

Modular reconfiguration of DNA origami assemblies using tile displacement

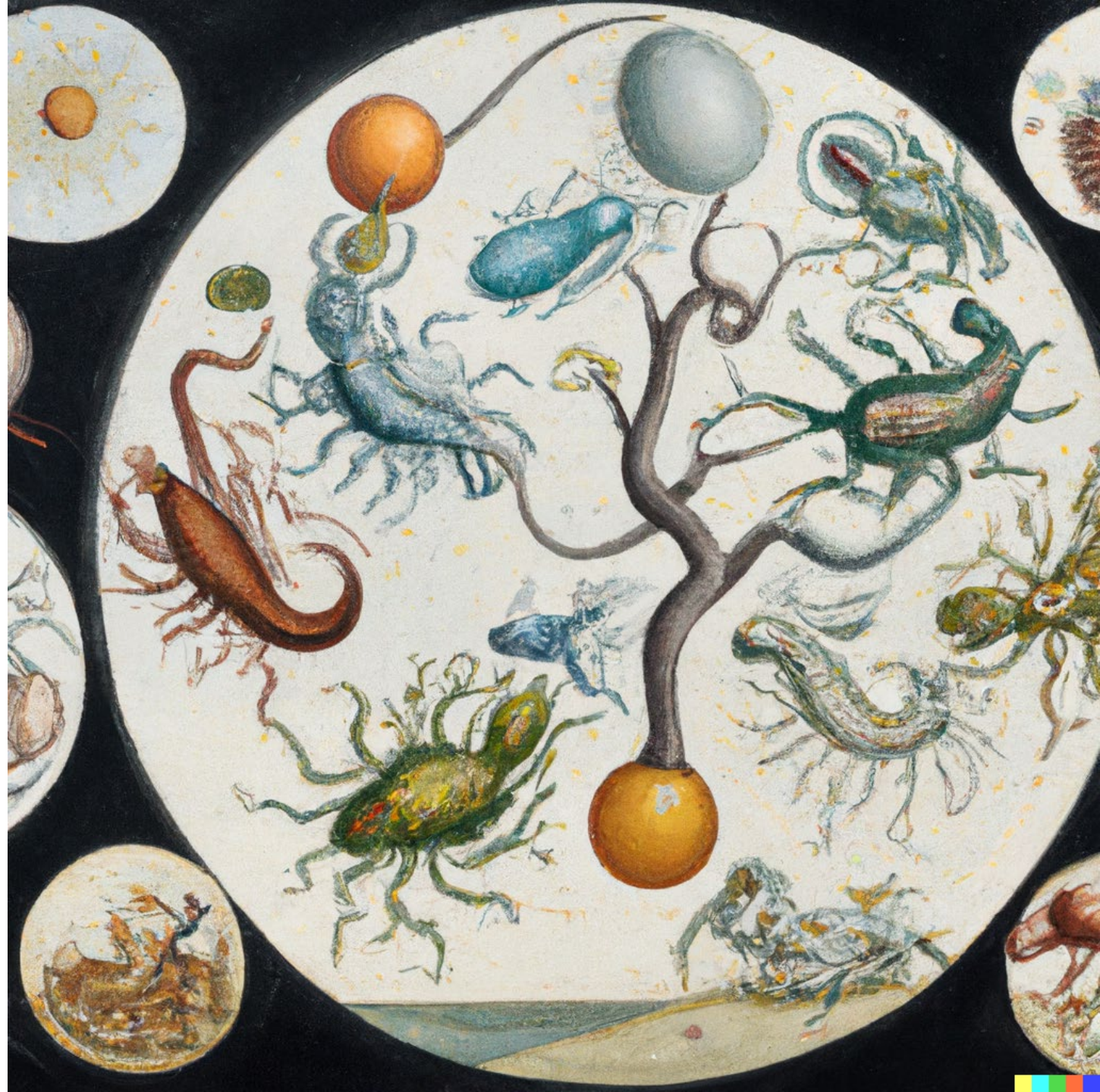
Namita Sarraf, Kellen Rodriguez, and Lulu Qian

Bioengineering
Computer Science
Computation & Neural Systems

Caltech

DNA29, September 14, 2023

The power of natural evolution lies in the adaptability of biological organisms but is constrained by the time scale of genetics and reproduction.



Engineering artificial molecular machines should not only include adaptability as a core feature but also apply it within a larger design space and at a faster time scale.



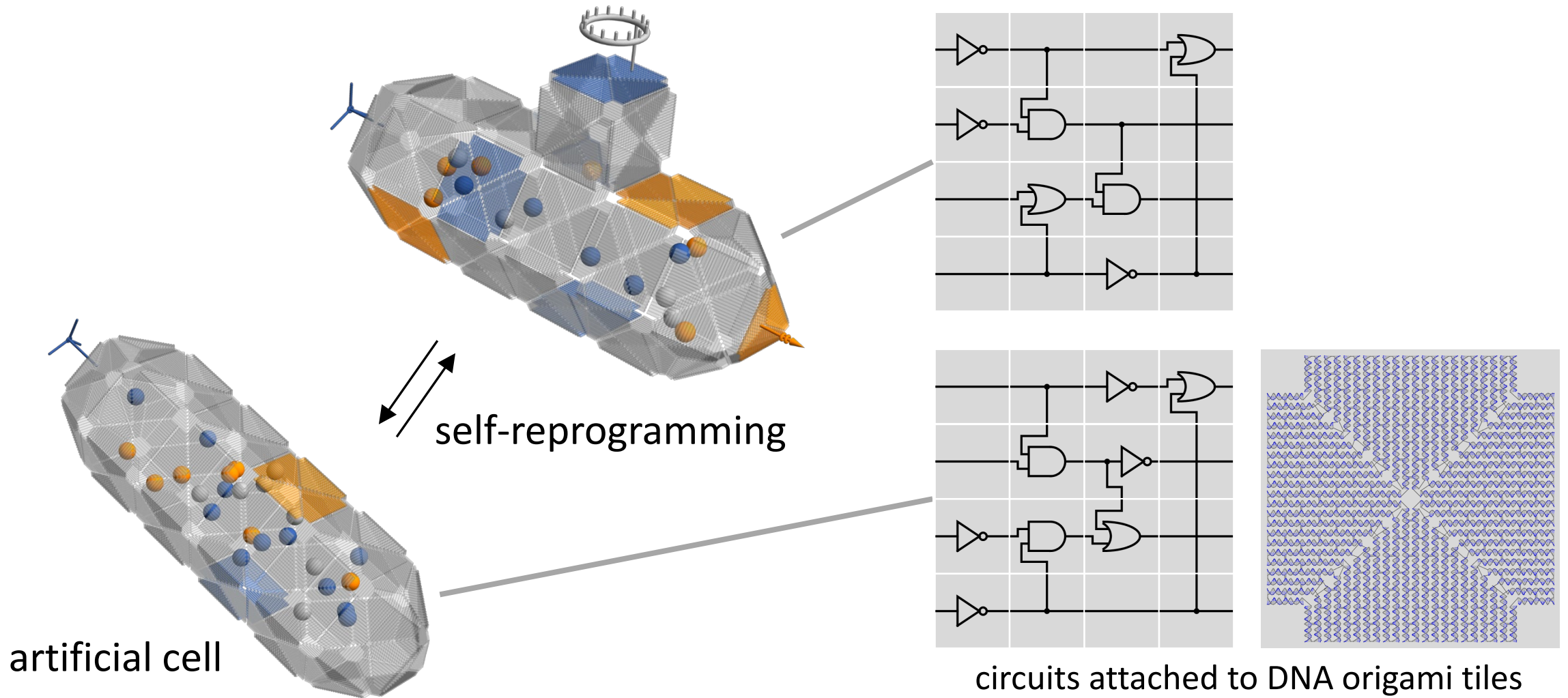
Modular electromechanical robots

CEBOT (Fukuda et al. 1988)
Crystalline (Rus et al. 2001)
MTRAN (Murata et al. 2002)
PolyBot (Yim et al. 2002)
Programmable Parts (Klavins et al. 2005)
Molecubes (Zykov et al. 2005)
SuperBot (Shen et al. 2006)
Miche (Rus et al. 2006)
SMORES (Davey et al. 2012)
M-Block (Romanishin et al. 2015)
ModQuad (Saldana et al. 2018)
⋮

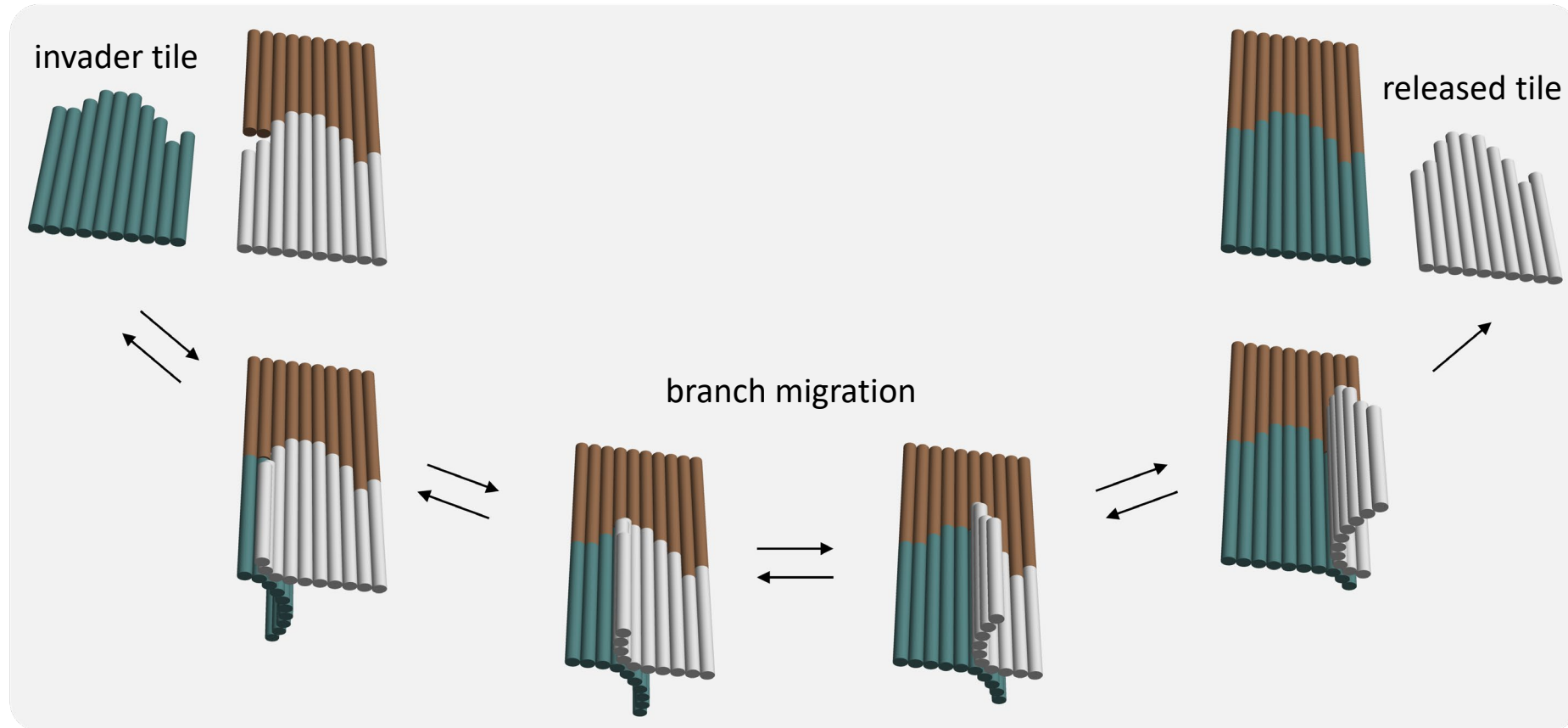


Cubelets

Future cell-scale molecular robots



Concept of DNA tile displacement



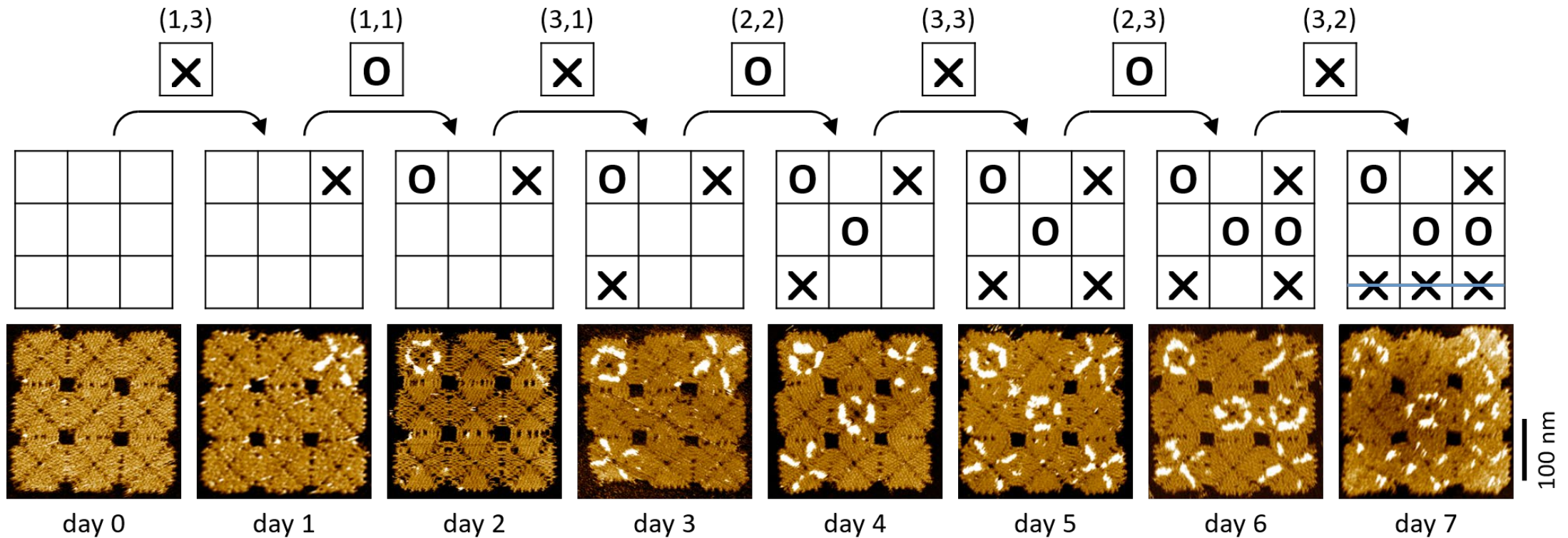
A tic-tac-toe game



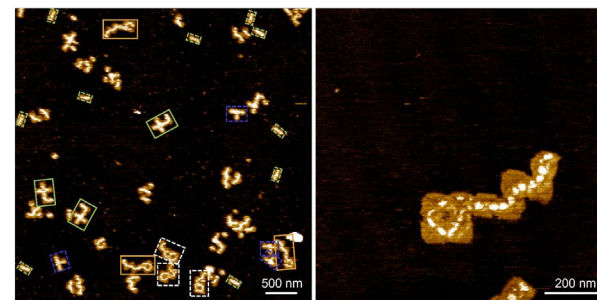
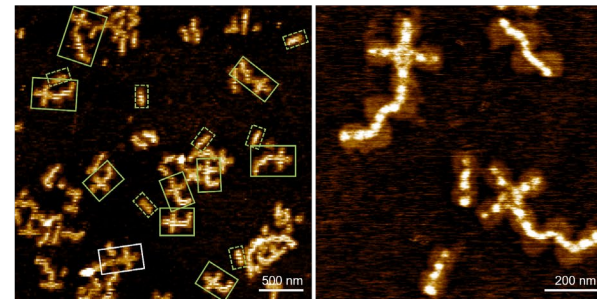
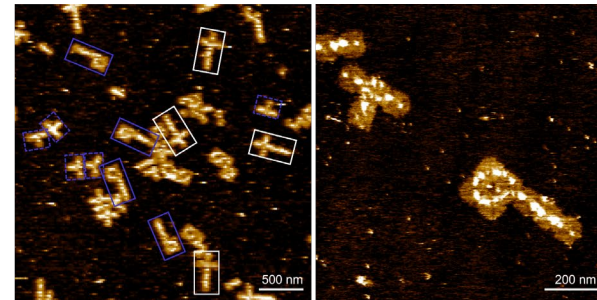
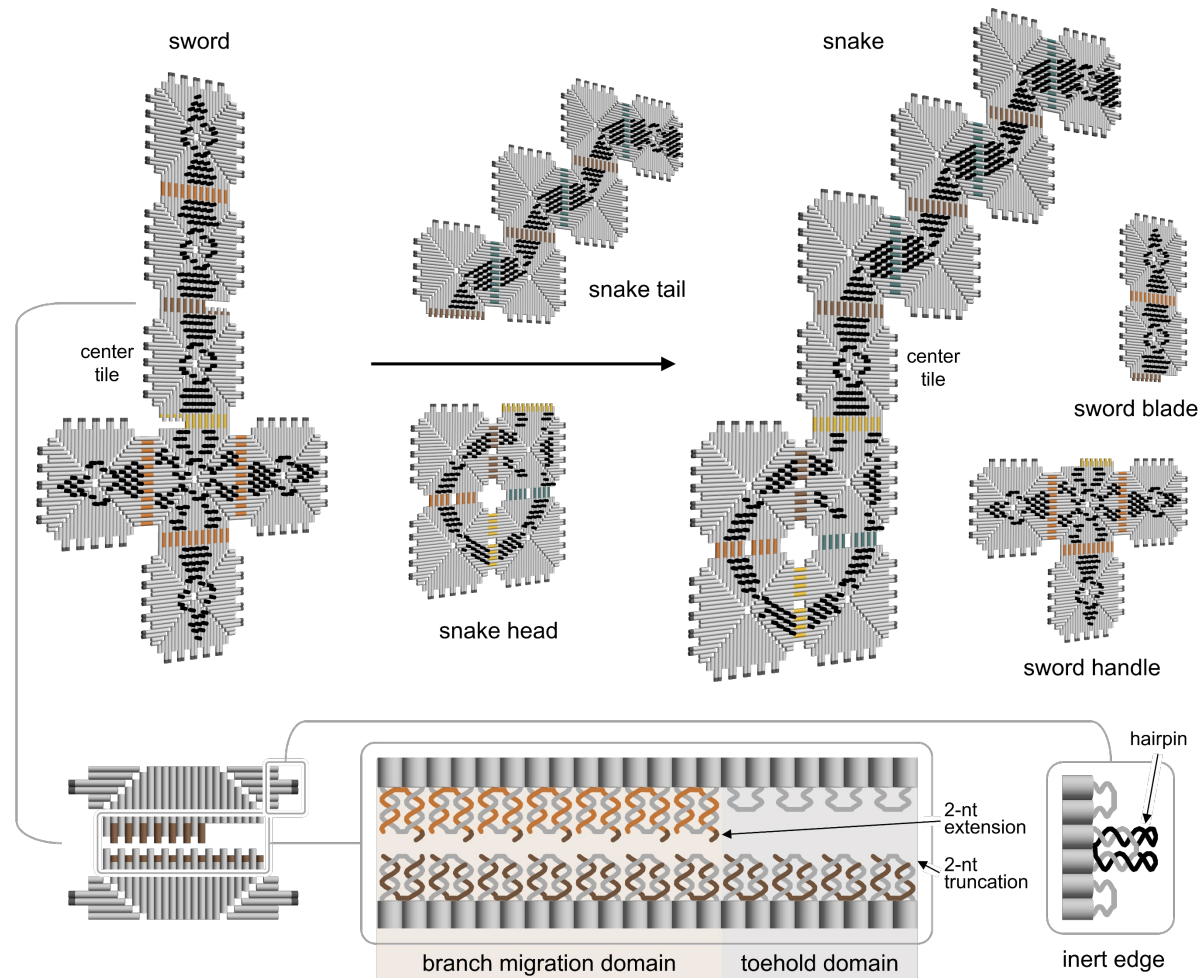
Philip Petersen



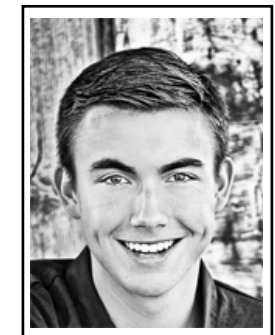
Greg Tikhomirov



Modular reconfiguration of DNA origami assemblies

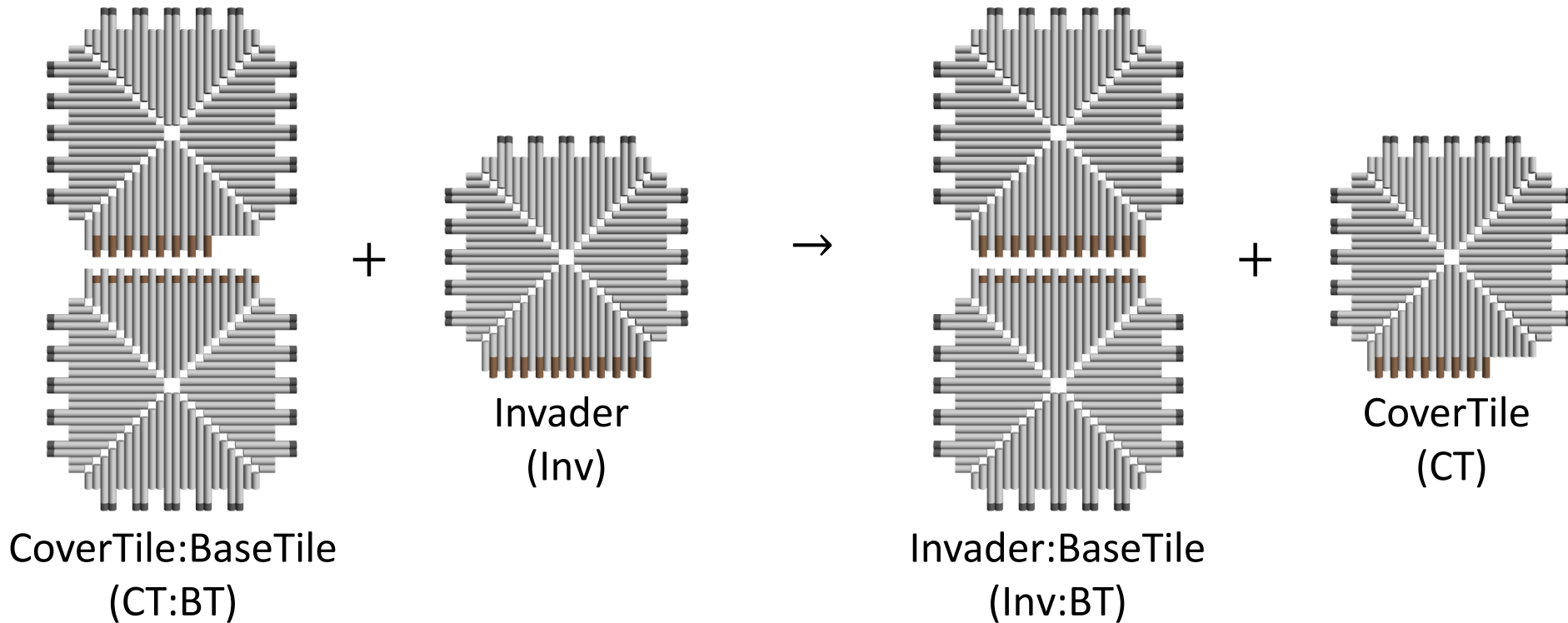
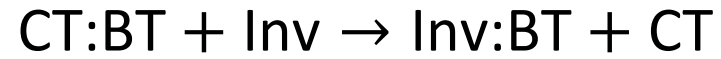


Namita Sarraf

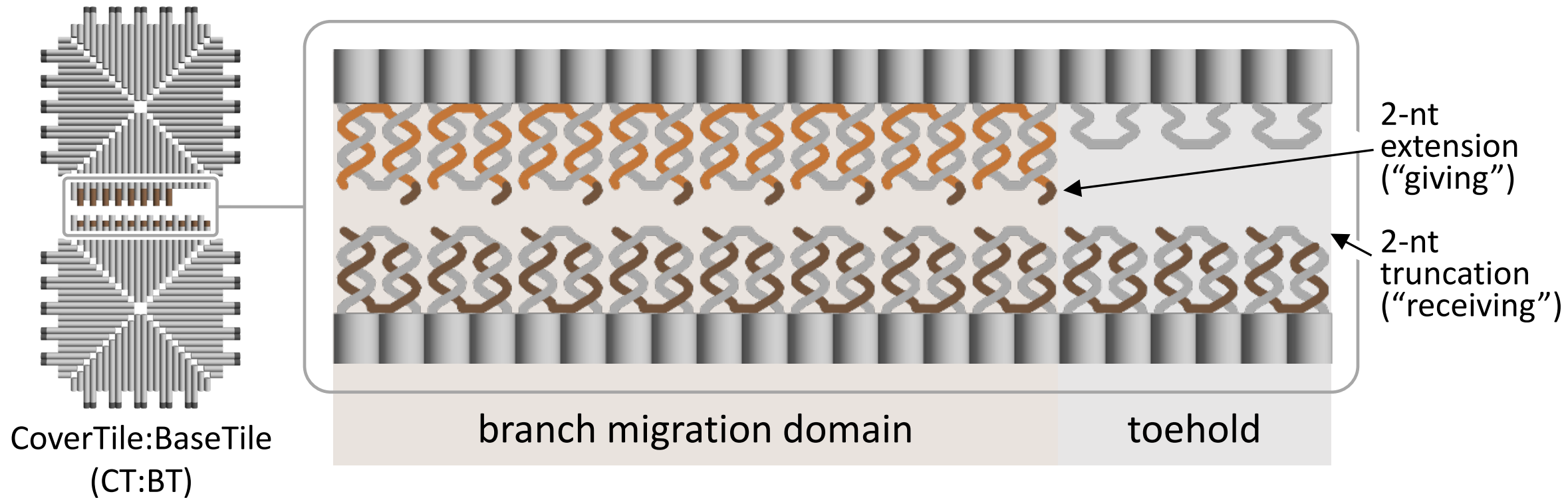


Kellen Rodriguez

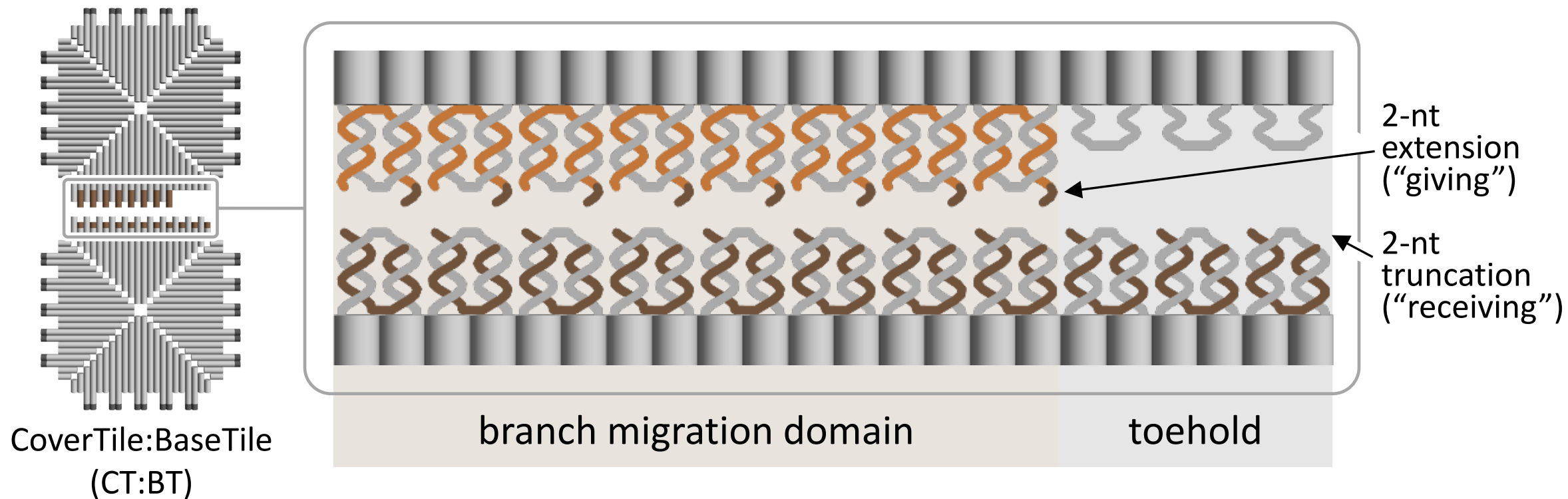
A simple tile displacement reaction



A simple tile displacement reaction



How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?



