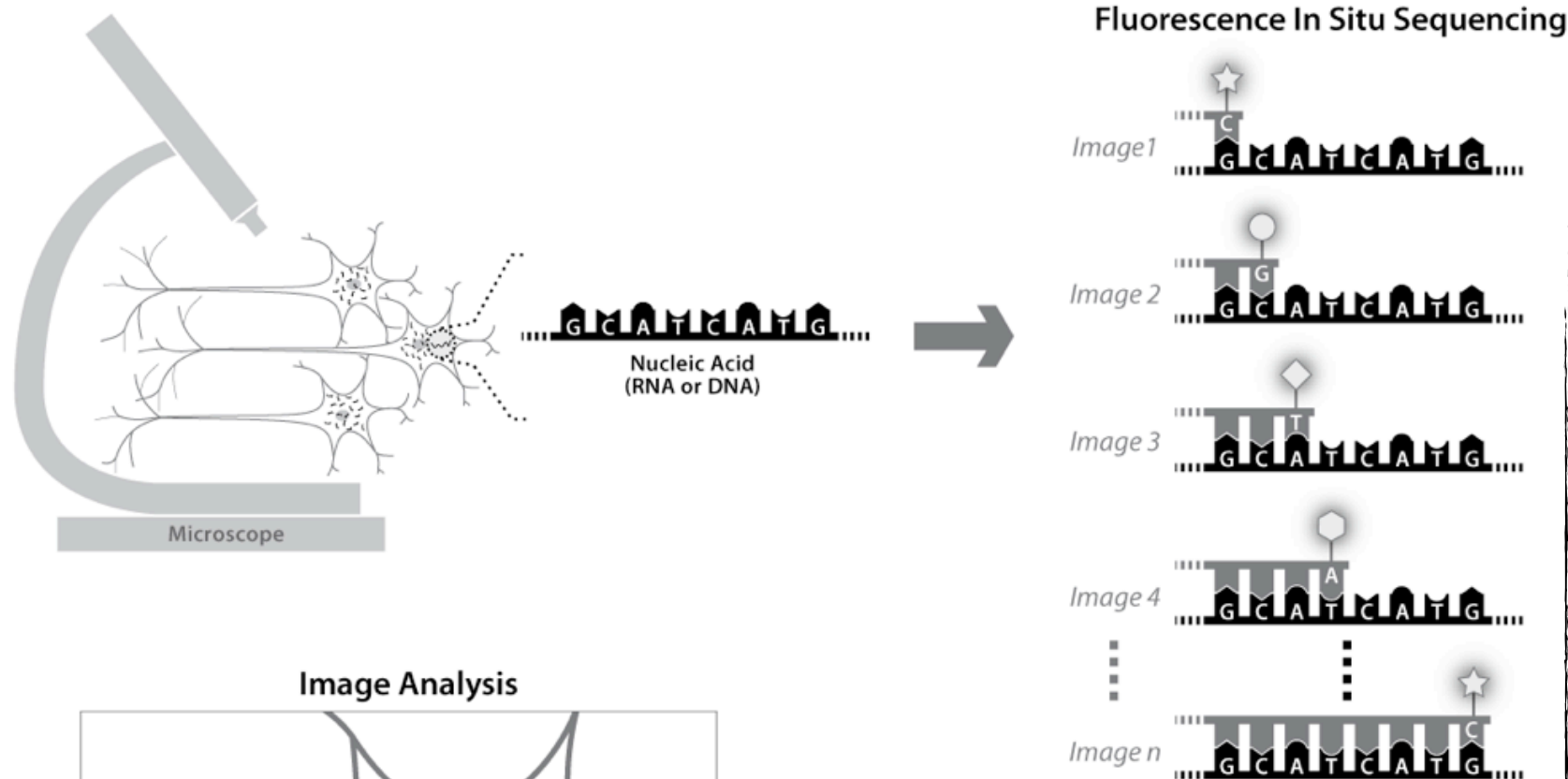
Read one letter of RNA
at a time, sequentially

digital 4^Ncolor microscopy

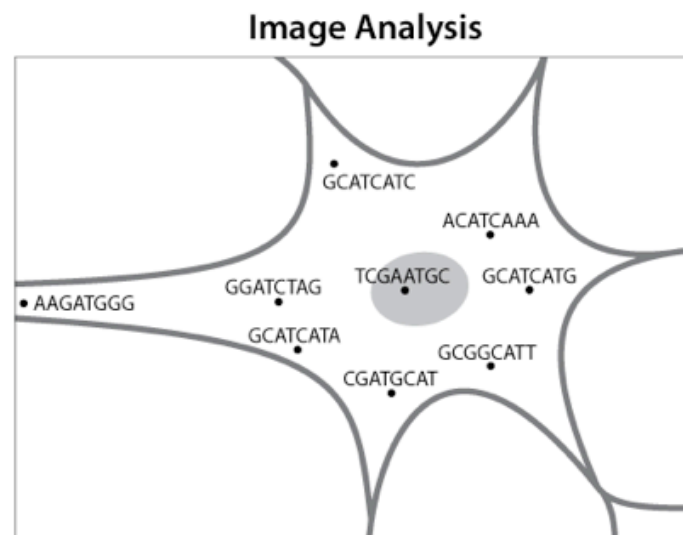
# of cycles	# of molecules discriminated
1	4
10	4 ¹⁰ , about 10 ⁶
30	4 ³⁰ , about 10 ¹⁸

Fluorescent In-Situ RNA Sequencing (FISSEQ):

A



B



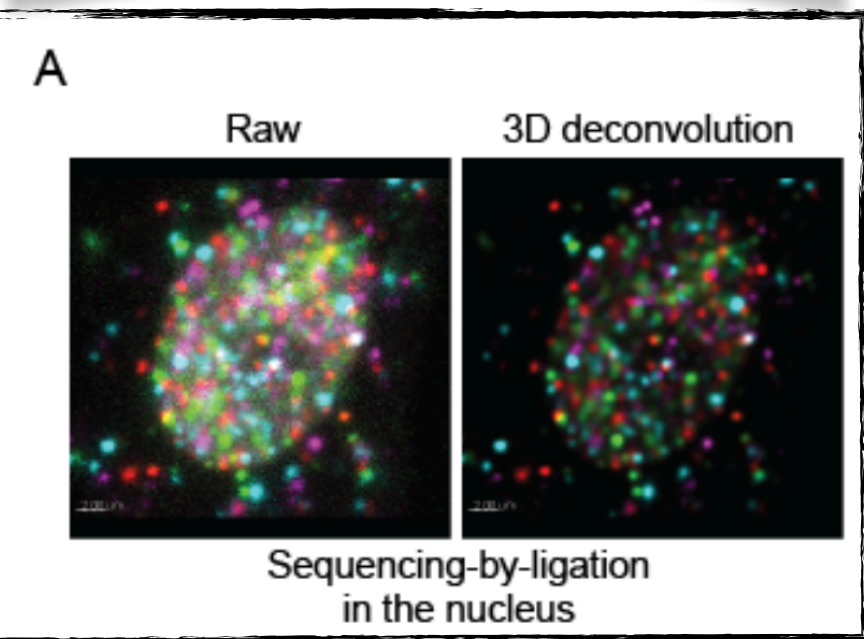
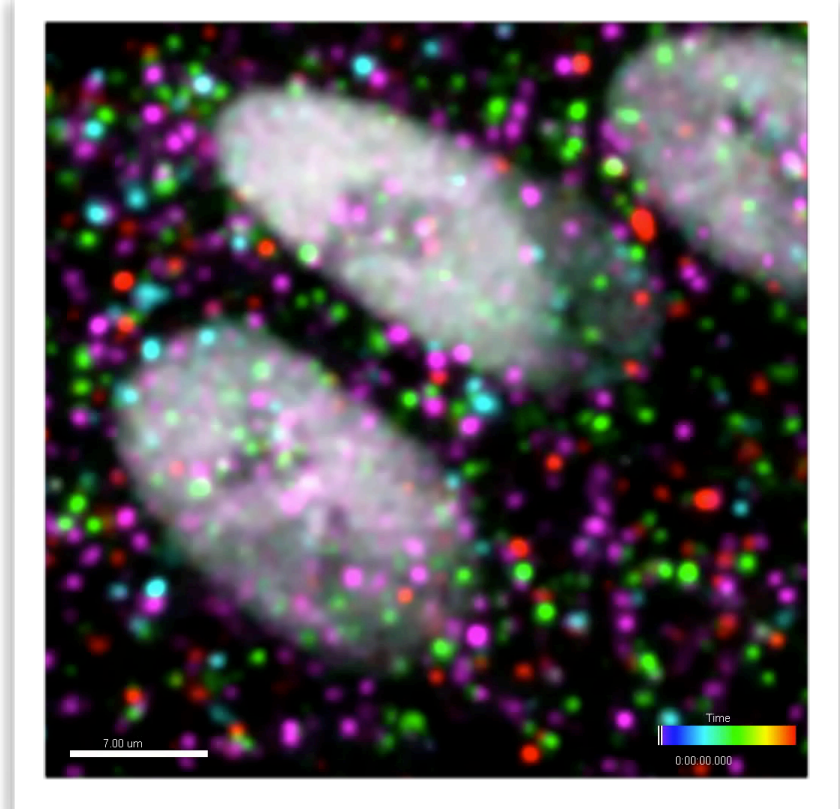
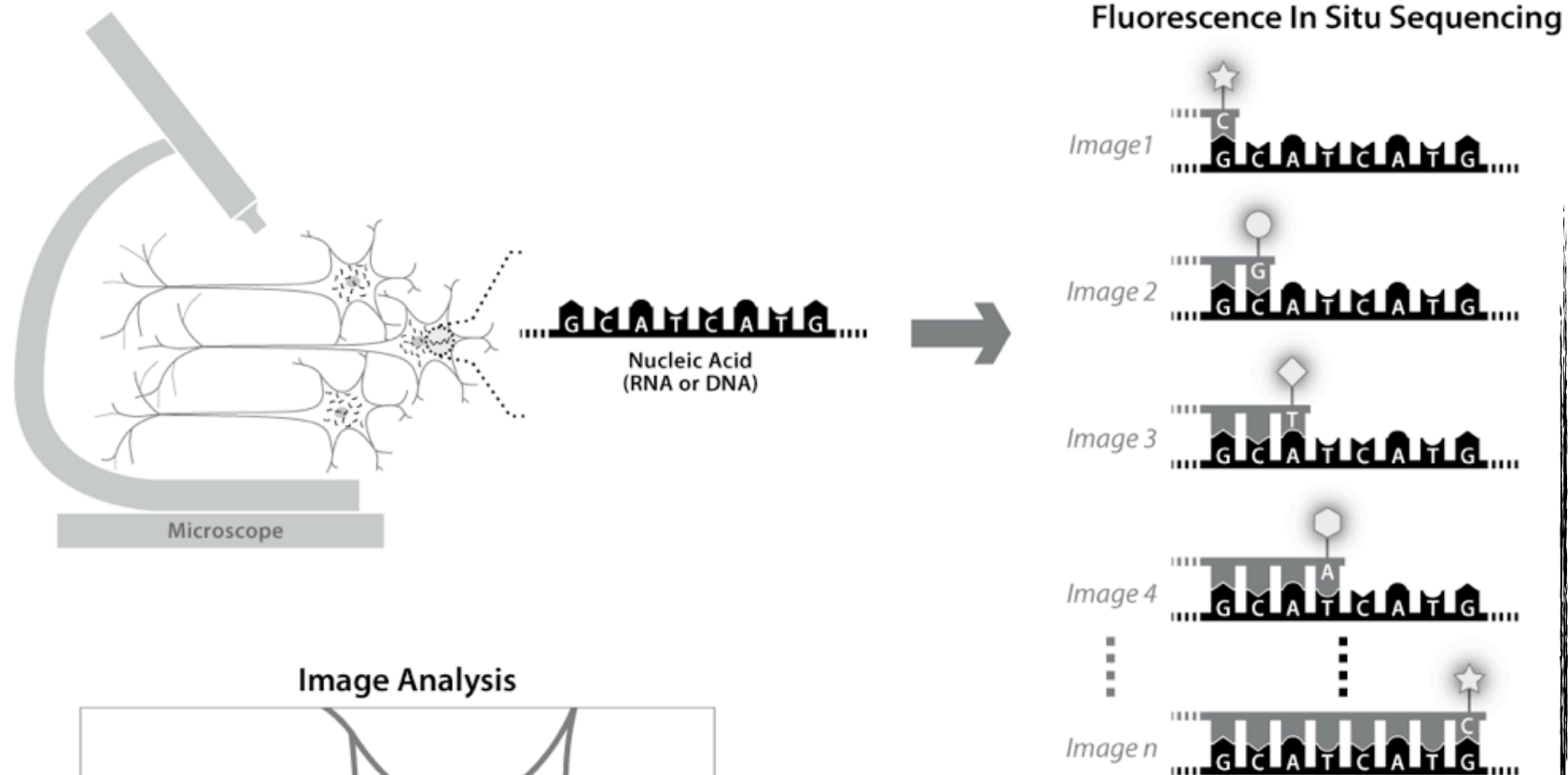
Highly Multiplexed Subcellular RNA Sequencing in Situ

Je Hyuk Lee,^{1,2,*†} Evan R. Daugharthy,^{1,2,4*} Jonathan Scheiman,^{1,2} Reza Kalhor,² Joyce L. Yang,² Thomas C. Ferrante,¹ Richard Terry,¹ Sauveur S. F. Jeanty,¹ Chao Li,¹ Ryoji Amamoto,³ Derek T. Peters,³ Brian M. Turczyk,¹ Adam H. Marblestone,^{1,2} Samuel A. Inverso,¹ Amy Bernard,⁵ Prashant Mali,² Xavier Rios,² John Aach,² George M. Church^{1,2,†}

digital 4^Ncolor microscopy

Fluorescent In-Situ RNA Sequencing (FISSEQ):

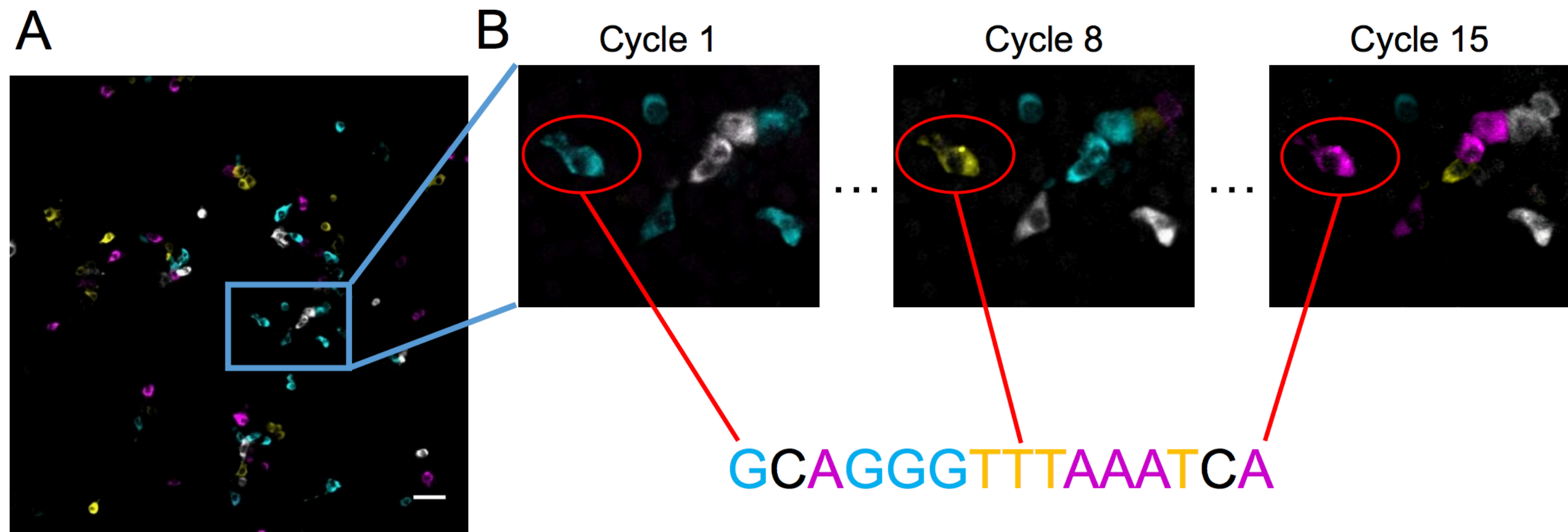
A



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In-situ readout of Zador barcodes



Efficient *in situ* barcode sequencing using padlock probe-based BaristaSeq

Xiaoyin Chen¹, Yu-Chi Sun¹, George M Church^{2,3}, Je Hyuk Lee¹, and Anthony M Zador¹

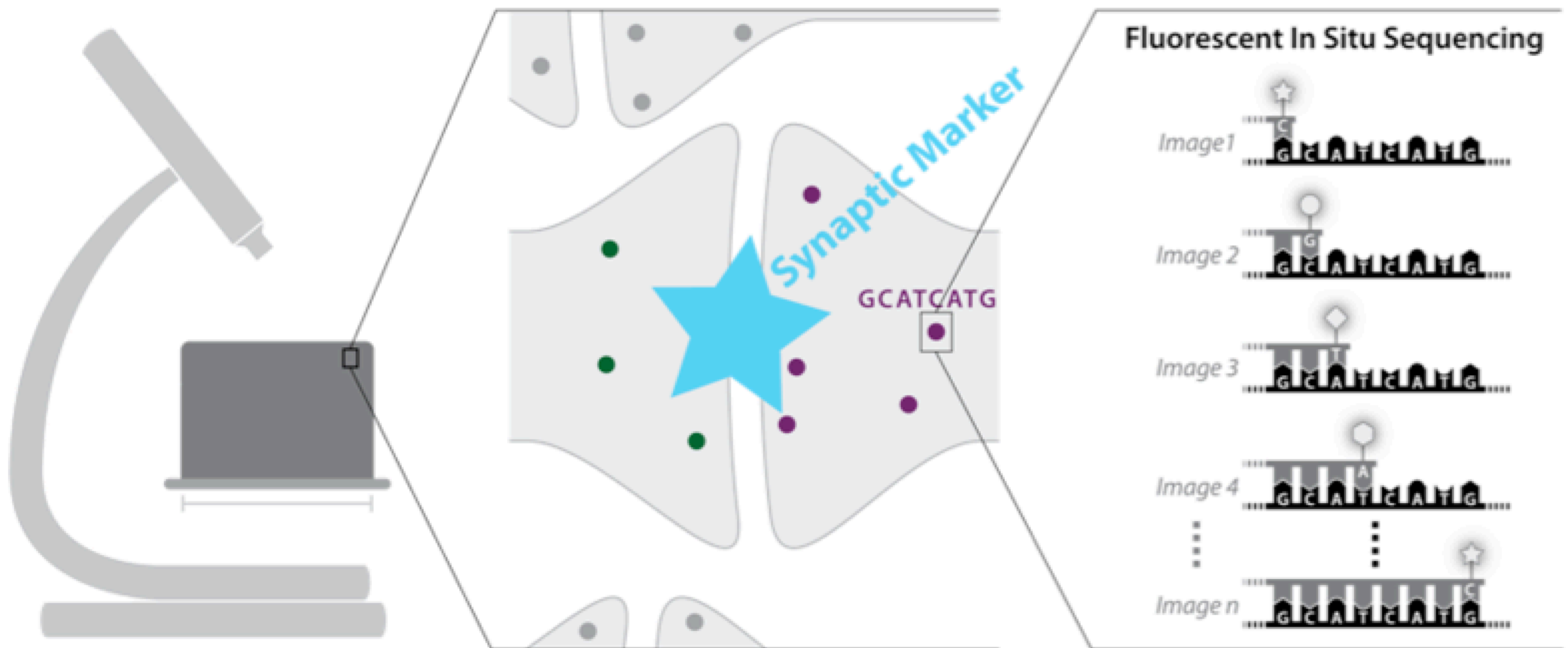
In-situ barcode connectomics

$x, y, z \sim 600 \text{ nm}$

$X, Y, Z > 1 \text{ cm}$

$c \sim \text{infinity}$

Synaptic resolution requires $x, y, z < 100 \text{ nm}$



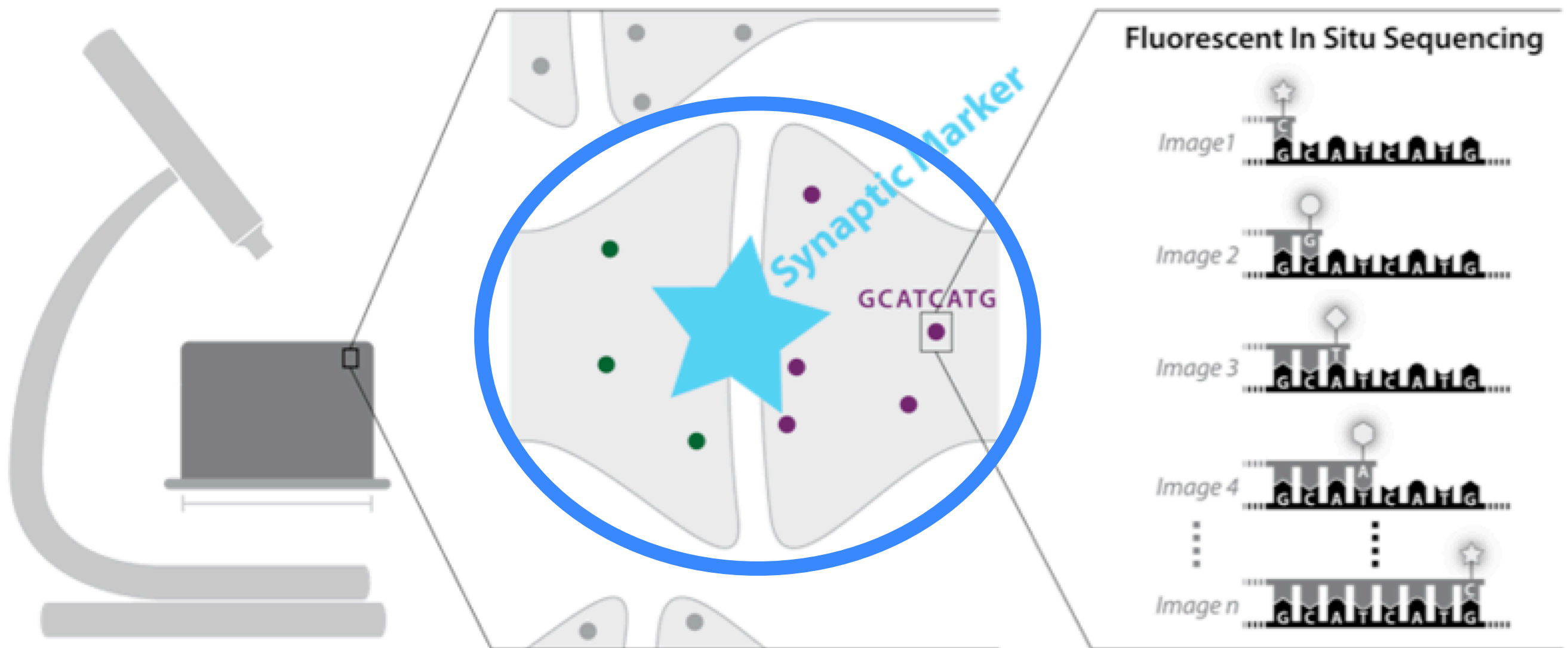
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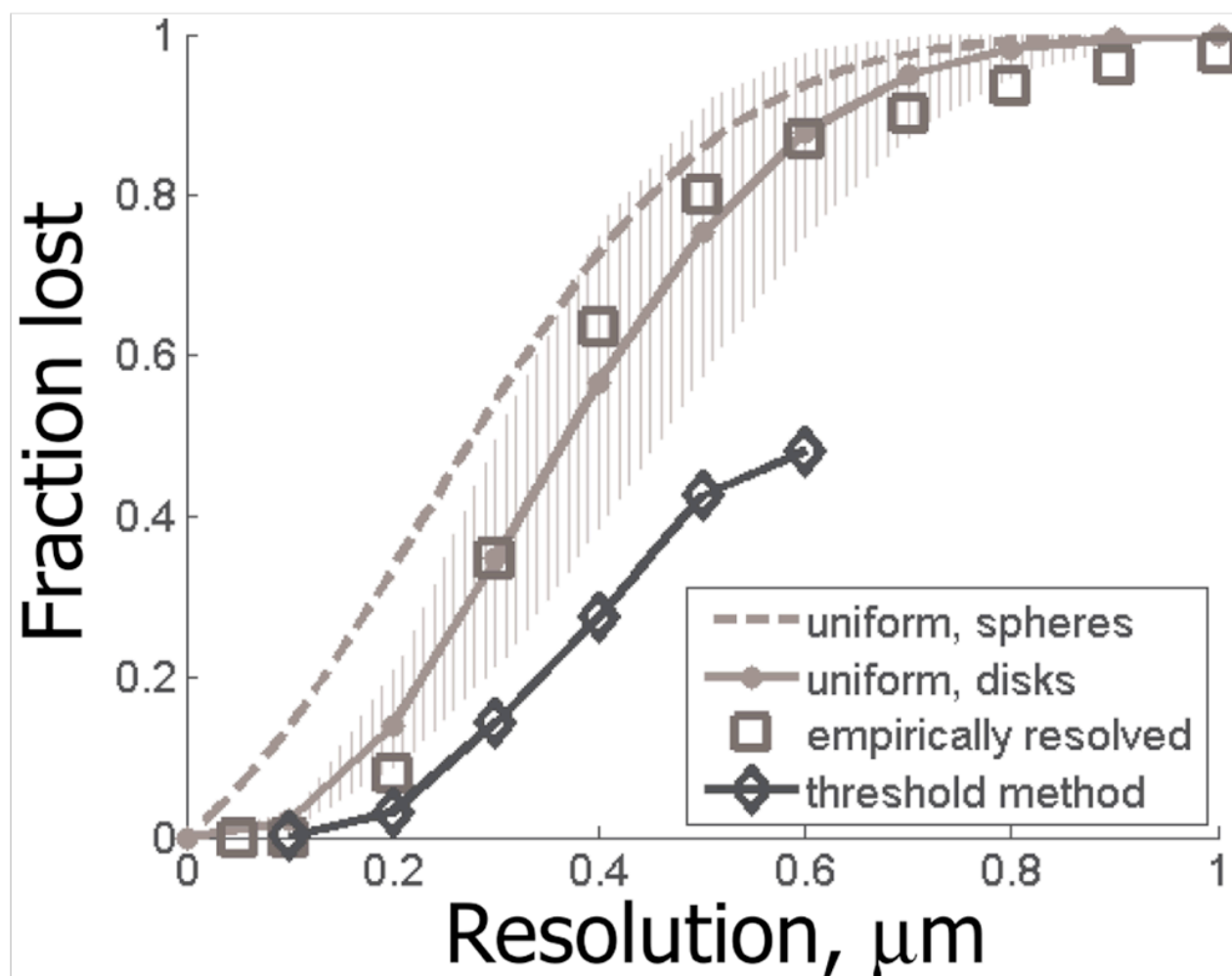
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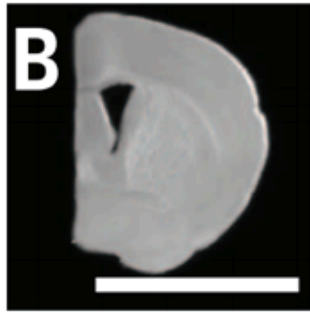
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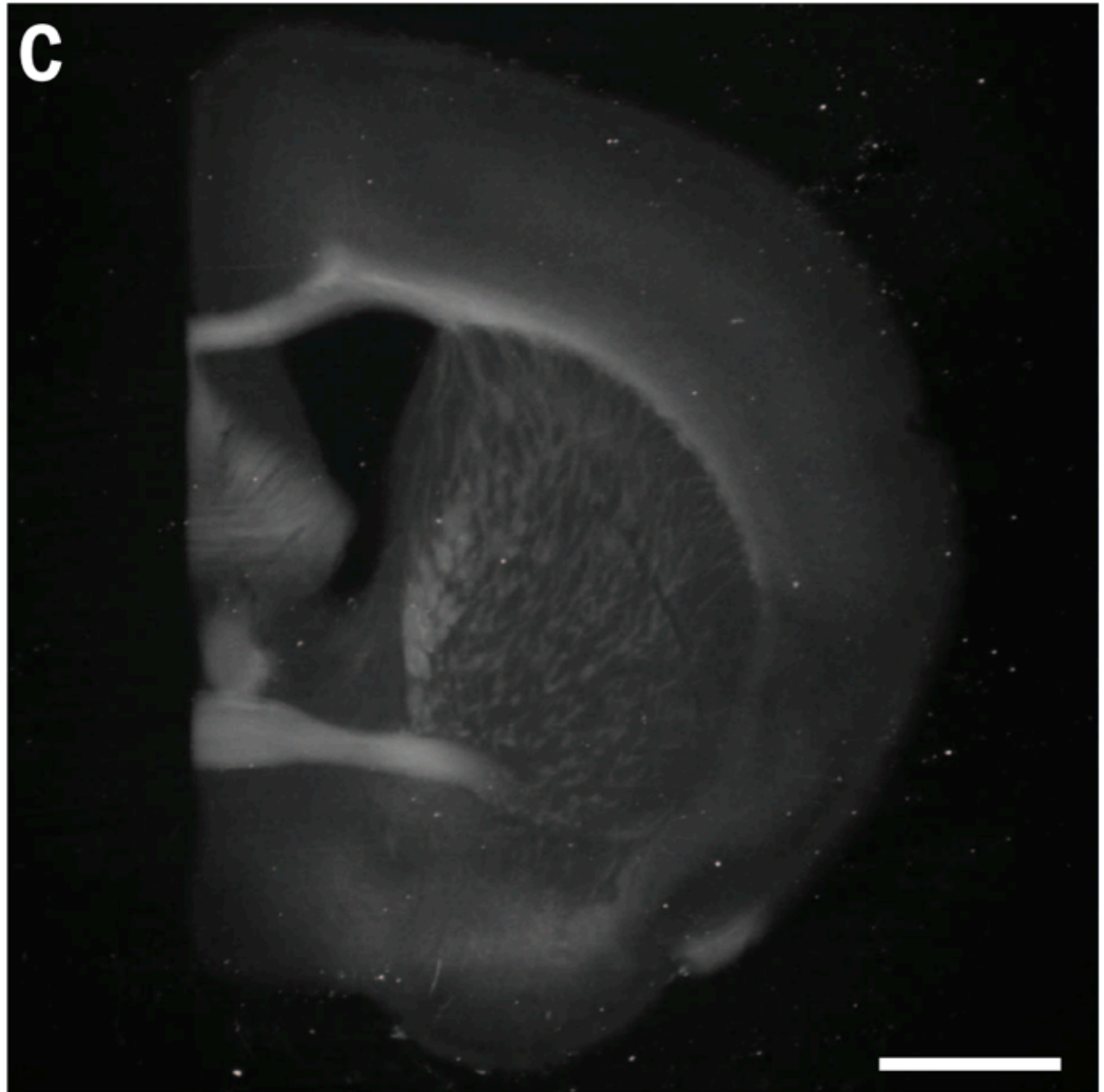
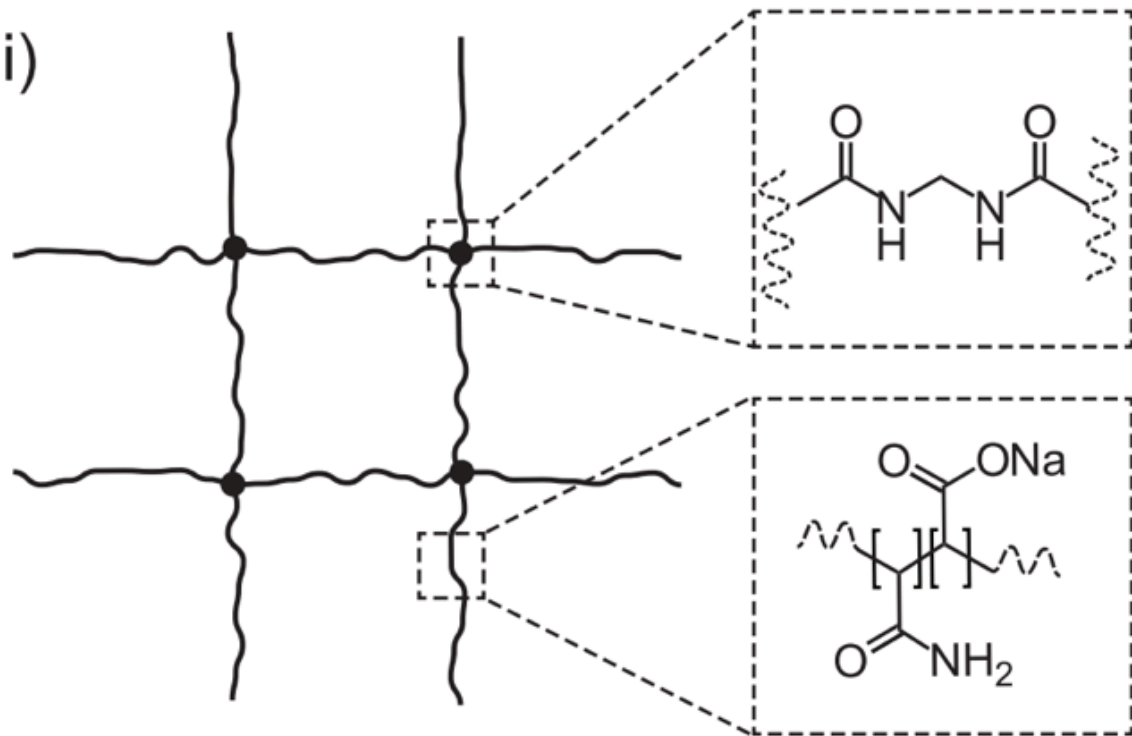
Synapse resolvability vs.
spatial resolution:
Yuriy Mishchenko, 2011

Expansion Microscopy (ExM)

A
(i)

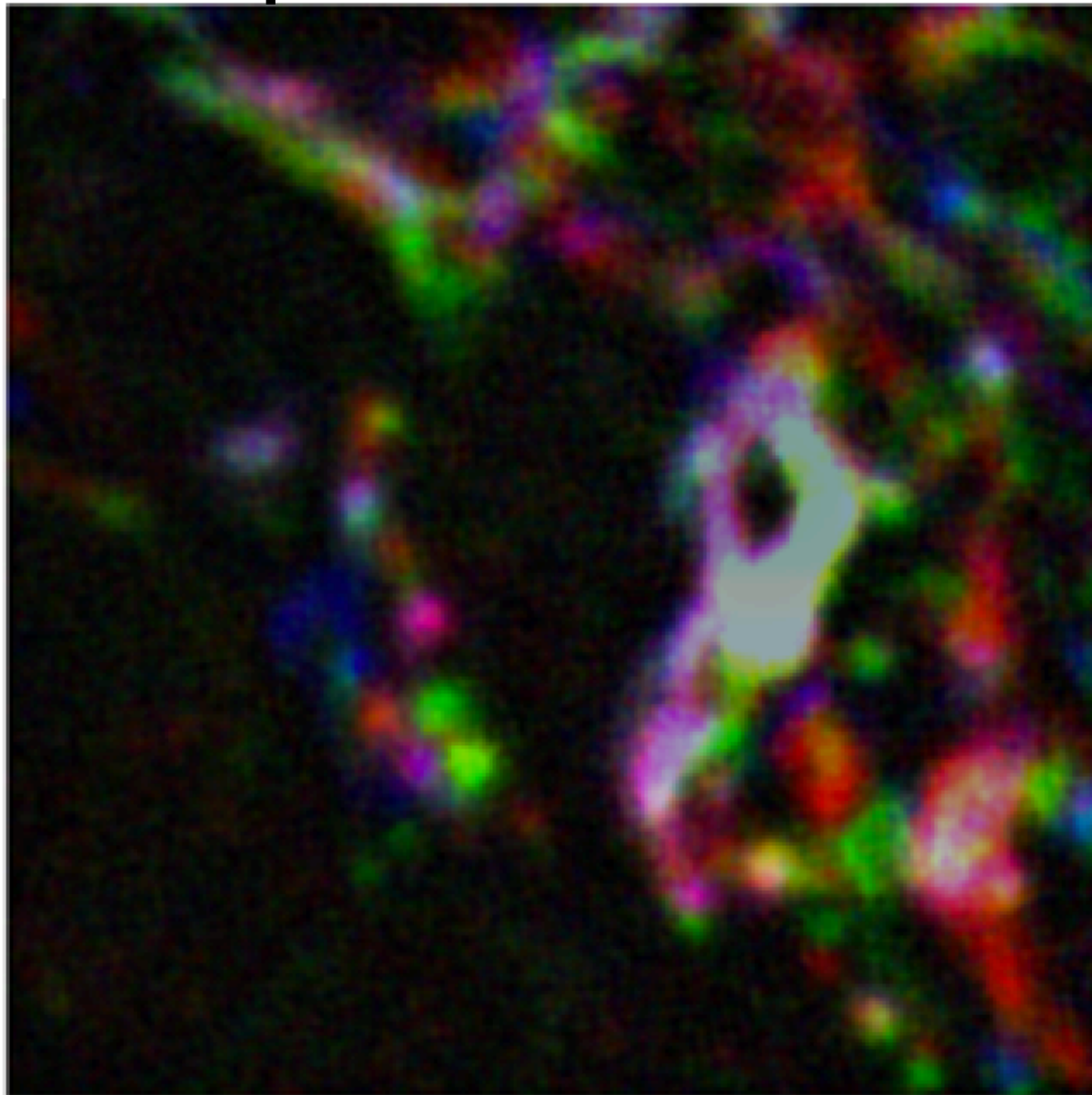


(ii)

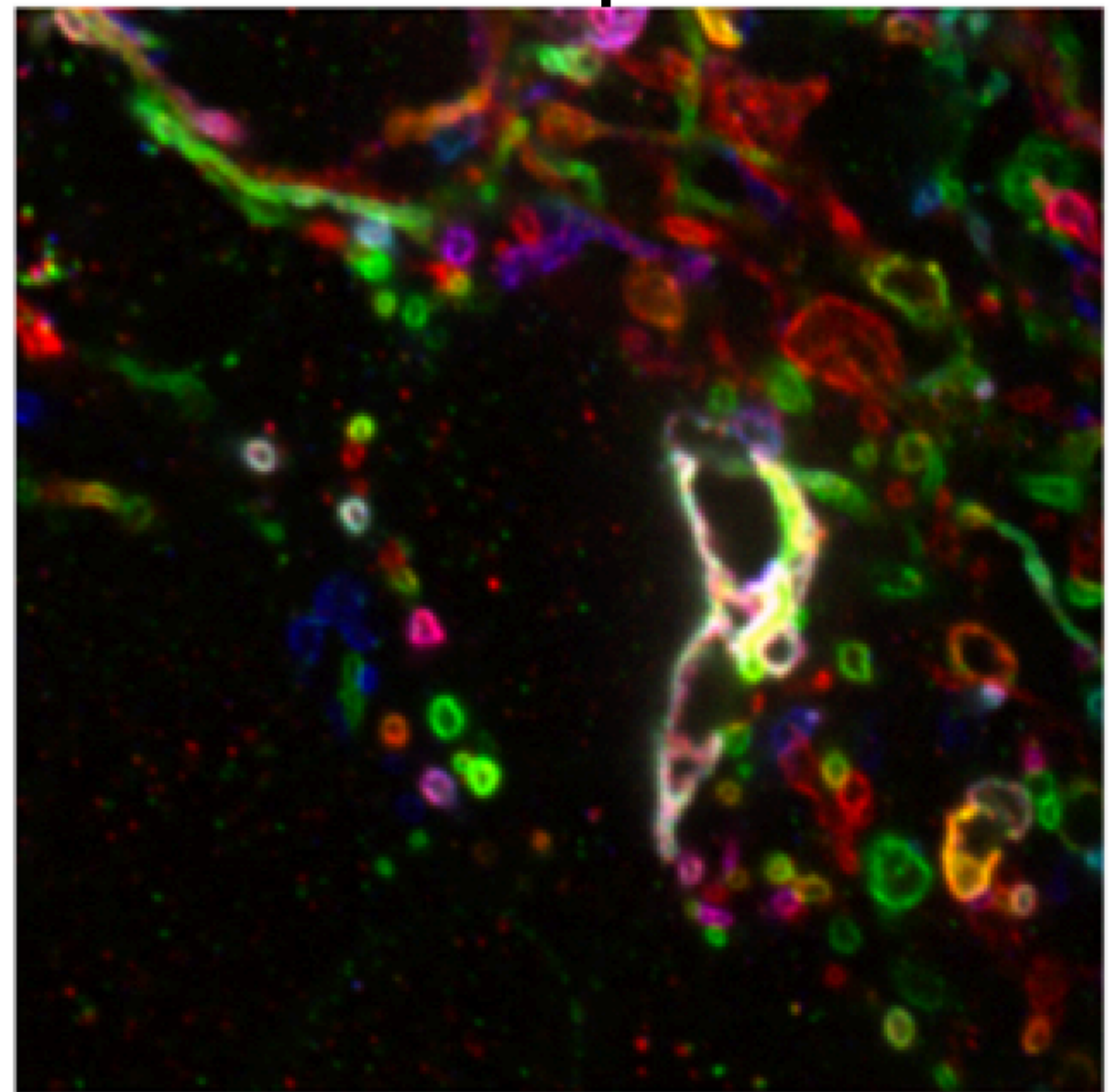


Expansion Microscopy (ExM)

no expansion



4.5x linear expansion



same microscope: a fast, diffraction-limited confocal

Expansion Microscopy (ExM)

Synapses at different levels of ExM expansion (simulated):

1x

2x

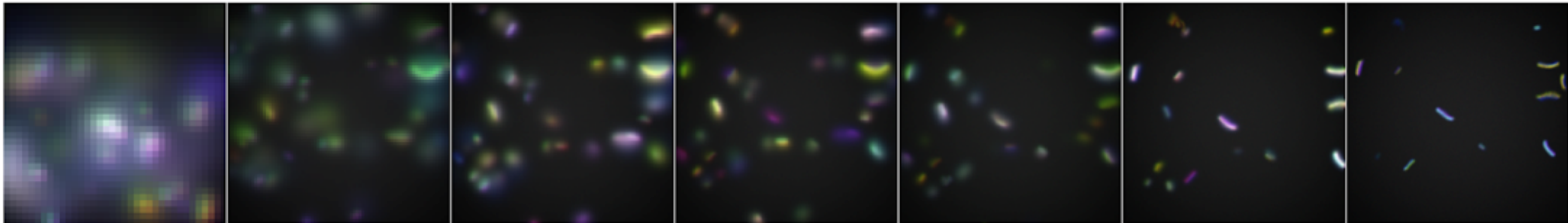
3x

4x

5x

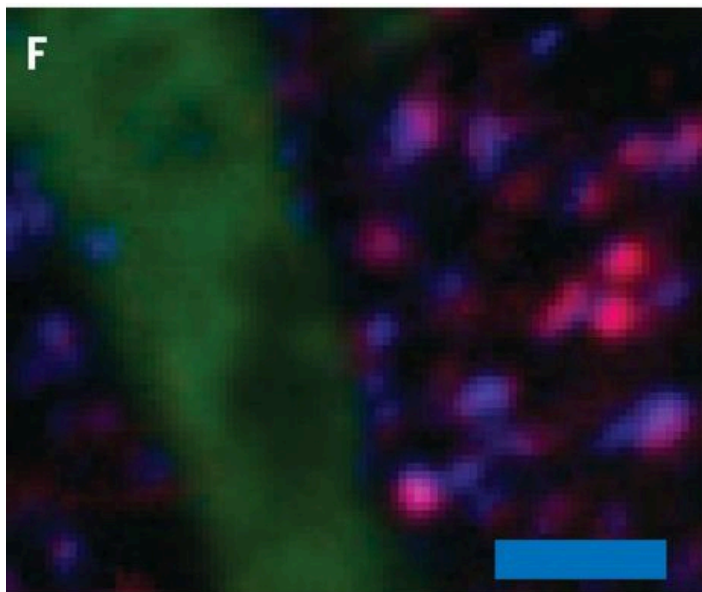
10x

20x

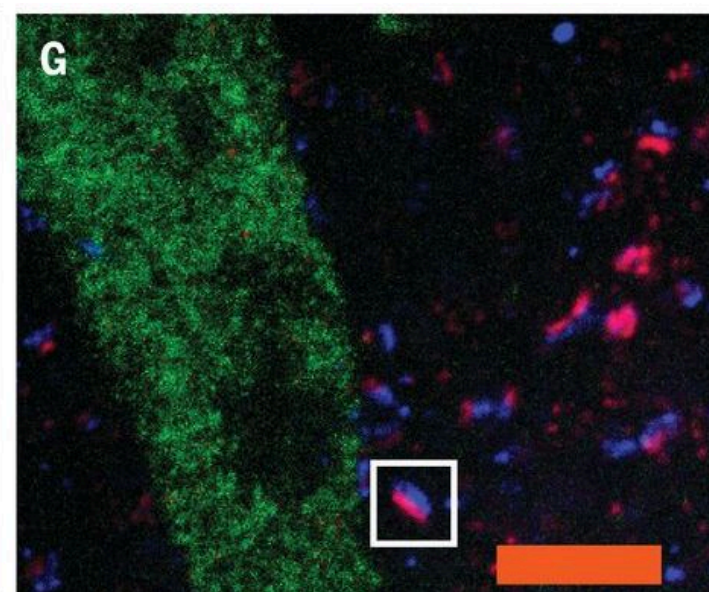


Simulation based on Kasthuri et al published dataset
Color indicates cell of origin

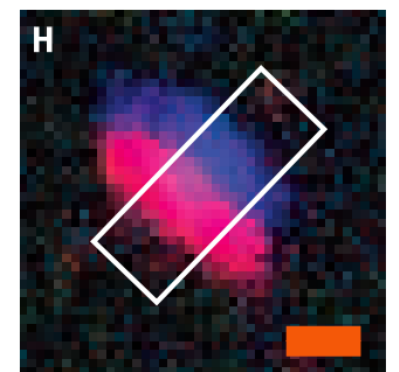
1x *real* Bassoon/Homer



4.5x *real* Bassoon/Homer

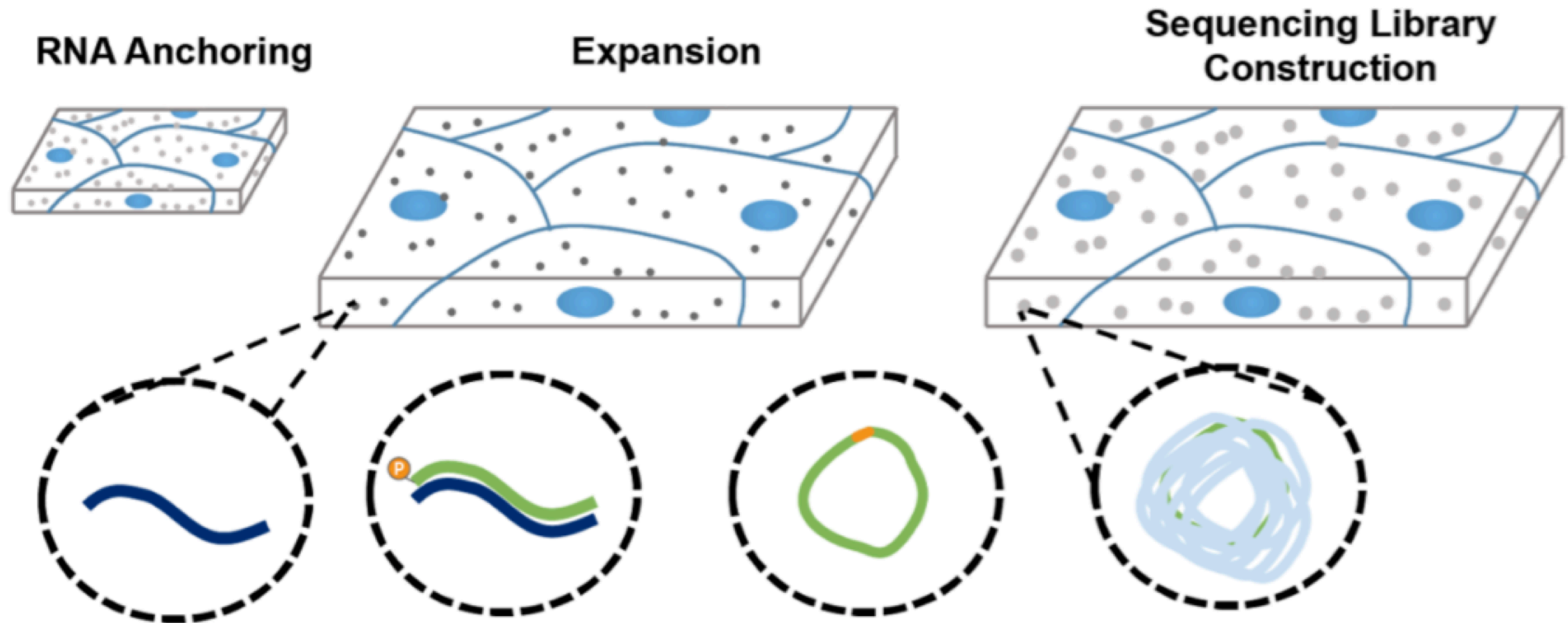


Pre/Post



4.5x ExM

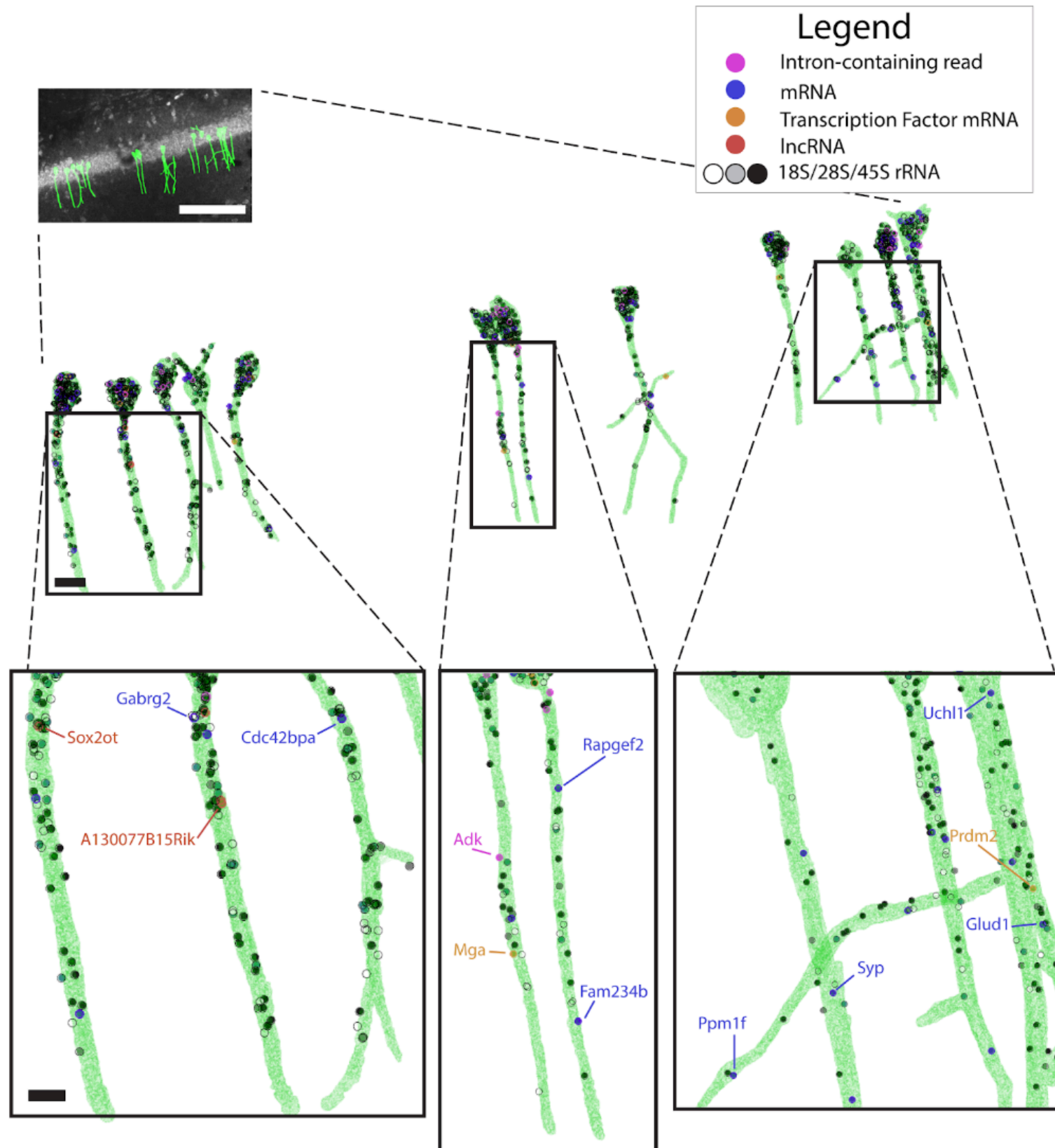
FISSEQ-ExM



Title: Expansion Sequencing: Spatially Precise *In Situ* Transcriptomics in Intact Biological Systems