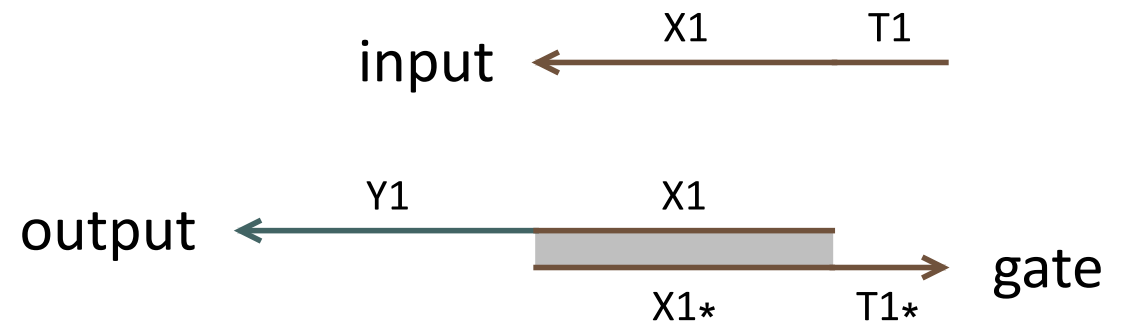
How many unique strand displacement reactions can be created using a gate strand that has a given length and sequence?

n unique reactions:

$X_i \rightarrow Y_i$ where $1 \leq i \leq n$

toehold = 6 nucleotides

branch migration = 16 nucleotides

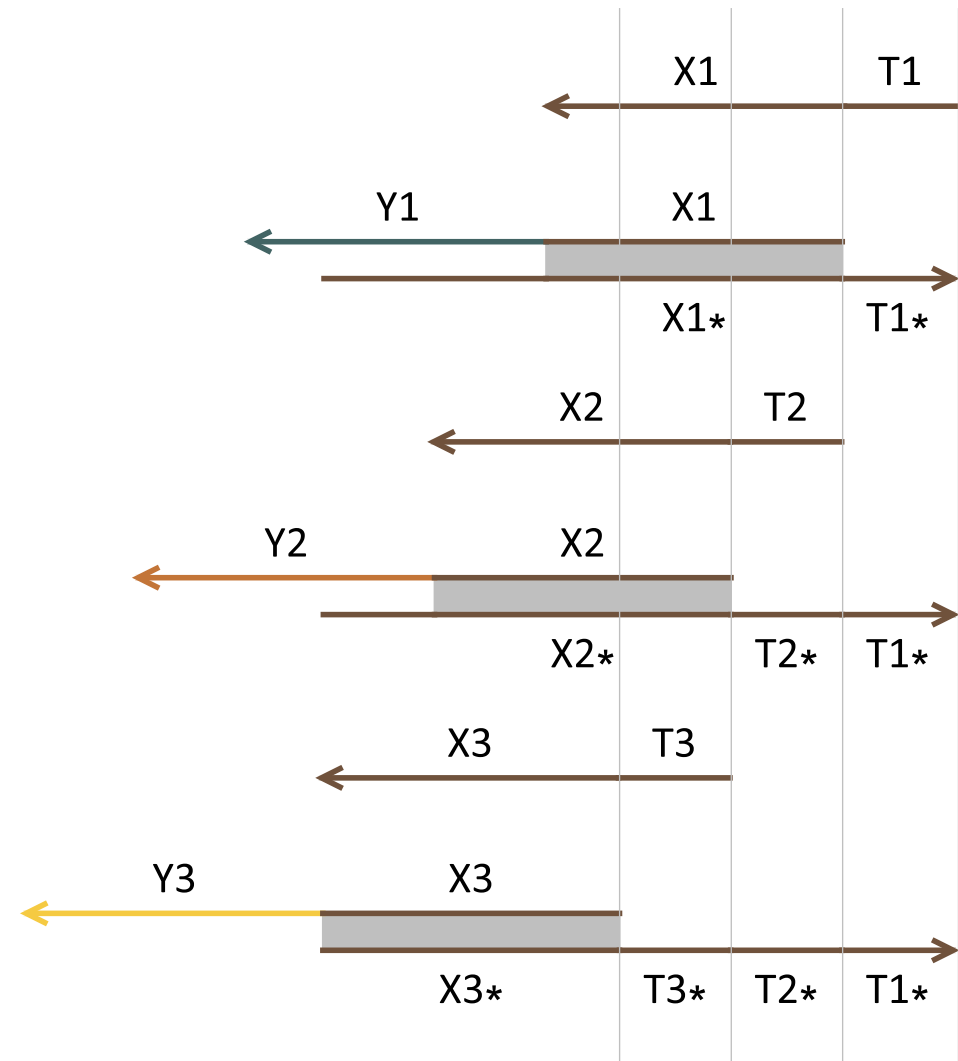


How many unique strand displacement reactions can be created using a gate strand that has a given length and sequence?

n unique reactions:
 $X_i \rightarrow Y_i$ where $1 \leq i \leq n$

toehold = 6 nucleotides
 branch migration = 16 nucleotides

34-nucleotide gate \Rightarrow 3 reactions



How many unique strand displacement reactions can be created using a gate strand that has a given length and sequence?

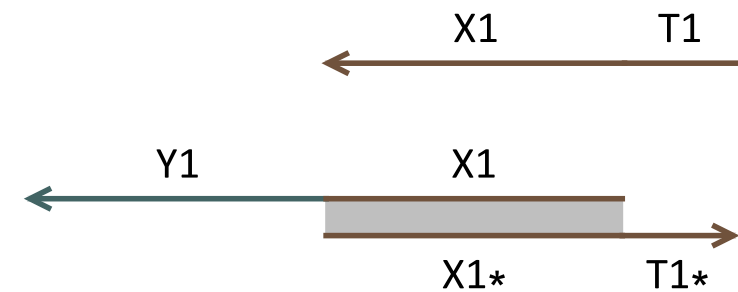
n unique reactions:

$X_i \rightarrow Y_i$ where $1 \leq i \leq n$

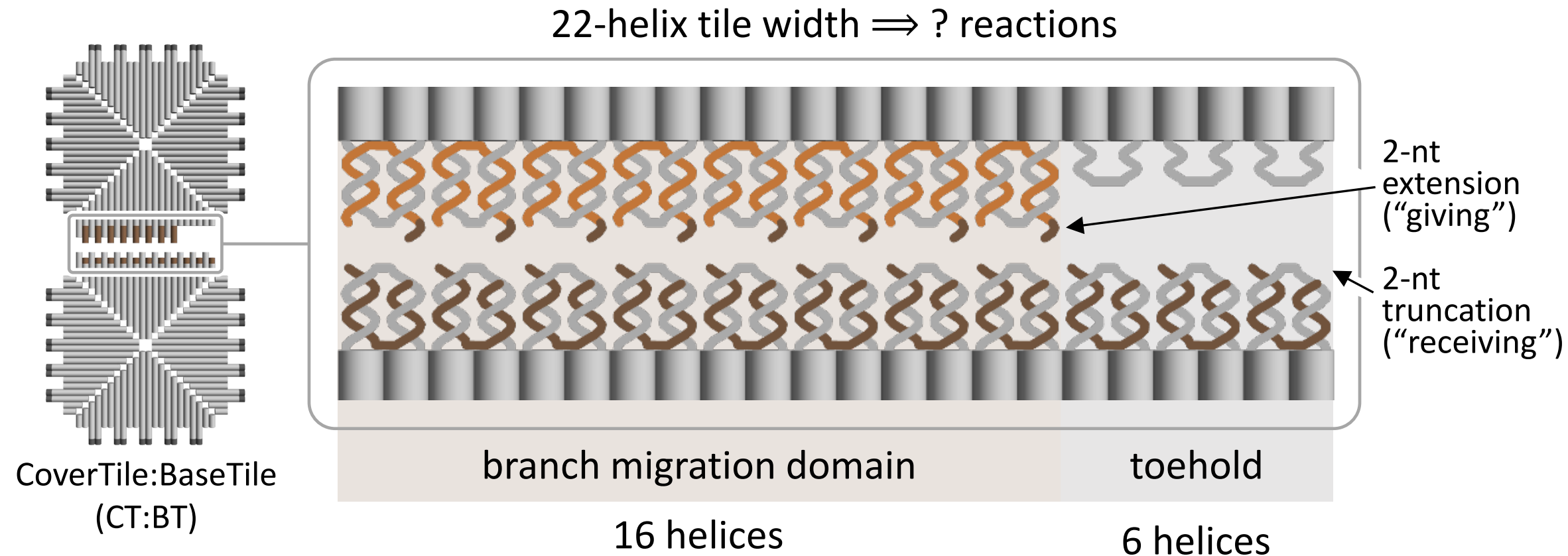
toehold = 6 nucleotides

branch migration = 16 nucleotides

22-nucleotide gate \Rightarrow 1 reaction

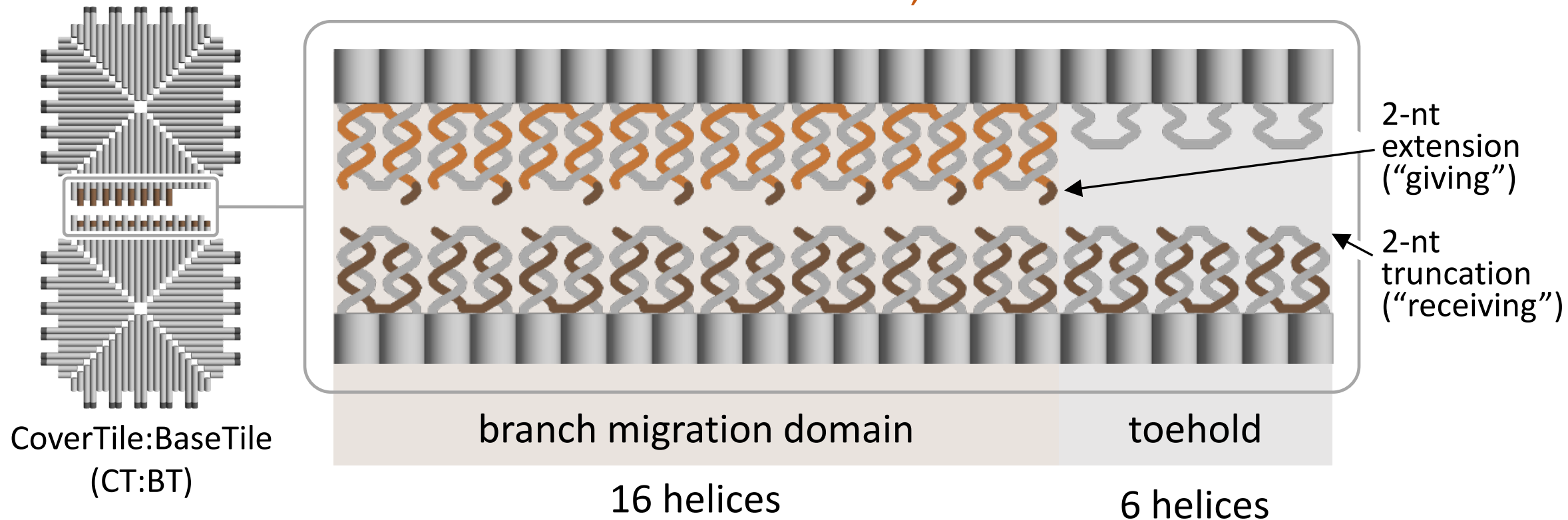


How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?

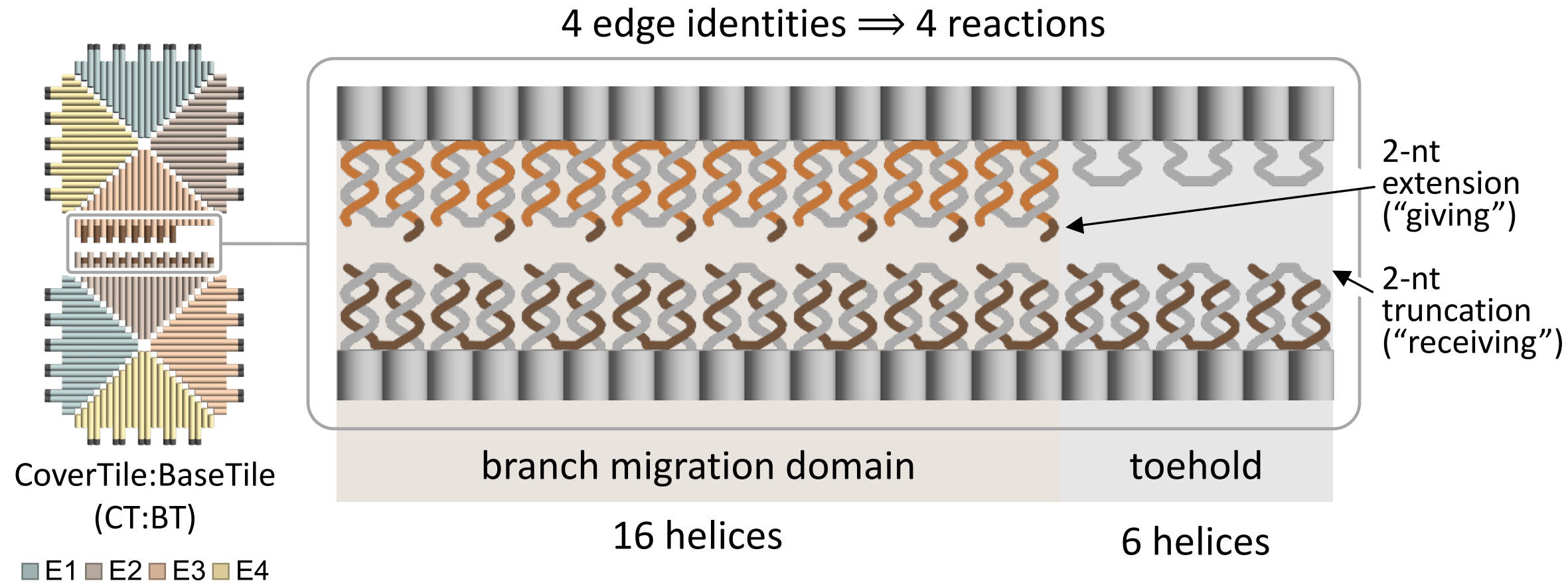


How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?

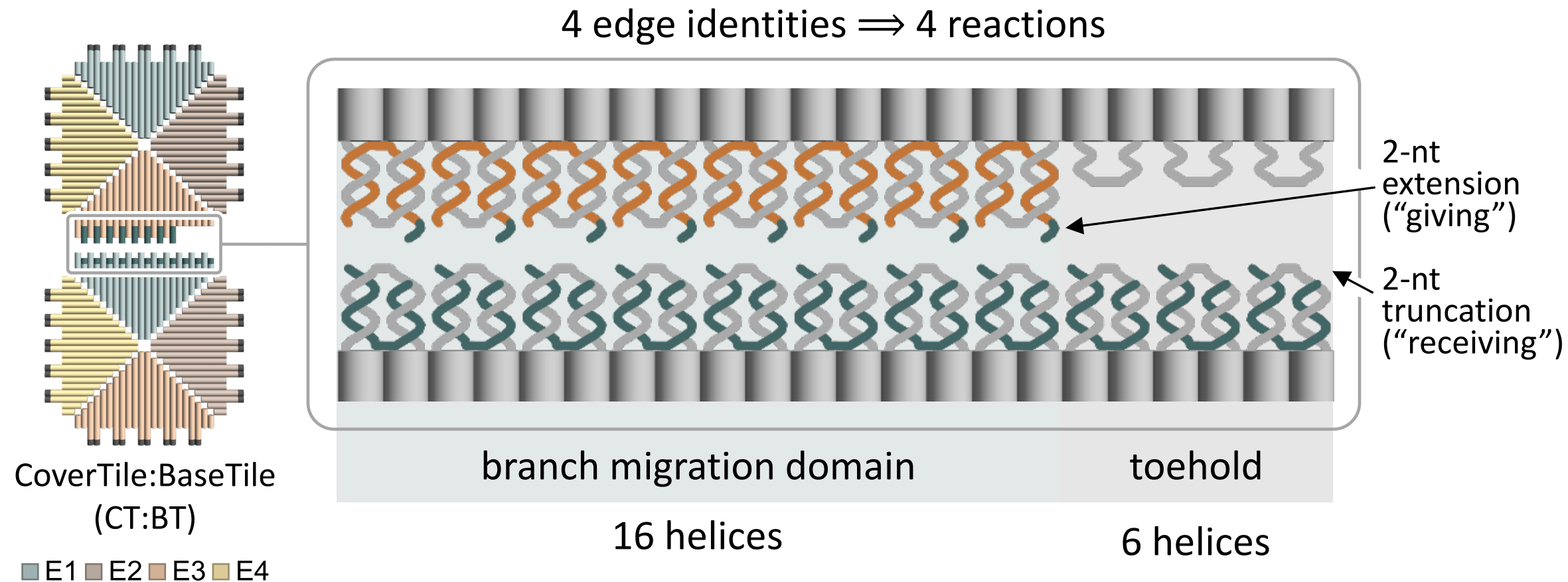
22-helix tile width \Rightarrow 1,104 reactions



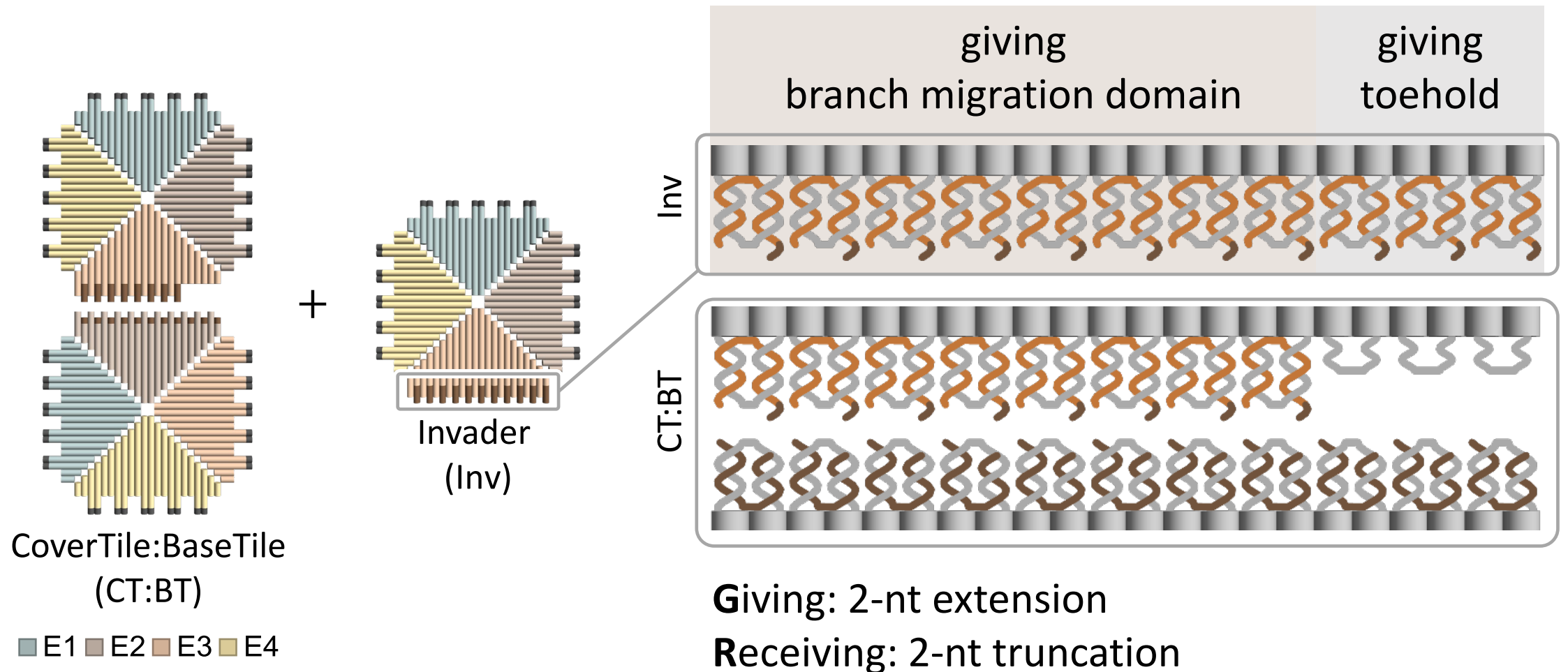
How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?



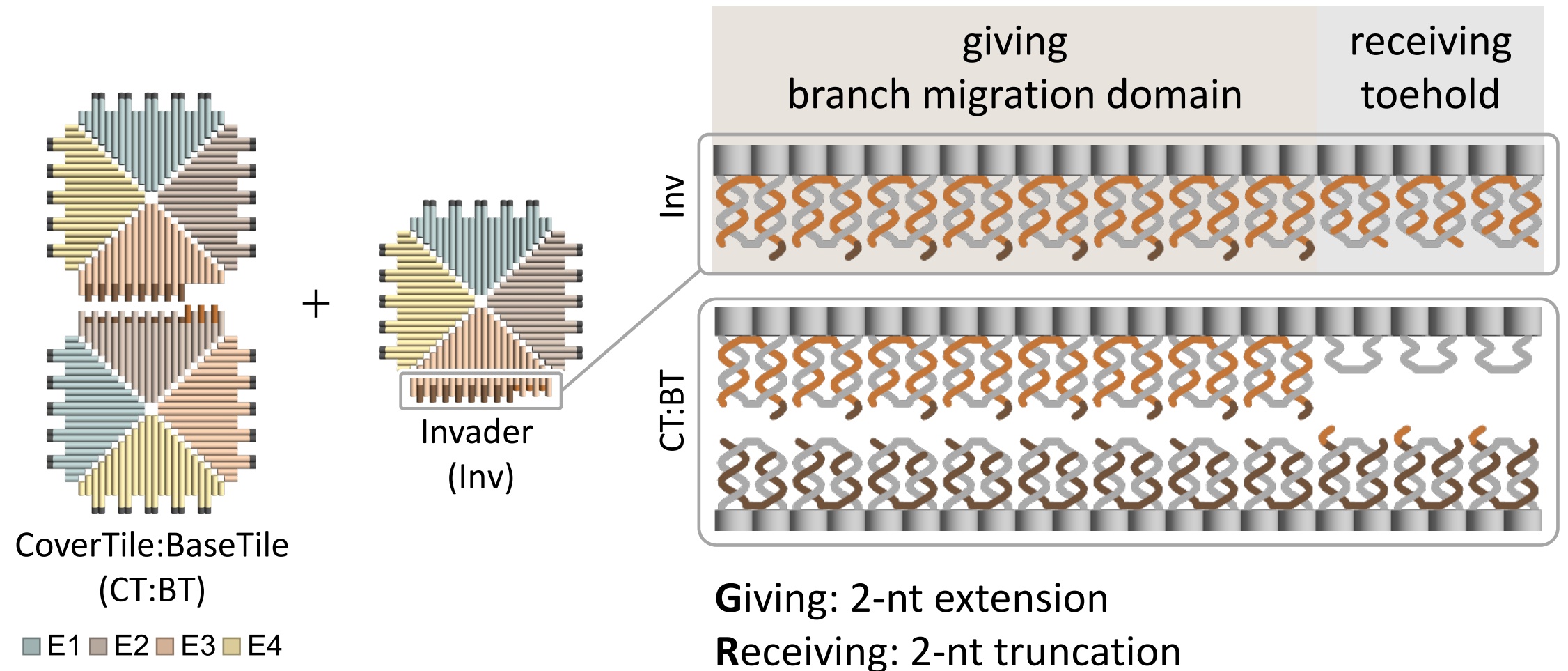
How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?



Same type of toehold and branch migration domains

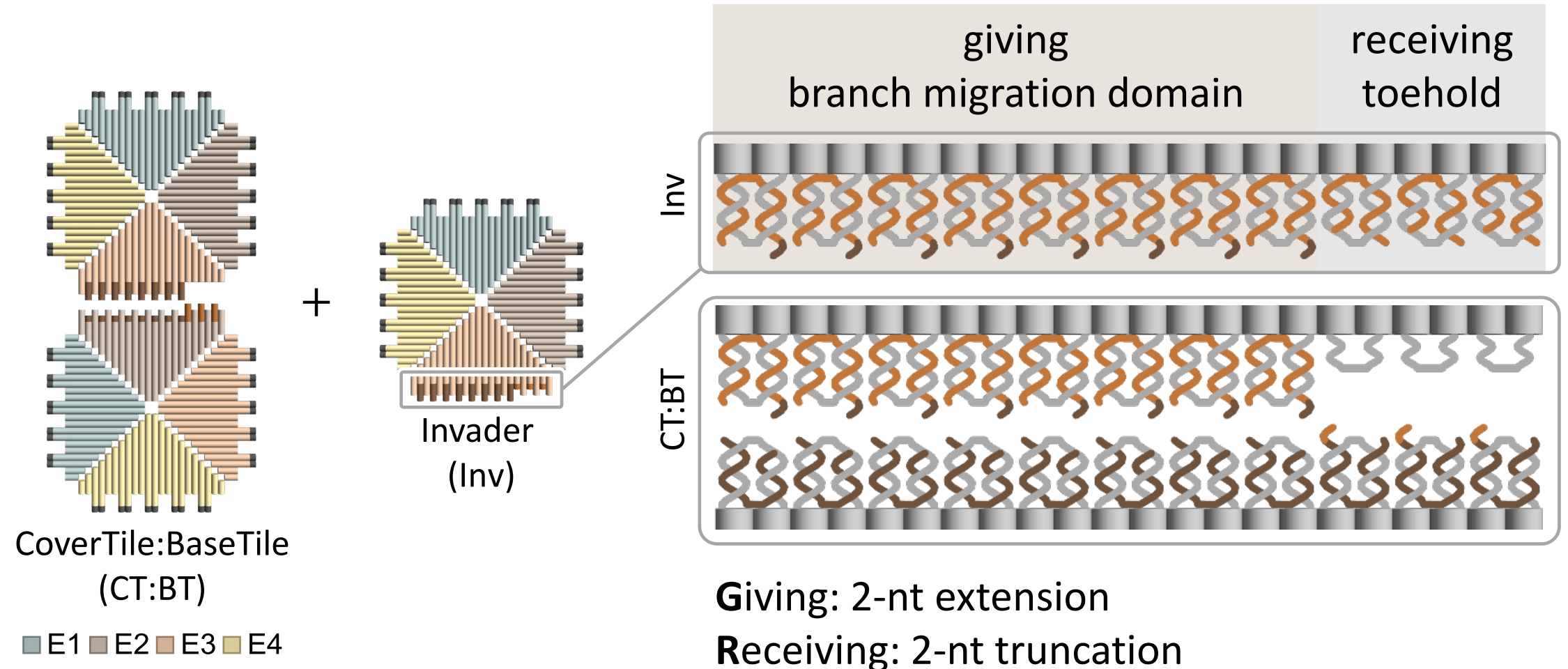


Mixed types of toehold and branch migration domains

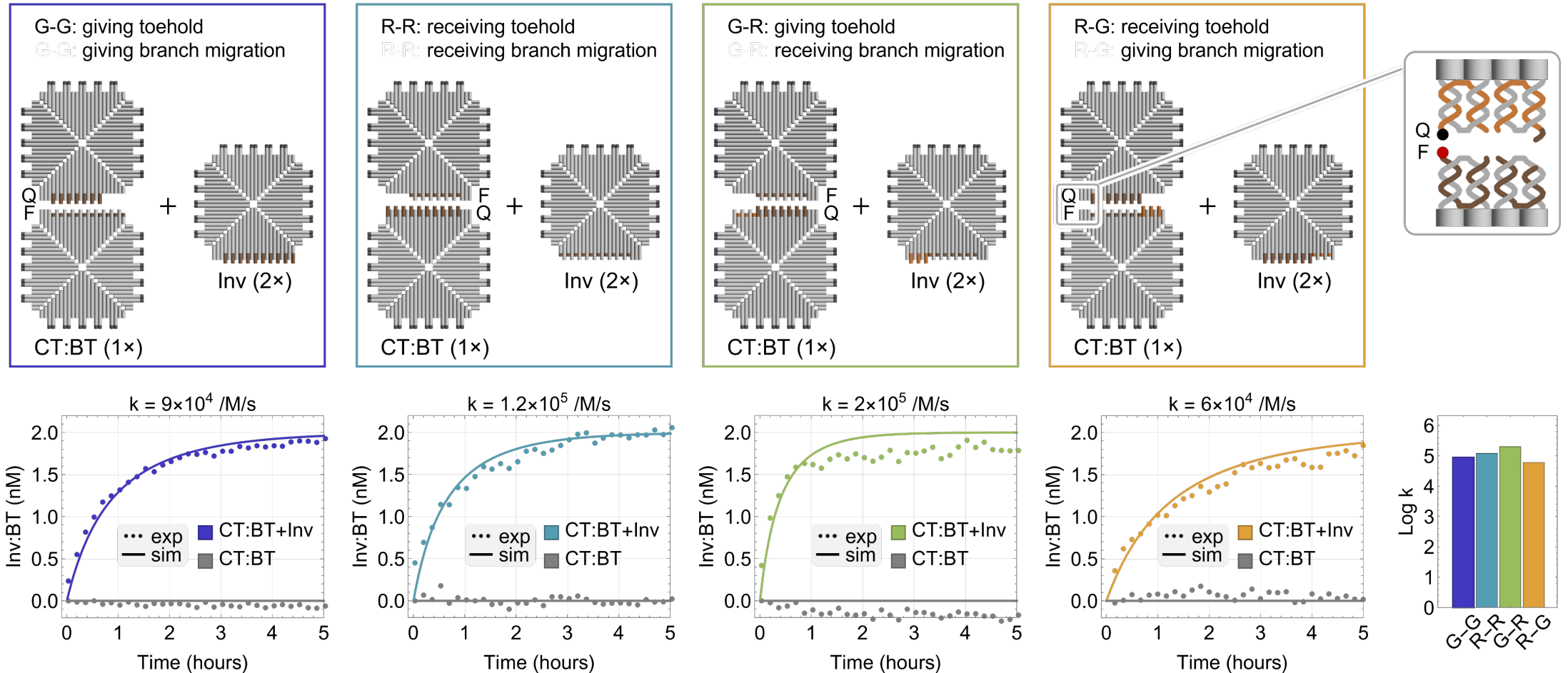


Mixed types of toehold and branch migration domains

4 toehold identities \times 4 branch migration identities \Rightarrow 16 reactions



All four giving and receiving combinations of toehold and branch migration domains exhibited similar kinetics



How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?

N_t : Number of toehold identities

N_b : Number of branch migration identities for a given toehold

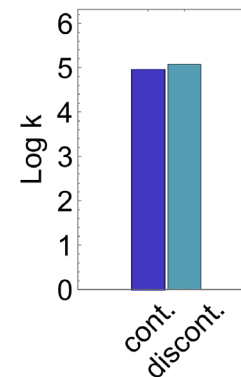
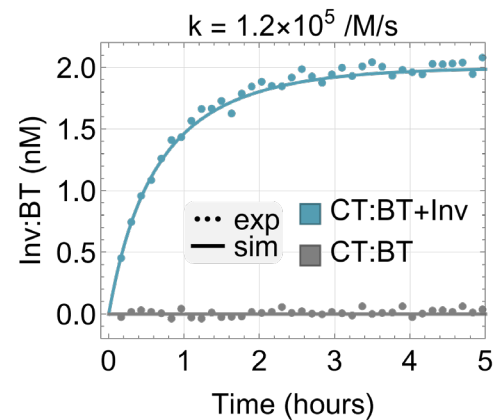
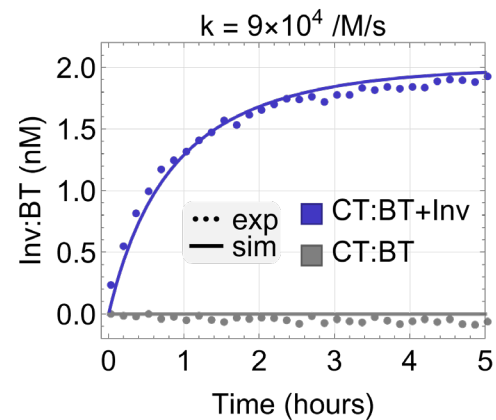
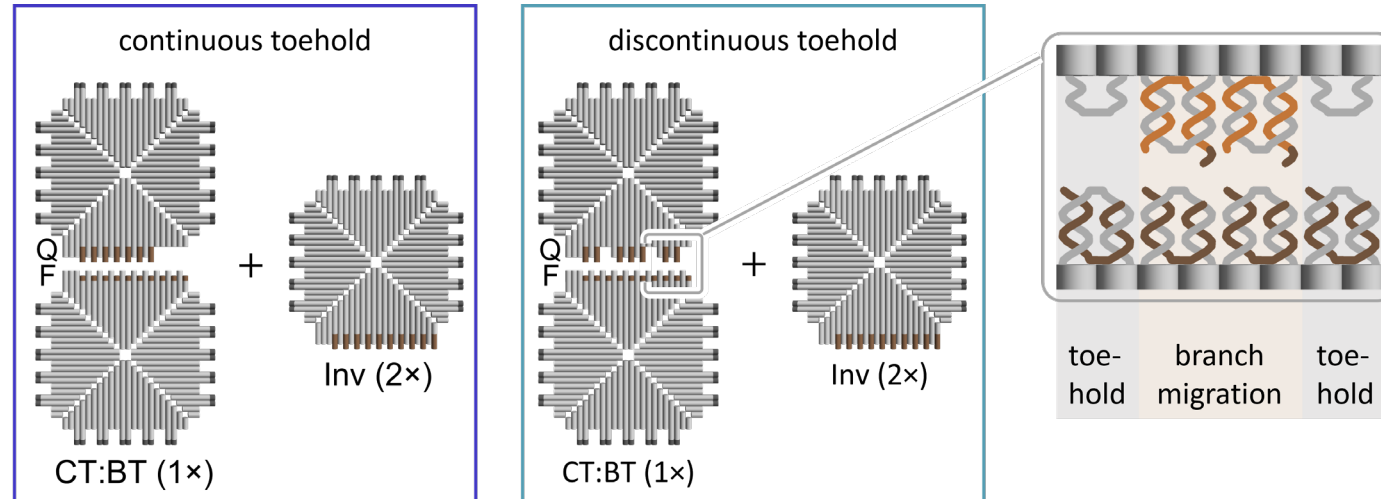
Number of distinct reactions: $N = N_t \times N_b$

	N_t	N_b	N
G-G	4	1	4
R-R	4	1	4
G-R	4	4	16
R-G	4	4	16
Total			40

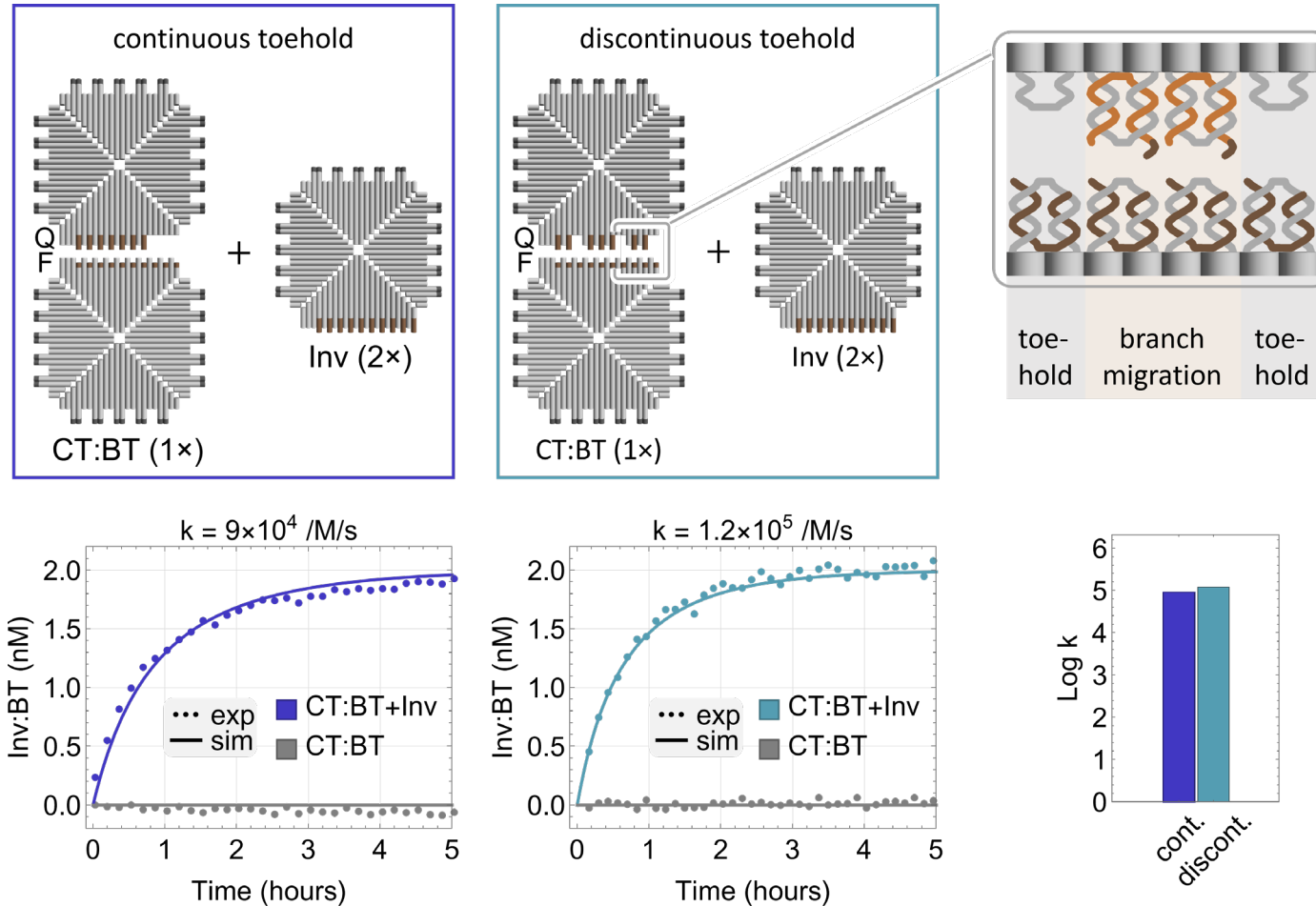
Giving toehold – **R**eceiving branch migration

Receiving toehold – **G**iving branch migration

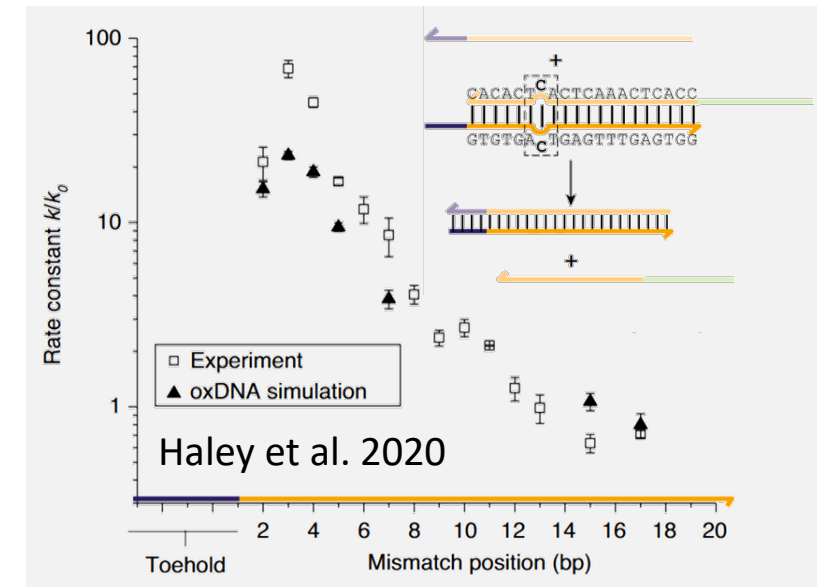
Continuous and discontinuous toeholds exhibited similar kinetics



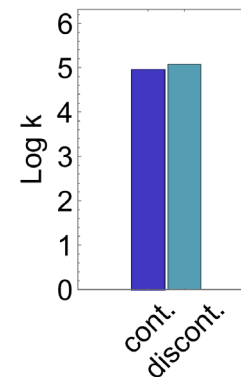
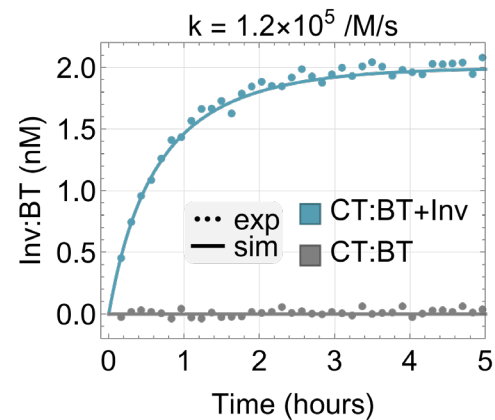
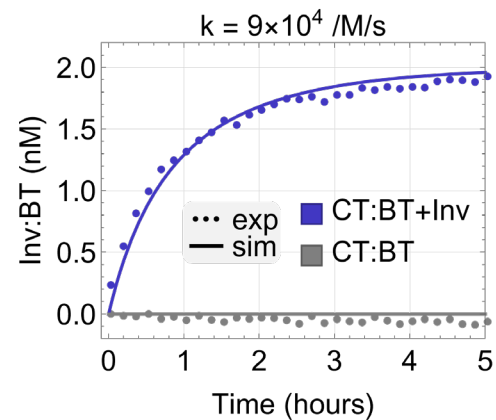
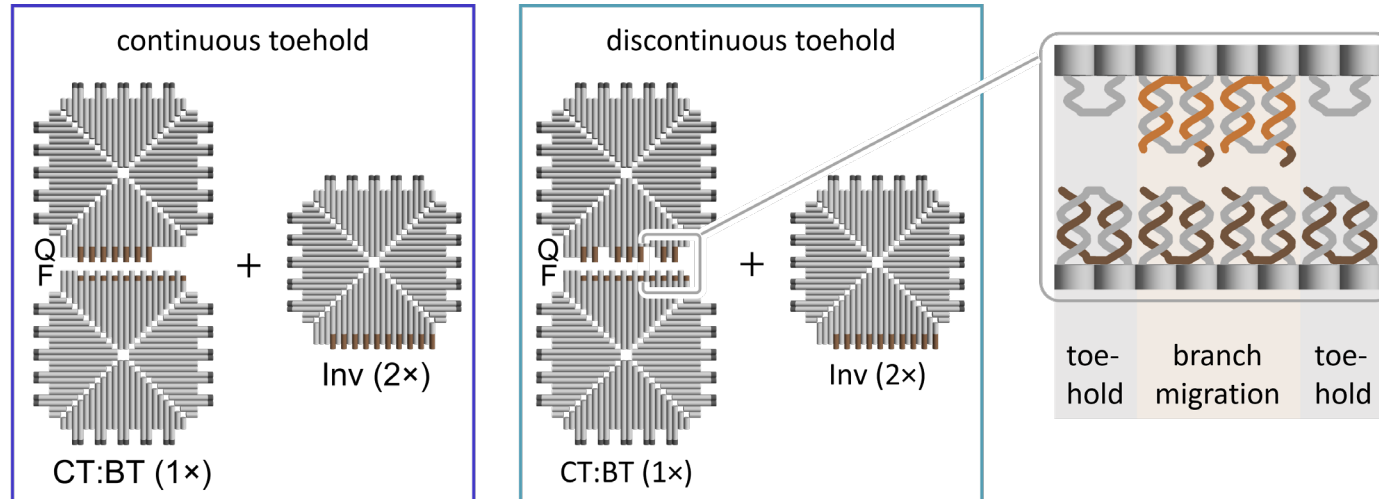
Continuous and discontinuous toeholds exhibited similar kinetics



A discontinuous toehold is conceptually similar to mismatch elimination in strand displacement, but in comparison it has much faster kinetics. Why?



Continuous and discontinuous toeholds exhibited similar kinetics

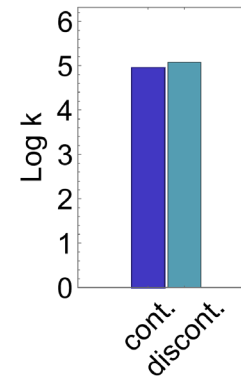
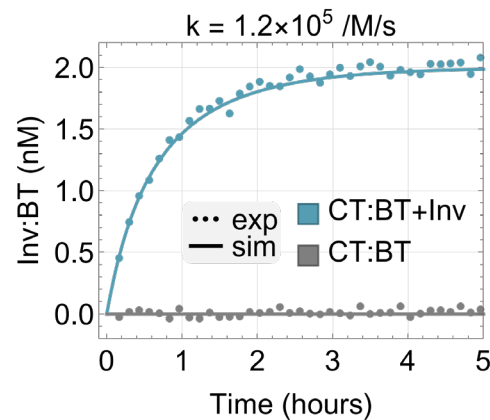
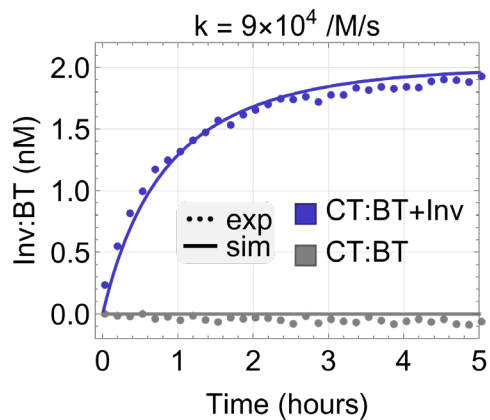
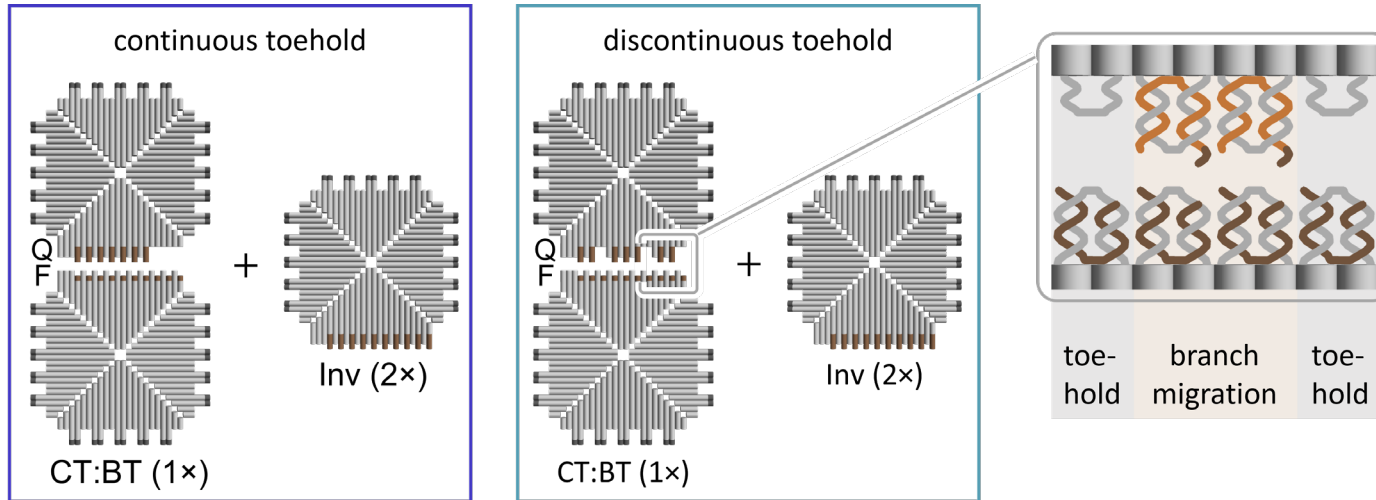


A discontinuous toehold is conceptually similar to mismatch elimination in strand displacement, but in comparison it has much faster kinetics. Why?

Explanations:

- less entropic cost

Continuous and discontinuous toeholds exhibited similar kinetics



A discontinuous toehold is conceptually similar to mismatch elimination in strand displacement, but in comparison it has much faster kinetics. Why?

Explanations:

- less entropic cost
- larger space

How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?

N_t : Number of toehold identities

N_b : Number of branch migration identities for a given toehold

N_p : Number of toehold locations

Number of distinct reactions: $N = N_t \times N_b \times N_p$

	N_t	N_b	N_p	N
G-G	4	1	1	4
R-R	4	1	1	4
G-R	4	4	17	272
R-G	4	4	17	272
Total				552

Toeholds consist of 3 out of 11 edge staples, no two share more than one staple in common.



How many unique tile displacement reactions can be created using a square DNA origami tile that has a given width and a given scaffold sequence?

N_t : Number of toehold identities

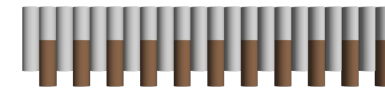
N_b : Number of branch migration identities for a given toehold

N_p : Number of toehold locations

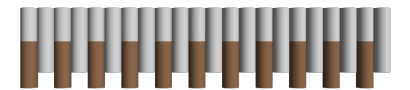
N_e : Number of staple extension locations

Number of distinct reactions: $N = N_t \times N_b \times N_p \times N_e$

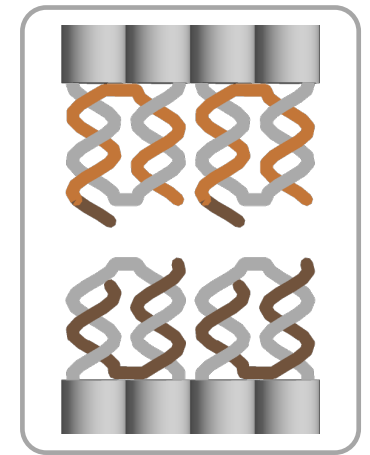
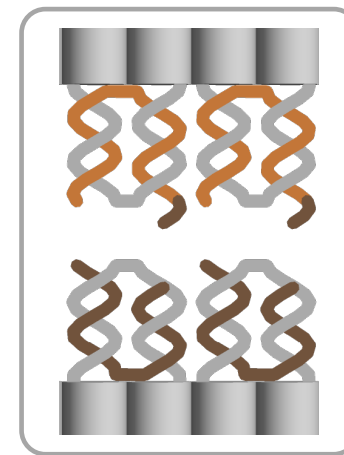
	N_t	N_b	N_p	N_e	N
G-G	4	1	1	2	8
R-R	4	1	1	2	8
G-R	4	4	17	2	544
R-G	4	4	17	2	544
Total					1104



5' staple extension
3' staple truncation



3' staple extension
5' staple truncation



$$N_e = 2$$

How robust are tile displacement reactions to spurious interactions such as cross-talk and occlusion?

N_t : Number of toehold identities

N_b : Number of branch migration identities for a given toehold

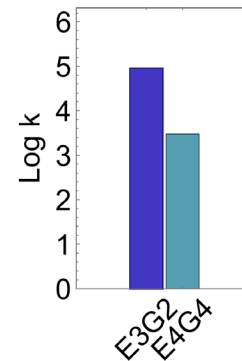
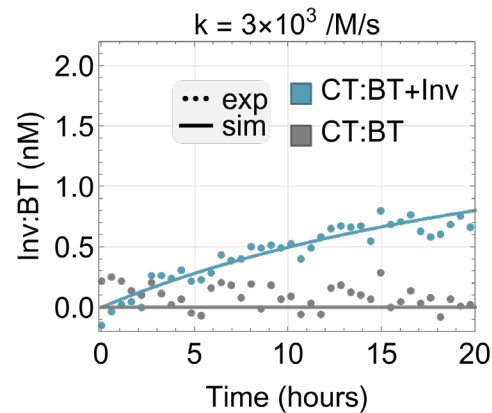
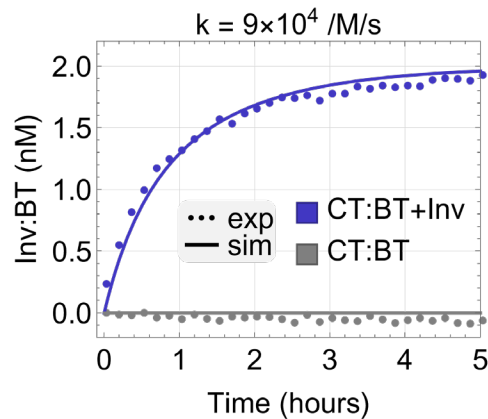
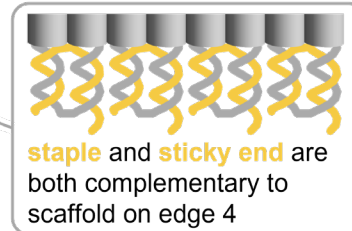
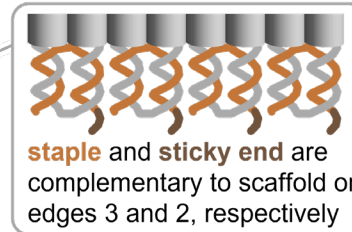
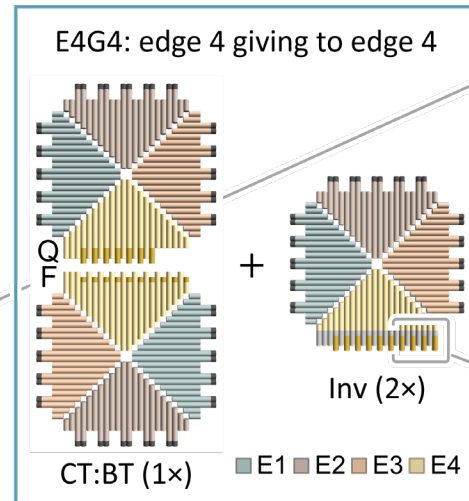
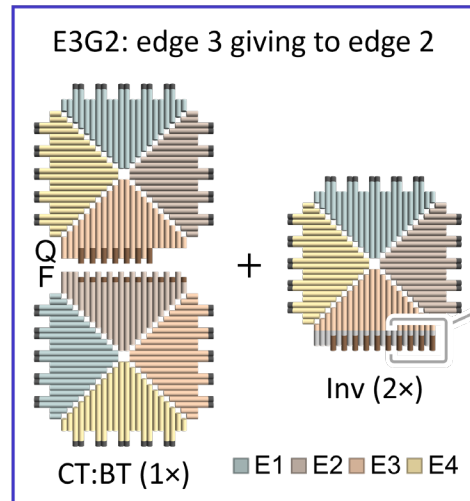
N_p : Number of toehold locations

N_e : Number of staple extension locations

Number of distinct reactions: $N = N_t \times N_b \times N_p \times N_e$

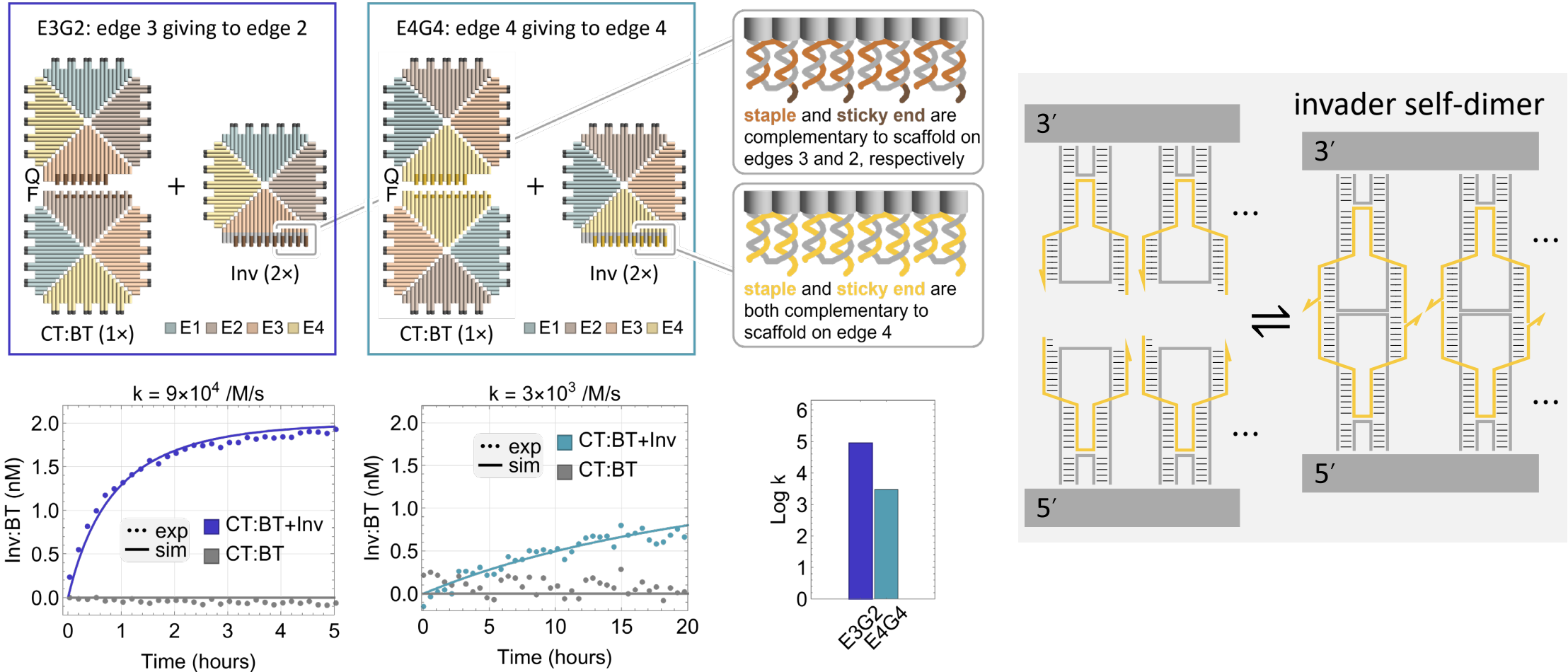
	N_t	N_b	N_p	N_e	N
G-G	4	1	1	2	8
R-R	4	1	1	2	8
G-R	4	4	17	2	544
R-G	4	4	17	2	544
Total					1104

Self-occluding edges exhibited slower kinetics



$ExGy$ indicates edge x giving to edge y , where $x, y \in \{1, 2, 3, 4\}$

Self-occluding edges exhibited slower kinetics



How robust are tile displacement reactions to spurious interactions such as cross-talk and occlusion?