Authors: Shahar Alon^{1,2,3†}, Daniel R Goodwin^{1,2†}, Anubhav Sinha^{1,2,4†}, Asmamaw T Wassie^{1,2,5†}, Fei Chen^{1,6†}, Evan R Daugharthy^{7,8††}, Yosuke Bando^{1,9}, Atsushi Kajita¹⁰, Andrew G Xue¹, Karl Marrett¹⁰, Robert Prior¹⁰, Yi Cui^{1,2}, Andrew C Payne^{1,6}, Chun-Chen Yao^{1,6}, Ho-Jun Suk^{1,2,4}, Ru Wang^{1,2}, Chih-Chieh (Jay) Yu^{1,2,5}, Paul Tillberg^{1†††}, Paul Reginato^{1,5,6,7,8}, Nikita Pak^{1,2,11}, Songlei Liu^{7,8}, Sukanya Punthambaker^{7,8}, Eswar P. R. Iyer⁸, Richie E Kohman^{7,8}, Jeremy A Miller¹², Ed S Lein¹², Ana Lako¹³, Nicole Cullen¹³, Scott Rodig¹³, Karla Helvie¹⁴, Daniel L Abravanel¹⁴, Nikhil Wagle¹⁴, Bruce E Johnson¹⁴, Johanna Klughammer⁶, Michal Slyper⁶, Julia Waldman⁶, Judit Jané-Valbuena⁶, Orit Rozenblatt-Rosen⁶, Aviv Regev^{6,15,16}, IMAXT Consortium¹⁷, George M Church^{7,8#*}, Adam H Marblestone^{1#†}, Edward S Boyden^{1,2,5,15,18#*}

FISSEQ-ExM

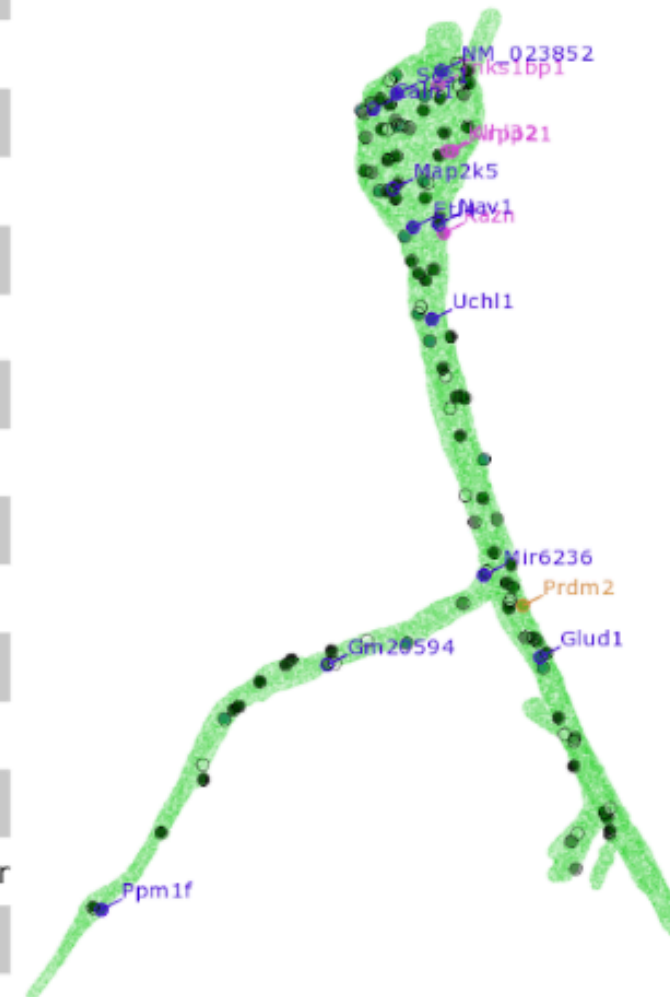


Alon*, Goodman*, Chen*, Daugharthy, ..., Church**, Marblestone**, Boyden**.

FISSEQ-ExM

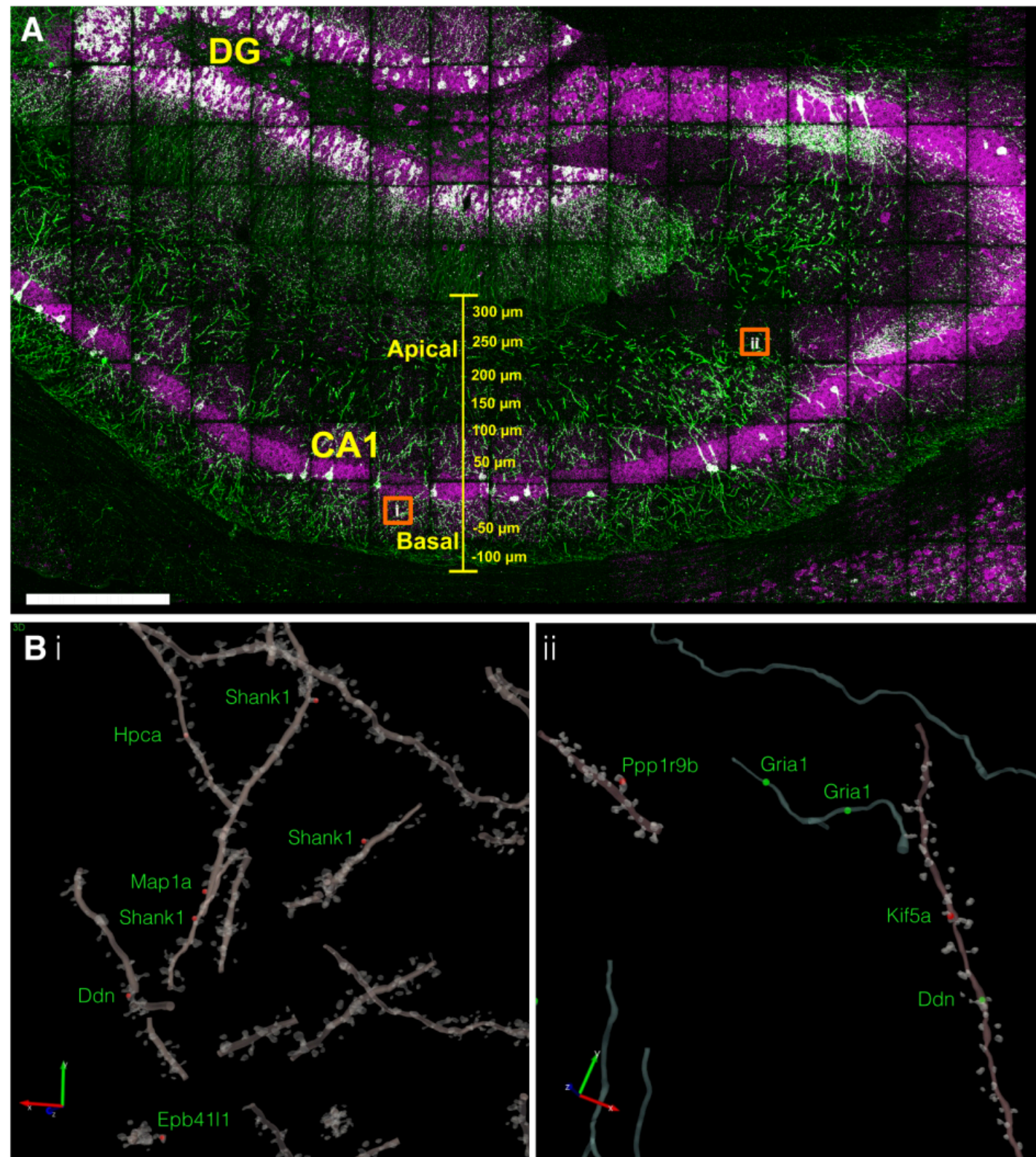
Neuron 13:

Gene Symbol	Gene name	Notes
Tnks1bp1	Tankyrase 1 Binding Protein 1	Intron
NM_023852	RAB3C, Member RAS Oncogene Family	
Kazn	Kazrin, Periplakin Interacting Protein	Intron
Etl4	Epilepsy, Occipitotemporal Lobe, And Migraine With Aura	
Caln1	Calneuron 1	
Nav1	Neuron Navigator 1	
Sos1	SOS Ras/Rac Guanine Nucleotide Exchange Factor 1	
Klhl32	Kelch Like Family Member 32	Intron
Arpp21	CAMP Regulated Phosphoprotein 21	Intron
Map2k5	Mitogen-Activated Protein Kinase Kinase 5	
Uchl1	Ubiquitin C-Terminal Hydrolase L1	
Mir6236		Probably rRNA
Prdm2	PR/SET Domain 2	Transcription Factor
Gm20594		Predicted gene
Glud1	Glutamate Dehydrogenase 1	
Ppm1f	Protein Phosphatase, Mg2+/Mn2+ Dependent 1F	



Alon*, Goodman*, Chen*, Daugharthy, ..., Church**, Marblestone**, Boyden**.

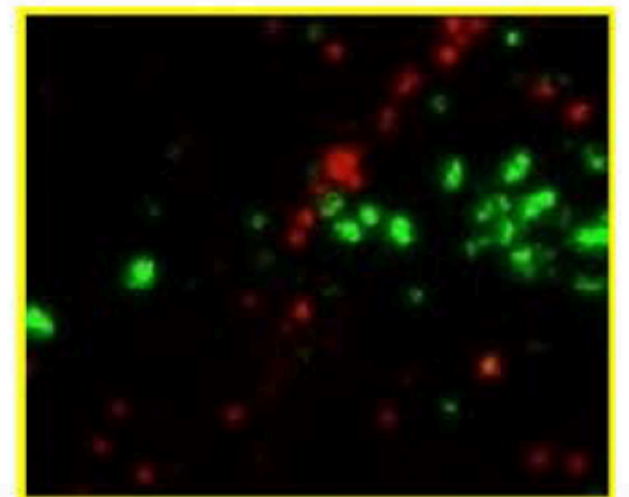
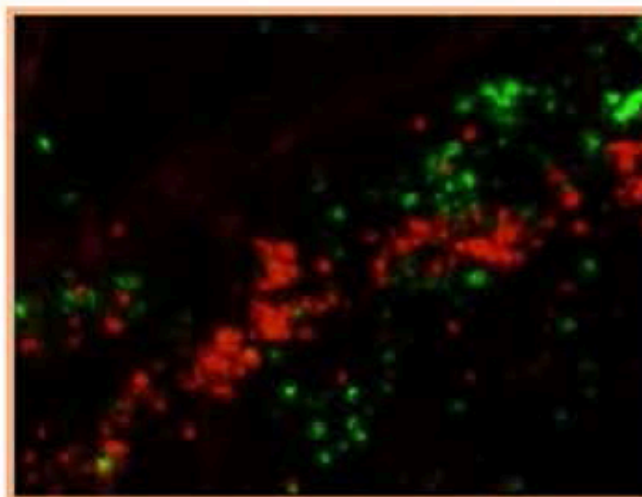
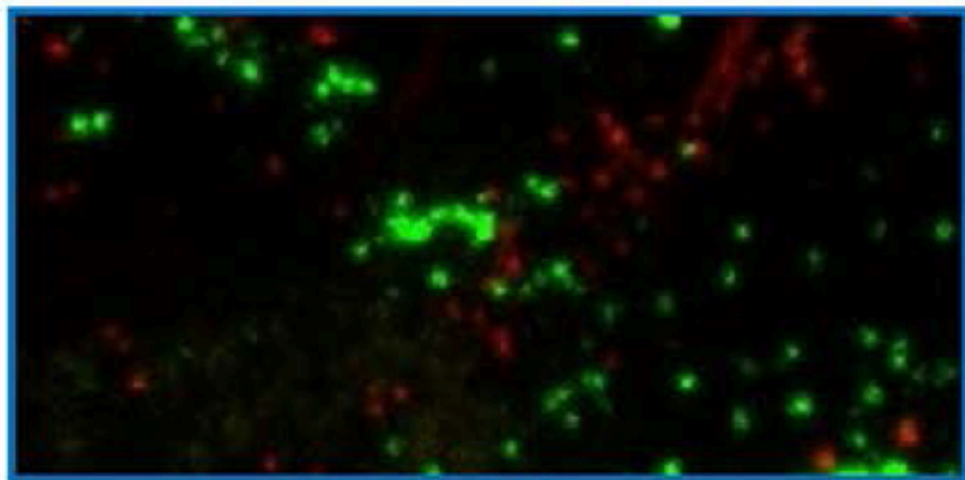
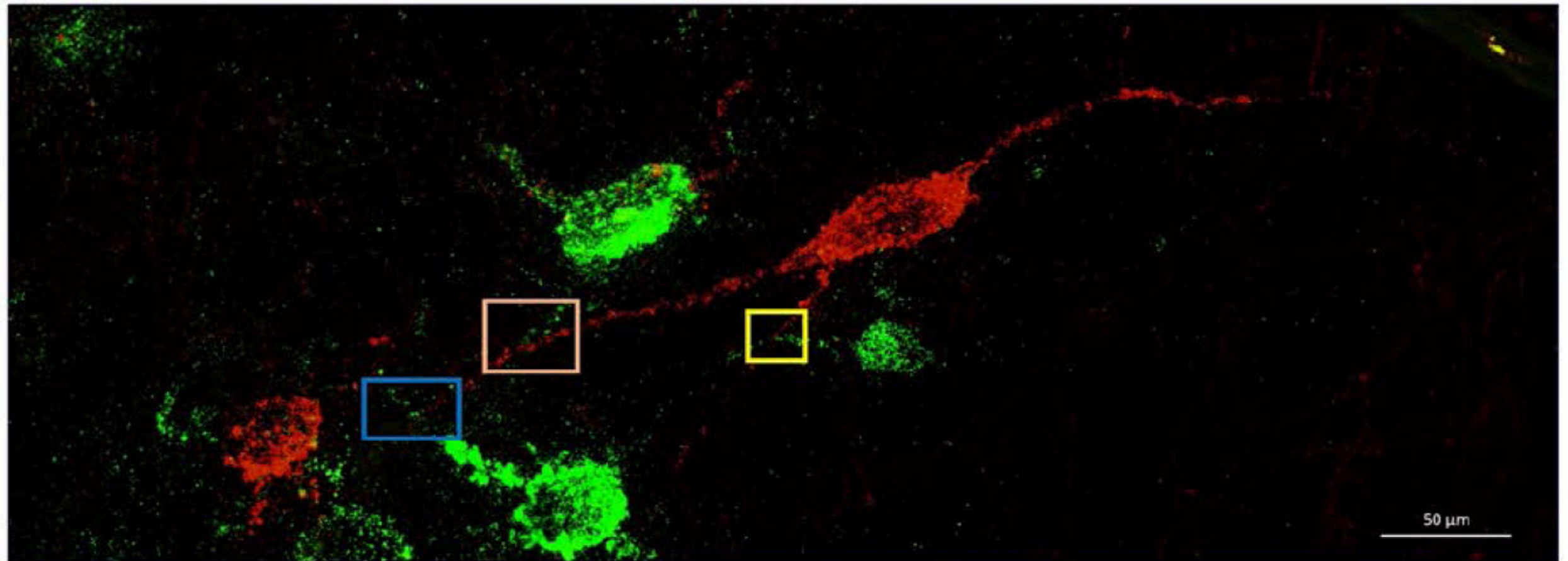
FISSEQ-ExM



Alon*, Goodman*, Chen*, Daugharthy, ..., Church**, Marblestone**, Boyden**.

Scalable brain mapping: unique ID's for structure

*Reading neuron barcode RNA sequences
in **physically expanded** brain tissue*

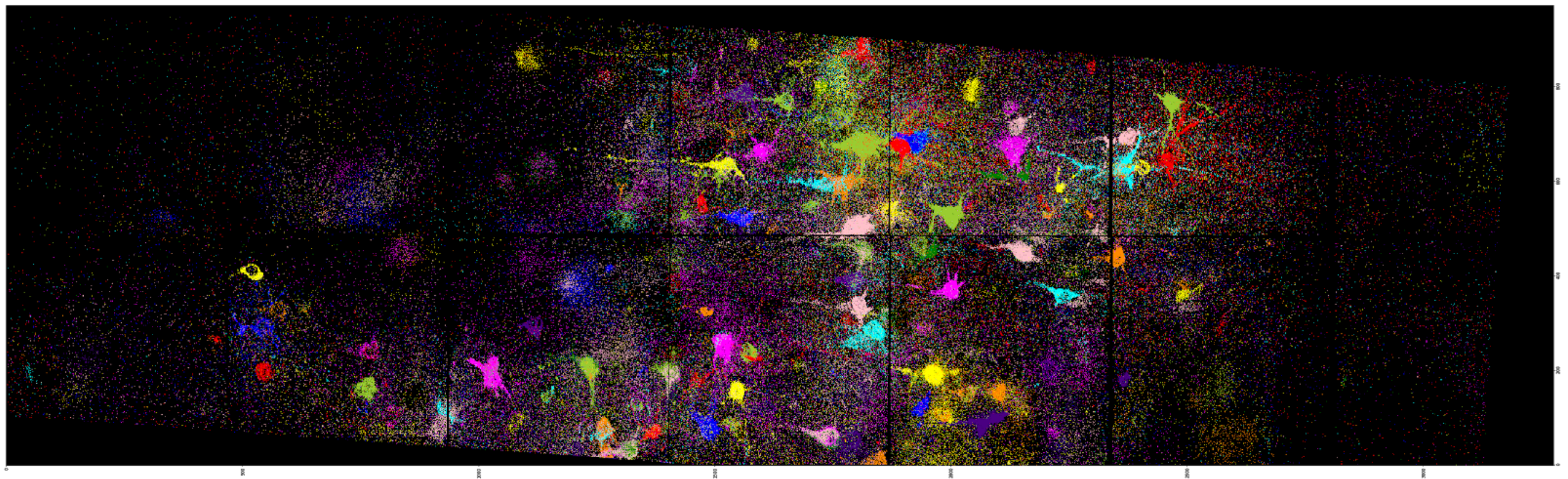


Data by Richie Kohman, analysis by Andrew Xue, Dan Goodwin, Ruihan Zhang

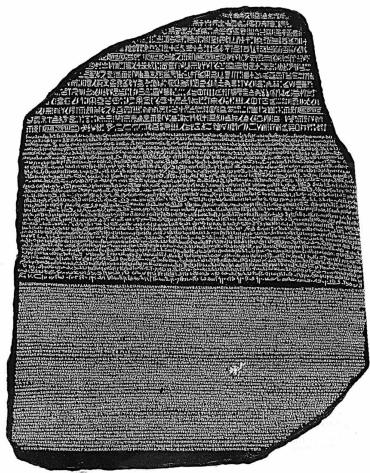
Scalable brain mapping: unique ID's for structure

*Reading neuron barcode RNA sequences
in **physically expanded** brain tissue*

full thickness of mouse cortex



(first-pass *automatic* barcode extraction)



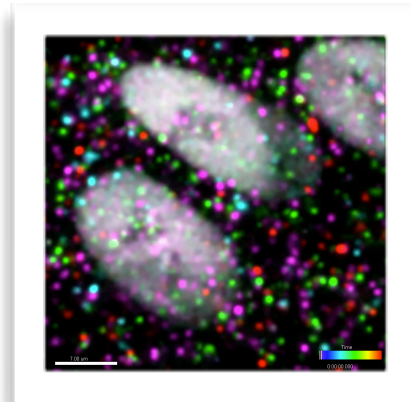
“Rosetta Brain”

Activity ? Molecular Tickertapes ?
Behavior
Connectivity
Development
Expression



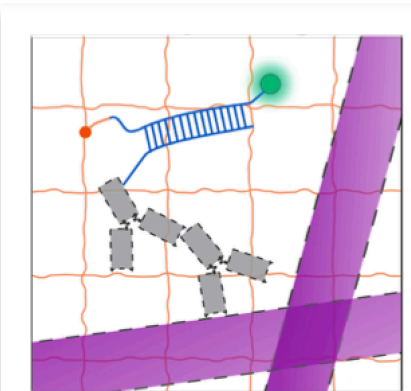
(in-vivo-generated)
Cell Barcodes
(update 1x per division)

RNA Transcripts +
DNA-barcoded **Antibodies**



FISSEQ
(Lee et al 2014)

+




ExM
(Chen et al 2014)

Rapidly evolving homing CRISPR barcodes

Reza Kalhor, Prashant Mali & George M Church

Large-scale simultaneous measurement of epitopes and transcriptomes in single cells.