N_t : Number of toehold identities

N_b : Number of branch migration identities for a given toehold

N_p : Number of toehold locations

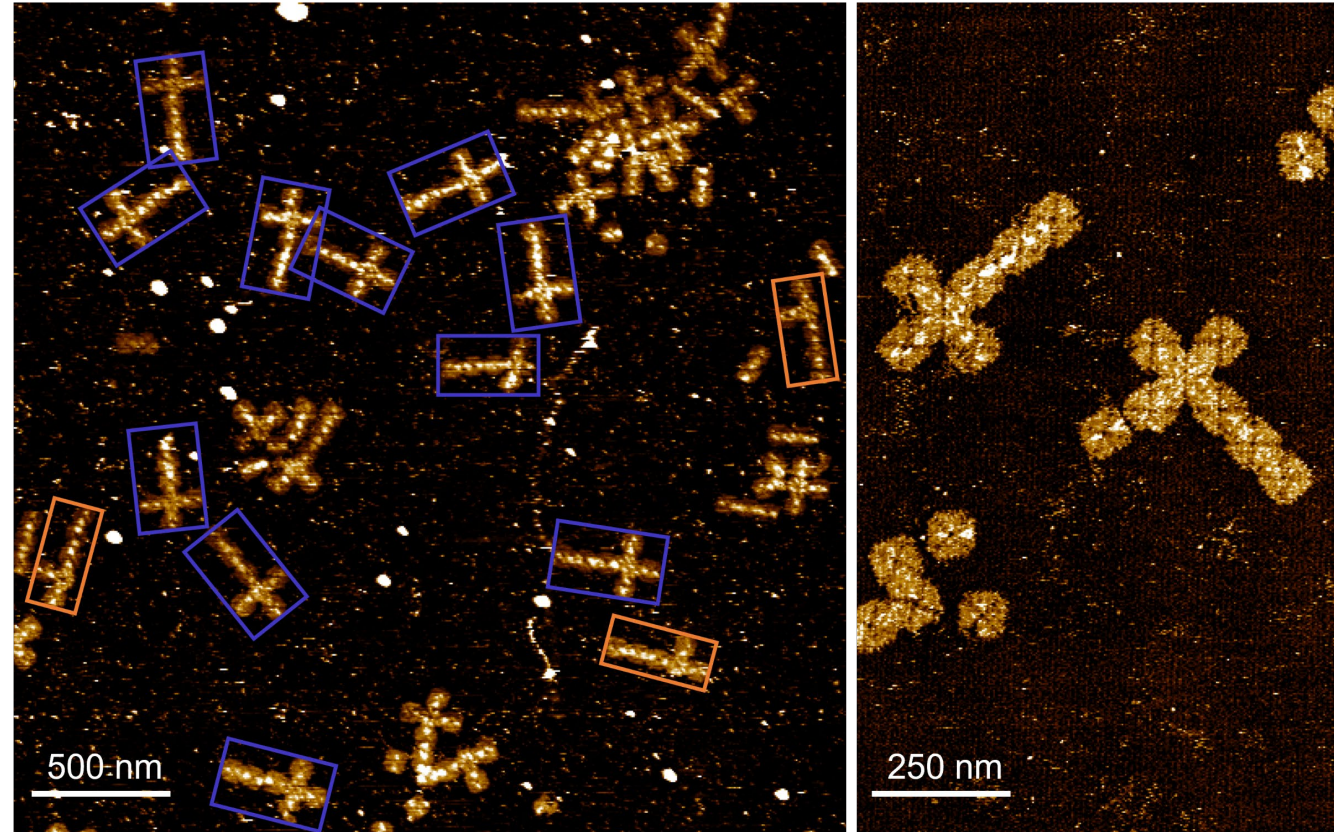
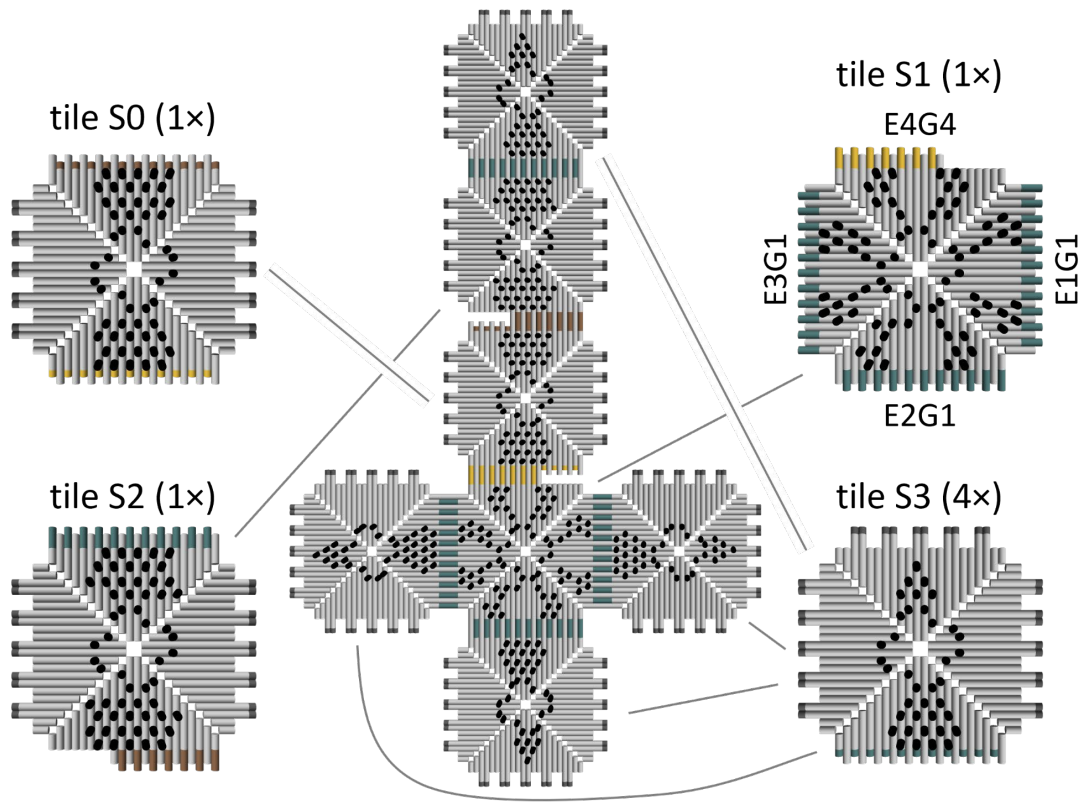
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Number of distinct reactions: $N = N_t \times N_b \times N_p \times N_e$

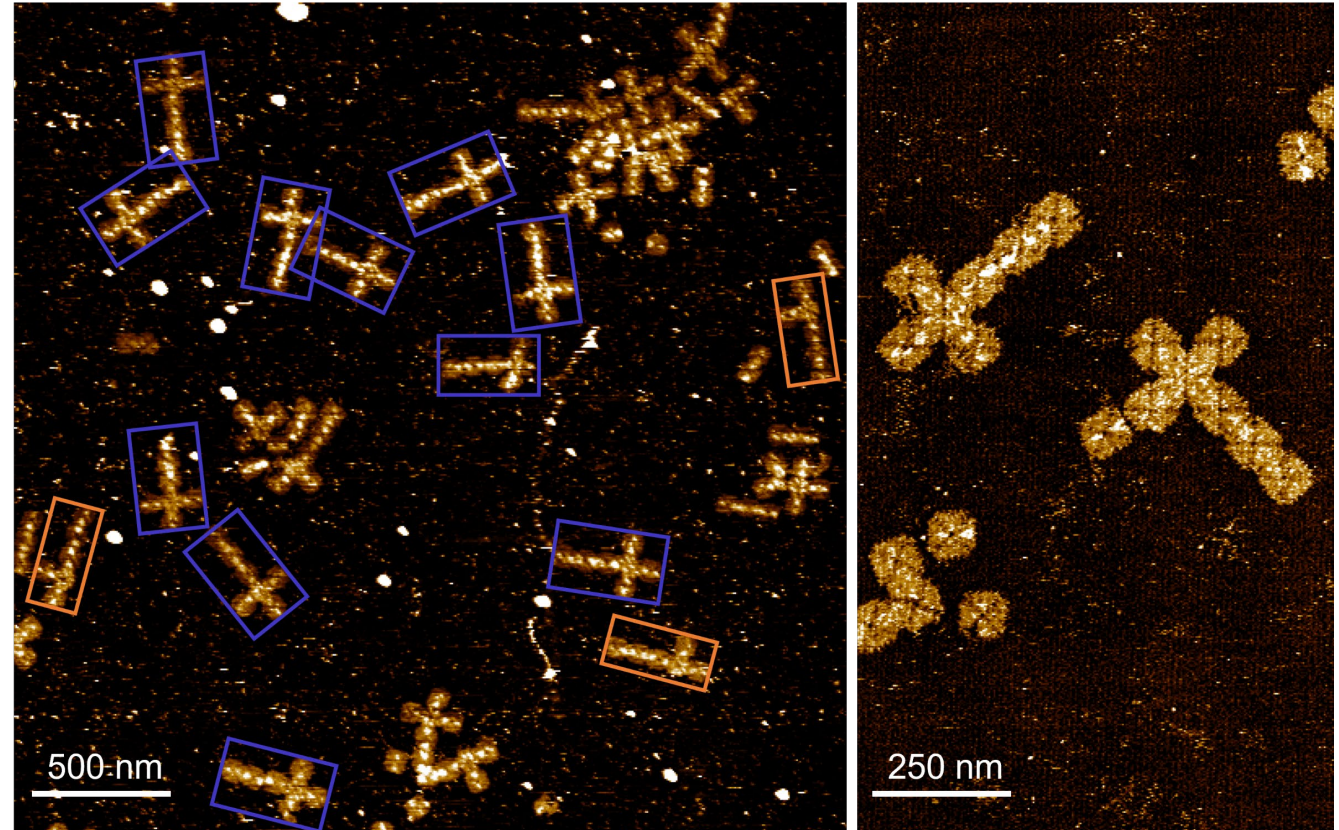
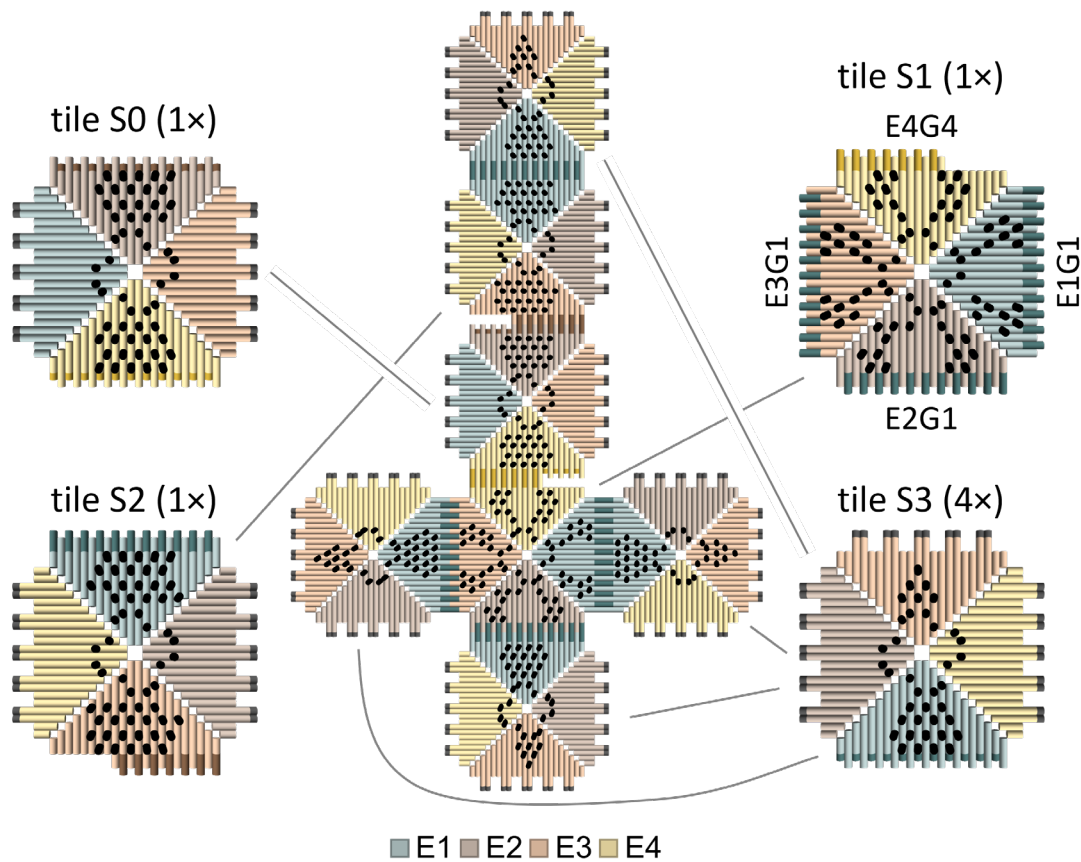
	N_t	N_b	N_p	N_e	N
G-G	4	1	1	2	8
R-R	4	1	1	2	8
G-R	4	3	17	2	408
R-G	4	3	17	2	408
Total					832

To maintain a controlled tile displacement rate, self-occluding edges should be avoided.

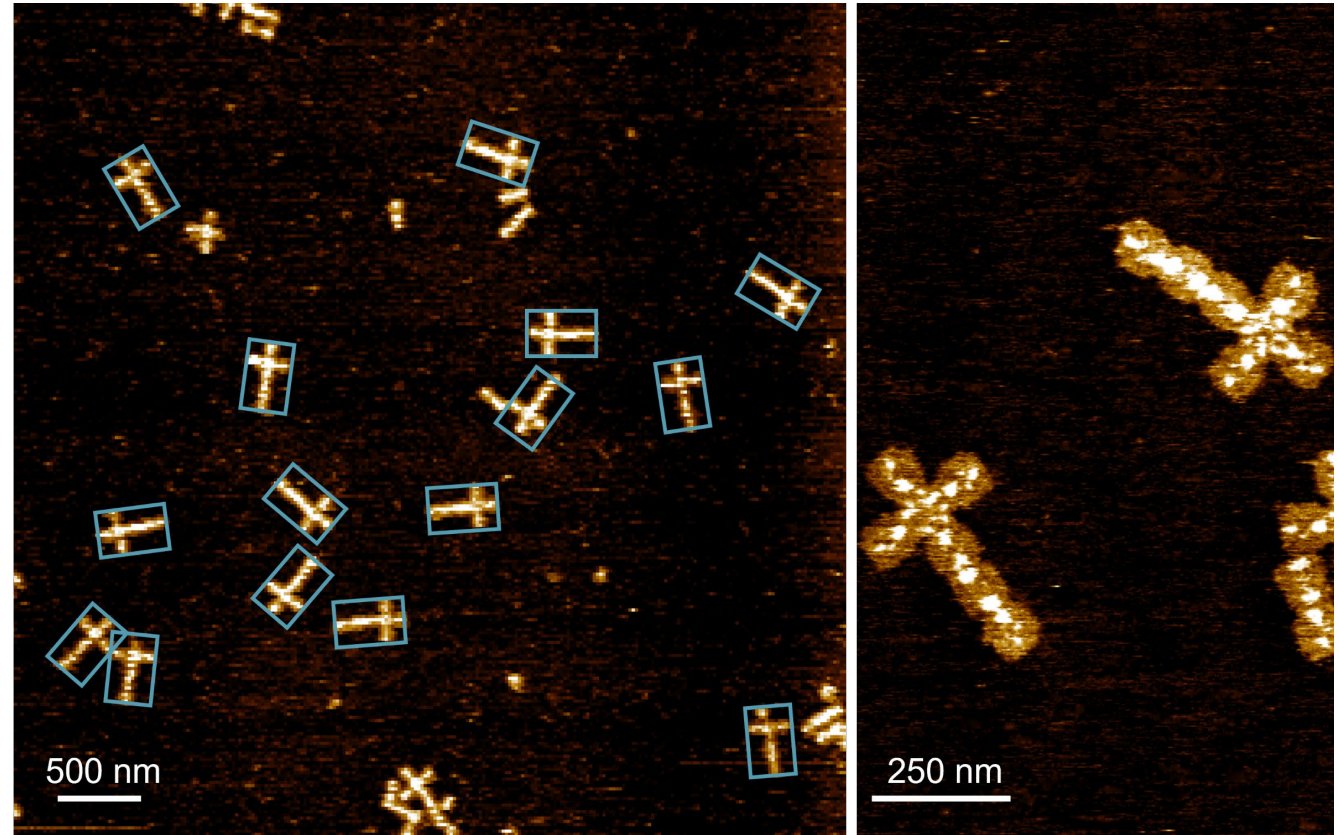
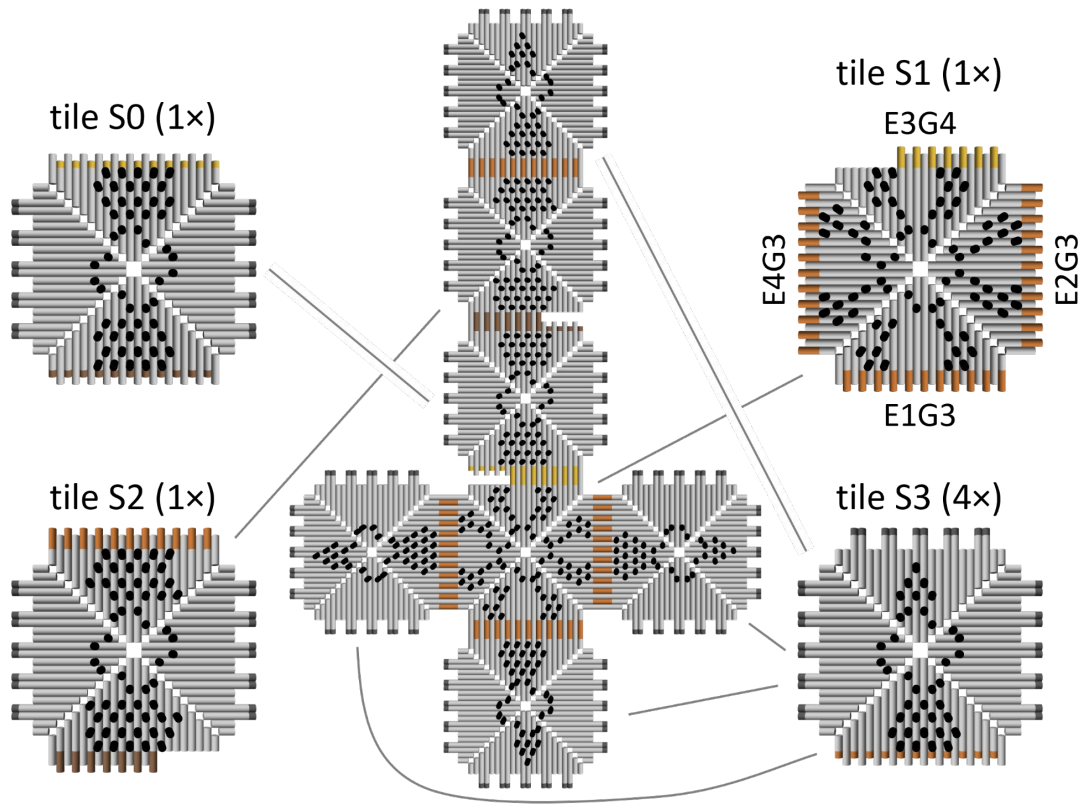
Does self-occluding edges affect the yield of tile assembly?



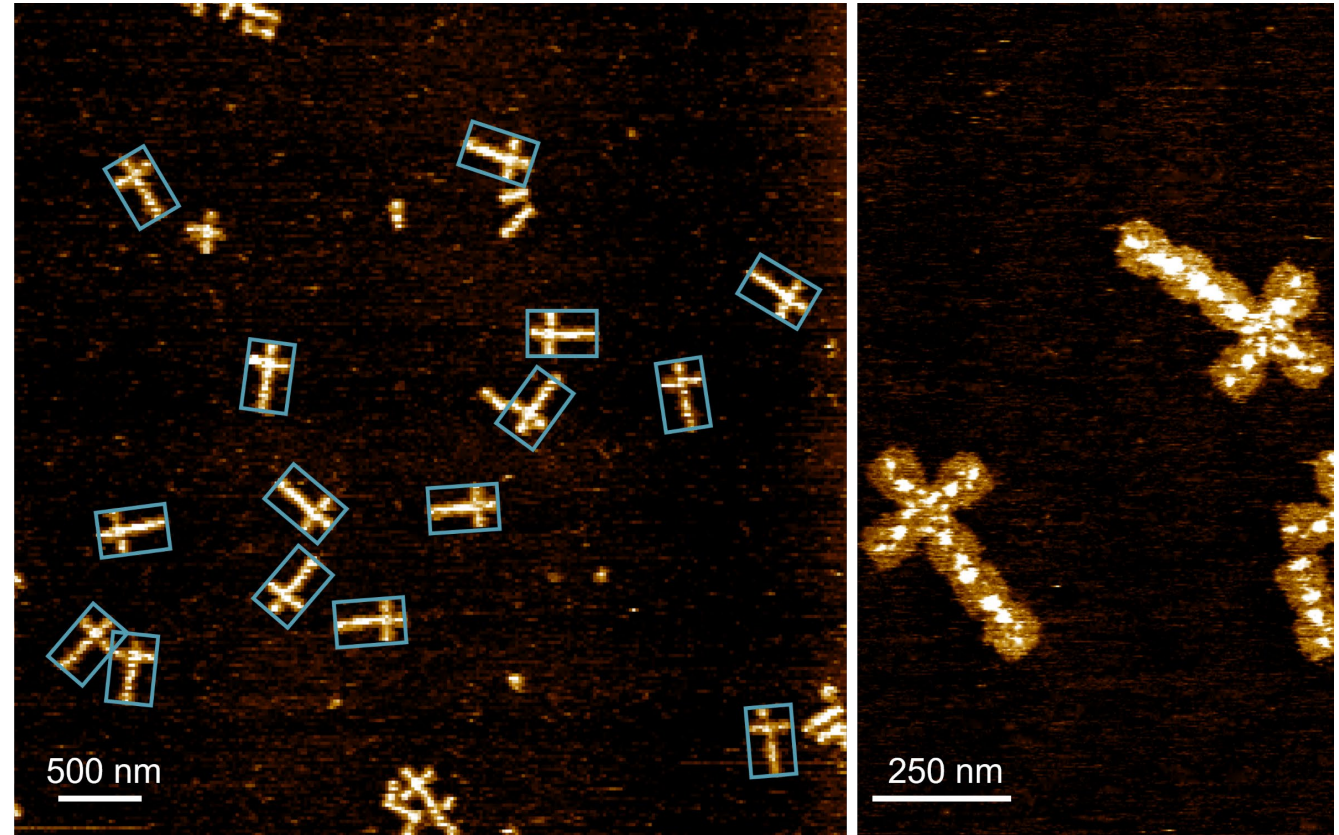
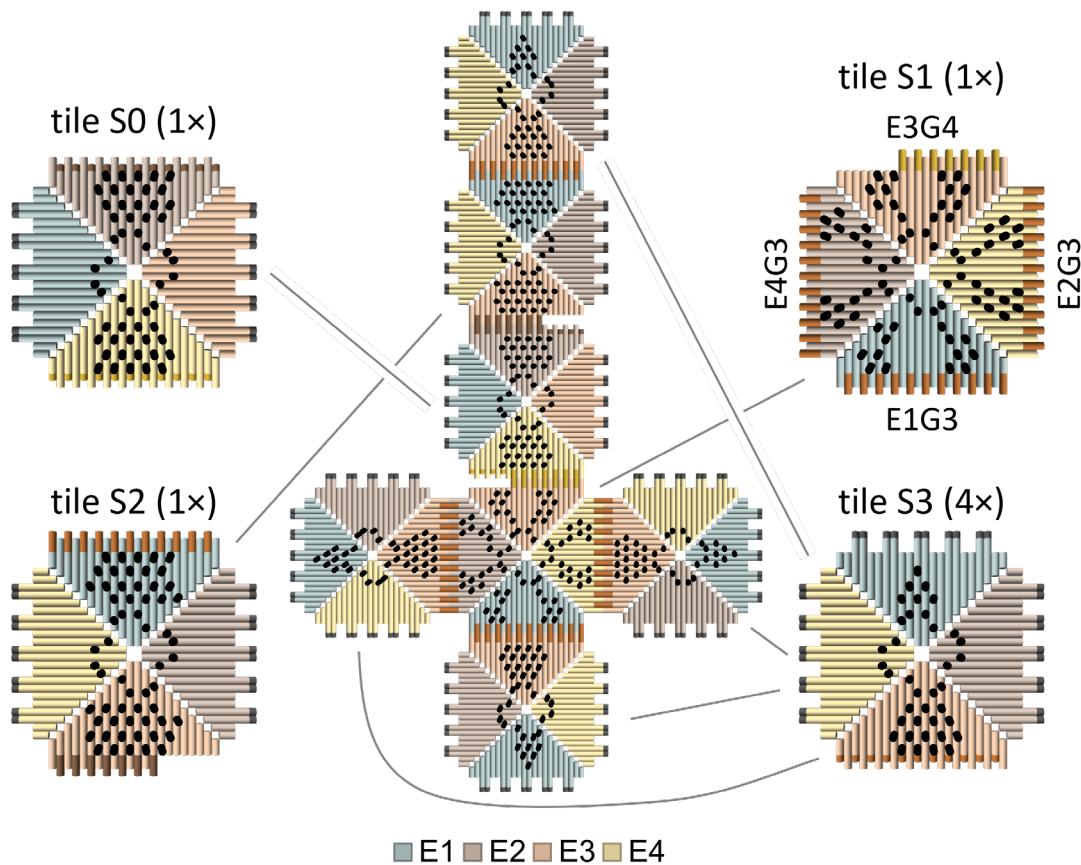
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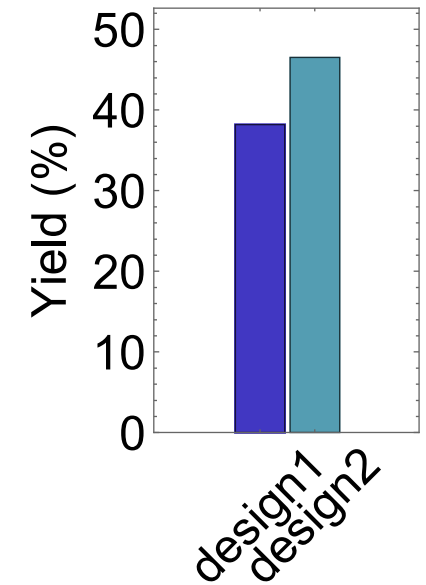
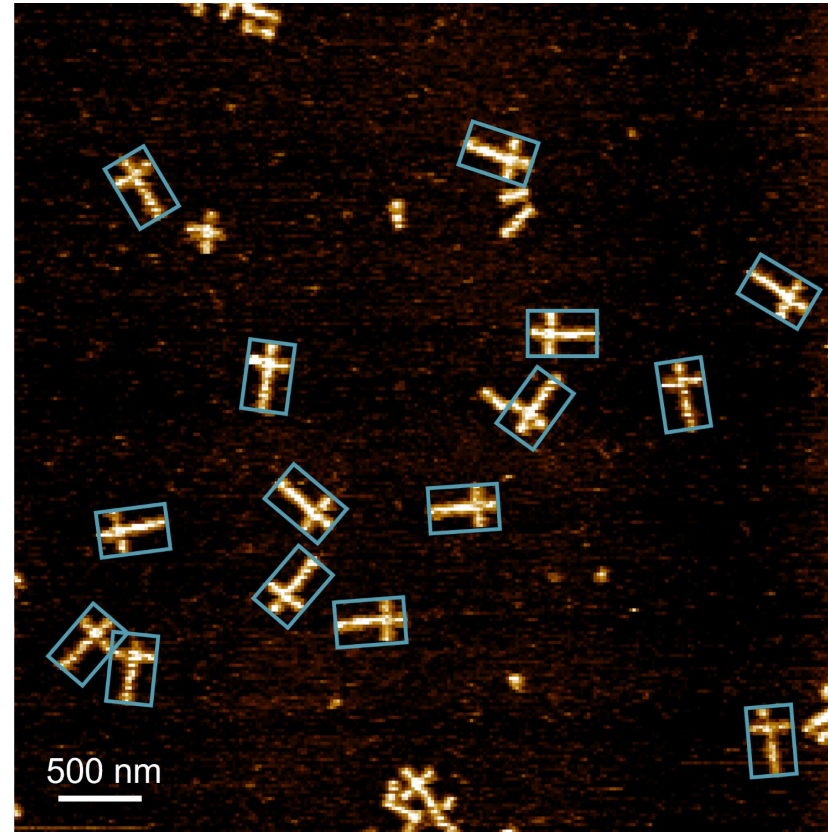
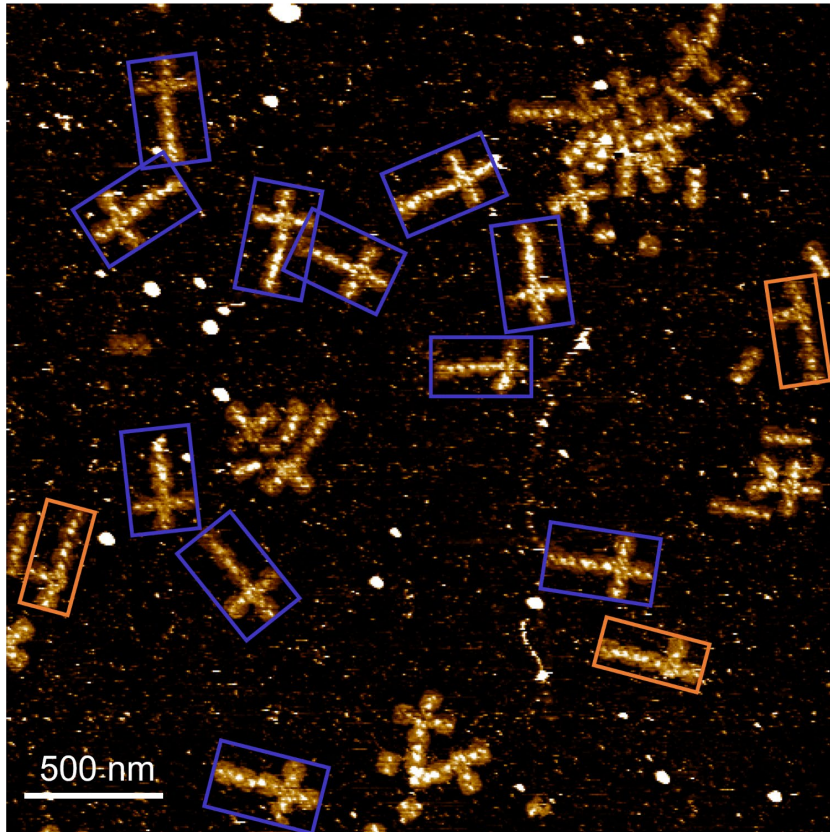
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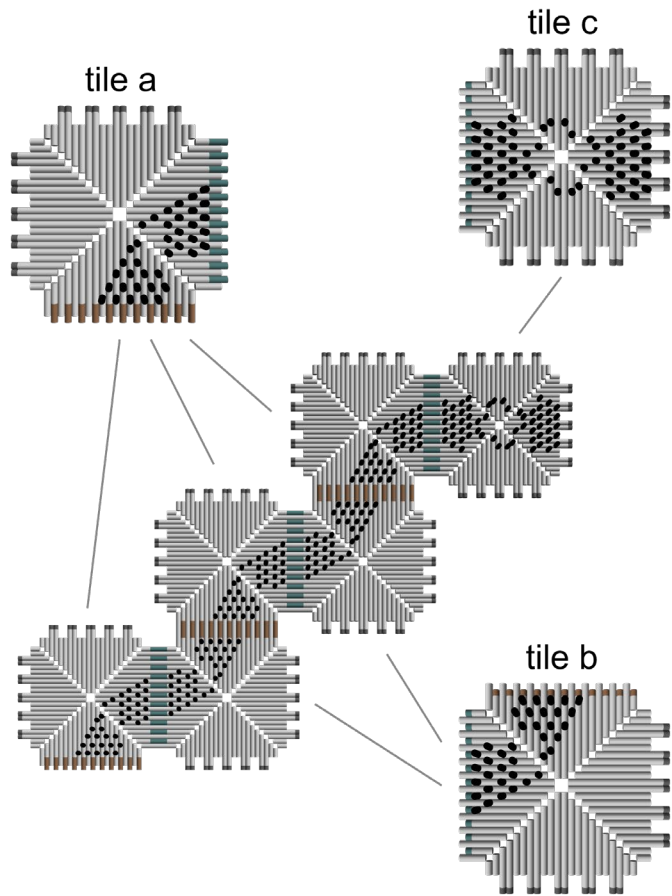
Does self-occluding edges affect the yield of tile assembly?