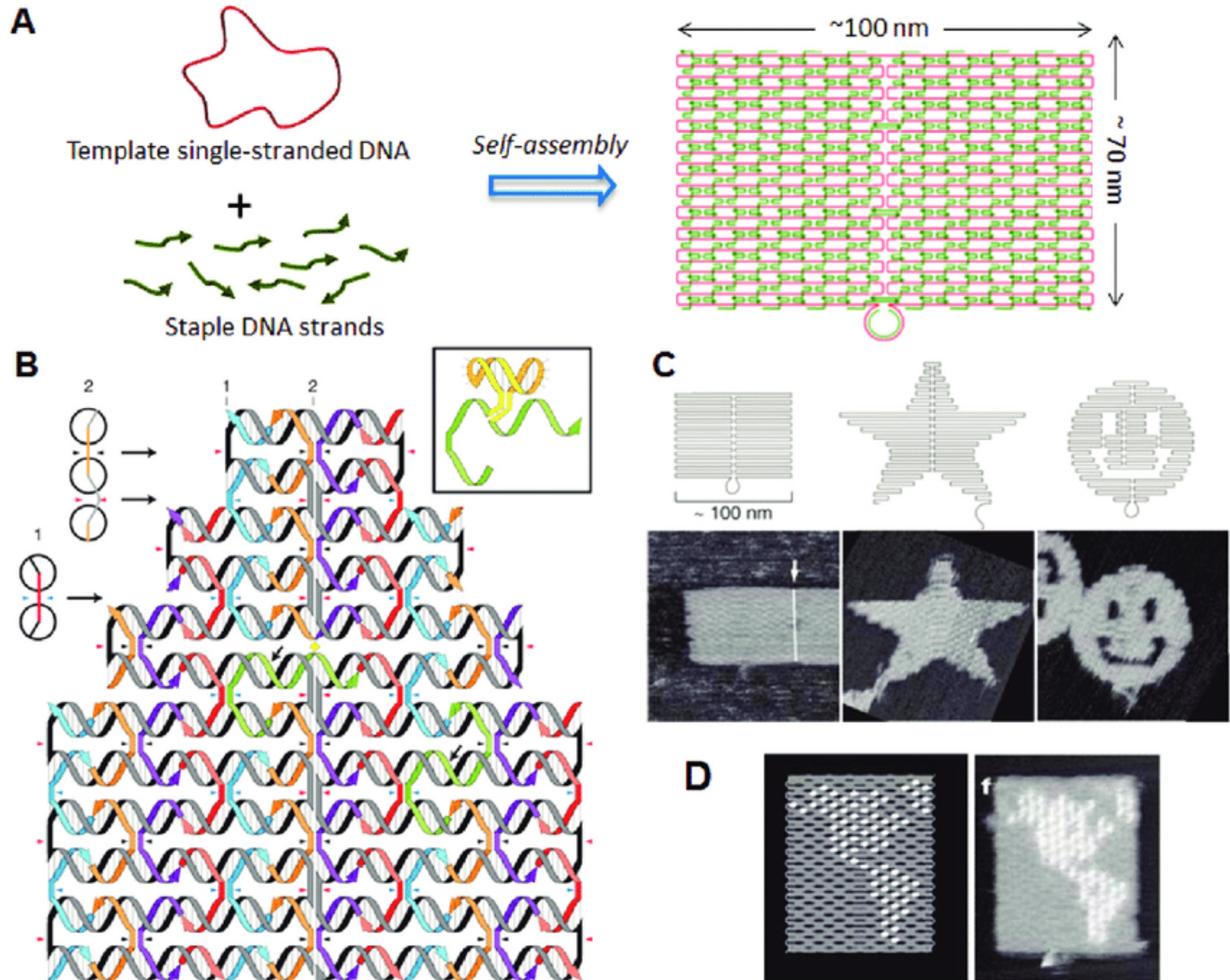
Marlon Stoeckius,  Christoph Hafemeister, William Stephenson, Brian Houck-Loomis, Harold Swerdlow, Rahul Satija, Peter Smibert

doi: [https://doi.org/ 10.1101/113068](https://doi.org/10.1101/113068)

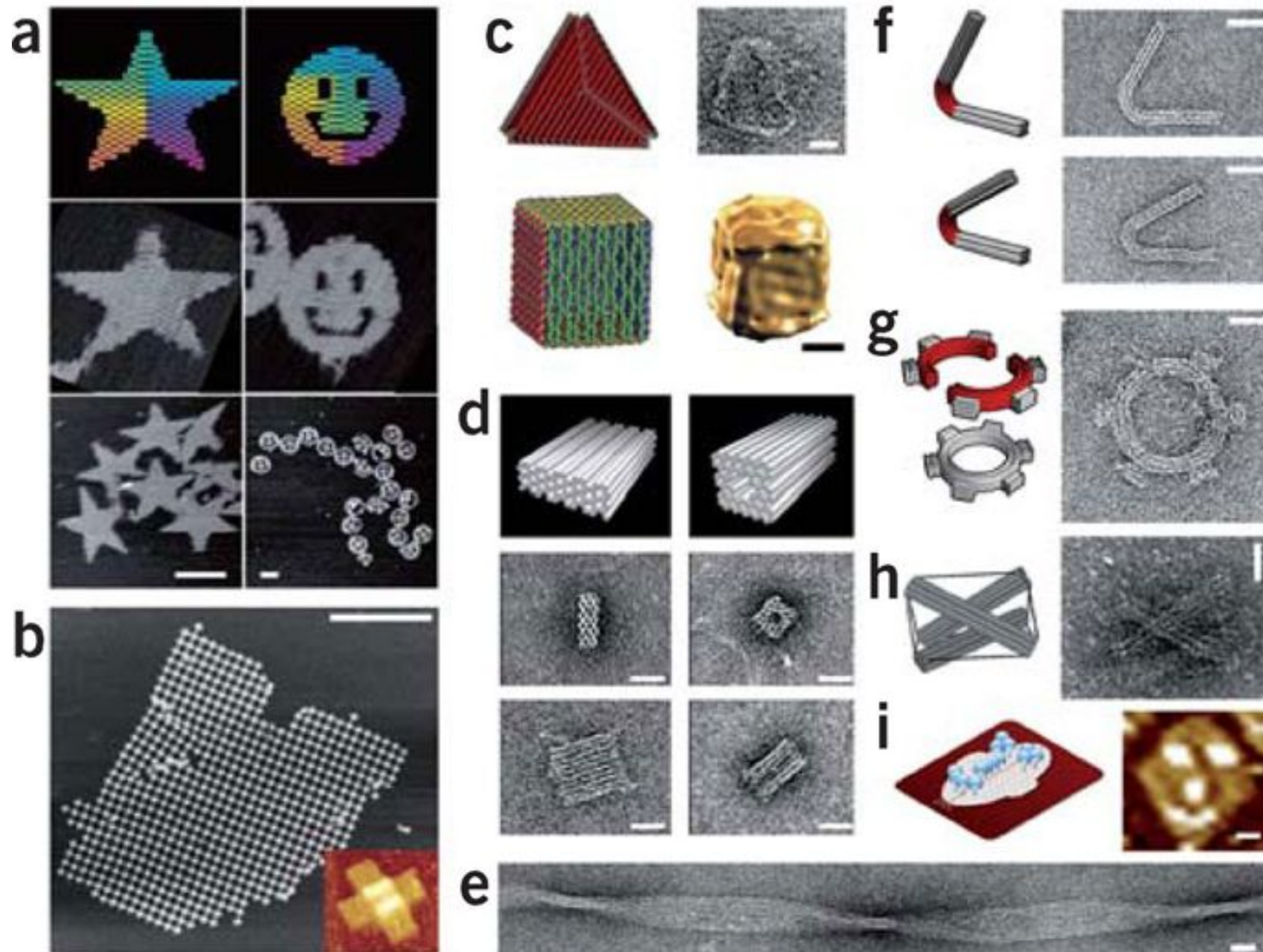
Part 2: construct

How to position molecules where we want

DNA origami

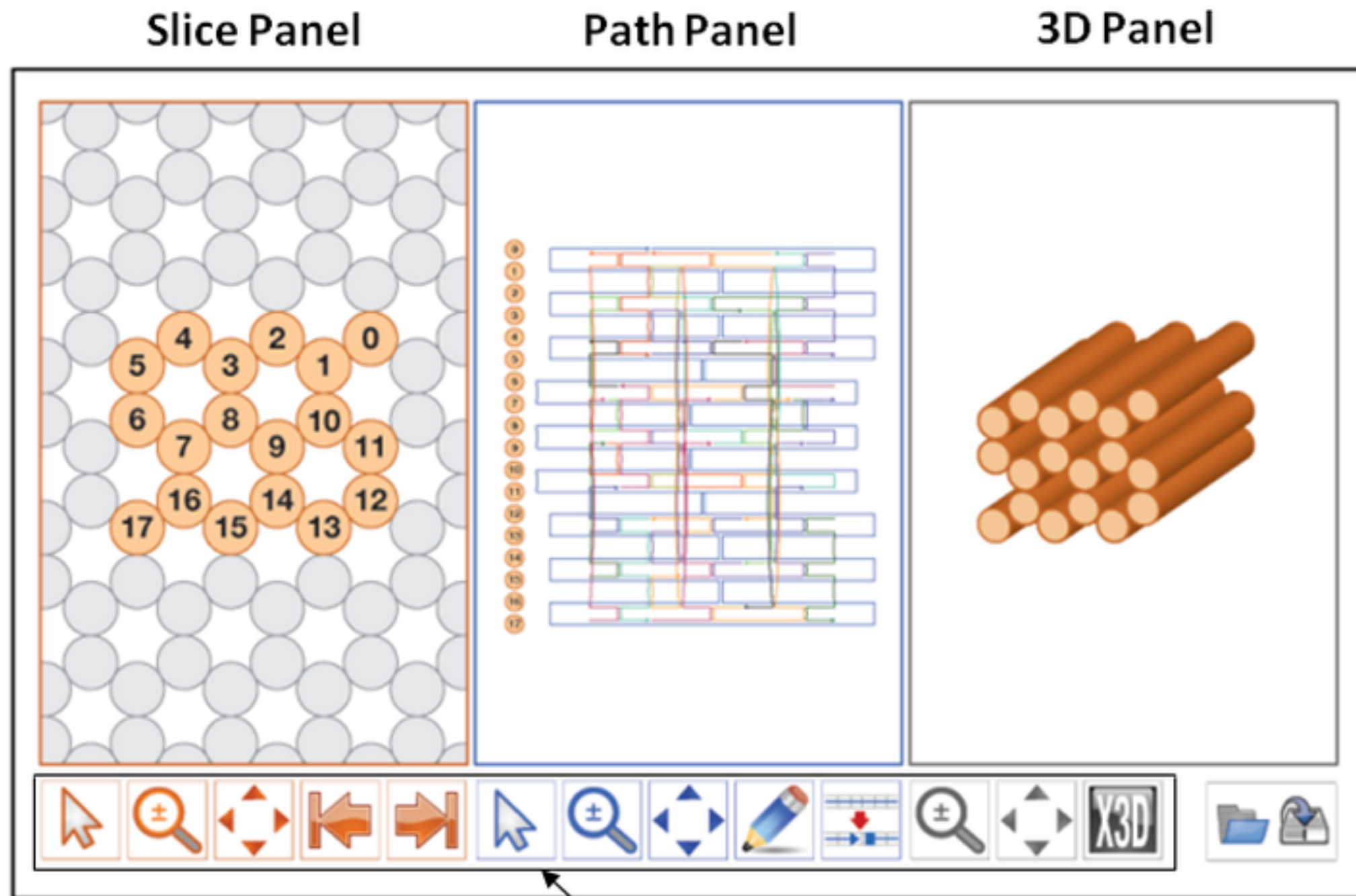


DNA origami



DNA origami

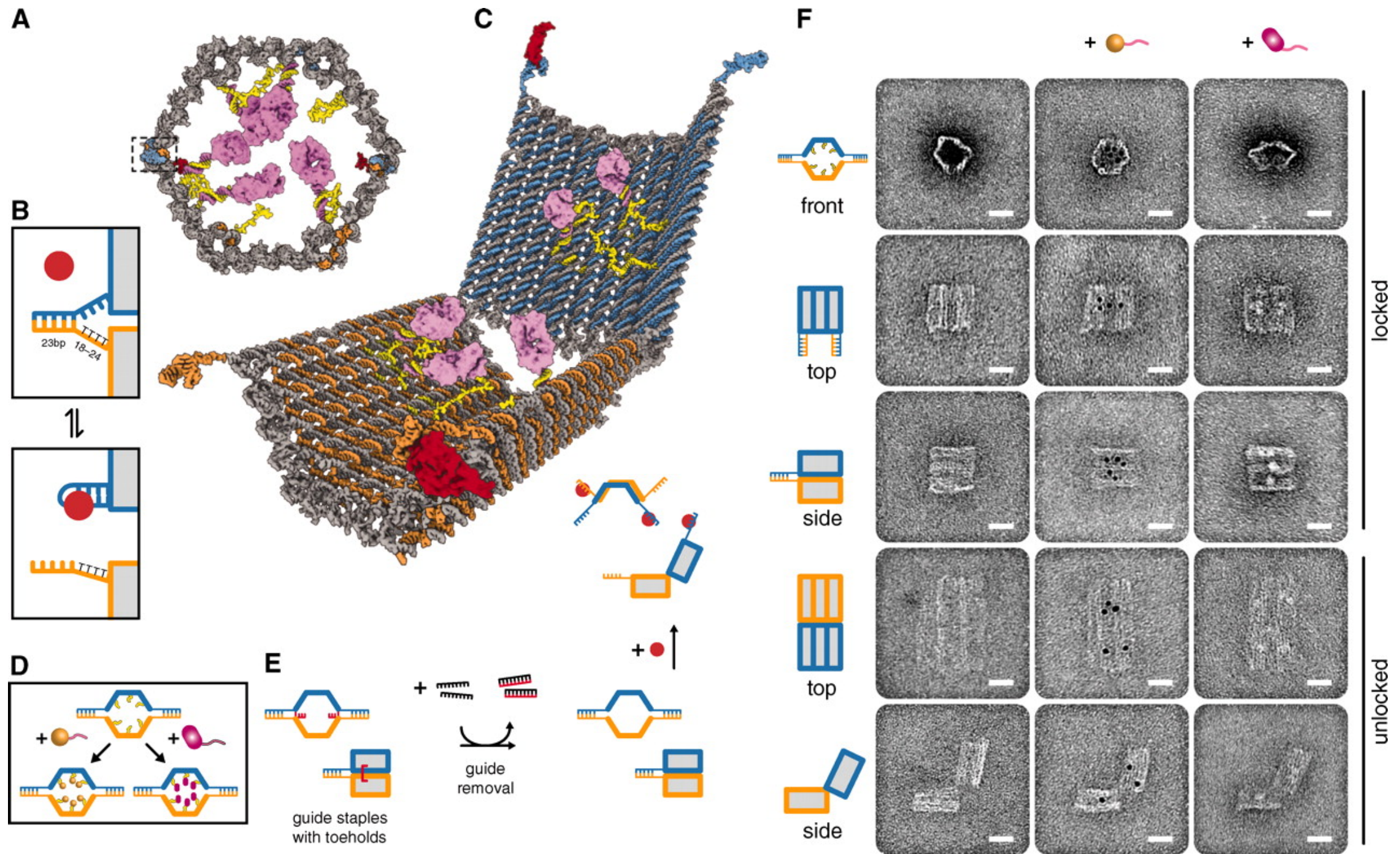
caDNAAno: www.cadnano.org



Tool box

Douglas, Marblestone et al, 2009

DNA origami



Douglas, Bachelet, 2012

DNA origami

$x, y, z \sim 5-10 \text{ nm}$

DNA base spacing = 0.3 nm

helical diameter = 2 nm

orderly manner on solid substrates^{11,12}. So far, few objects afford a design accuracy better than 5 nm¹³⁻¹⁶, and the sub-nanometre scale has been reached only within the unit cells of designed DNA crystals¹⁷. Here, we report a molecular position-

$X, Y, Z > 100 \text{ nm}$

$c \sim \text{no practical limit}$

NOT quite *small* enough for covalent “APM”

NOT quite *big* enough for integration into devices

DNA origami

$x, y, z \sim 5-10 \text{ nm}$

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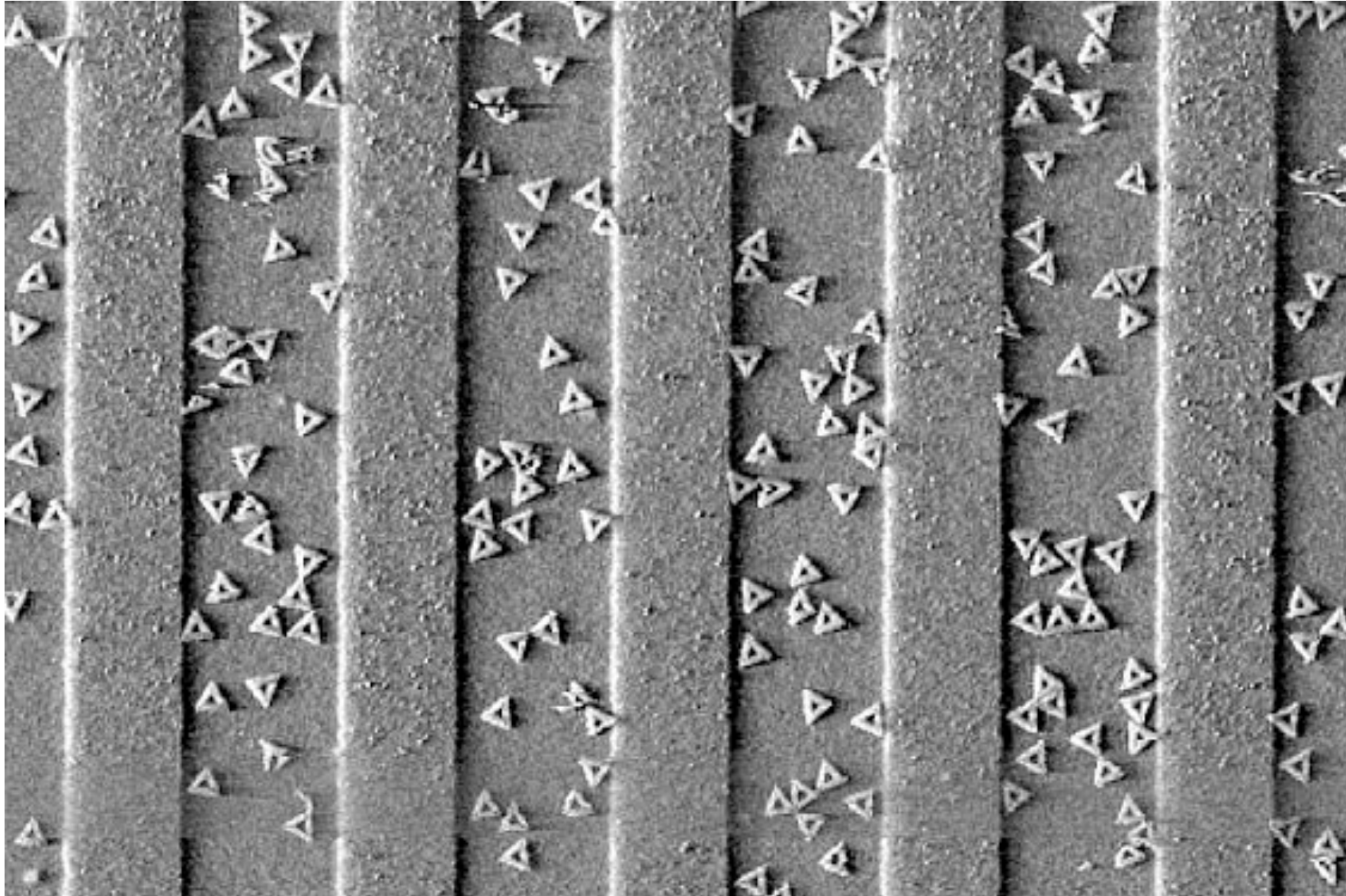
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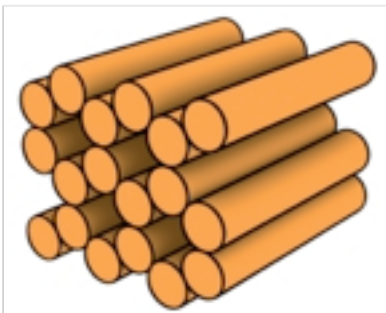
NOT quite *big* enough for integration into devices

How to combine “top-down” with “bottom-up” in nanotechnology?



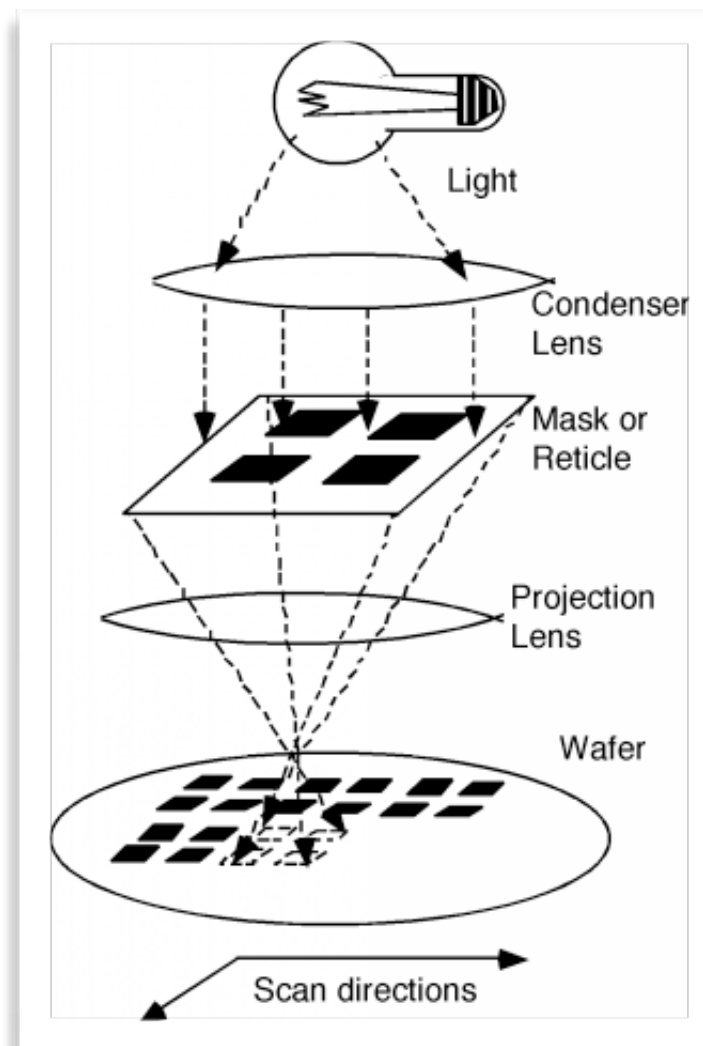
How to combine “top-down” with “bottom-up” in nanotechnology?

DNA origami



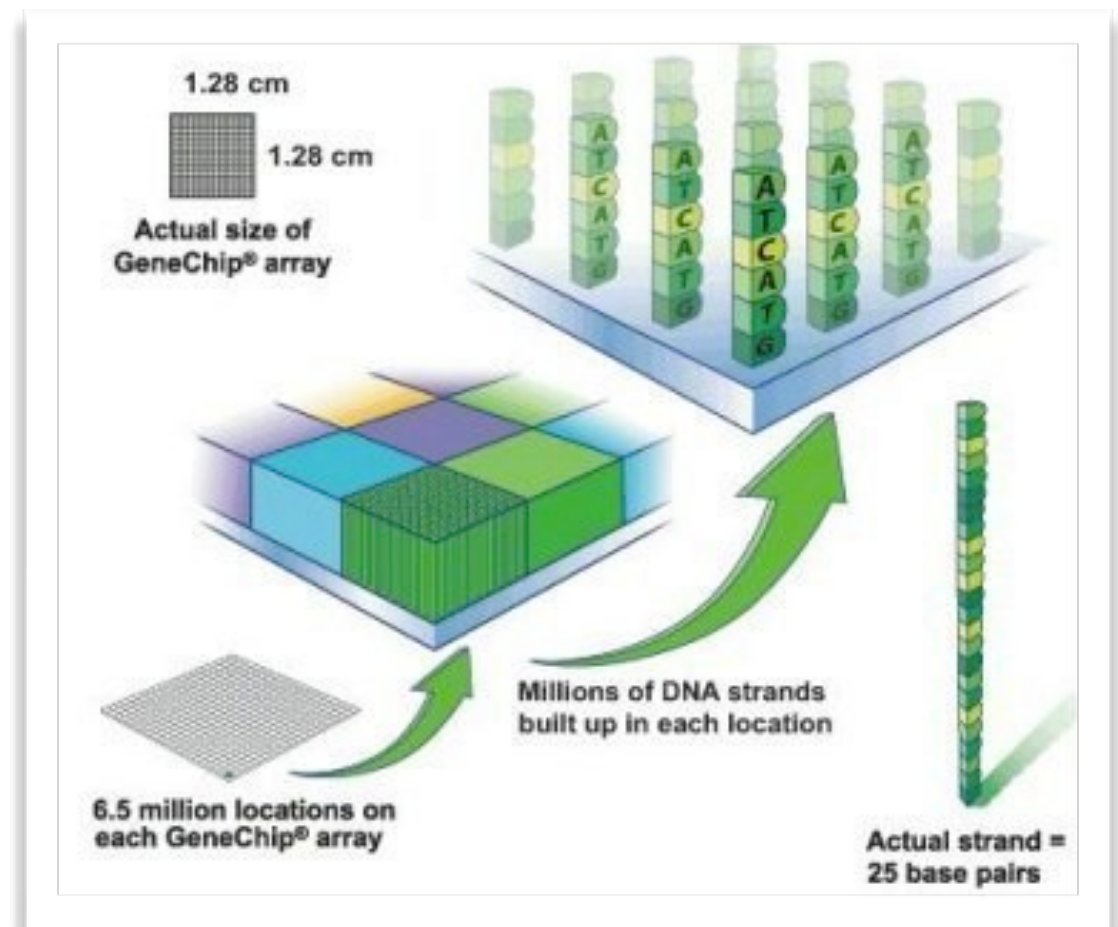
+

photolithography



+

DNA micro-arrays



= **chip-scale** programmable nano-fabrication

How to combine “top-down” with “bottom-up” in nanotechnology?

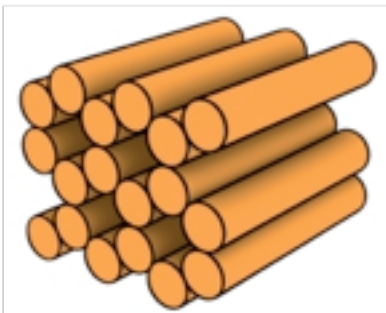
e.g., light-directed DNA synthesis on chip



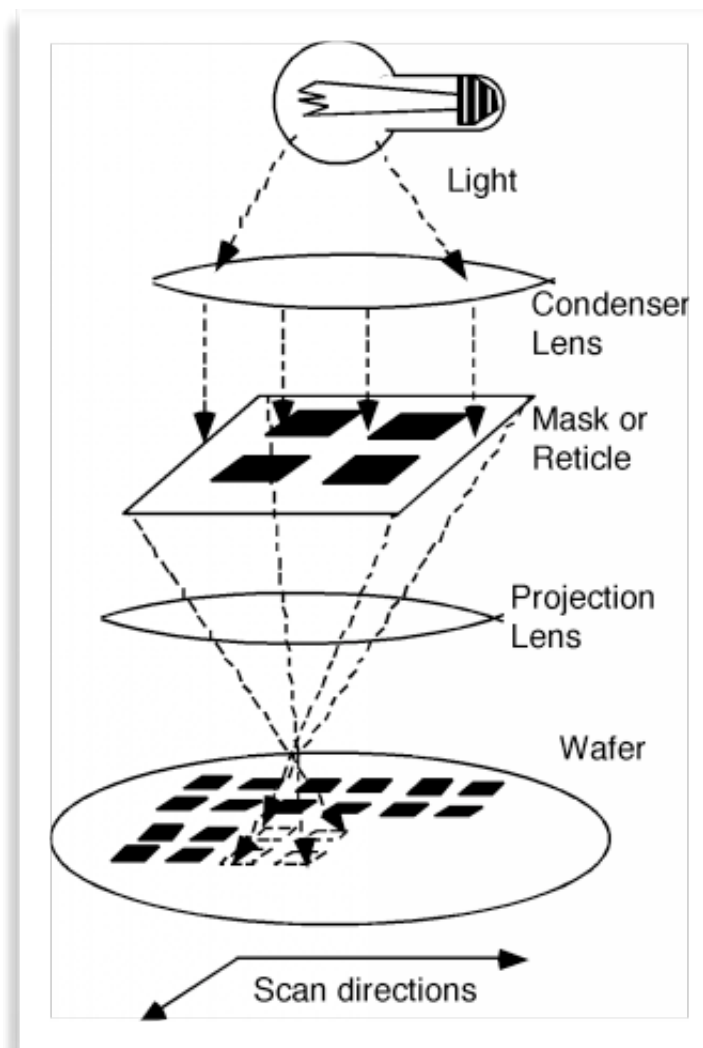
photolithography

DNA micro-arrays

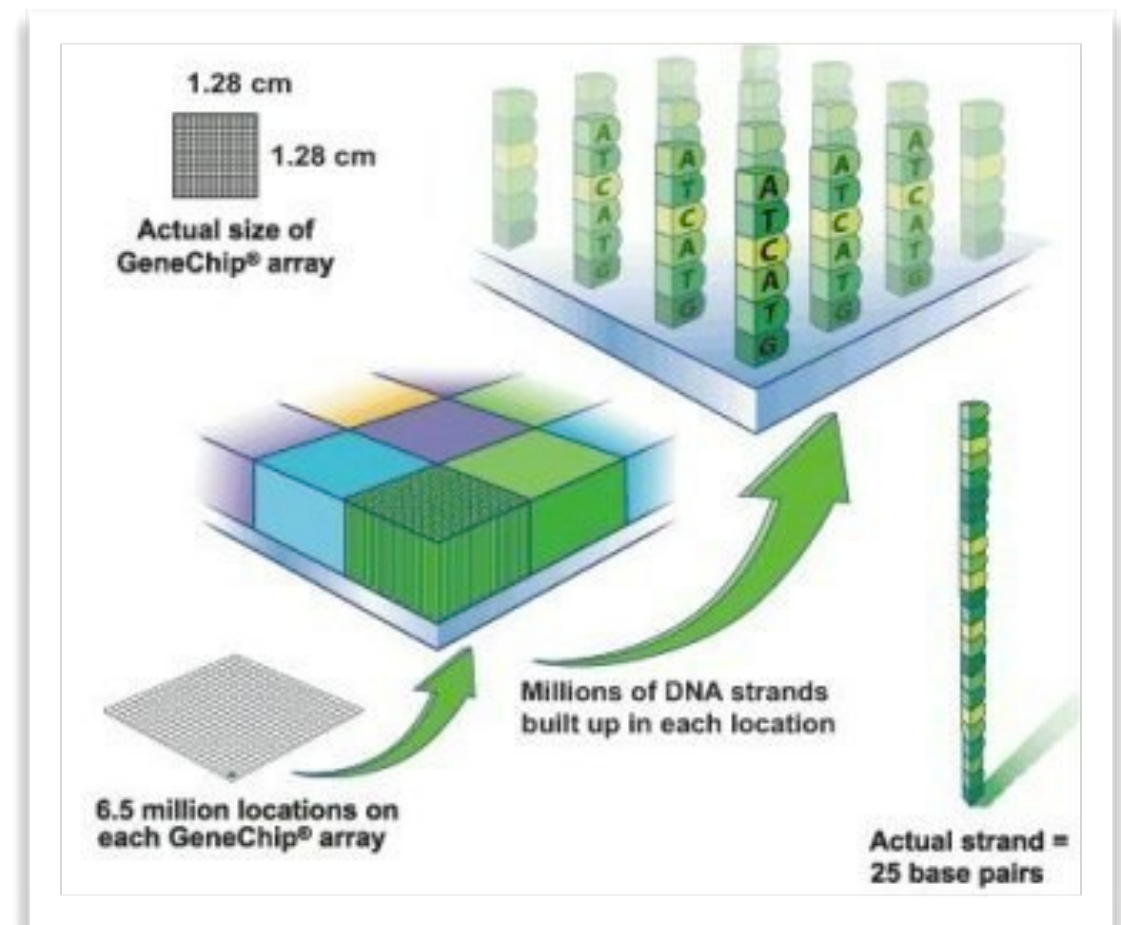
DNA origami



+



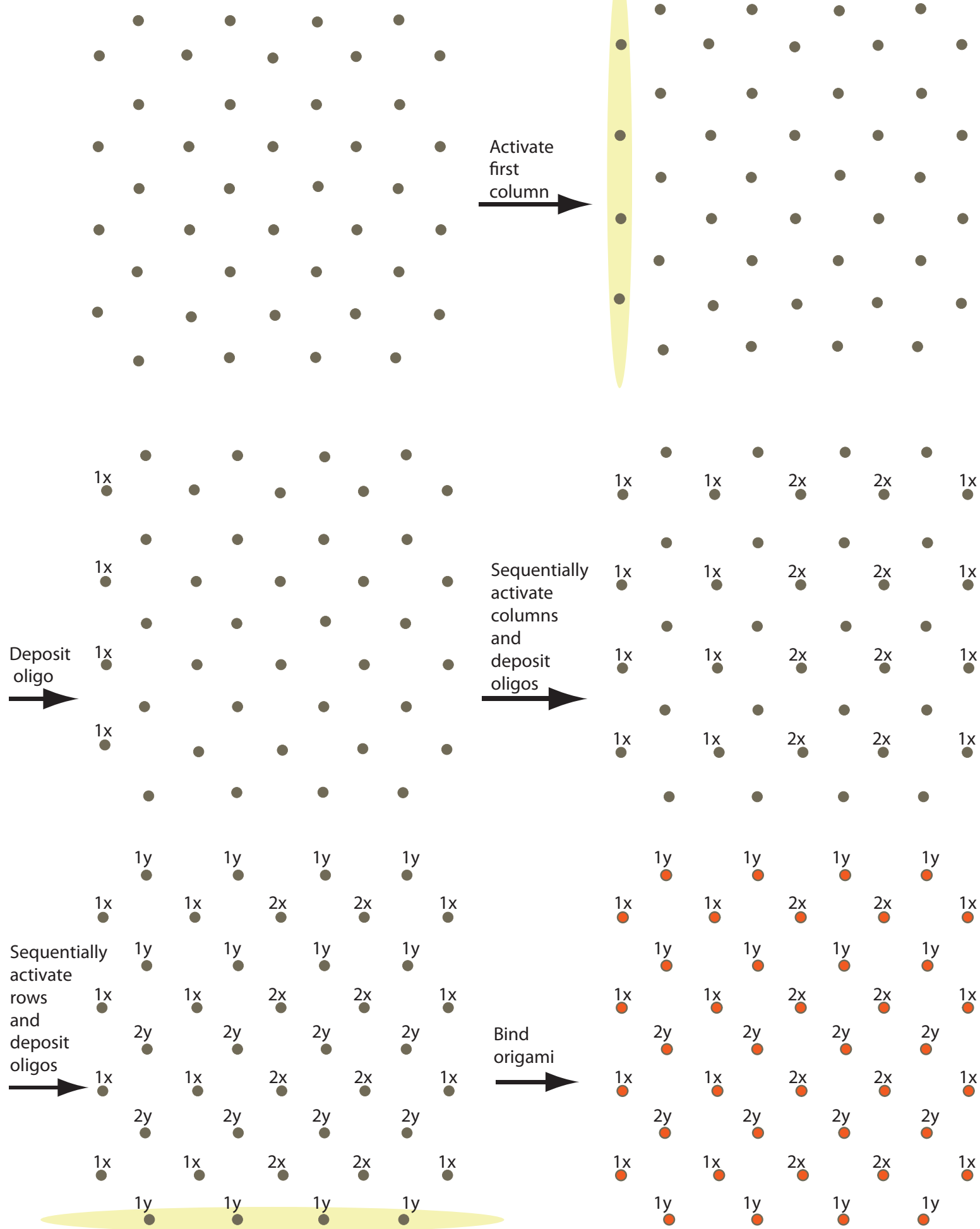
+



= **chip-scale** programmable nano-fabrication

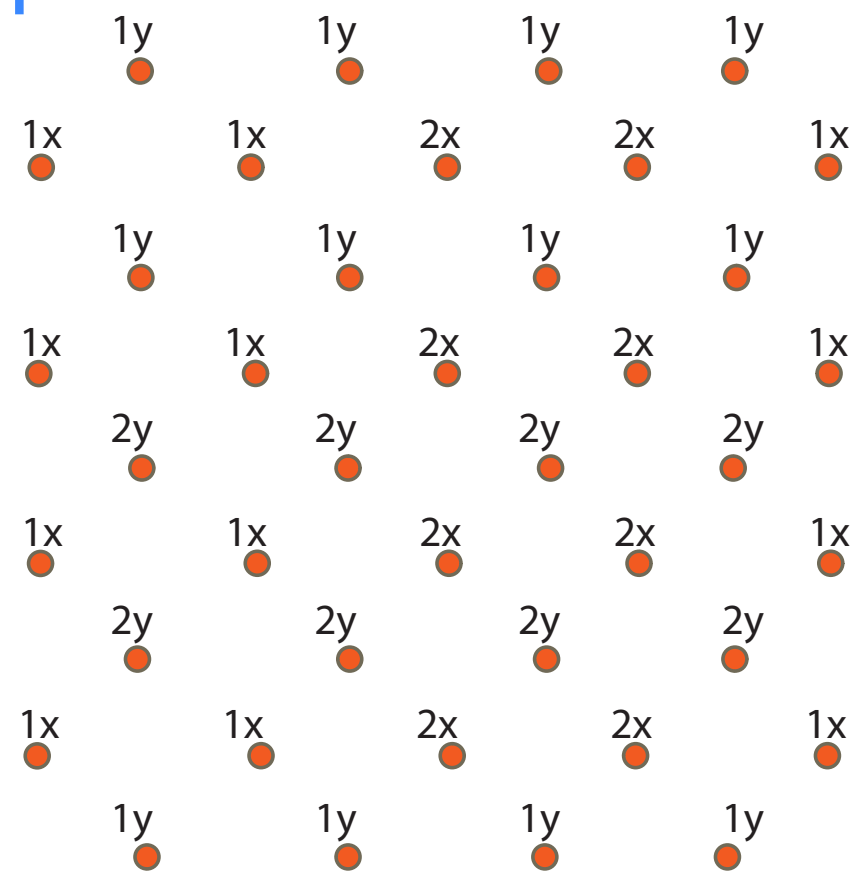
early “nm2cm”

Interferometric array

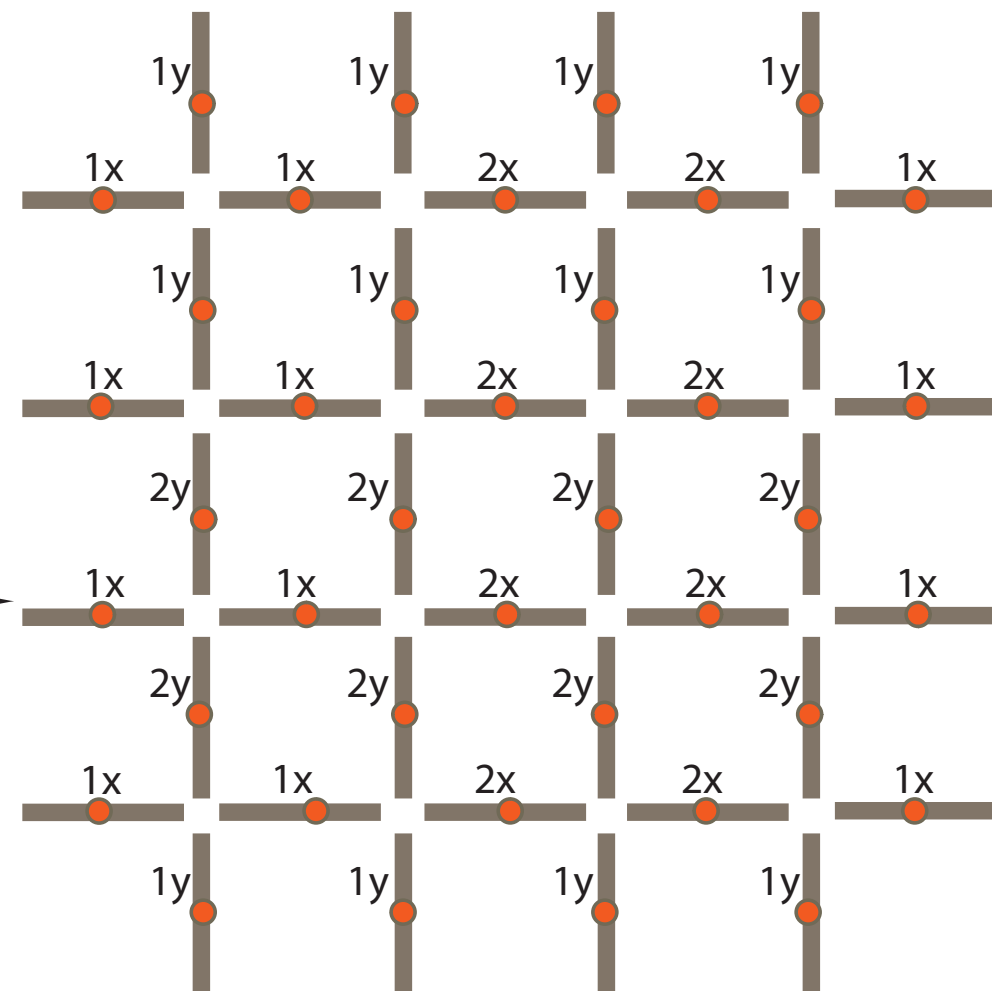


early “nm2cm”

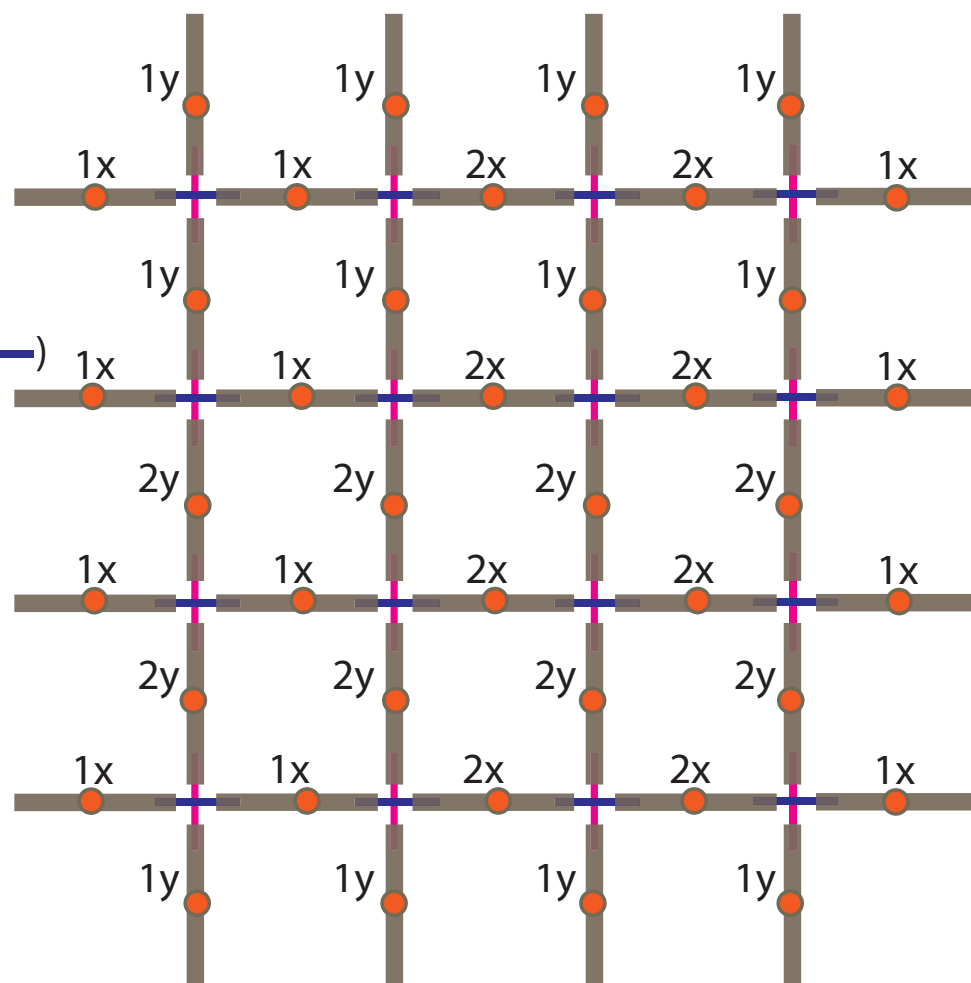
DNA
nano-array
synthesis
→



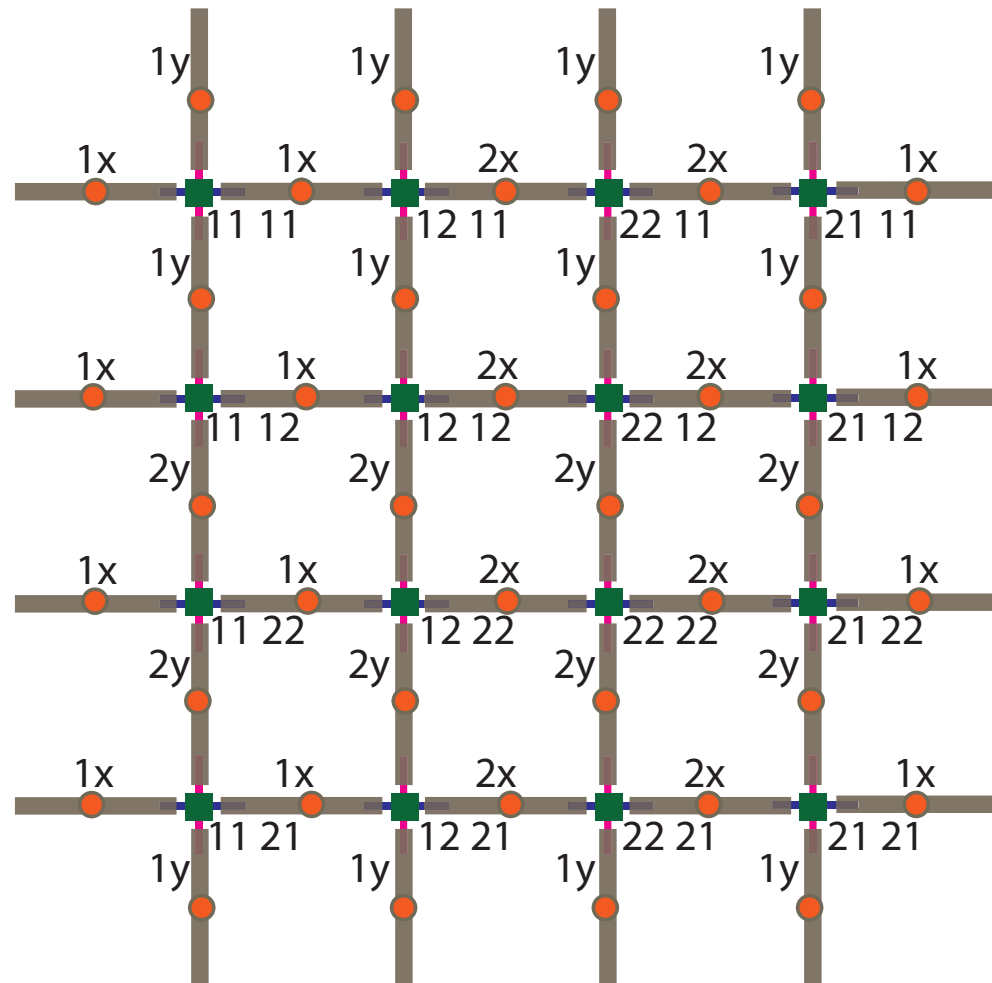
Bind DNA
nano-rods
→



Add
vertical (|) and
horizontal (—) rod
coupling
DNAs (RCDs)
→



Add
2nd order
rod
coupling
DNAs (■)
(to couple
RCD pairs)
→



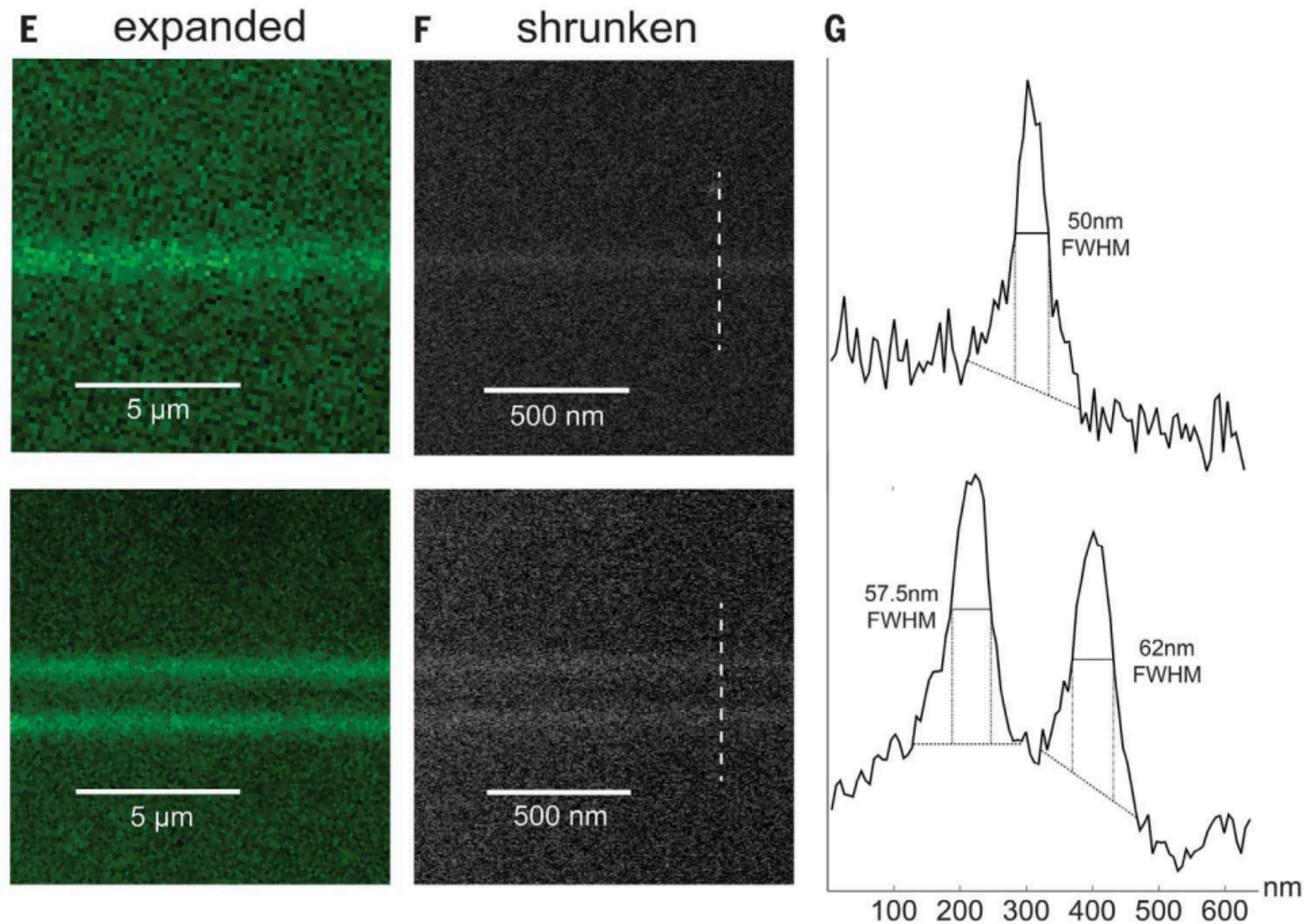
How to combine “top-down” with “bottom-up” in nanotechnology?