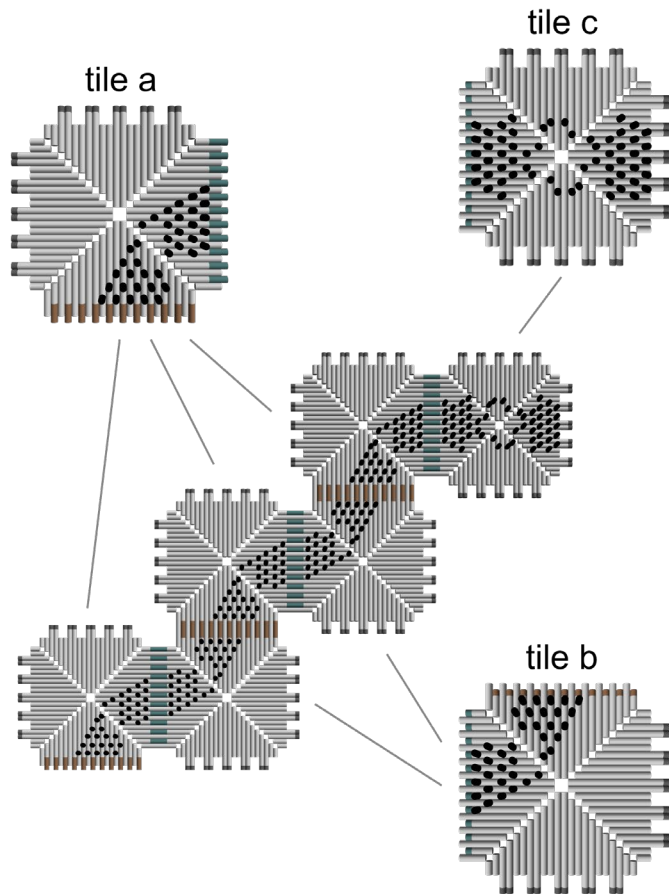
Does self-occluding edges affect the yield of tile assembly? **Yes**



Invaders with variable sizes



Invaders with variable sizes



monomers = $\{a, b, c\}$

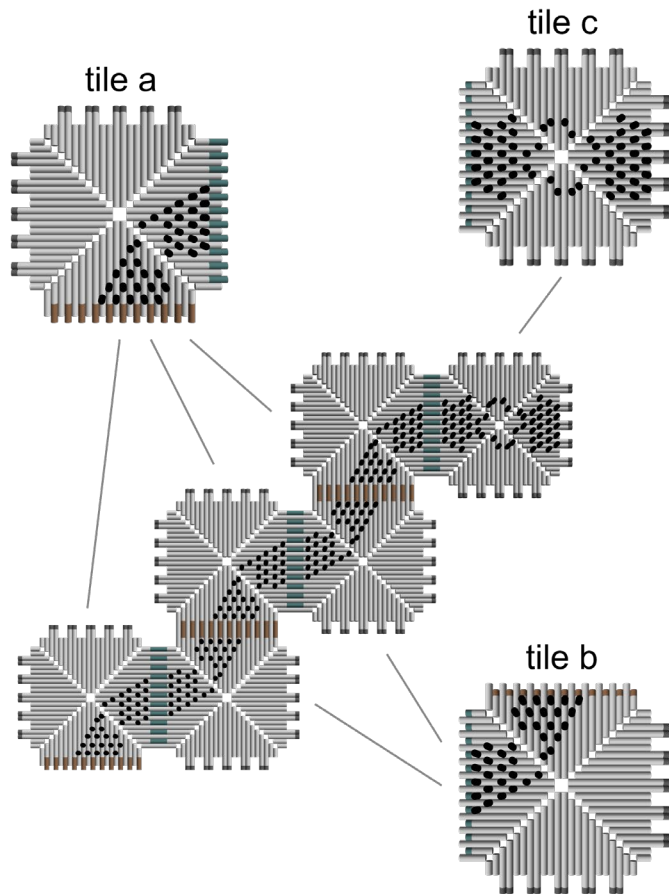
rules = $\{\{a, b\}, \{a, c\}, \{b, a\}\}$

rates = $\{k, k, k\}$, where $k = 4.5 \times 10^5$

maxlength = 20

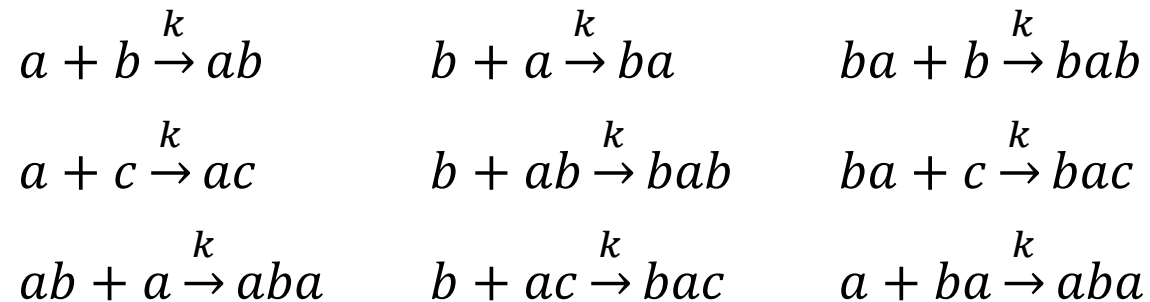
reactions = `polymerCRN[monomers, rules, rates, maxlength]`

Invaders with variable sizes

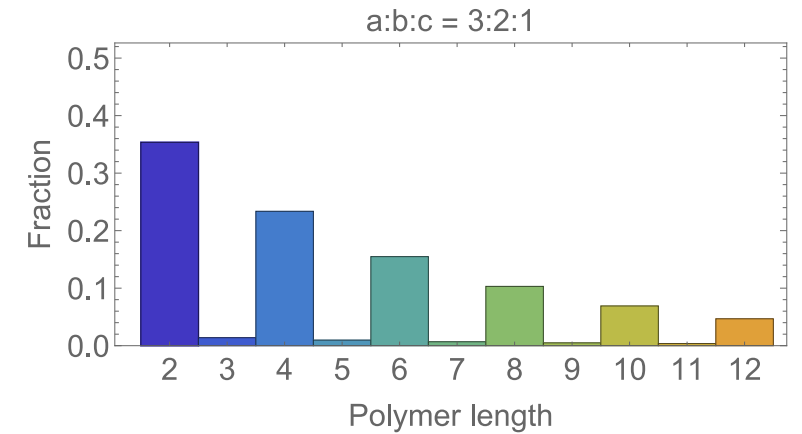
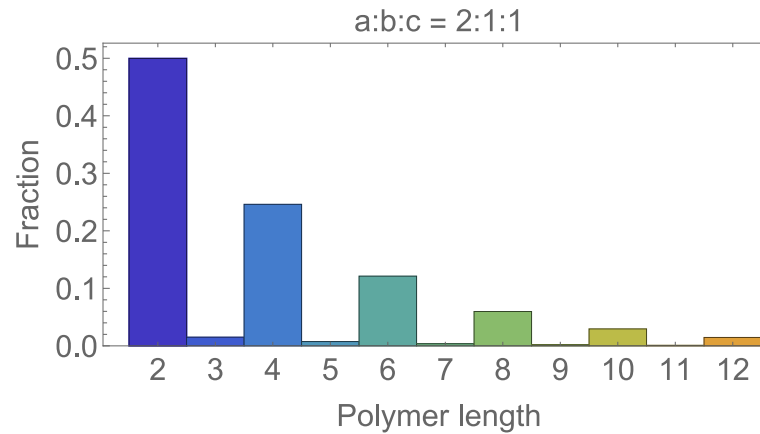
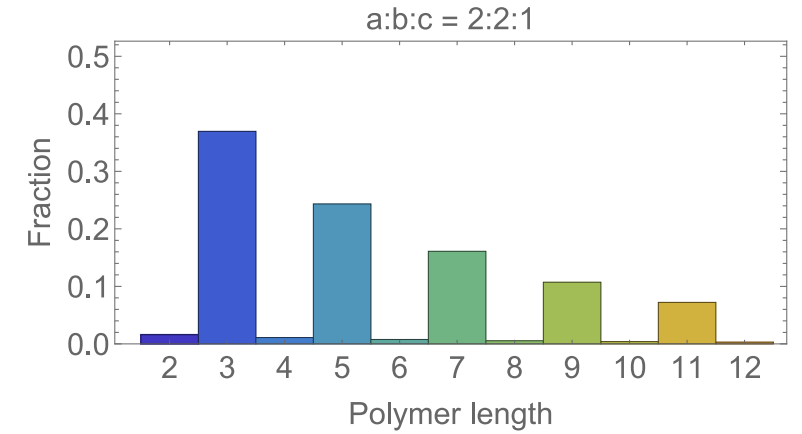
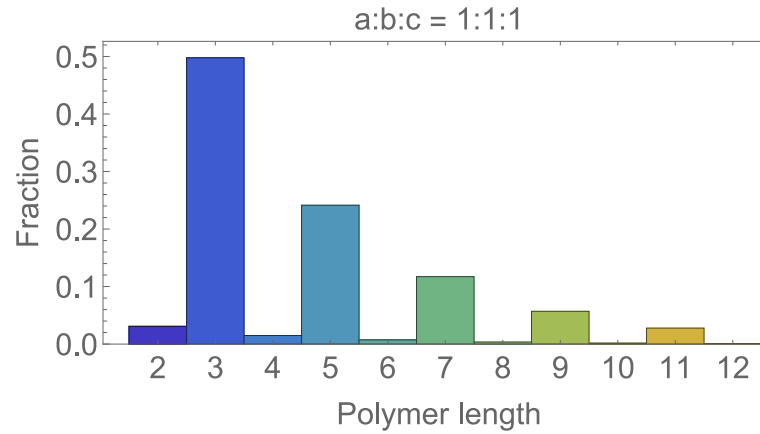
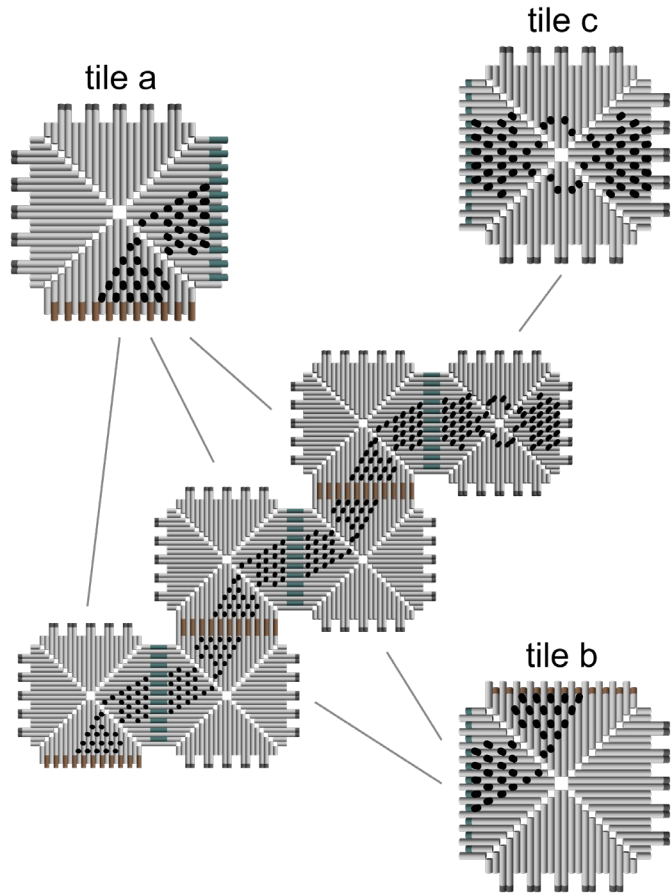


monomers = $\{a, b, c\}$
rules = $\{\{a, b\}, \{a, c\}, \{b, a\}\}$
rates = $\{k, k, k\}$, where $k = 4.5 \times 10^5$
maxlength = 20
reactions = `polymerCRN[monomers, rules, rates, maxlength]`

Example reactions enumerated with maxlength = 3:

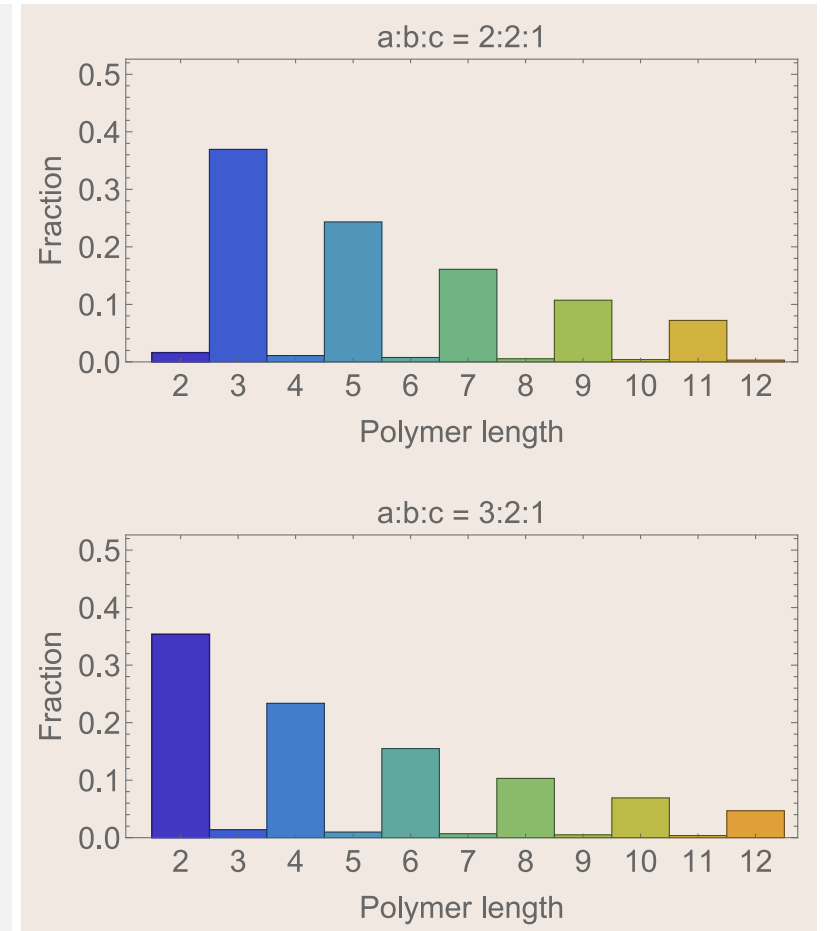
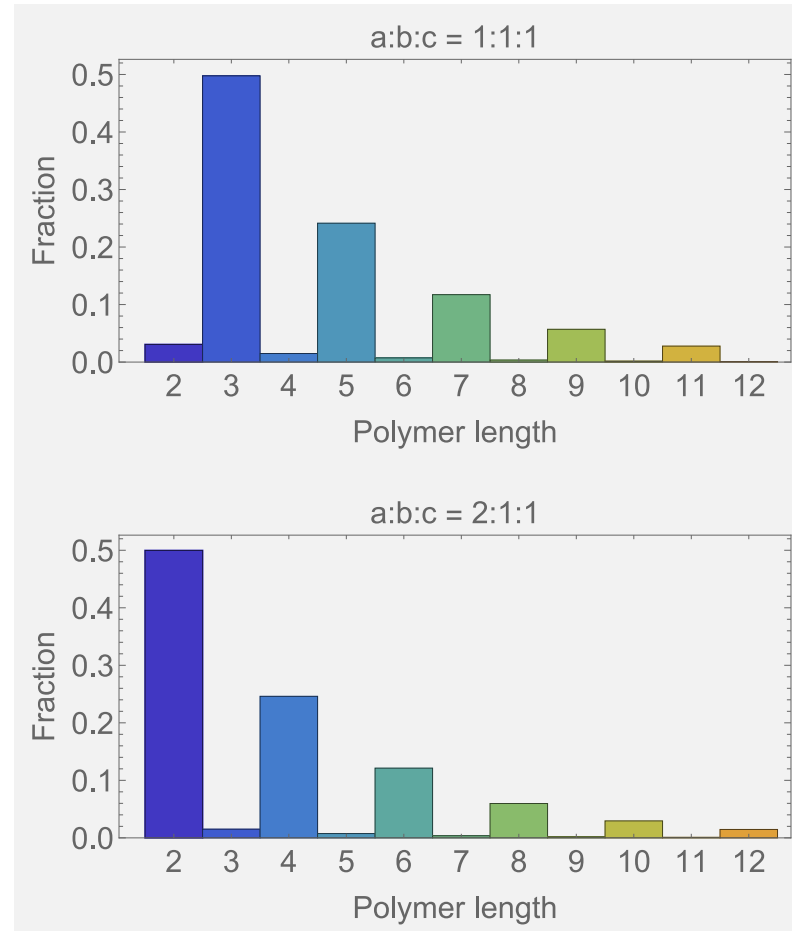
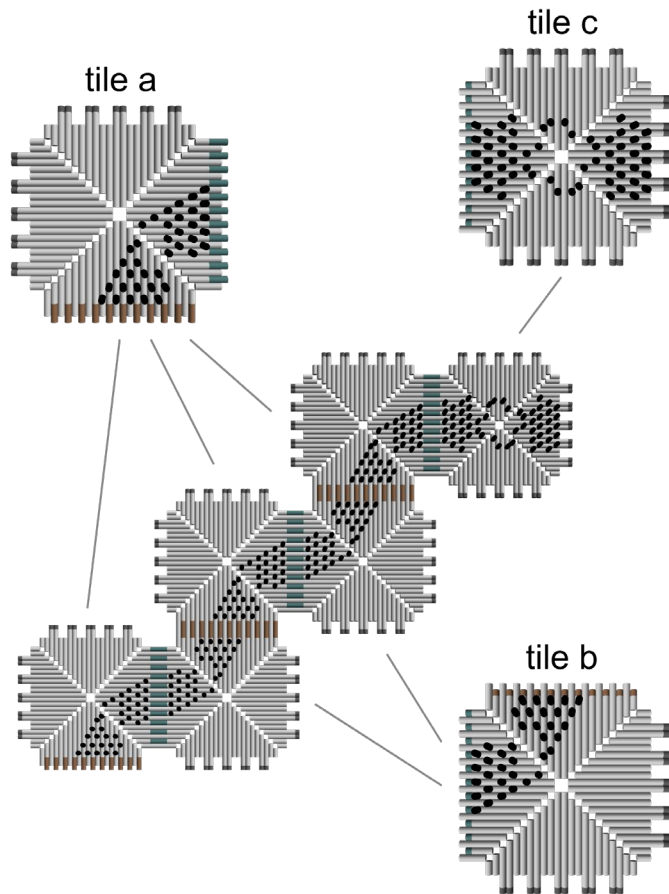


Invaders with variable sizes



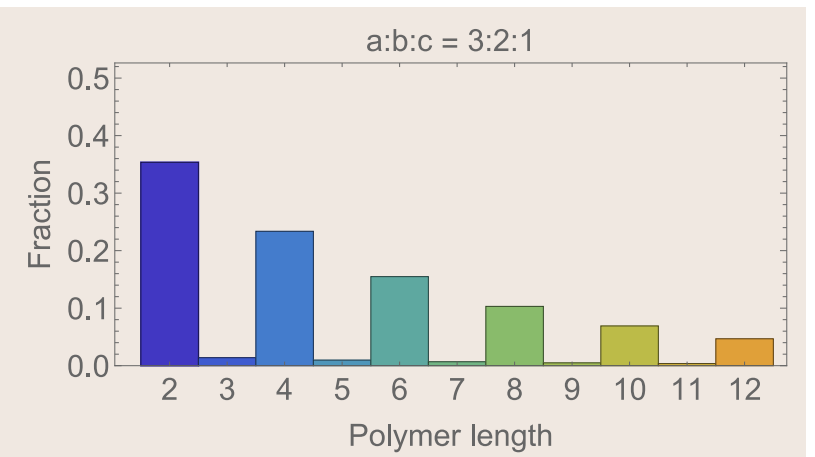
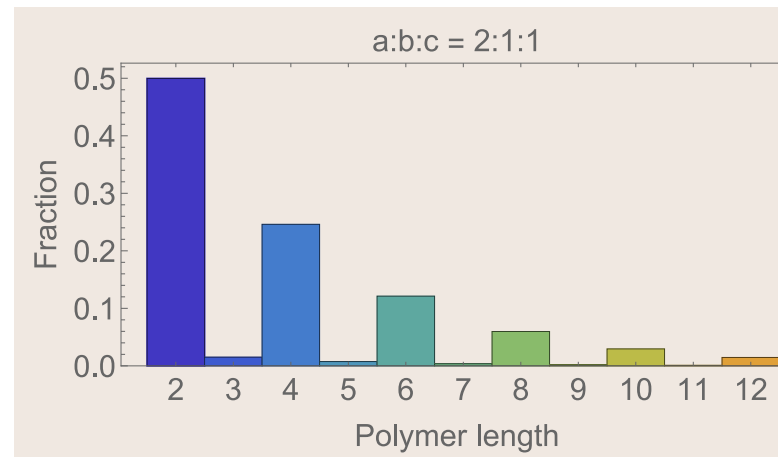
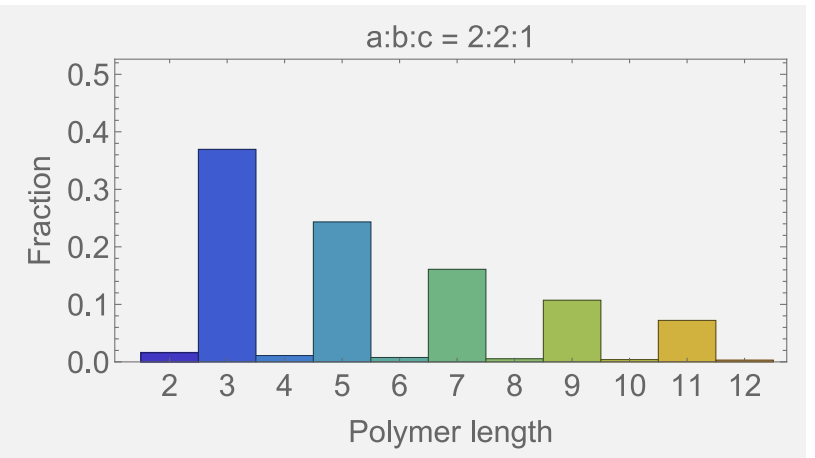
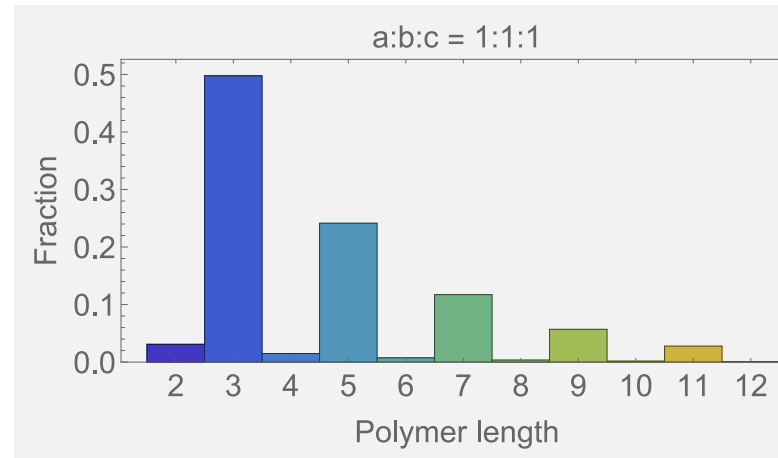
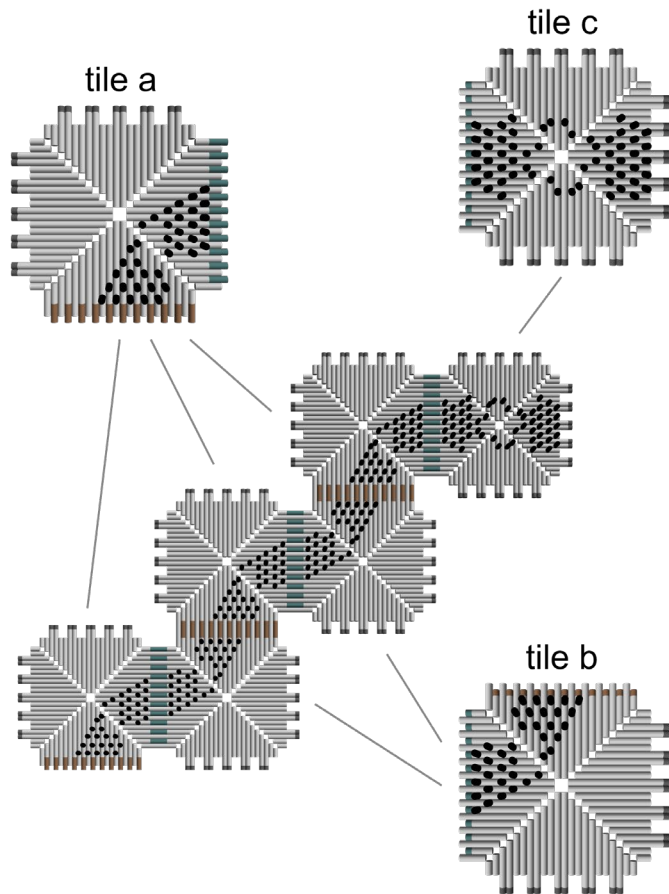
Invaders with variable sizes

lower tile ratio $c : (a + b)$ results in longer polymers

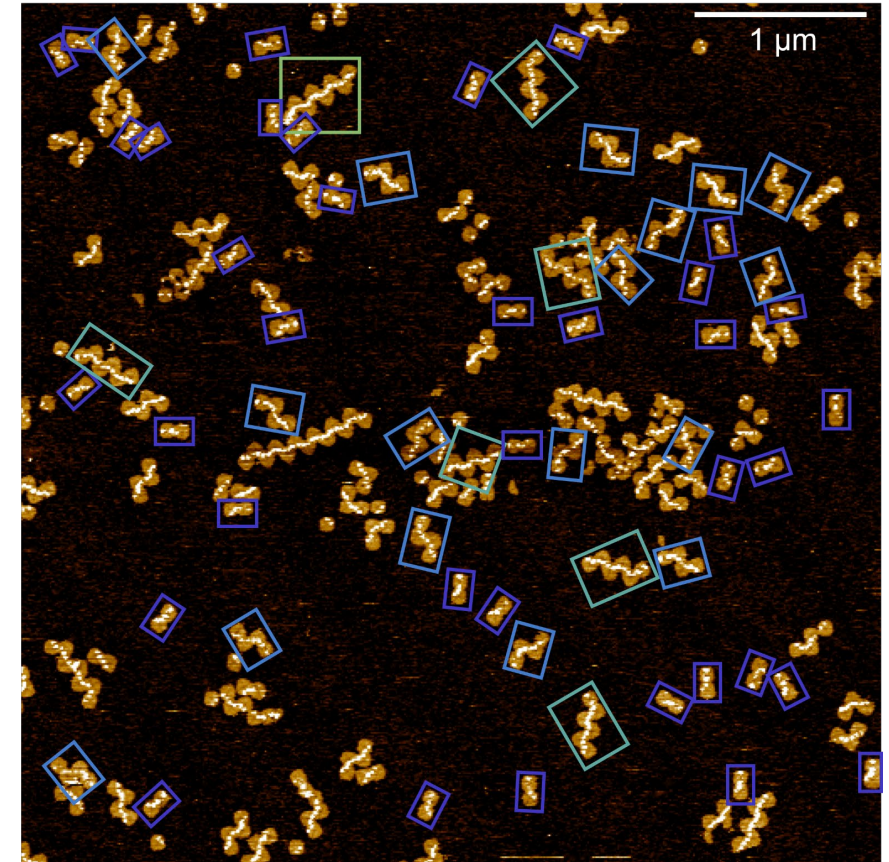
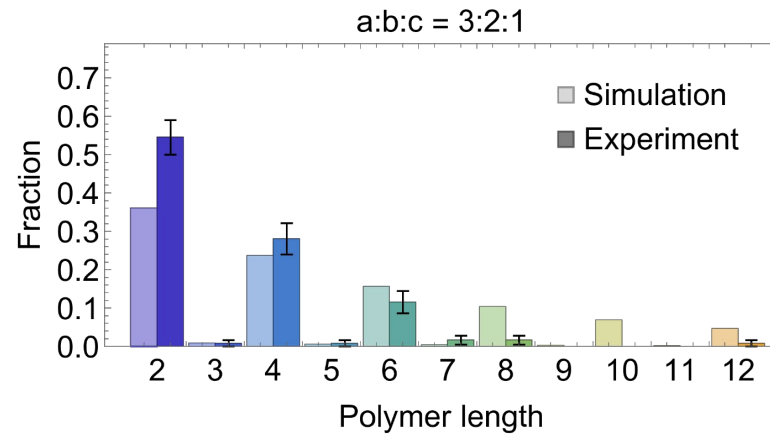
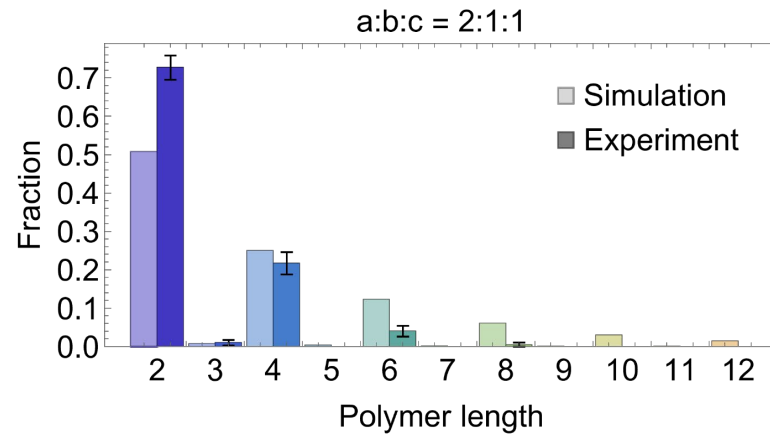
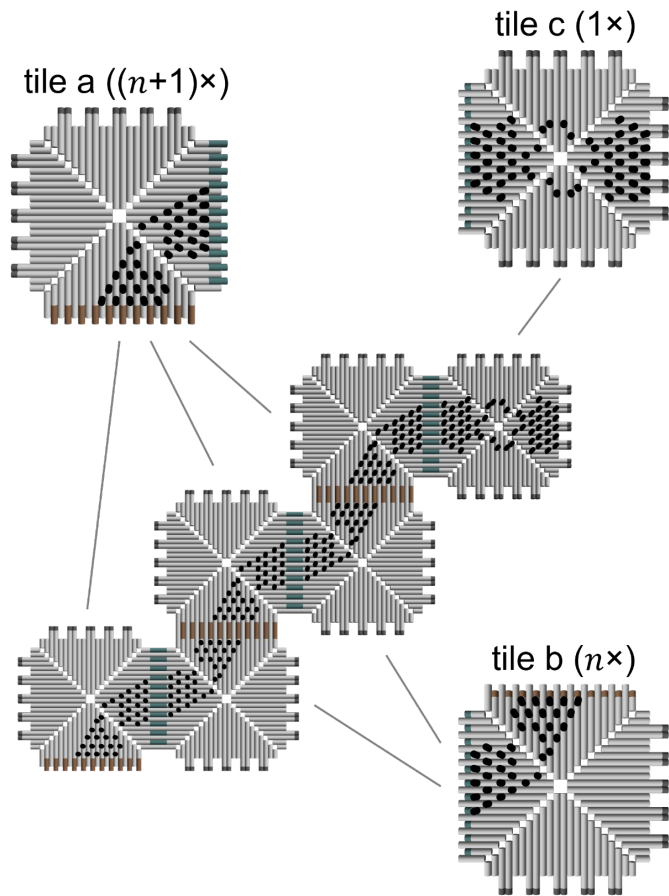


Invaders with variable sizes

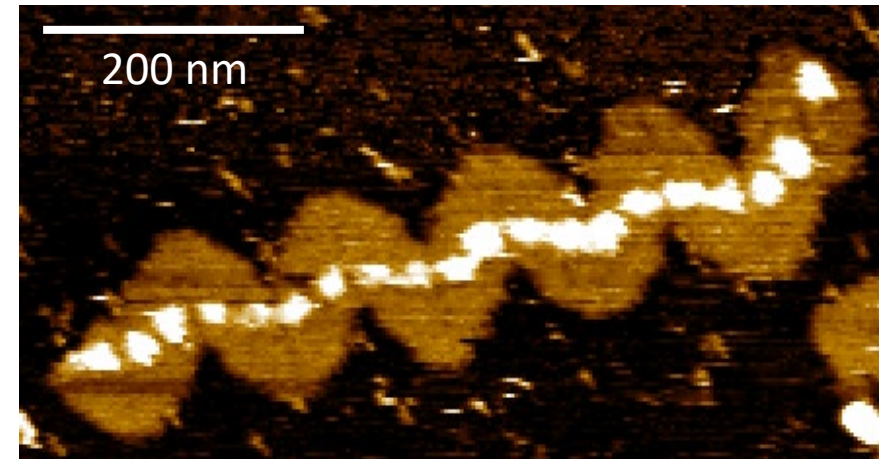
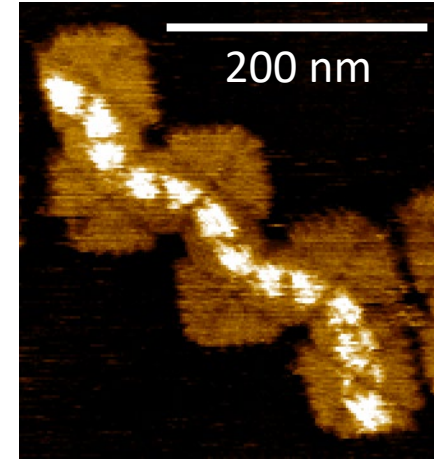
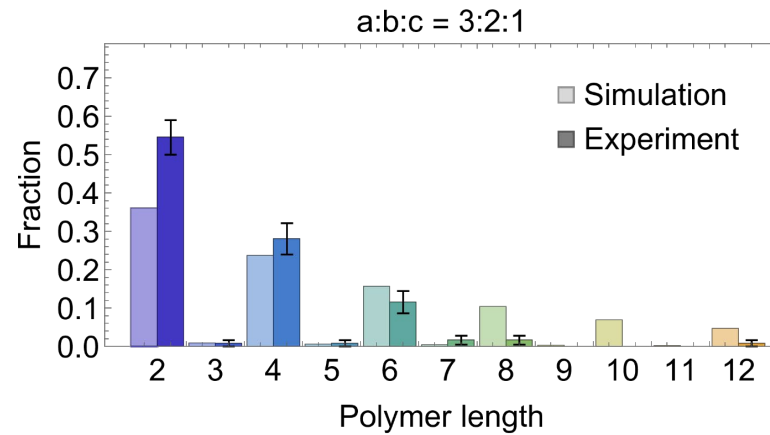
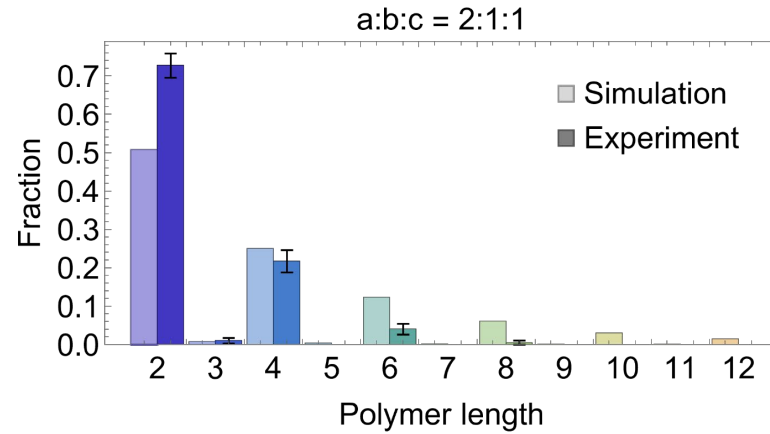
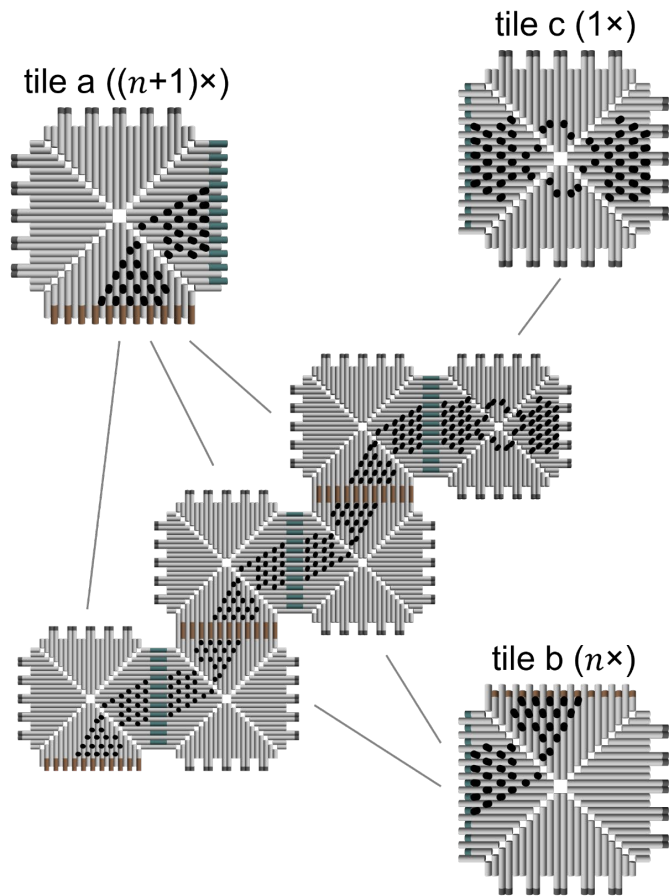
tile ratio $a:b$ determines whether even or odd-length polymers are favored



Invaders with variable sizes

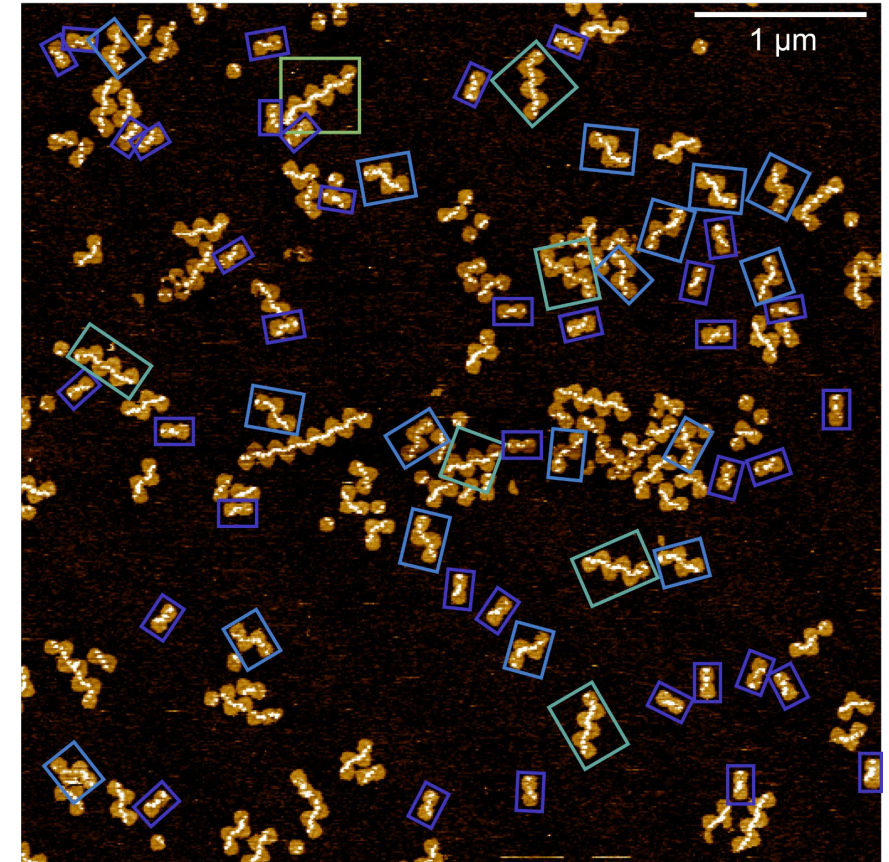
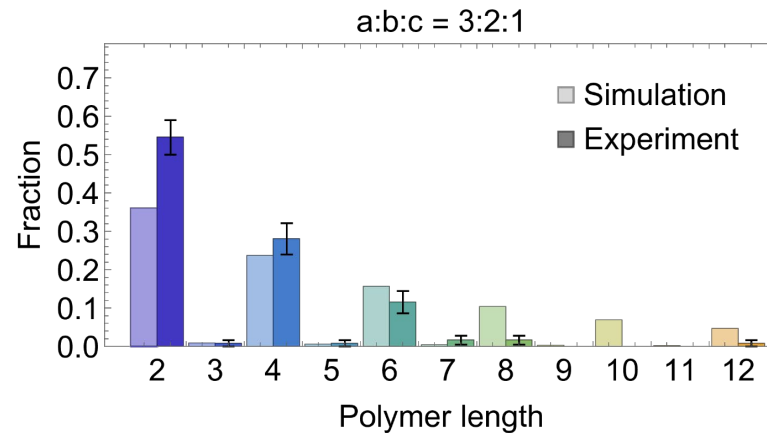
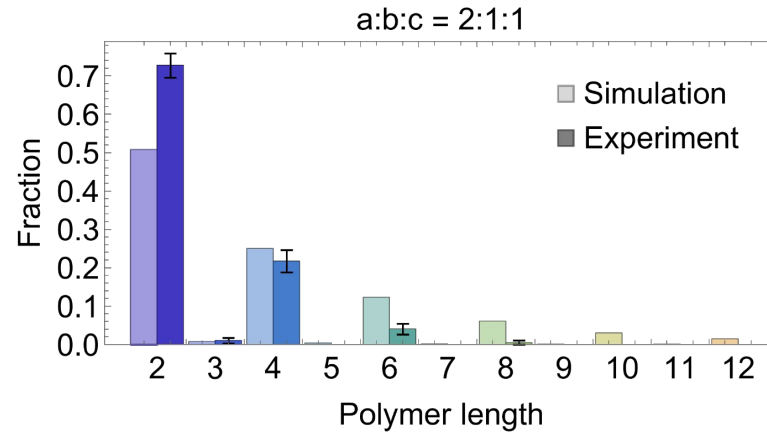
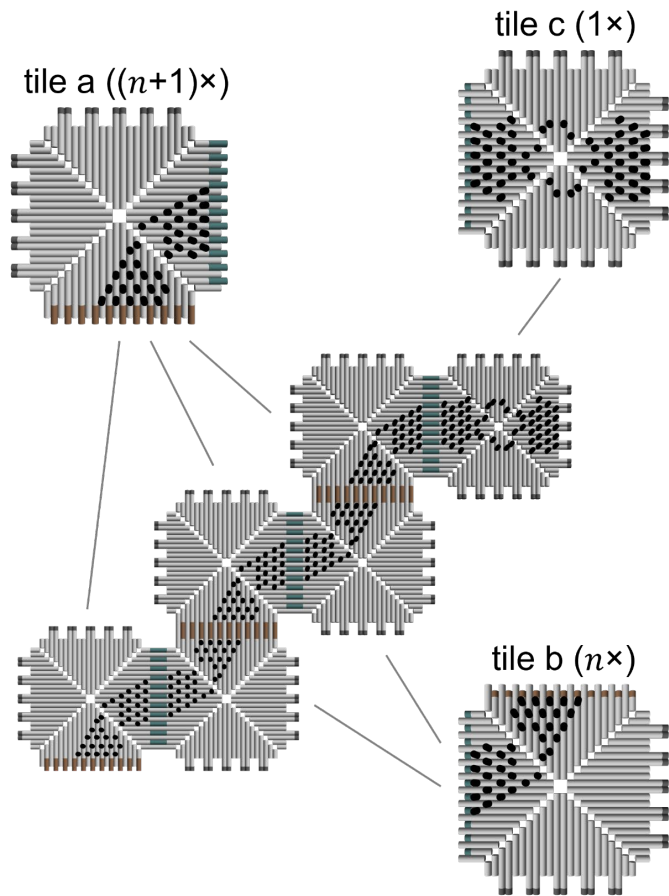


Invaders with variable sizes

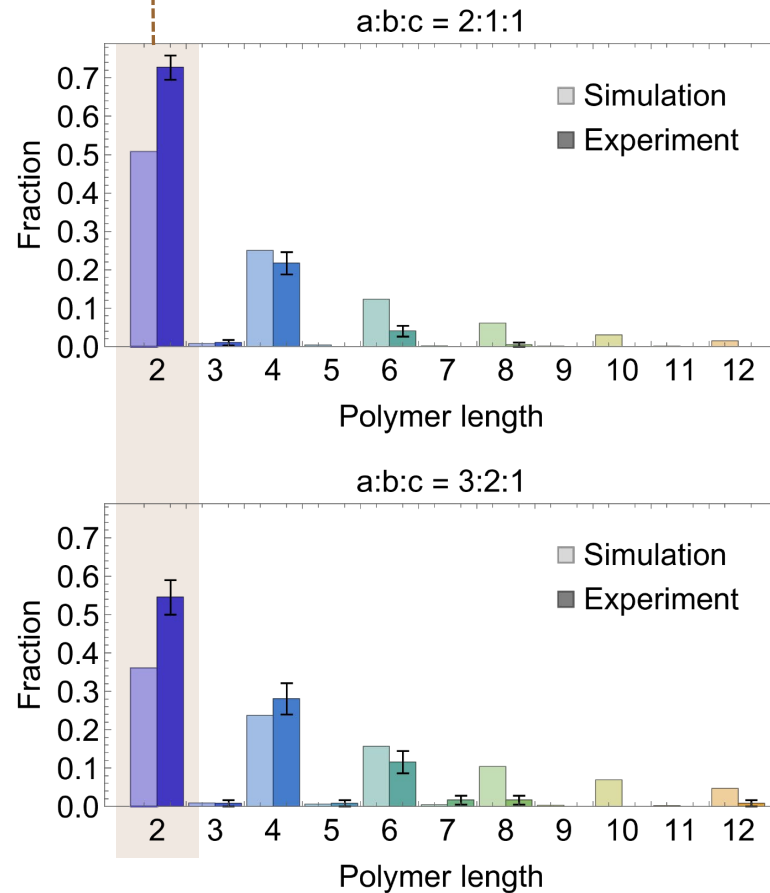
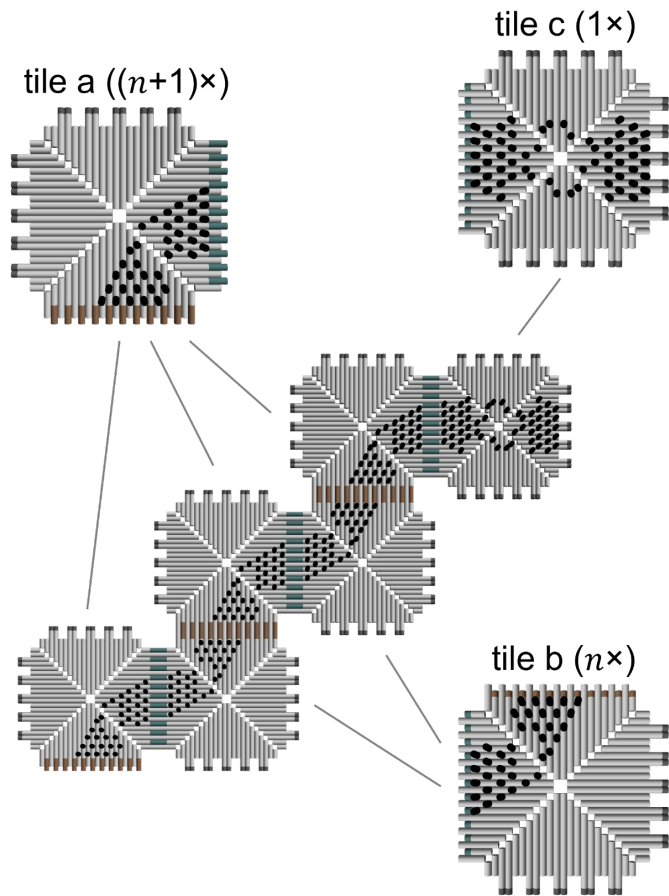


Invaders with variable sizes

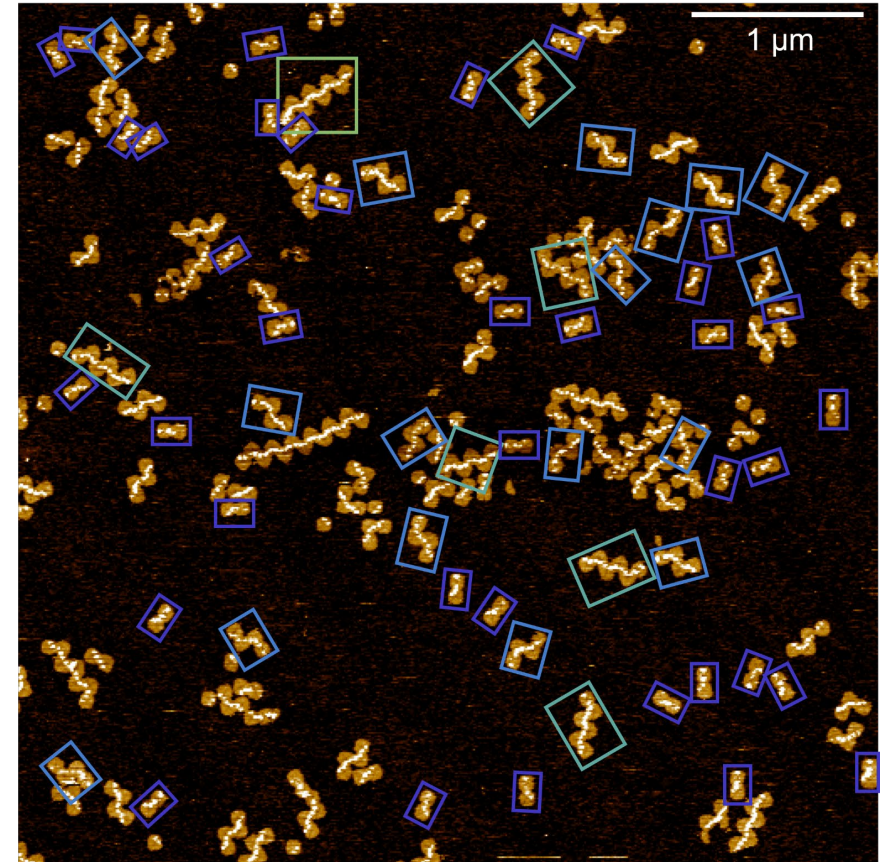
Mystery 1: roughly 50% of the structures contained just tiles a and b, contradictory to the simulation prediction that the concentrations of ab-only polymers should be approximately zero.



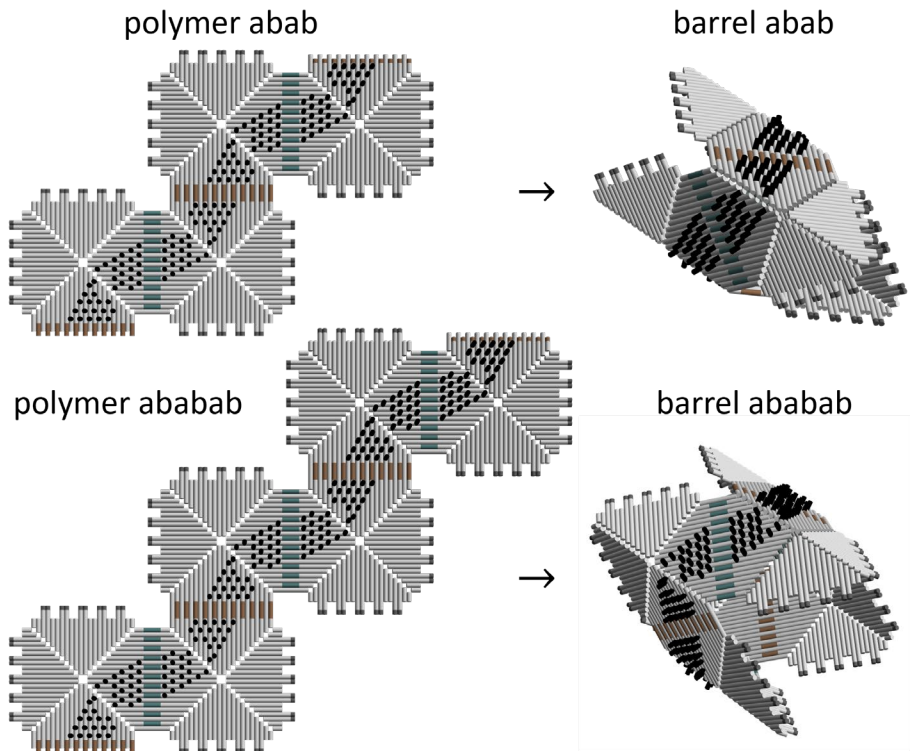
Invaders with variable sizes



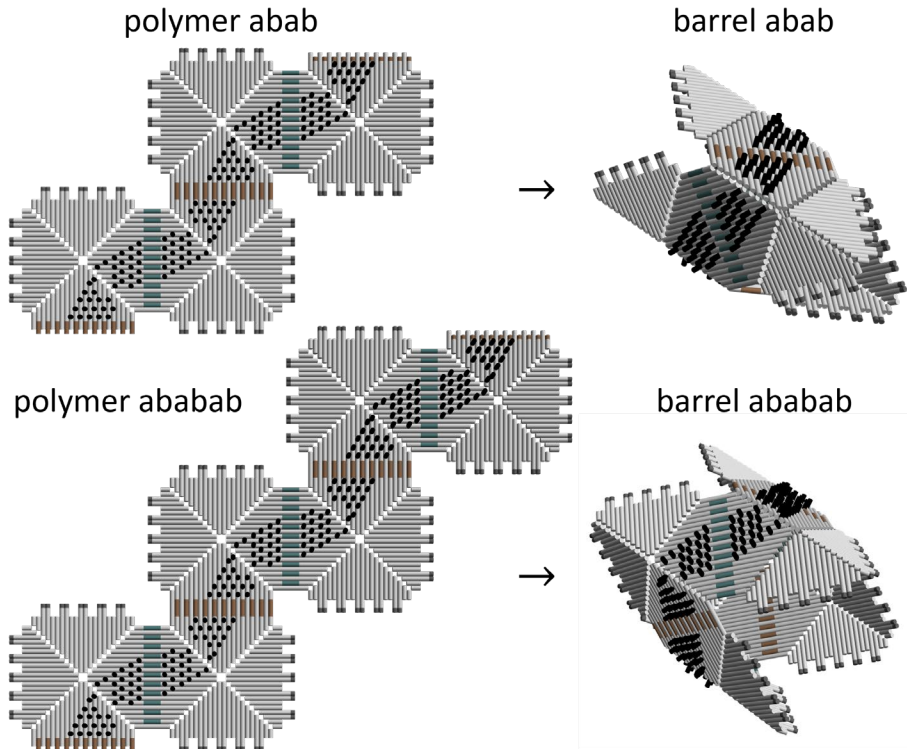
Mystery 2: more ac dimers (length = 2) were observed in experiments than what simulations predicted.