3D nanofabrication by volumetric deposition and controlled shrinkage of patterned scaffolds

Daniel Oran^{1,*}, Samuel G. Rodrigues^{1,2,*}, Ruixuan Gao¹, Shoh Asano^{1,3}, Mark A. Skylar-Scott^{4,5}, Fei Chen^{1,6}, Paul W. Tillberg^{1,7,†}, Adam H. Marblestone^{1,‡}, Edward S. Boyden^{1,6,8,9,10,‡,§}

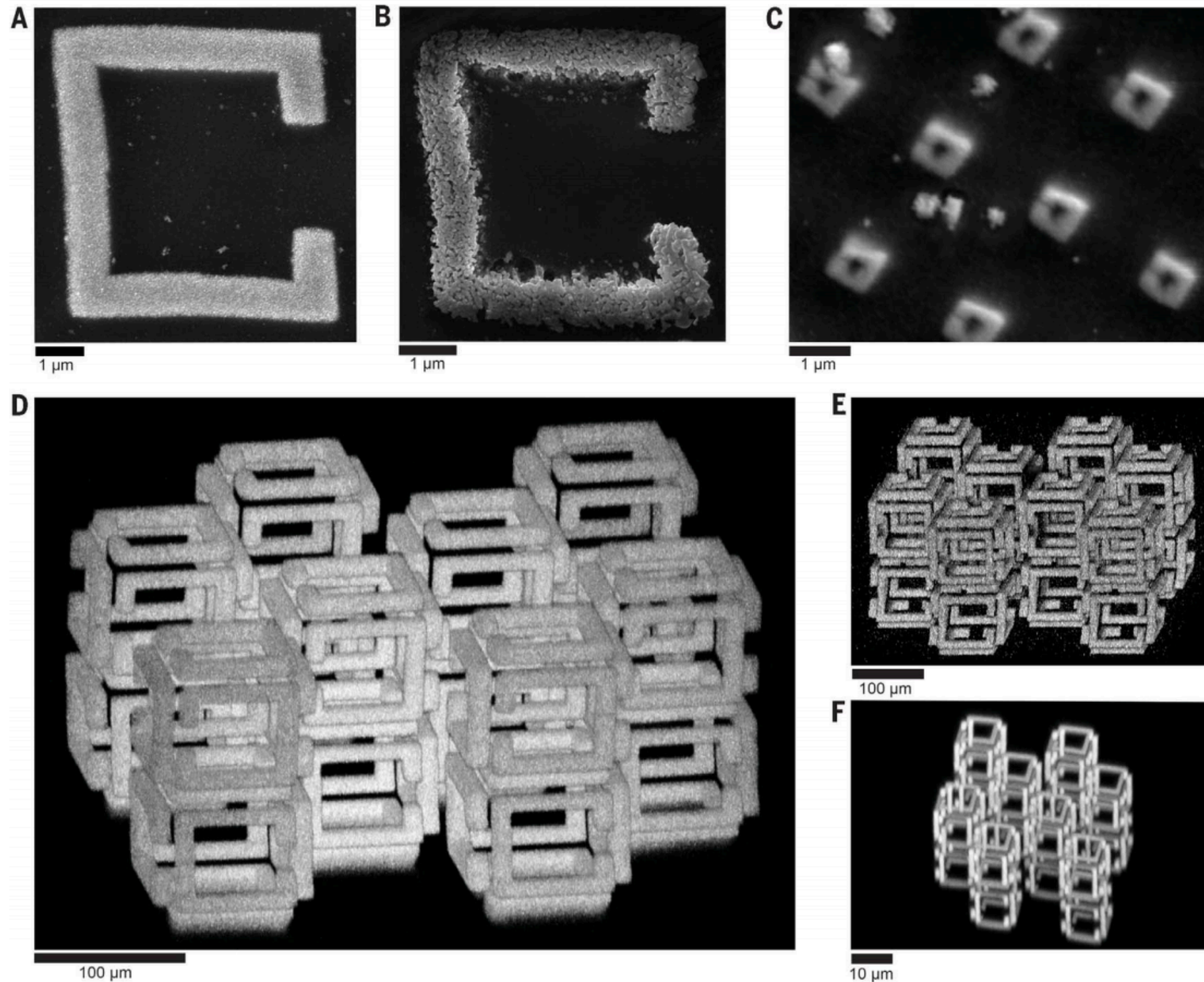
How to combine “top-down” with “bottom-up” in nanotechnology?



3D nanofabrication by volumetric deposition and controlled shrinkage of patterned scaffolds

Daniel Oran^{1,*}, Samuel G. Rodrigues^{1,2,*}, Ruixuan Gao¹, Shoh Asano^{1,3}, Mark A. Skylar-Scott^{4,5}, Fei Chen^{1,6}, Paul W. Tillberg^{1,7,†}, Adam H. Marblestone^{1,‡}, Edward S. Boyden^{1,6,8,9,10,‡,§}

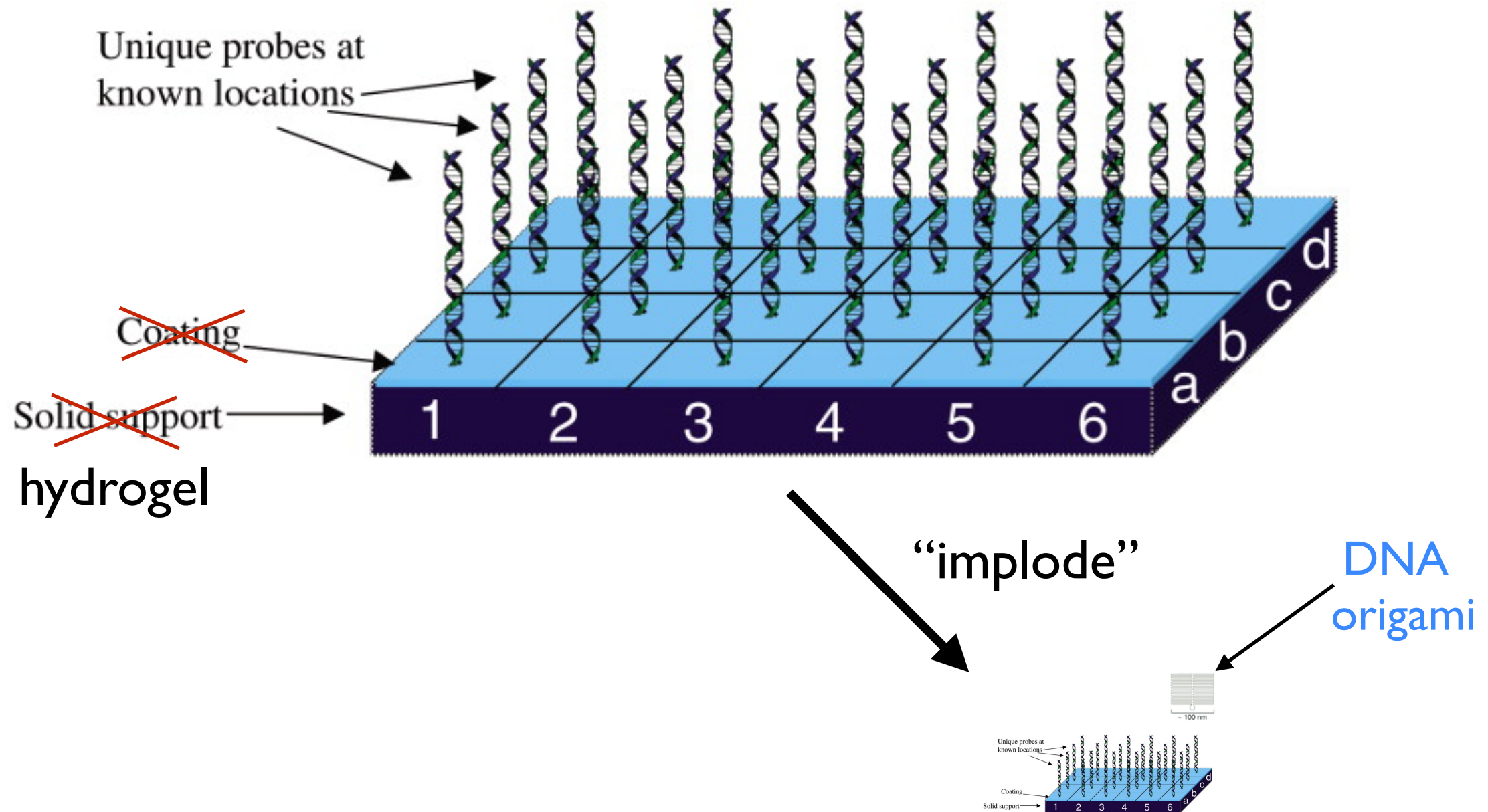
How to combine “top-down” with “bottom-up” in nanotechnology?



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DNA origami

$x, y, z \sim 5-10 \text{ nm}$

DNA base spacing = 0.3 nm

helical diameter = 2 nm

orderly manner on solid substrates^{11,12}. So far, few objects afford a design accuracy better than 5 nm¹³⁻¹⁶, and the sub-nanometre scale has been reached only within the unit cells of designed DNA crystals¹⁷. Here, we report a molecular position-

$X, Y, Z > 100 \text{ nm}$

$c \sim \text{no practical limit}$

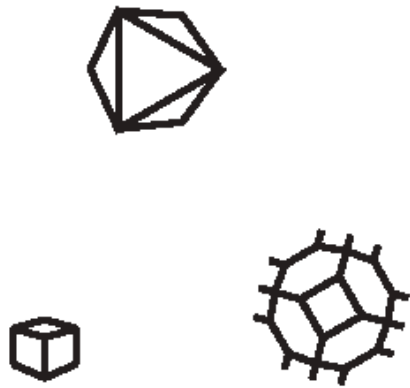
NOT quite *small* enough for covalent “APM”

NOT quite *big* enough for integration into devices

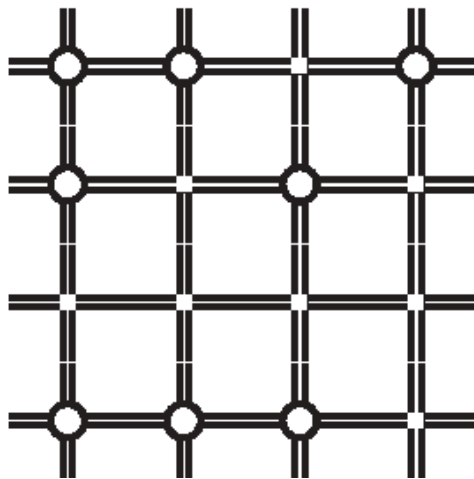
Going smaller...

previous work

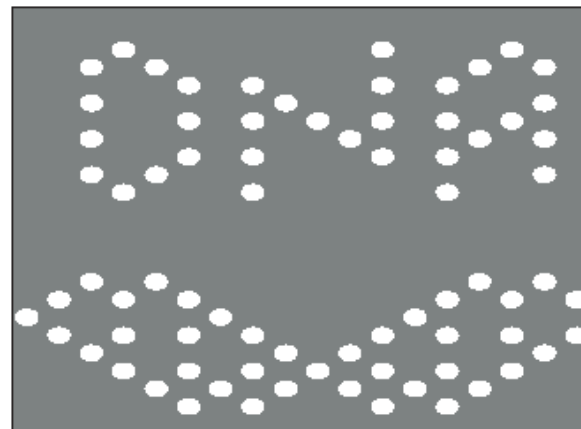
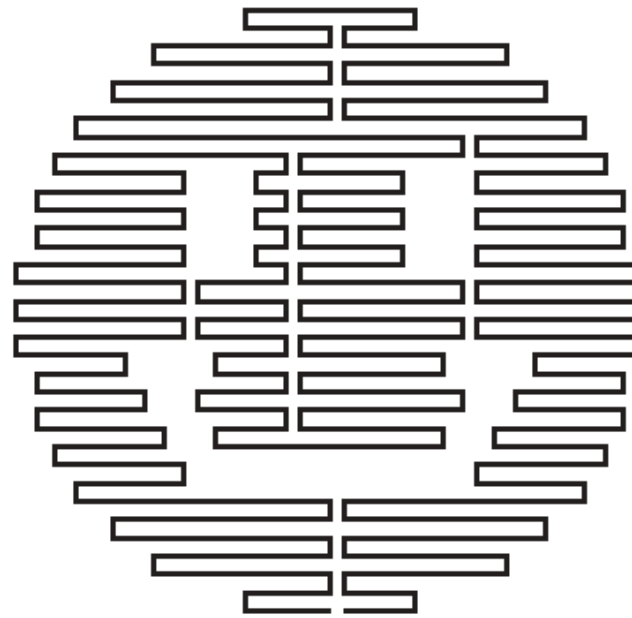
shapes



patterns



scaffolded origami



the ribosome



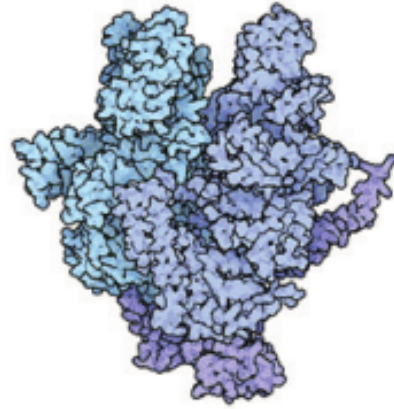
100 nm

top-down patterning

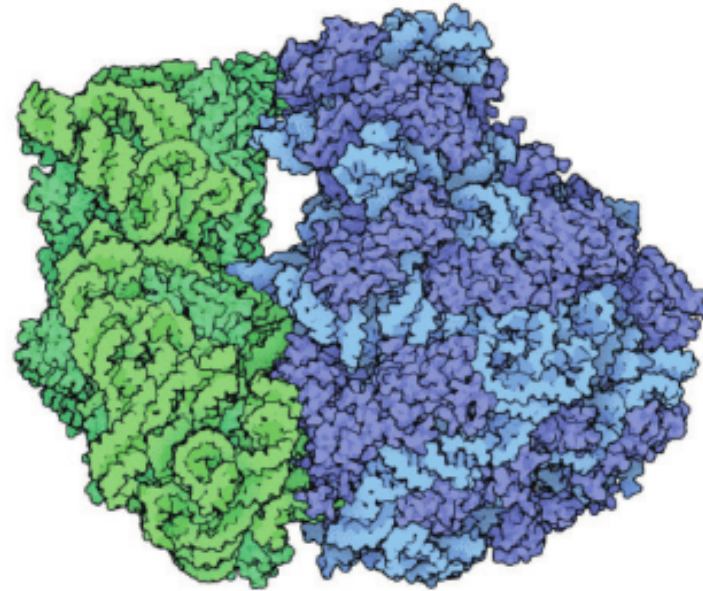
IBM

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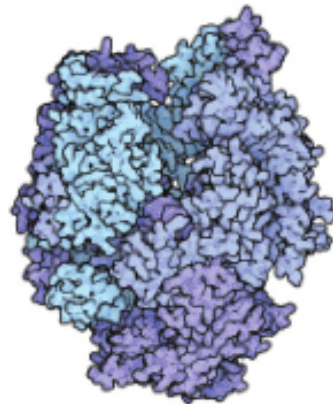
prokaryotic
RNA polymerase (4kmu)



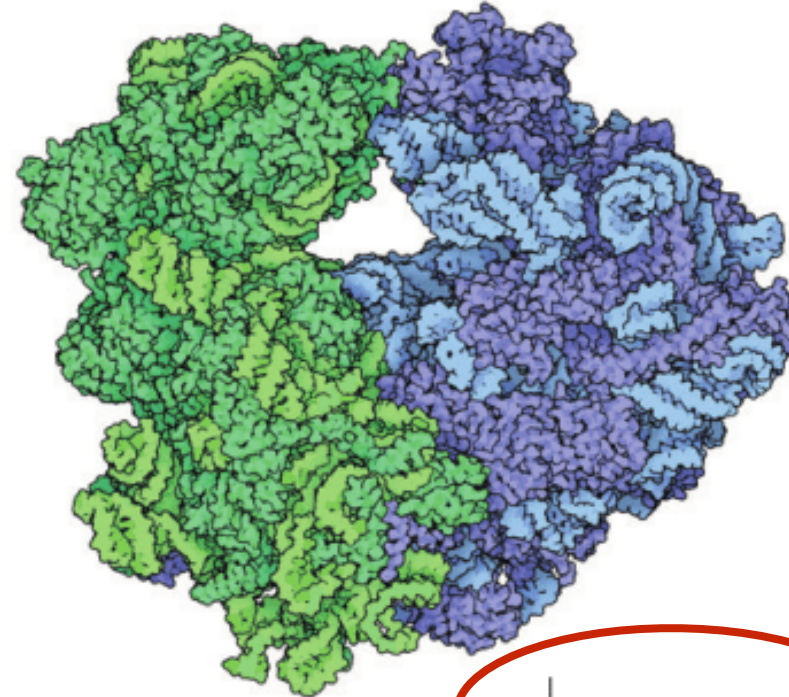
prokaryotic
ribosome (2wdk+2wdl)



eukaryotic
RNA polymerase (1i6h)

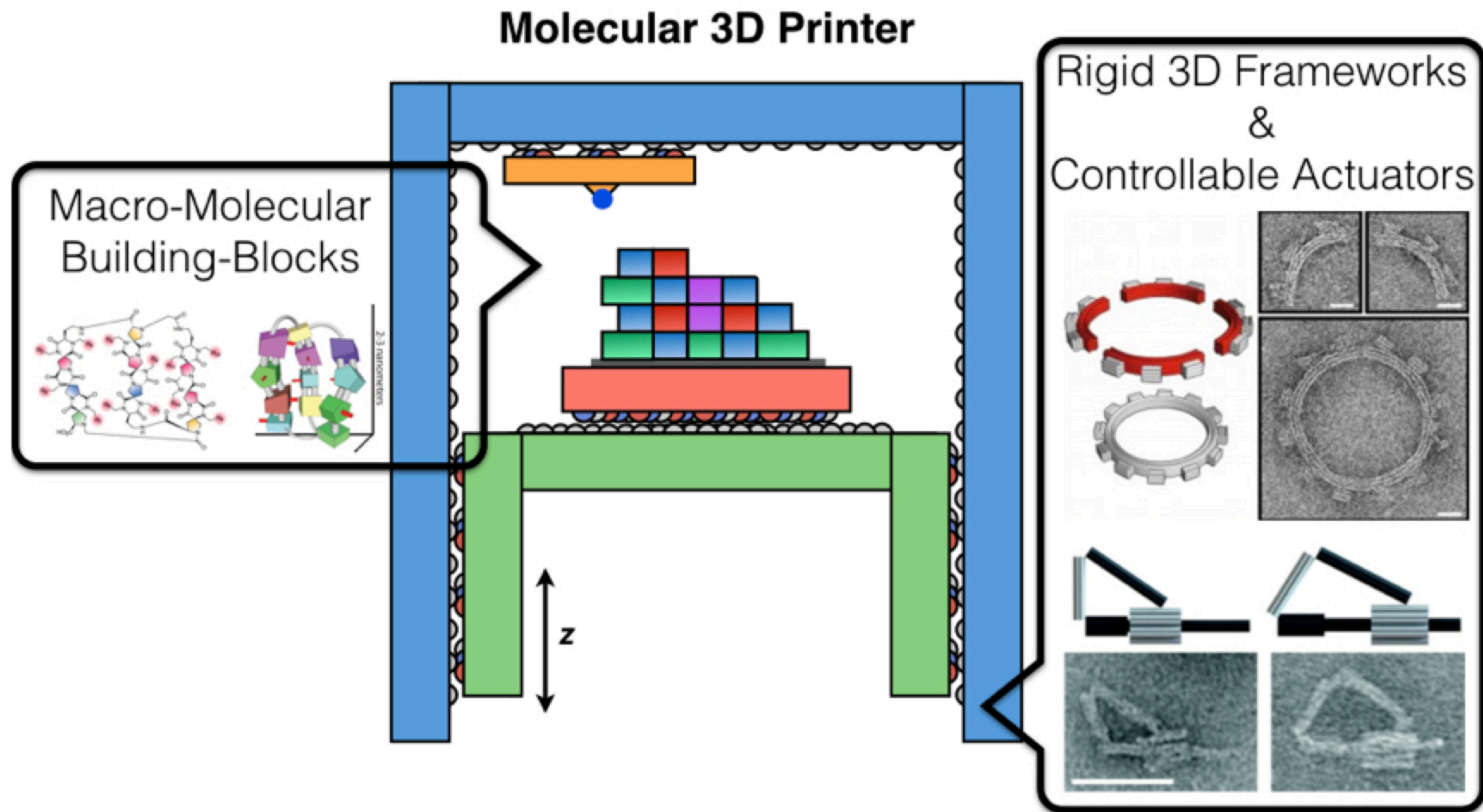


eukaryotic ribosome
(3u5b+3u5c+3u5d+3u5e)

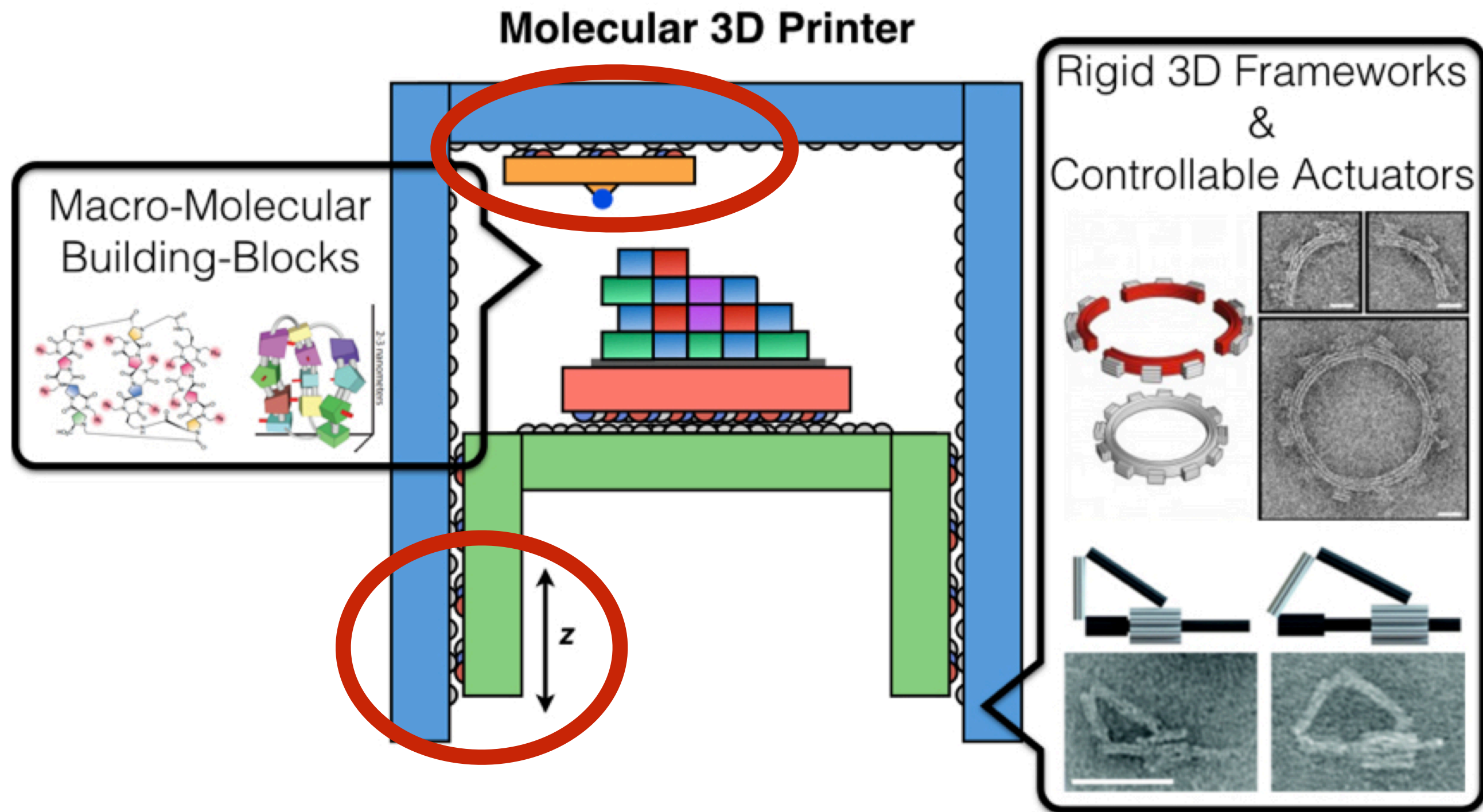


10 nm

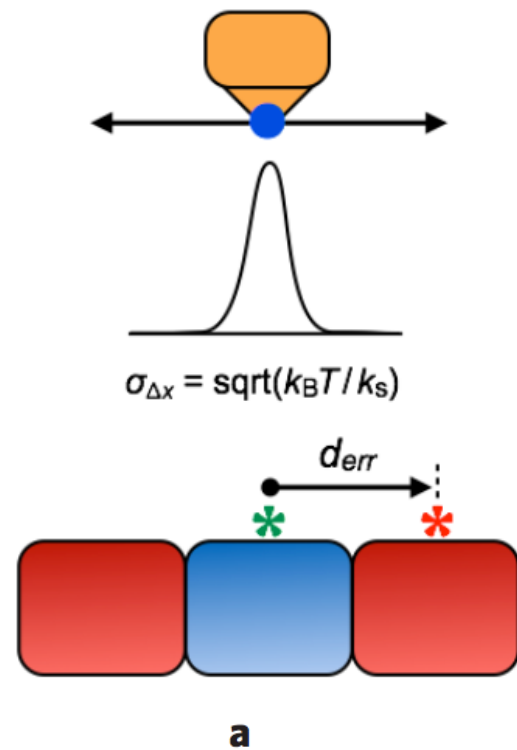
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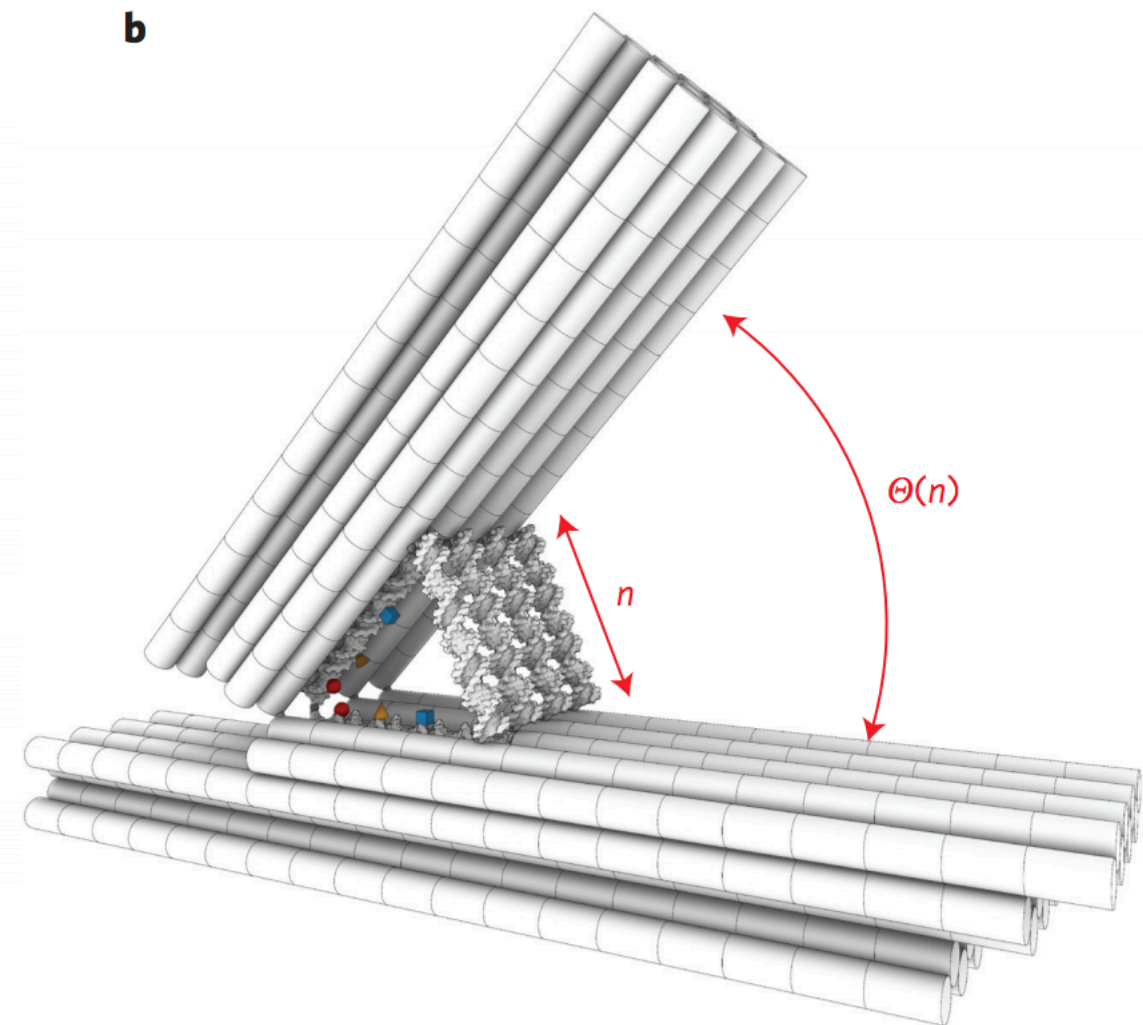
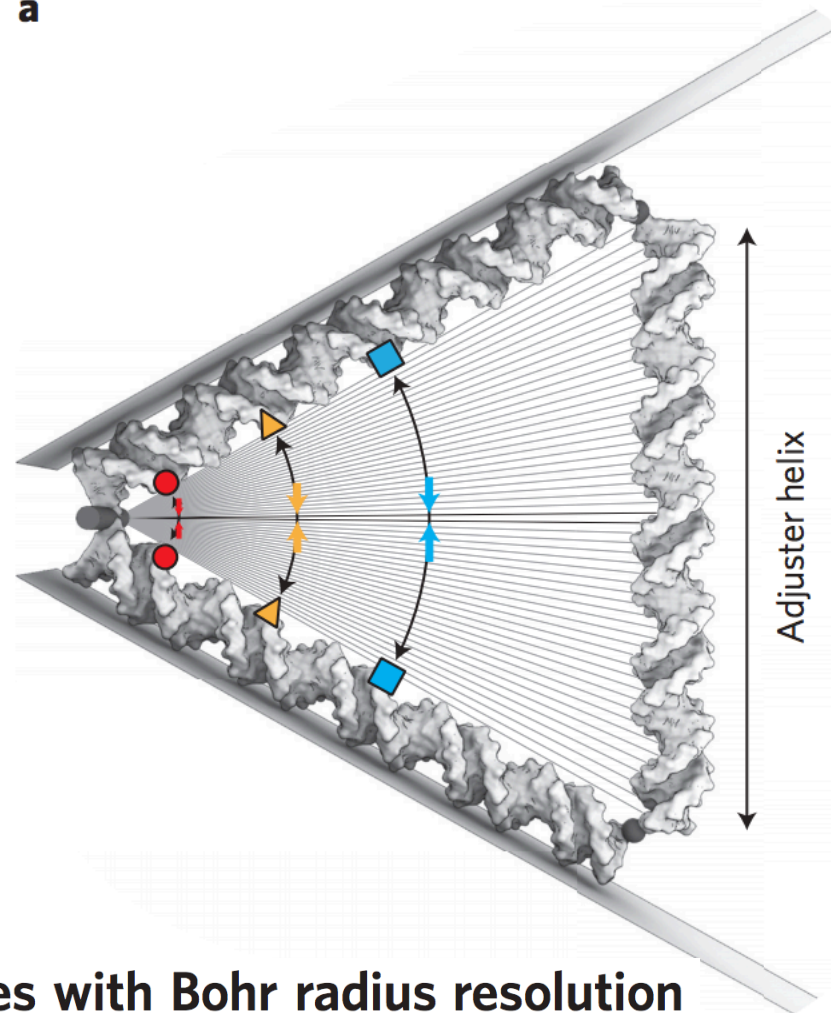
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Going smaller...

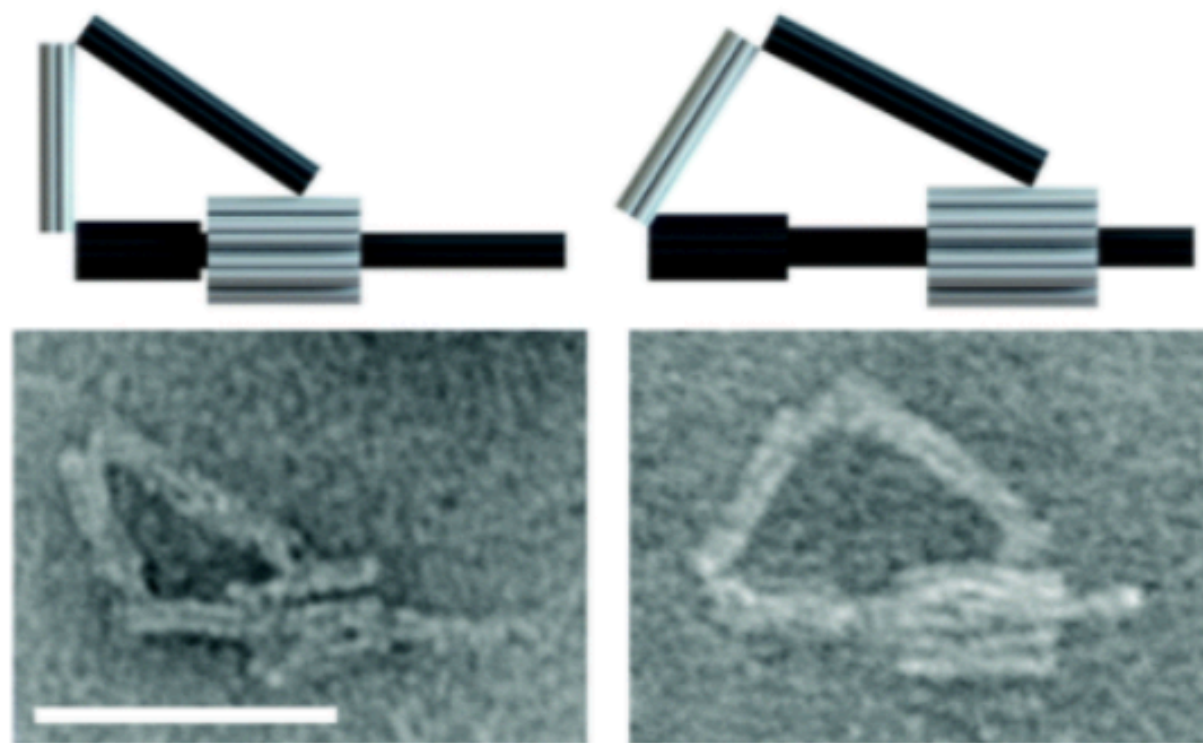
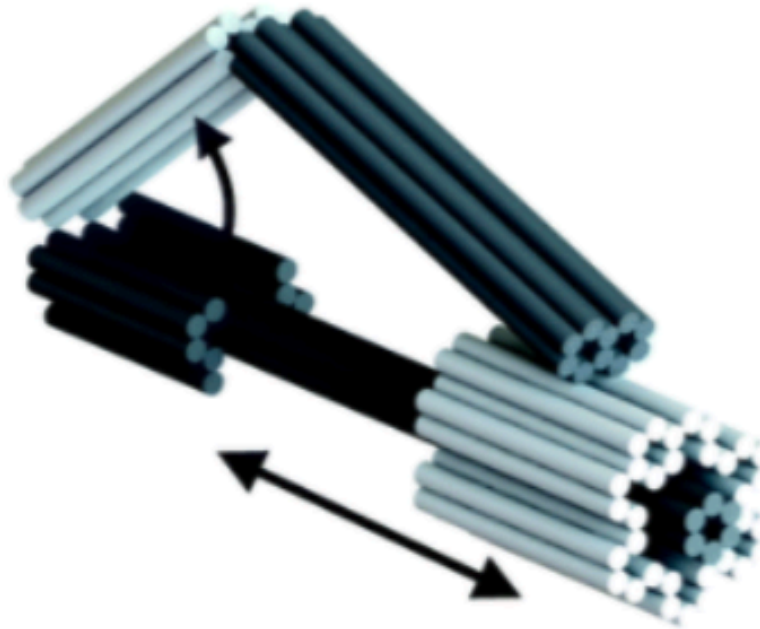
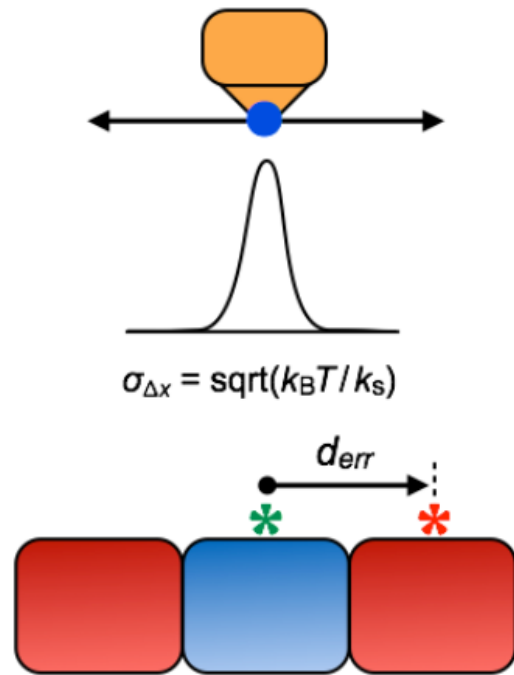


Using this combination of placement and analysis, we rationally adjusted the average distance between fluorescent molecules and reactive groups from 1.5 to 9 nm in 123 discrete displacement steps. The smallest displacement step possible was 0.04 nm, which is slightly less than the Bohr radius. The fluctuation amplitudes in the distance coordinate were also small (± 0.5 nm), and within a factor of two to three of the amplitudes found in protein structures¹⁸.



Placing molecules with Bohr radius resolution using DNA origami

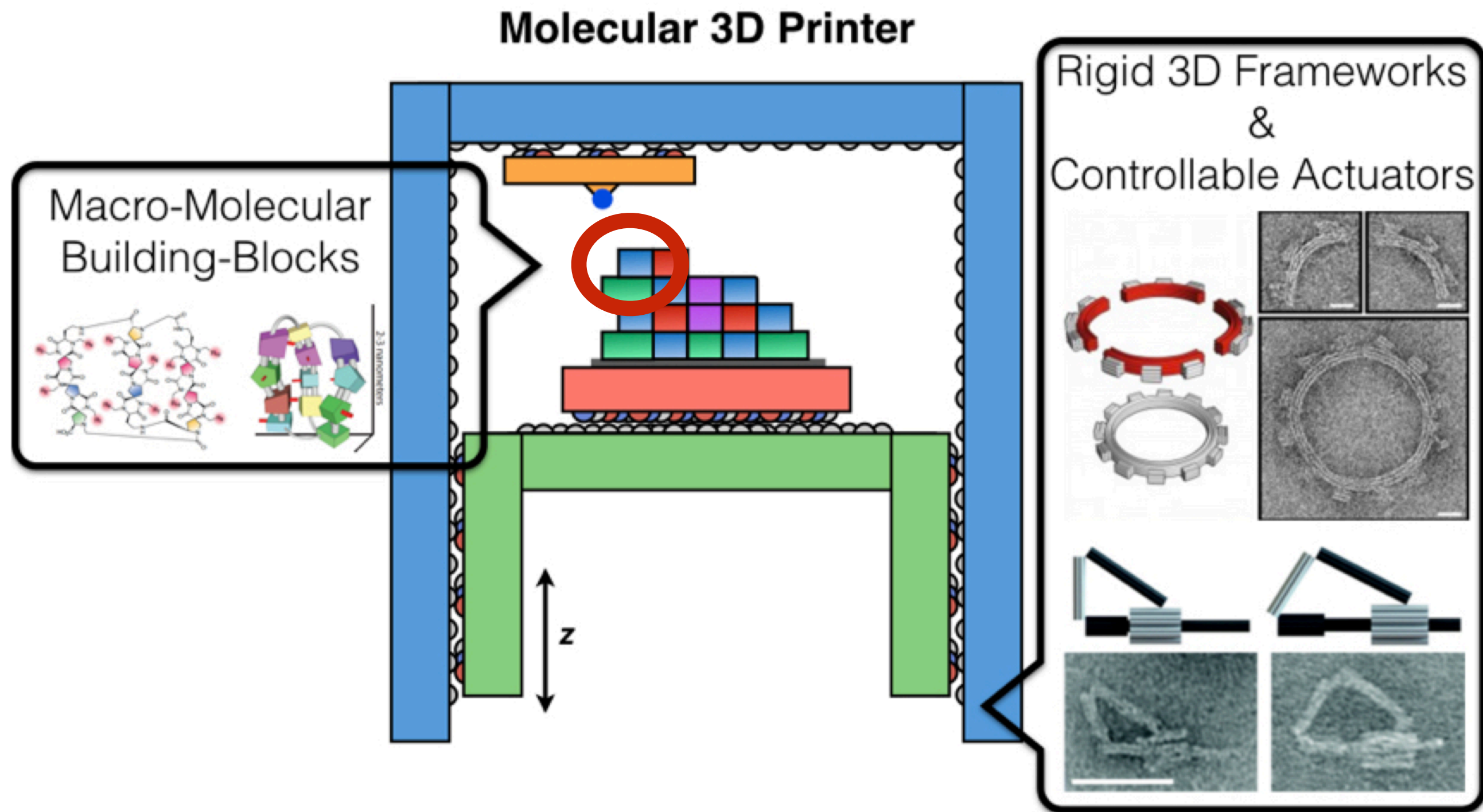
Going smaller...



Programmable motion of DNA origami mechanisms

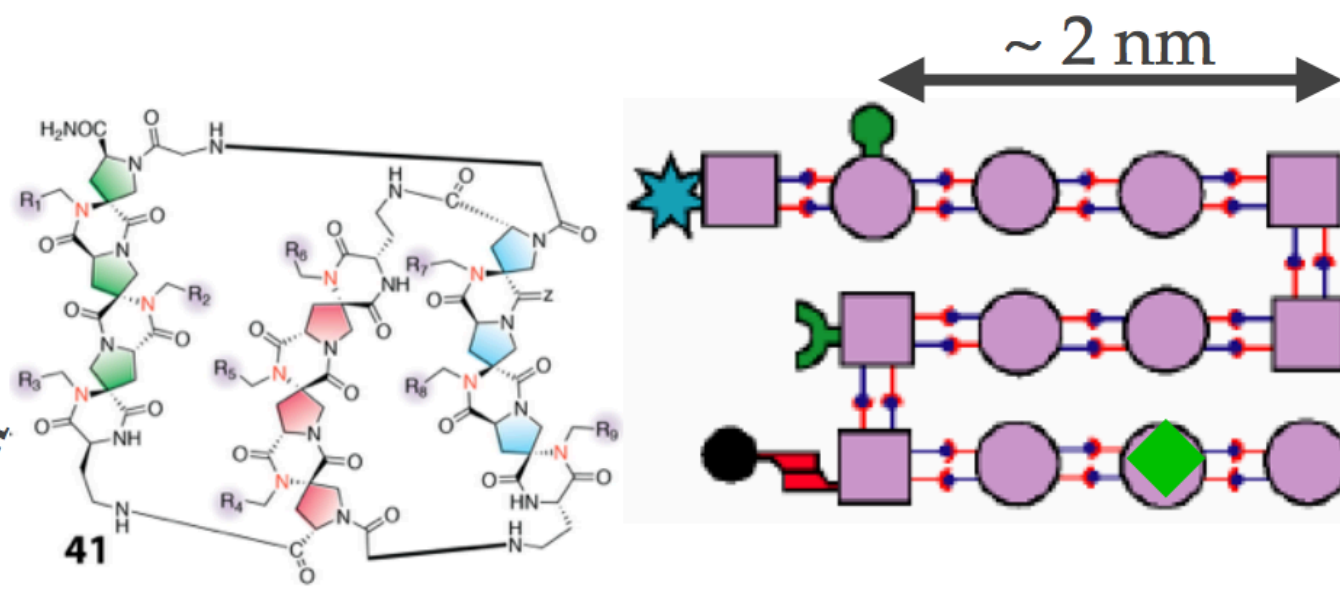
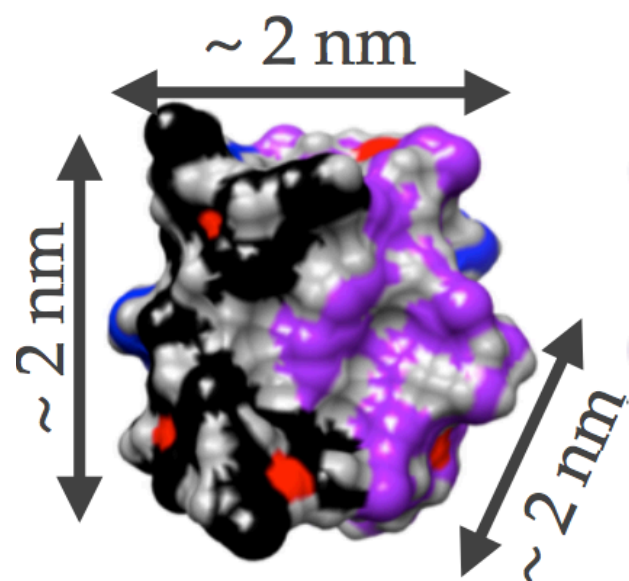
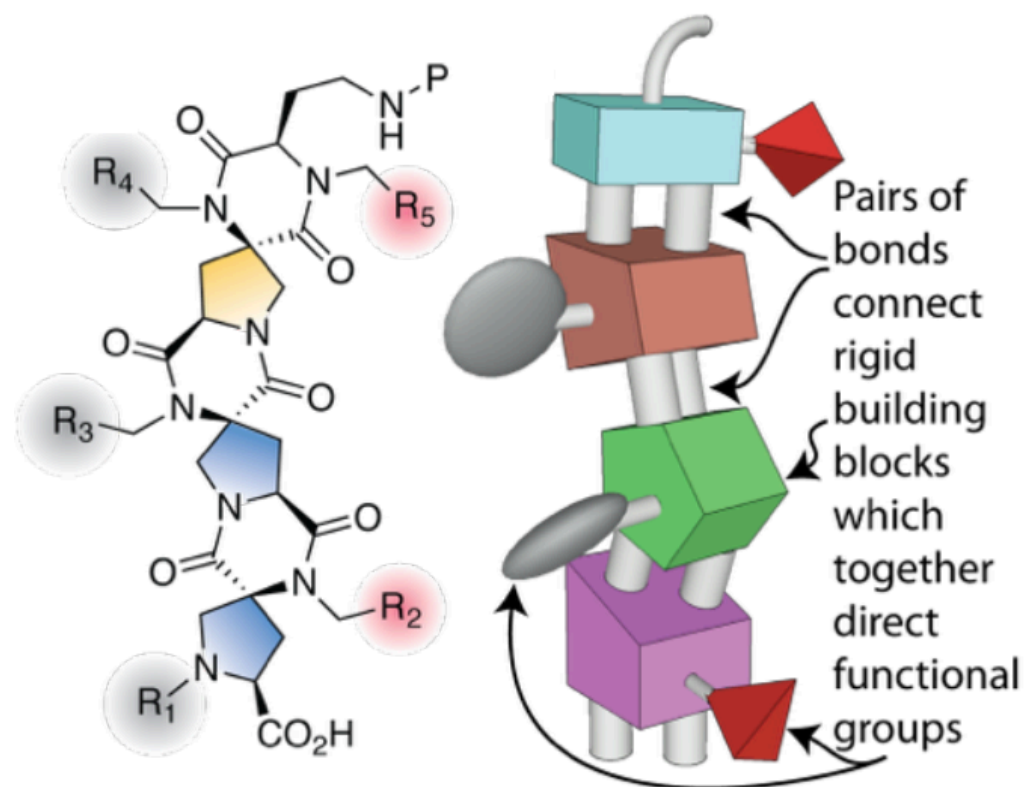
Alexander E. Marras, Lifeng Zhou, Hai-Jun Su, and Carlos E. Castro¹

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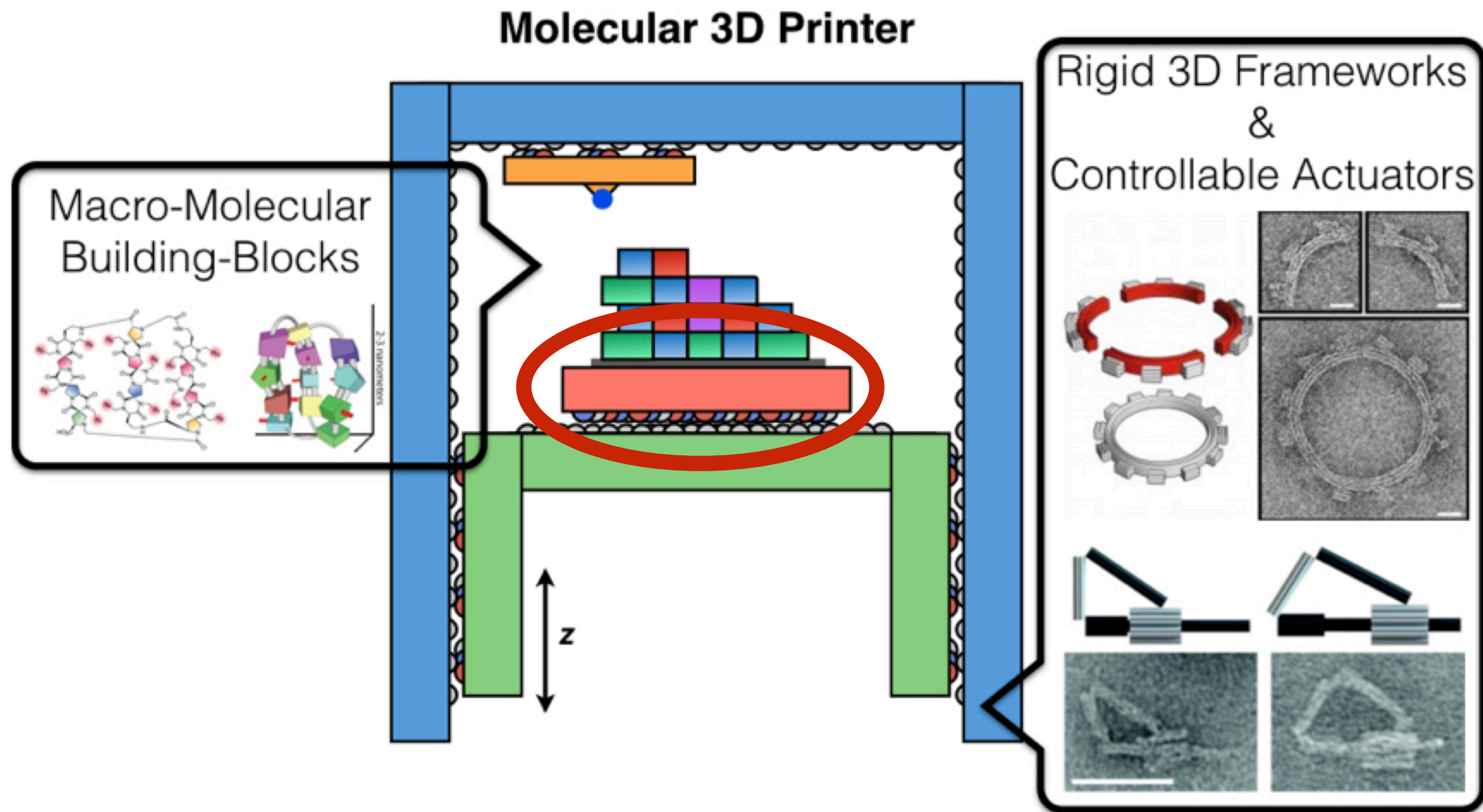


Going smaller...