Hypothesis: barrel formation



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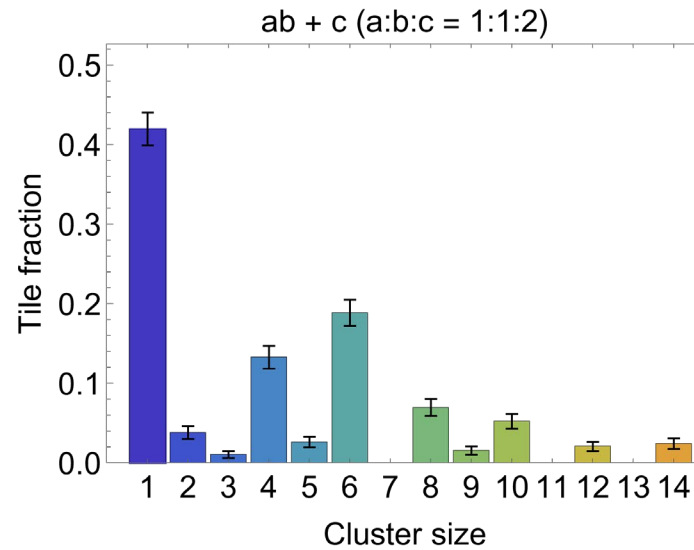
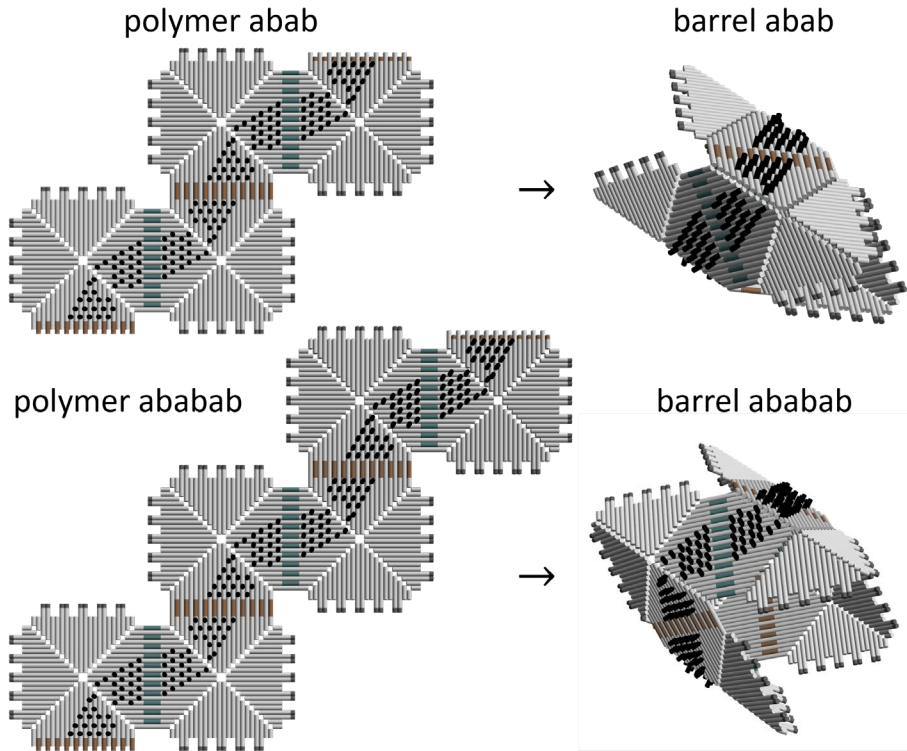


Mystery 1: roughly 50% of the structures contained just tiles a and b, contradictory to the simulation prediction that the concentrations of ab-only polymers should be approximately zero. ✓

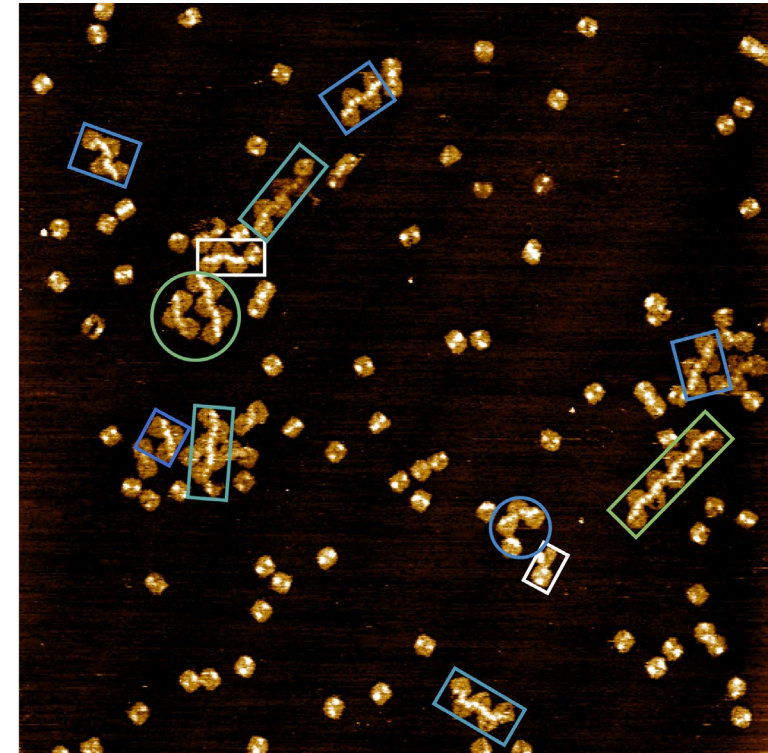
Mystery 2: more ac dimers (length = 2) were observed in experiments than what simulations predicted. ✓

Reactions like $abab + ac \rightarrow ababac$ cannot take place if polymers like $abab$ have formed barrel structures.

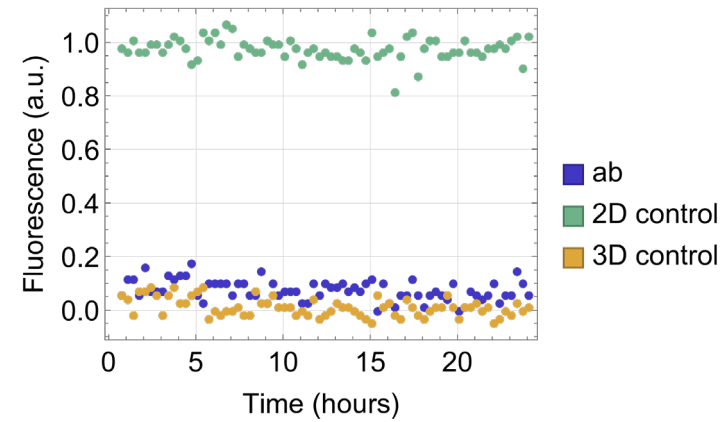
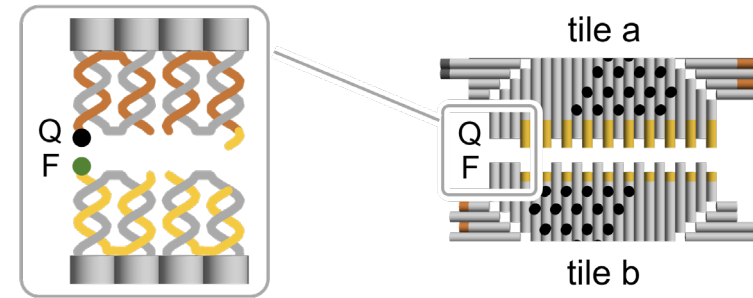
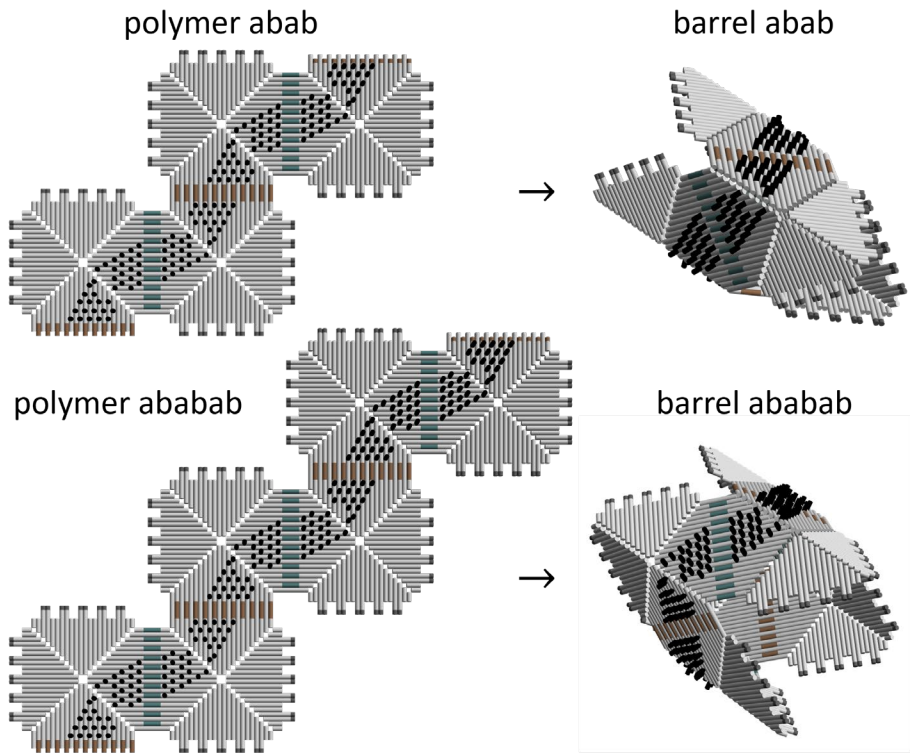
Hypothesis: barrel formation



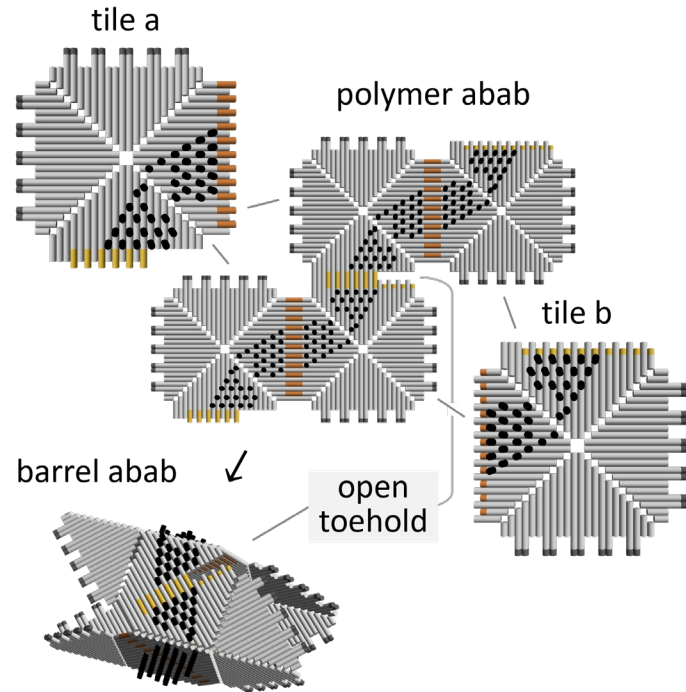
annealed tiles a and b at 1:1 ratio
and then added tile c to the mixture



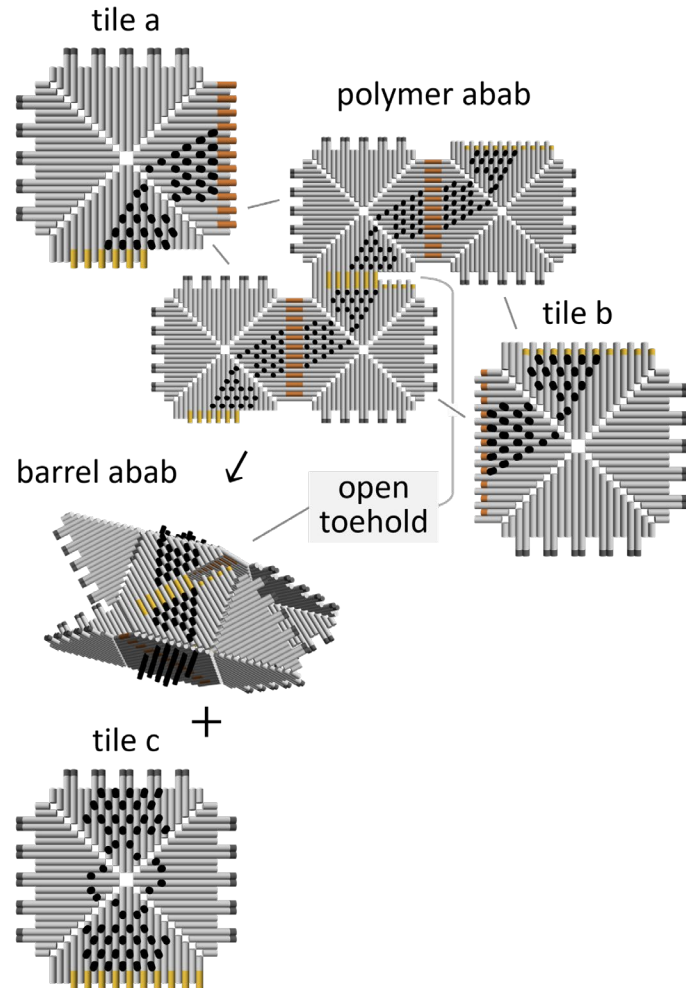
Hypothesis: barrel formation ✓



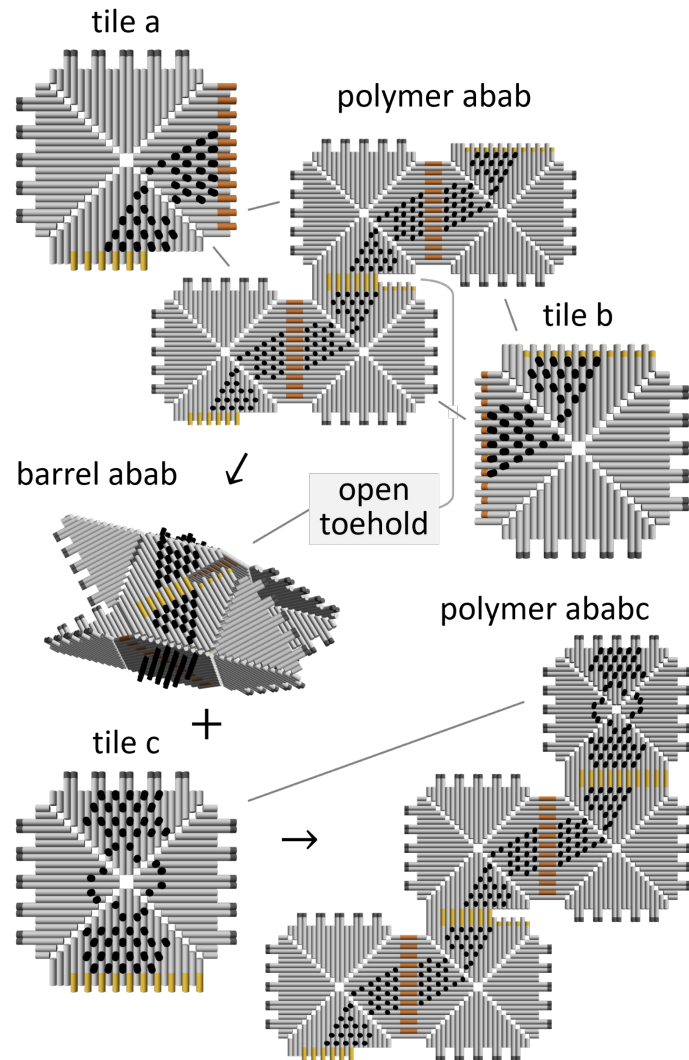
Reconfiguration of barrels to flat structures



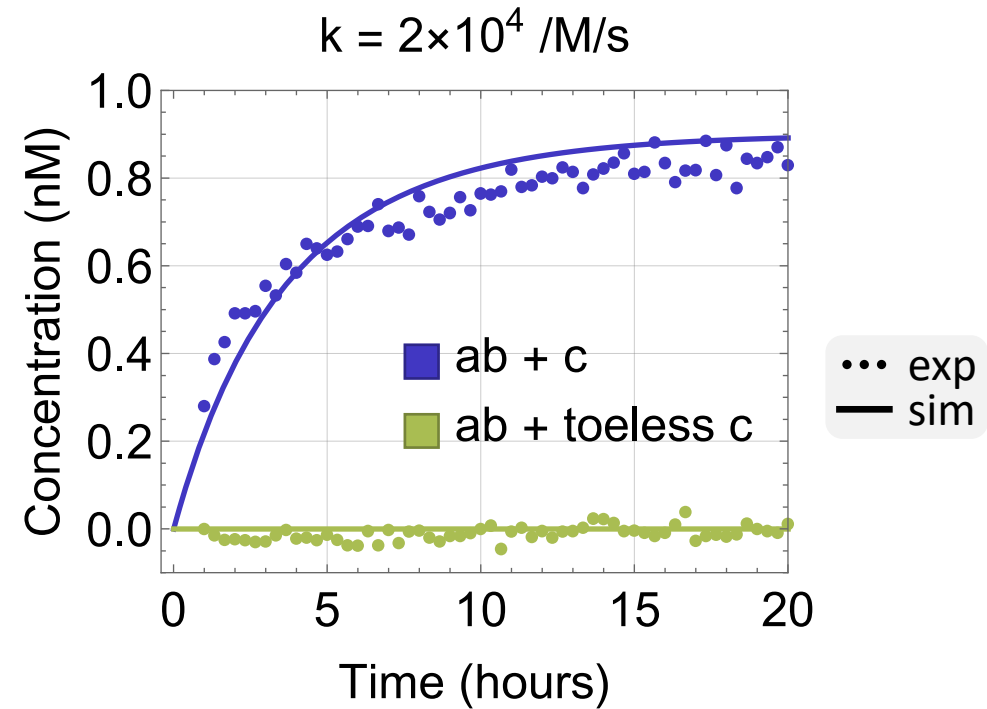
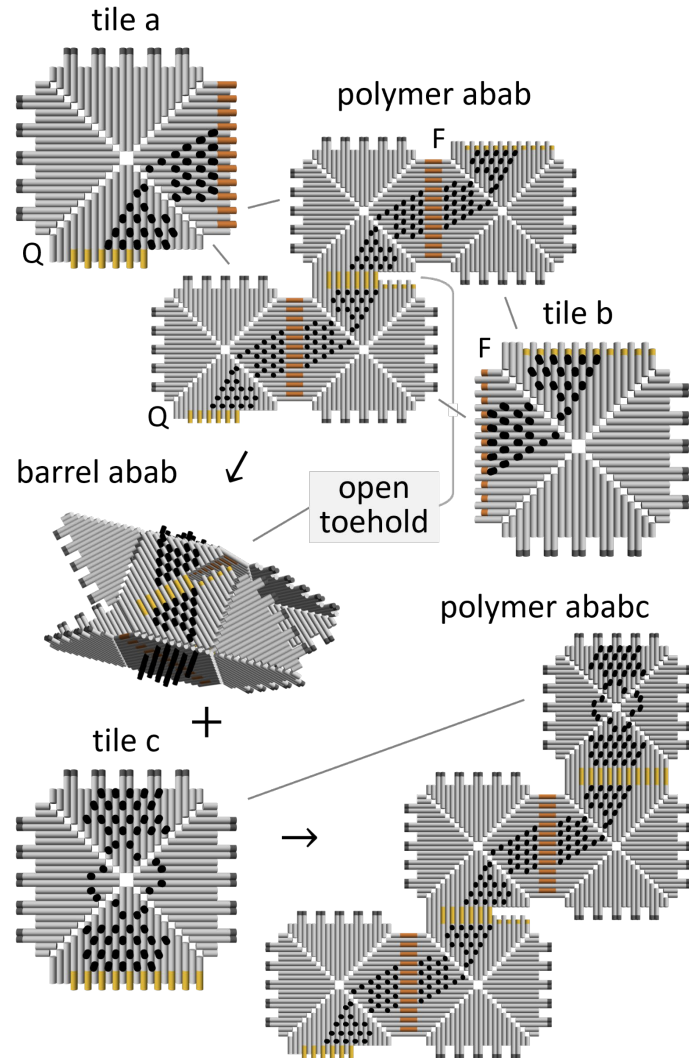
Reconfiguration of barrels to flat structures



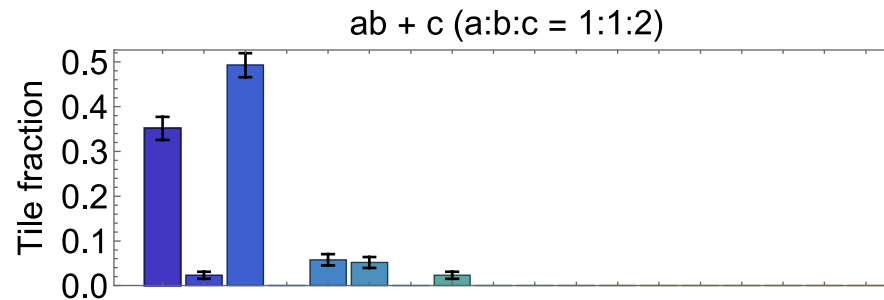
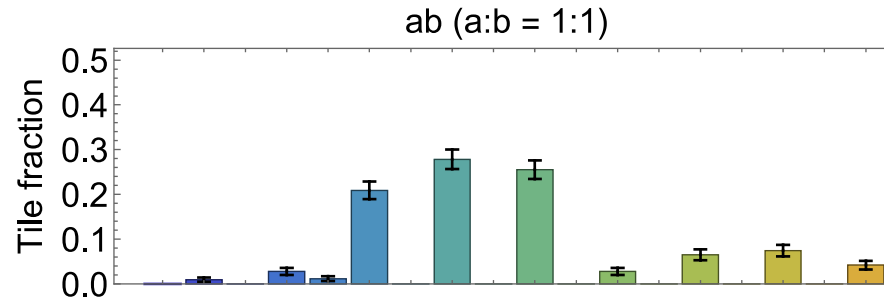
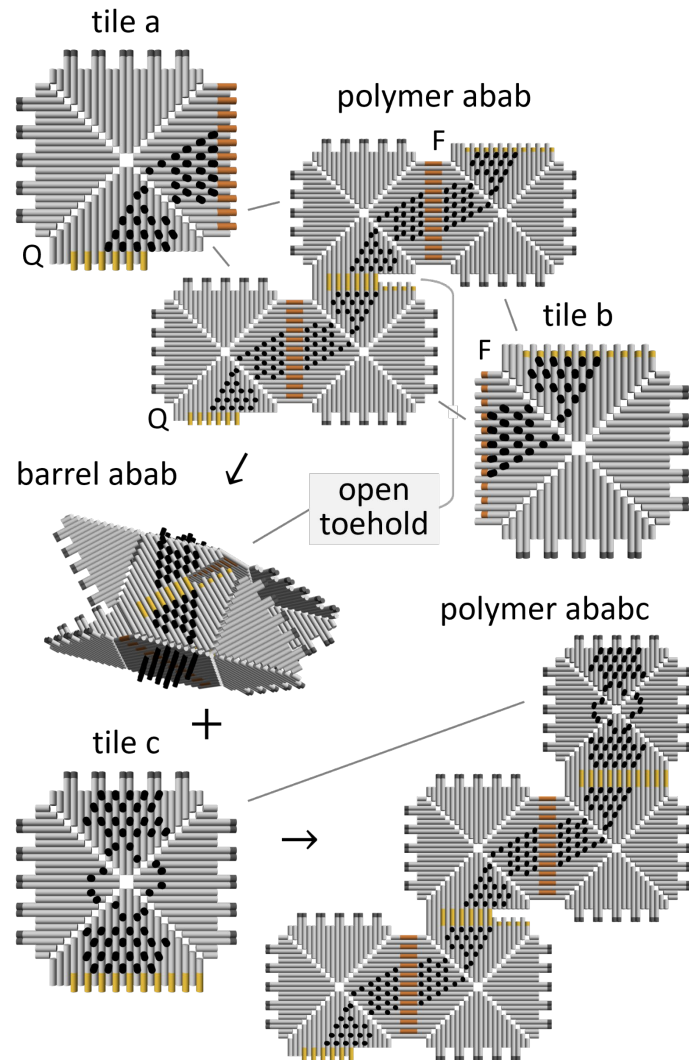
Reconfiguration of barrels to flat structures



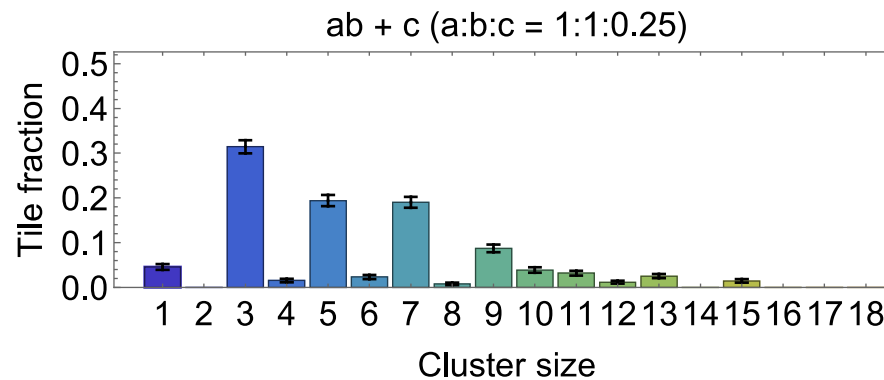
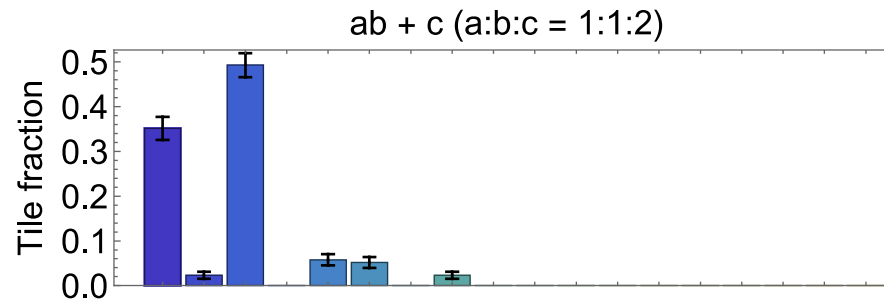
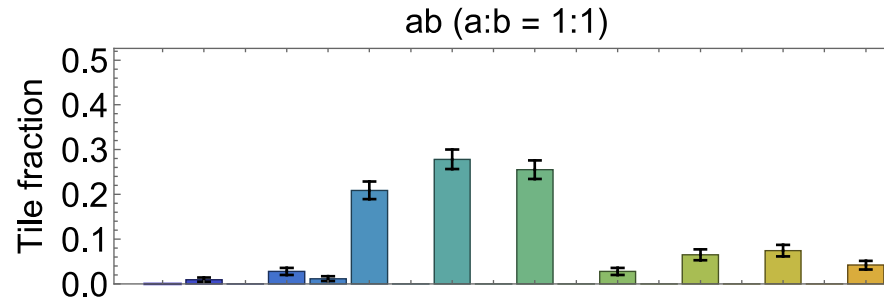
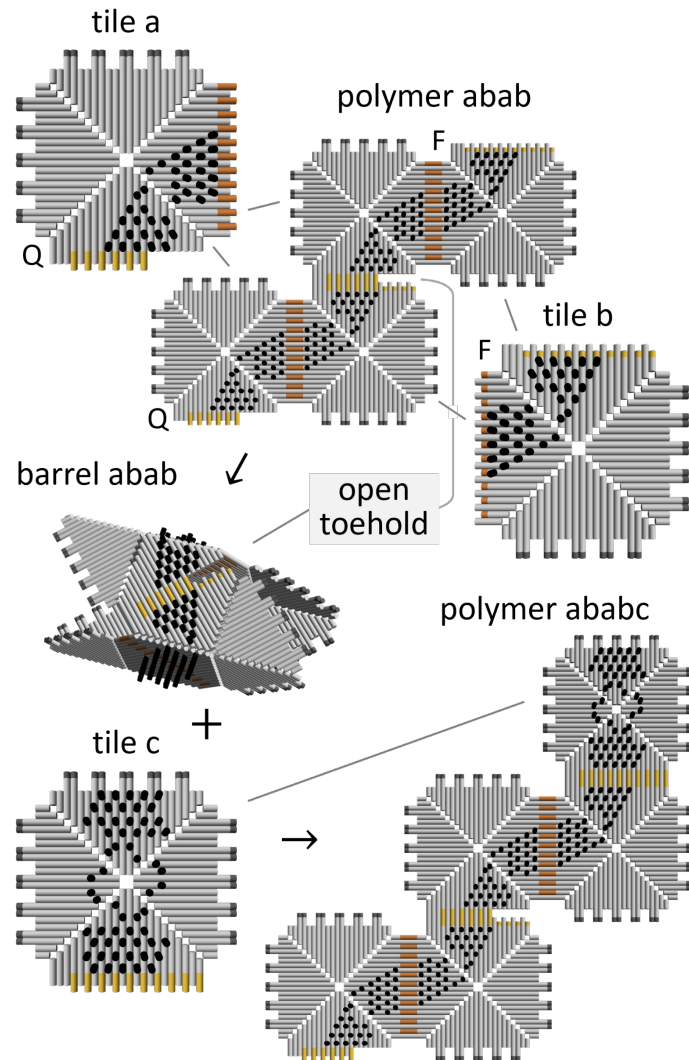
Reconfiguration of barrels to flat structures