Spiroligomer “bricks” (Schafmeister):



Going smaller...

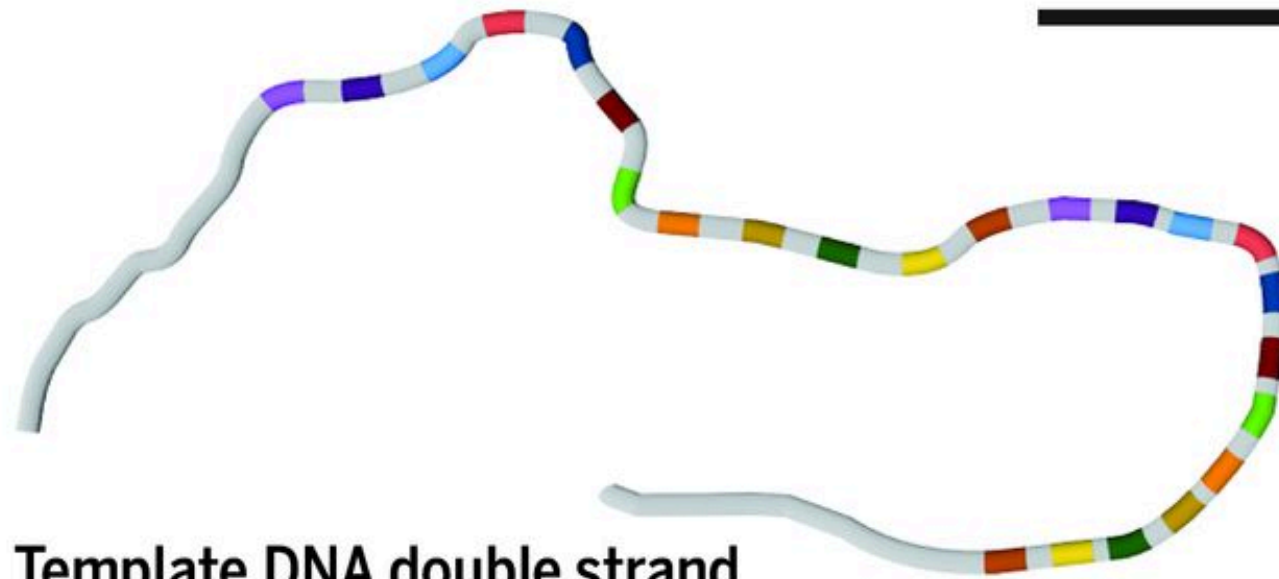
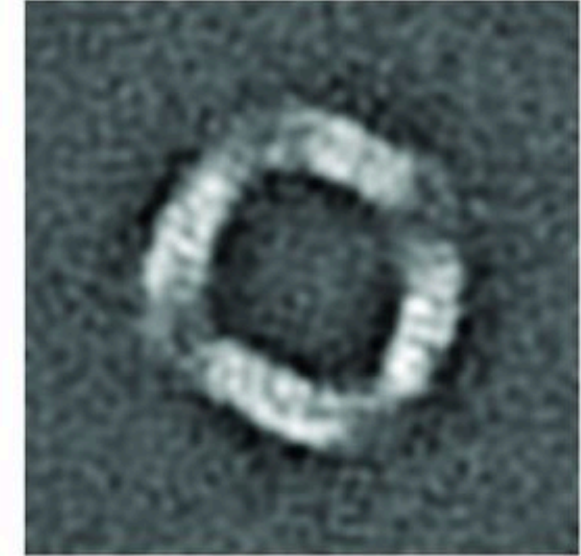
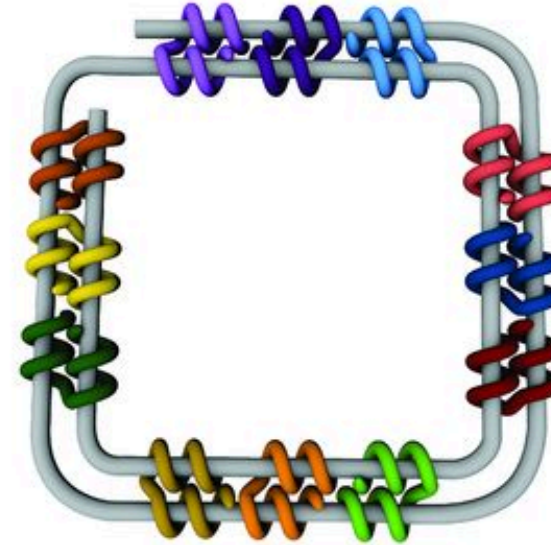


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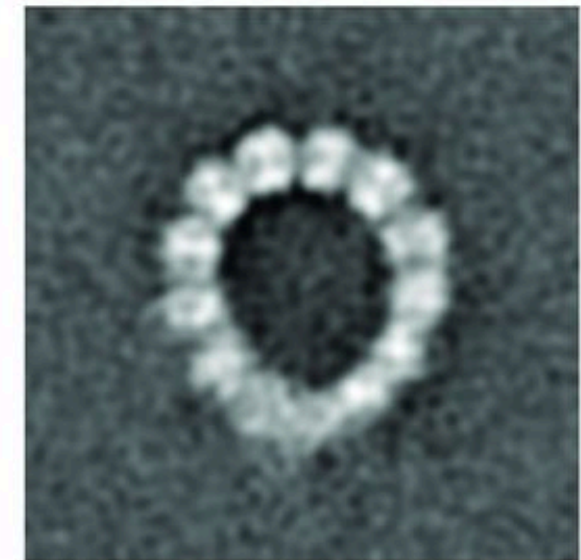
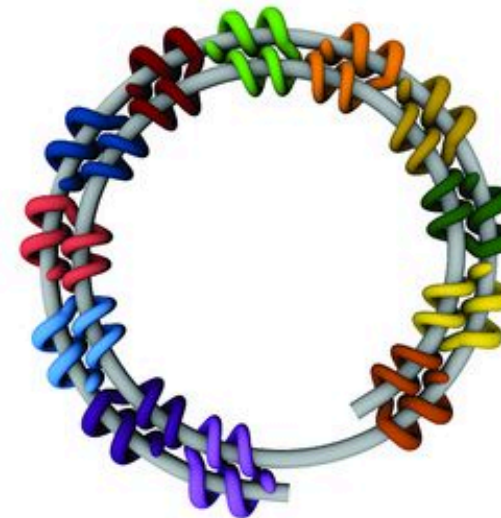
Double-TAL staple proteins



Self-assembly



Template DNA double strand

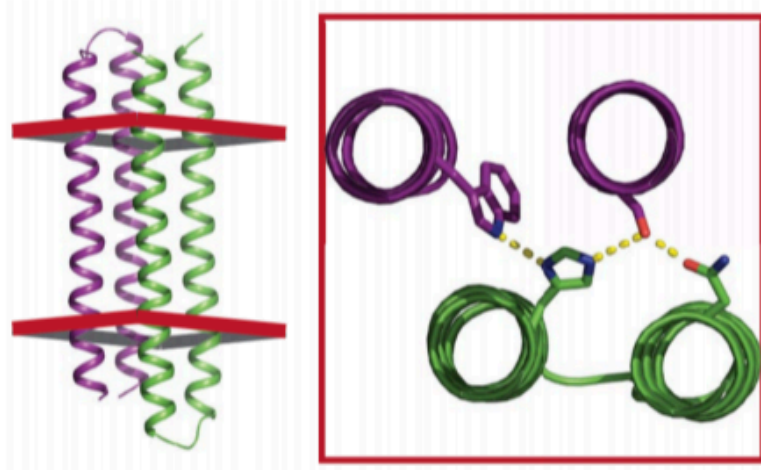


Self-assembly of genetically encoded DNA-protein hybrid nanoscale shapes

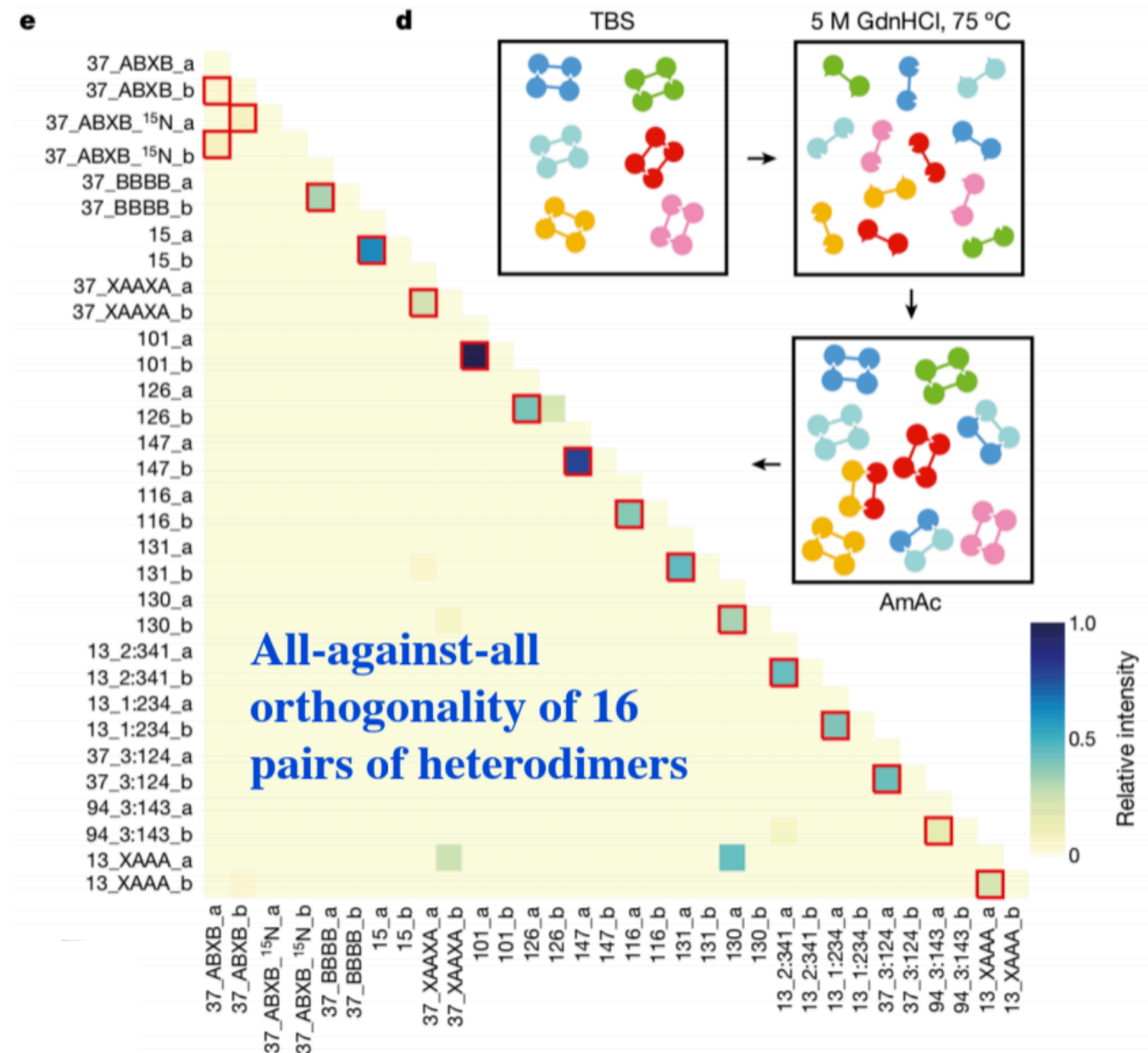
Going smaller...

Design of orthogonal protein heterodimers (Nature, 2018)

...we show that protein–protein **interaction specificity** can be achieved using extensive and **modular side-chain hydrogen-bond networks**.



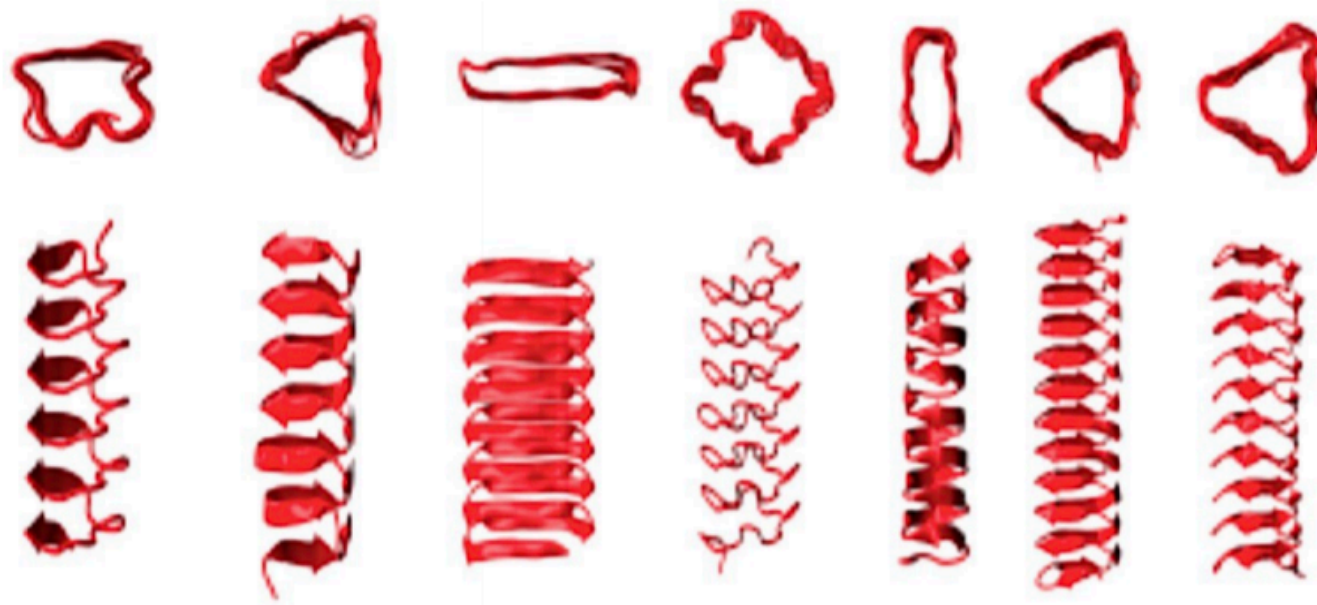
Chen, Z., Boyken, S. E., Jia, M., Busch, F., Flores-Solis, D., Bick, M. J., ... & Bermeo, S. ...Baker, D (2019). Programmable design of orthogonal protein heterodimers. *Nature*, 565(7737), 106-111.



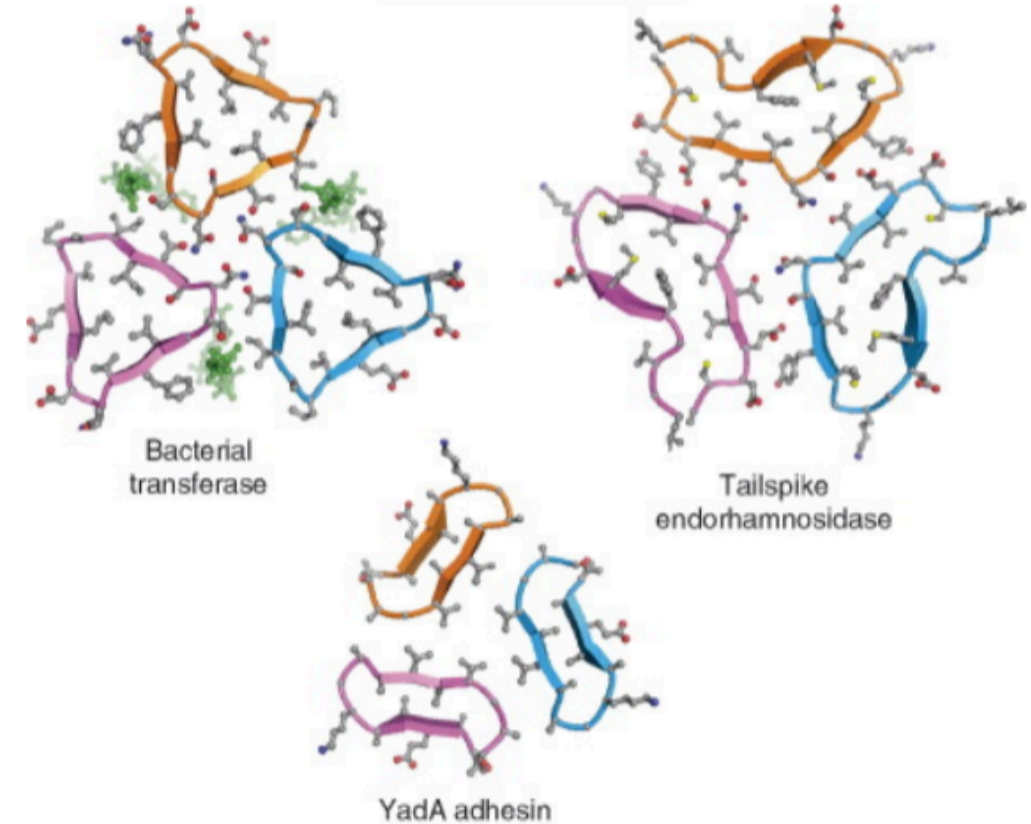
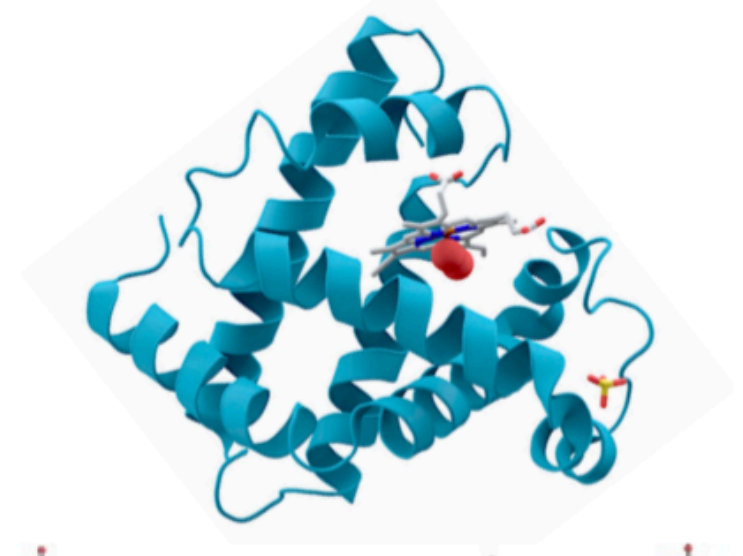
Going smaller... *beta solenoid proteins (BSPs)*

Diverse shapes among natural proteins:

Extensive diversity
even among BSP proteins/domains:

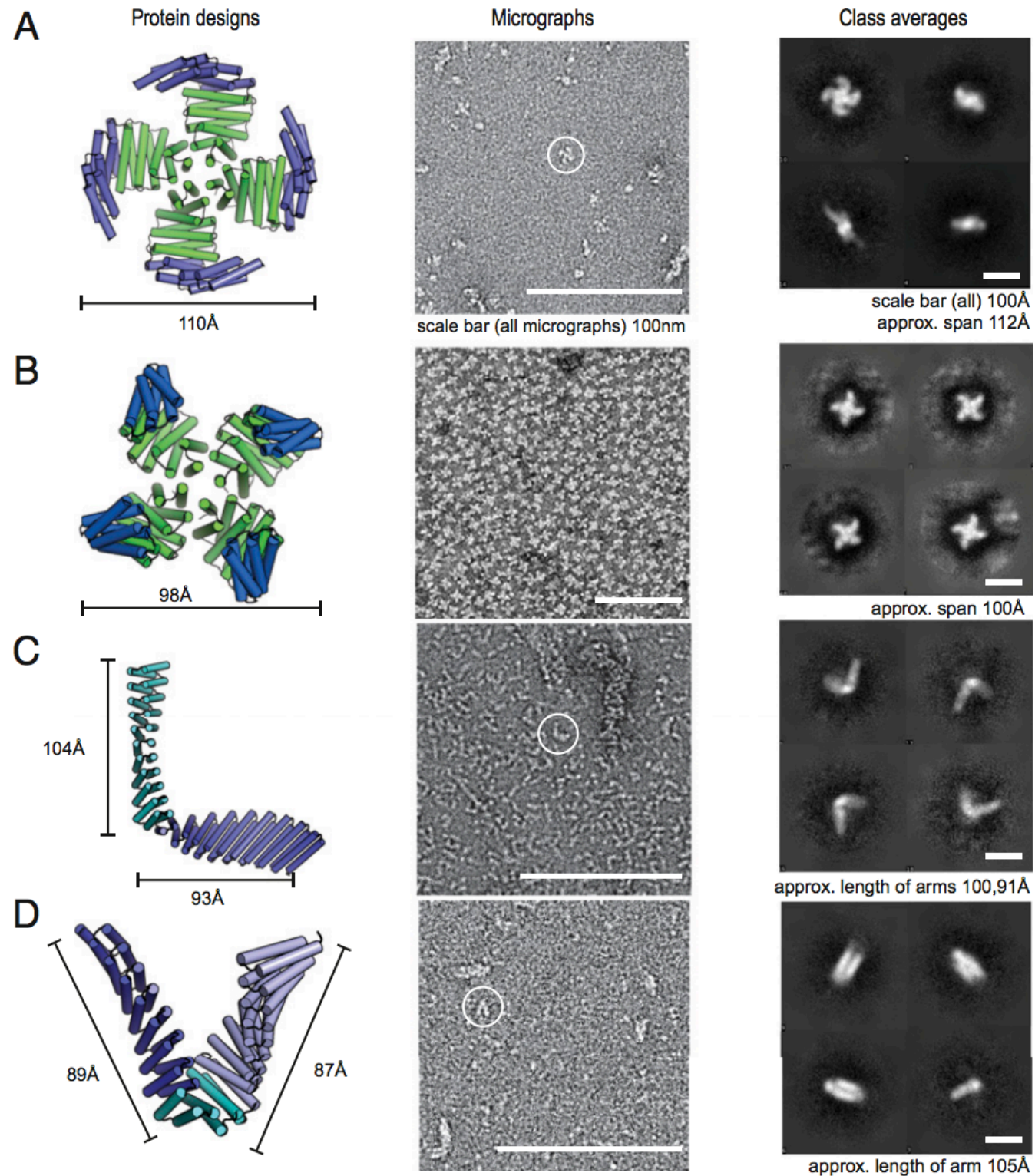


Parker, A., Ravikumar, K., & Cox, D. (2017). Molecular dynamics-based strength estimates of beta solenoid proteins. *Soft matter*, 13(36), 6218-6226.



Kajava, A. V., & Steven, A. C. (2006). β -rolls, β -helices, and other β -solenoid proteins. *Advances in protein chemistry*, 73, 55-96.

Going smaller...



Modular repeat protein sculpting using rigid helical junctions

TJ Brunette^{a,b,1}, Matthew J. Bick^{a,b}, Jesse M. Hansen^{a,c}, Cameron M. Chow^{a,b}, Justin M. Kollman^a, and David Baker^{a,b,d}

Summary

Image:

- Using expansion microscopy and in-situ optical sequencing of DNA, we are on path to “*arbitrary resolution, infinite color microscopy*” for bio
- Sequencing neuron-indexing RNA barcodes this way should allow *full mammalian brain connectomes* for ~\$30M

Construct:

- DNA origami allows ~5 nm patterning of diverse materials over ~100 nm length scales by self-assembly, with trivial/facile design
- We should be able to organize DNA origami into larger systems by patterning them on *shrunk* DNA microarrays
- A “*molecular 3D printer*”, made through various steps involving DNA origami, DNA templating of proteins / peptides, and modular protein engineering with fixed backbones and *programmable interfaces*, could be an interesting first step to explore and demo “APM” principles