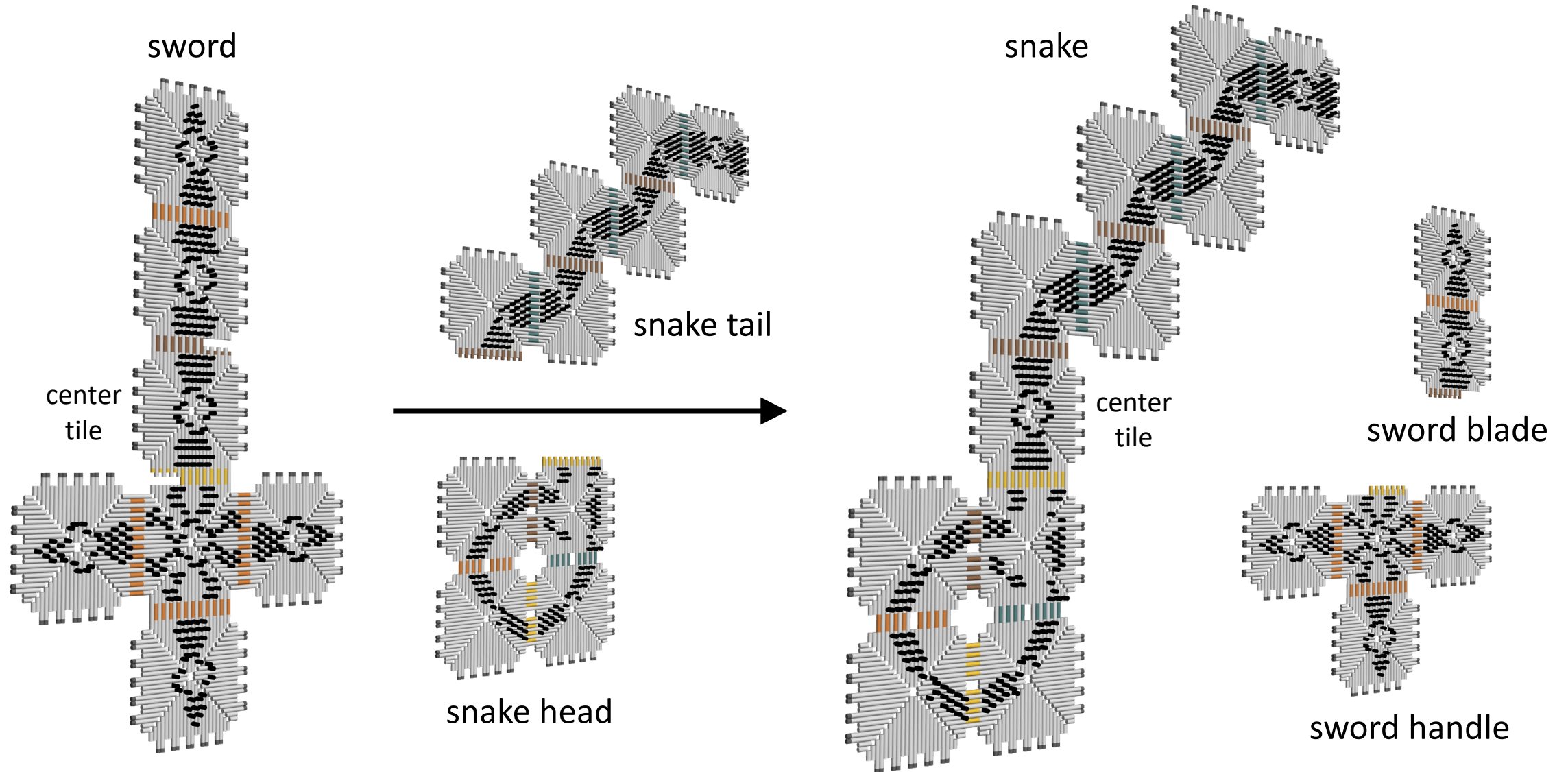
Reconfiguration of barrels to flat structures



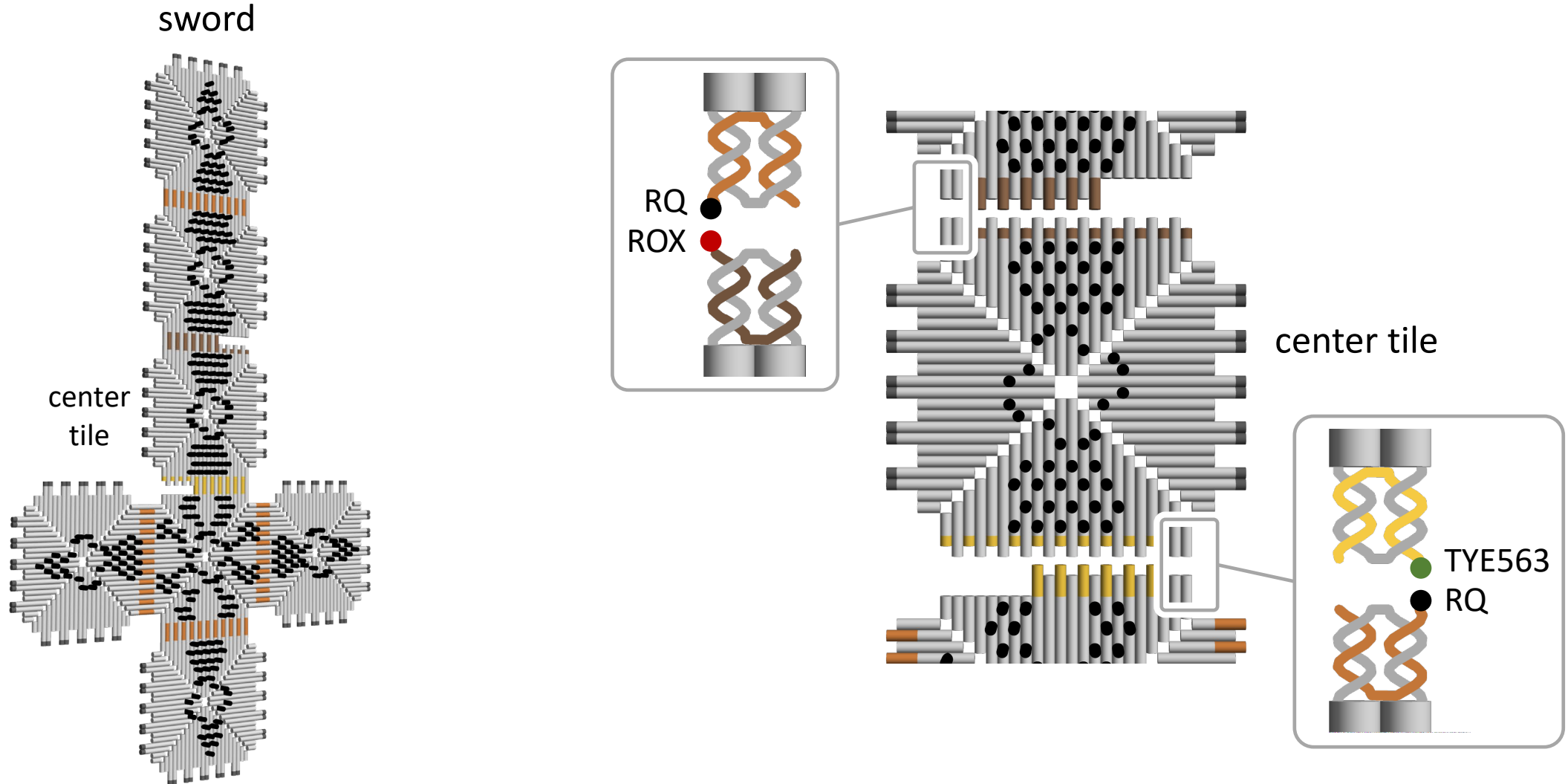
Reconfiguration of barrels to flat structures



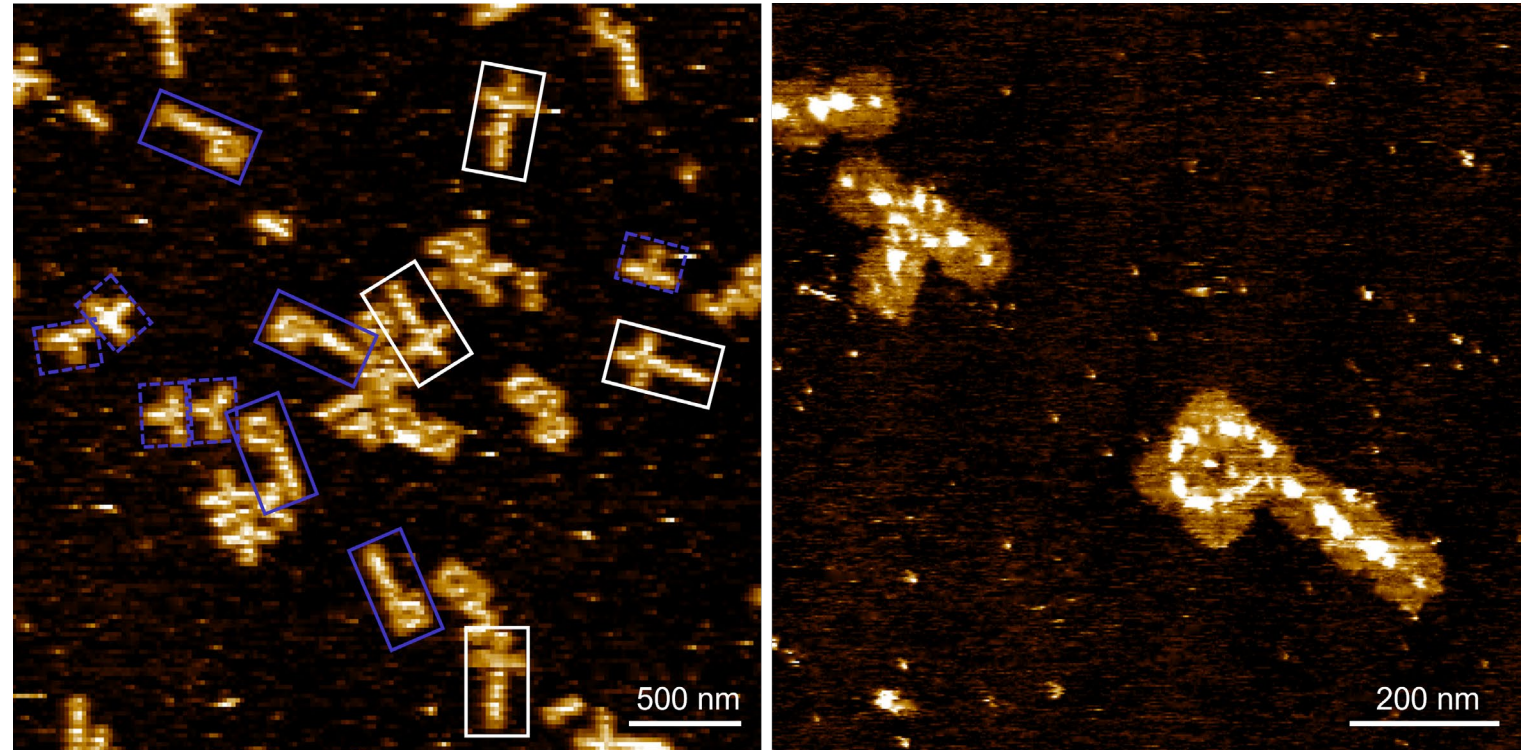
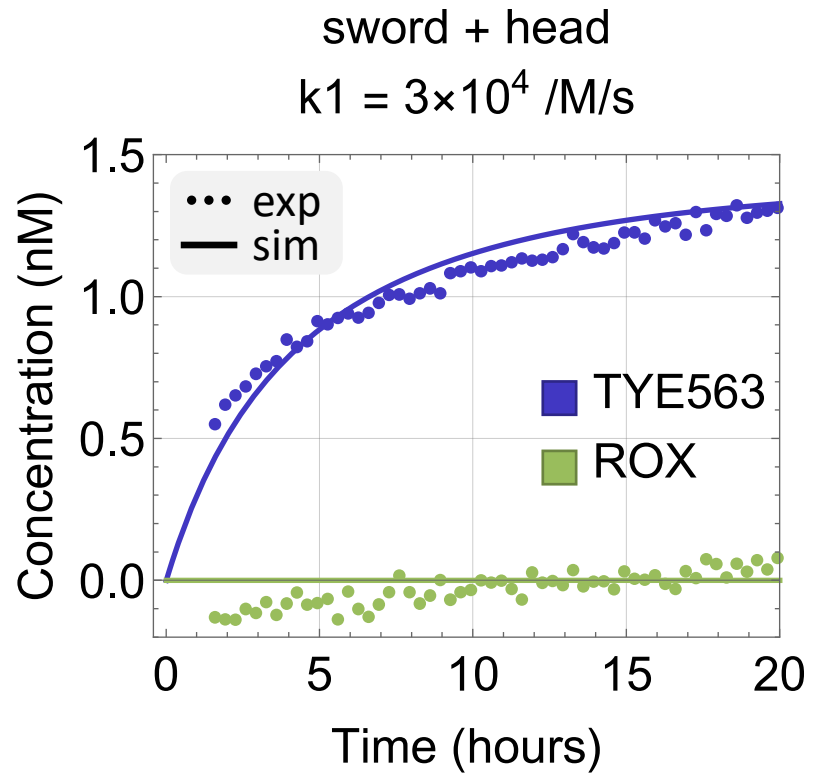
Simultaneous tile displacement



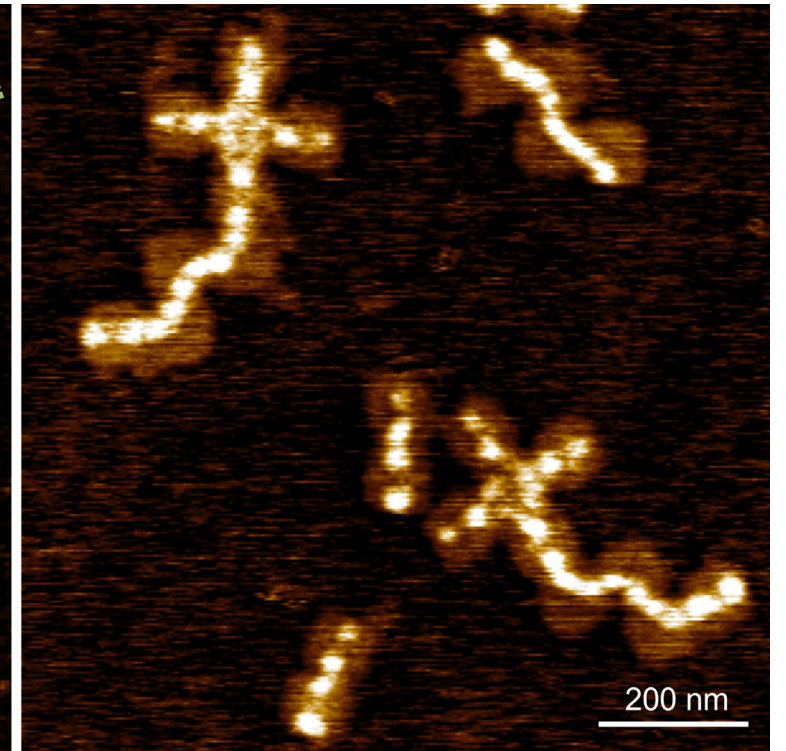
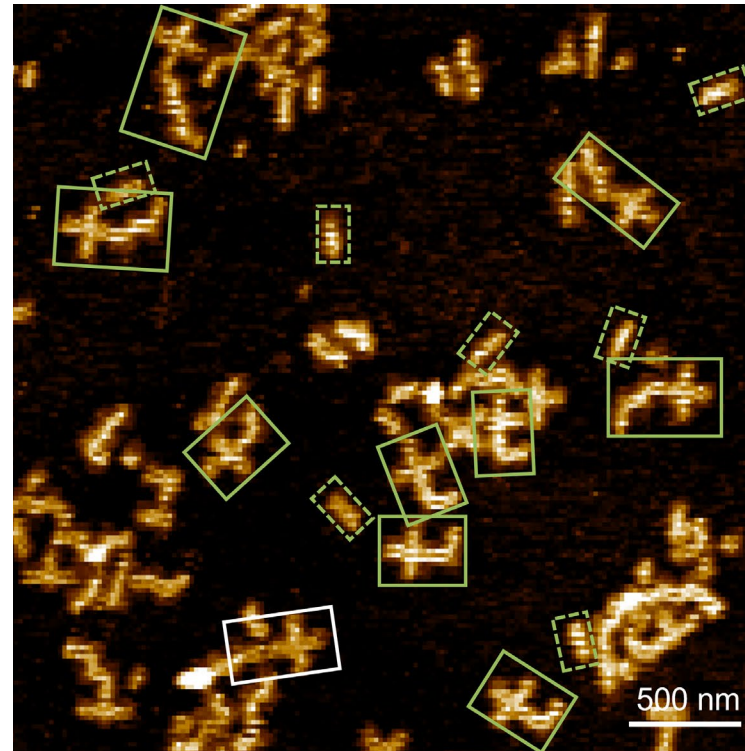
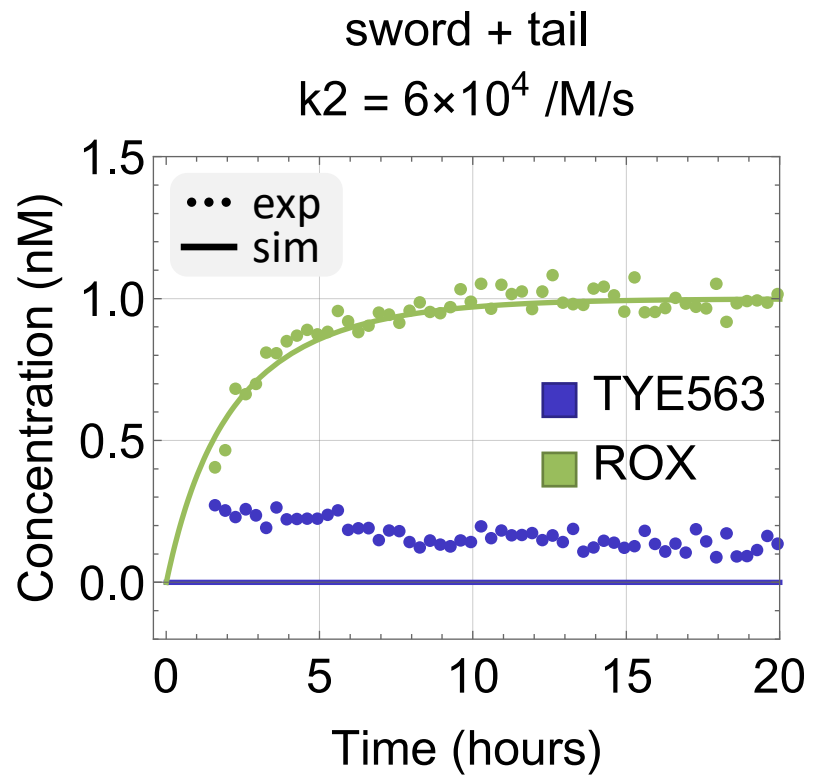
Simultaneous tile displacement



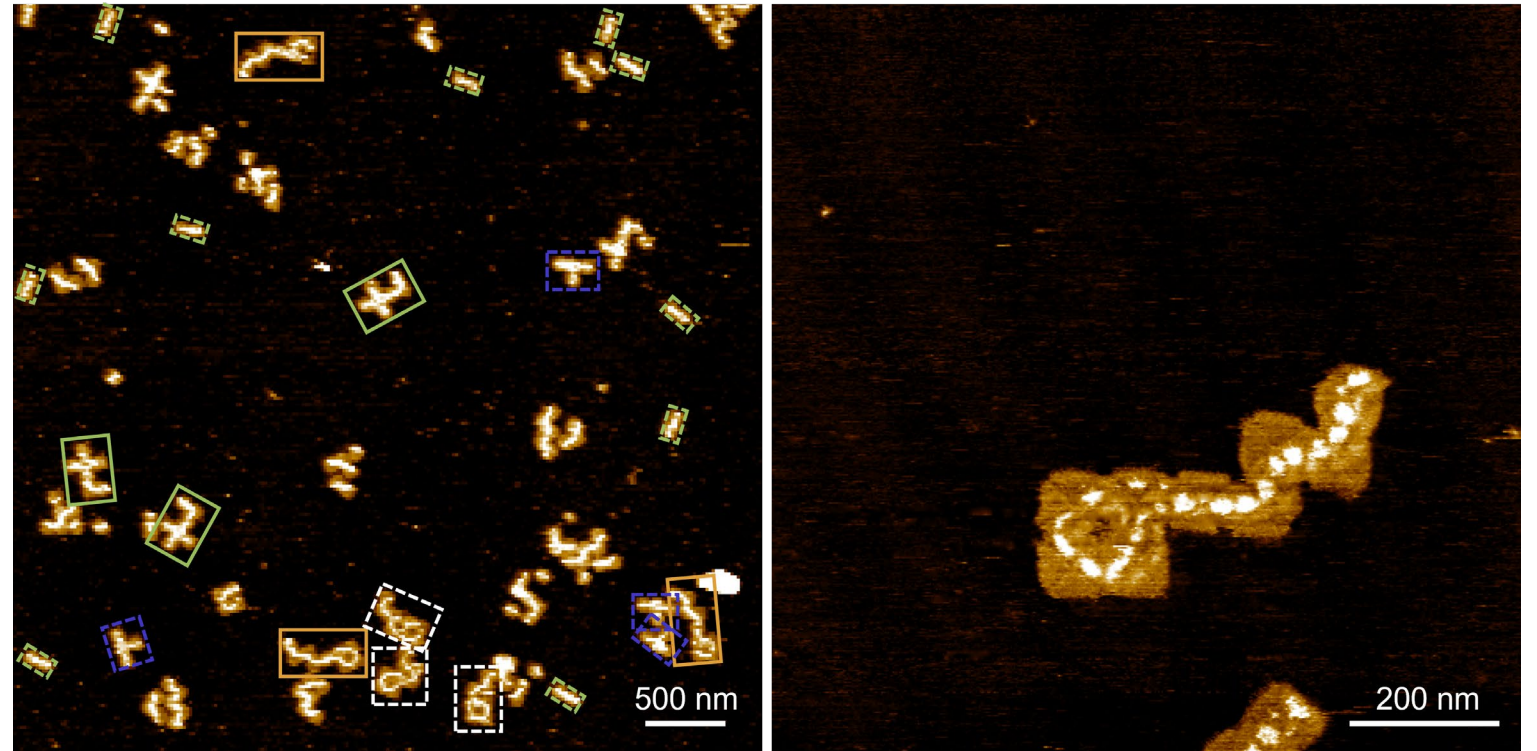
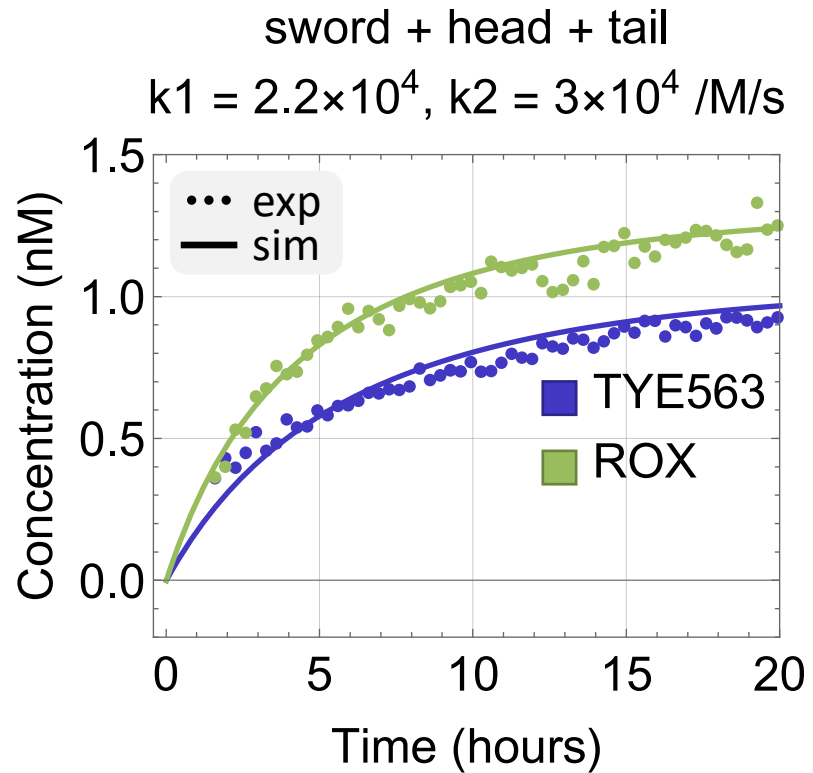
Simultaneous tile displacement



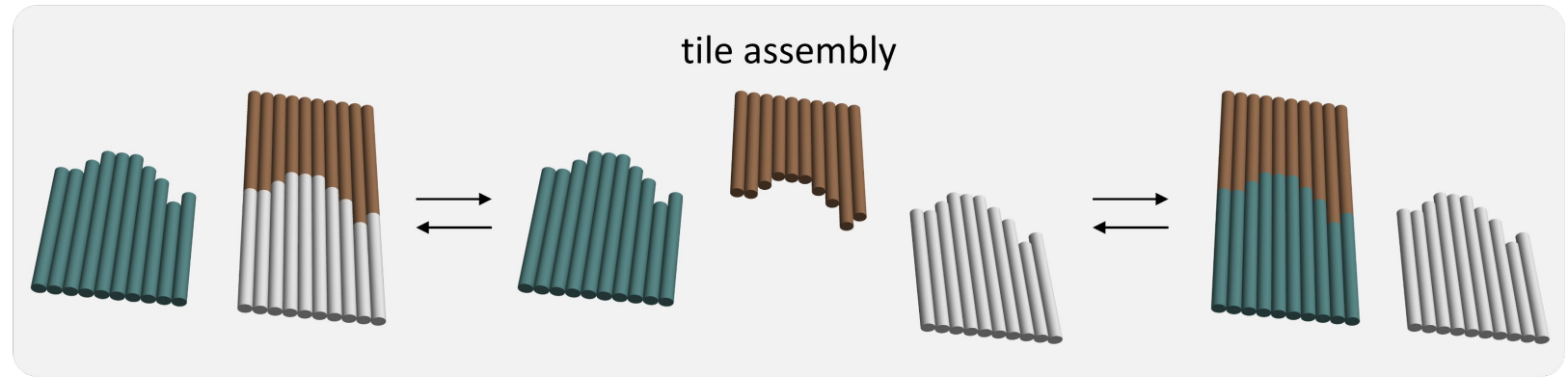
Simultaneous tile displacement



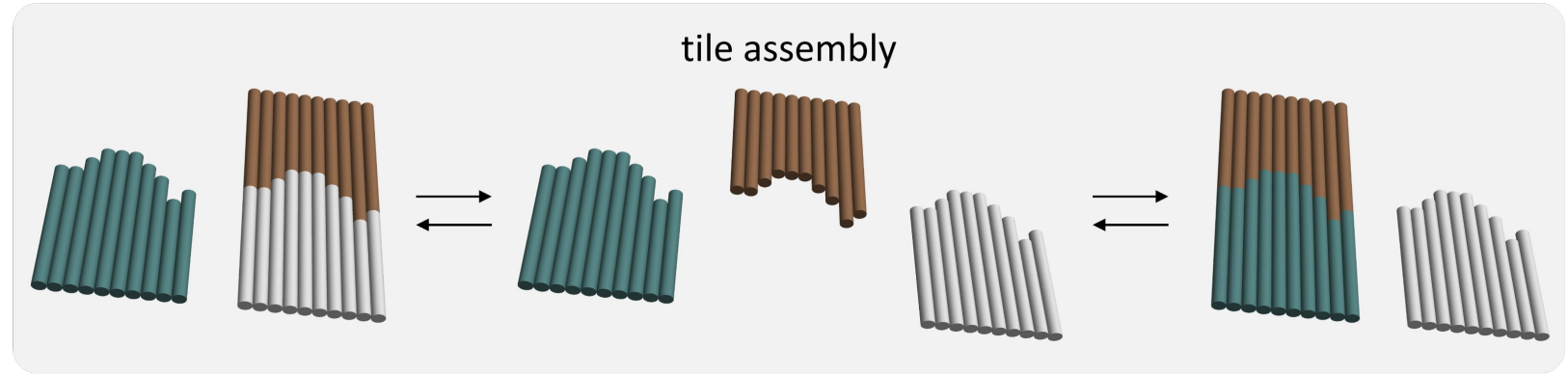
Simultaneous tile displacement



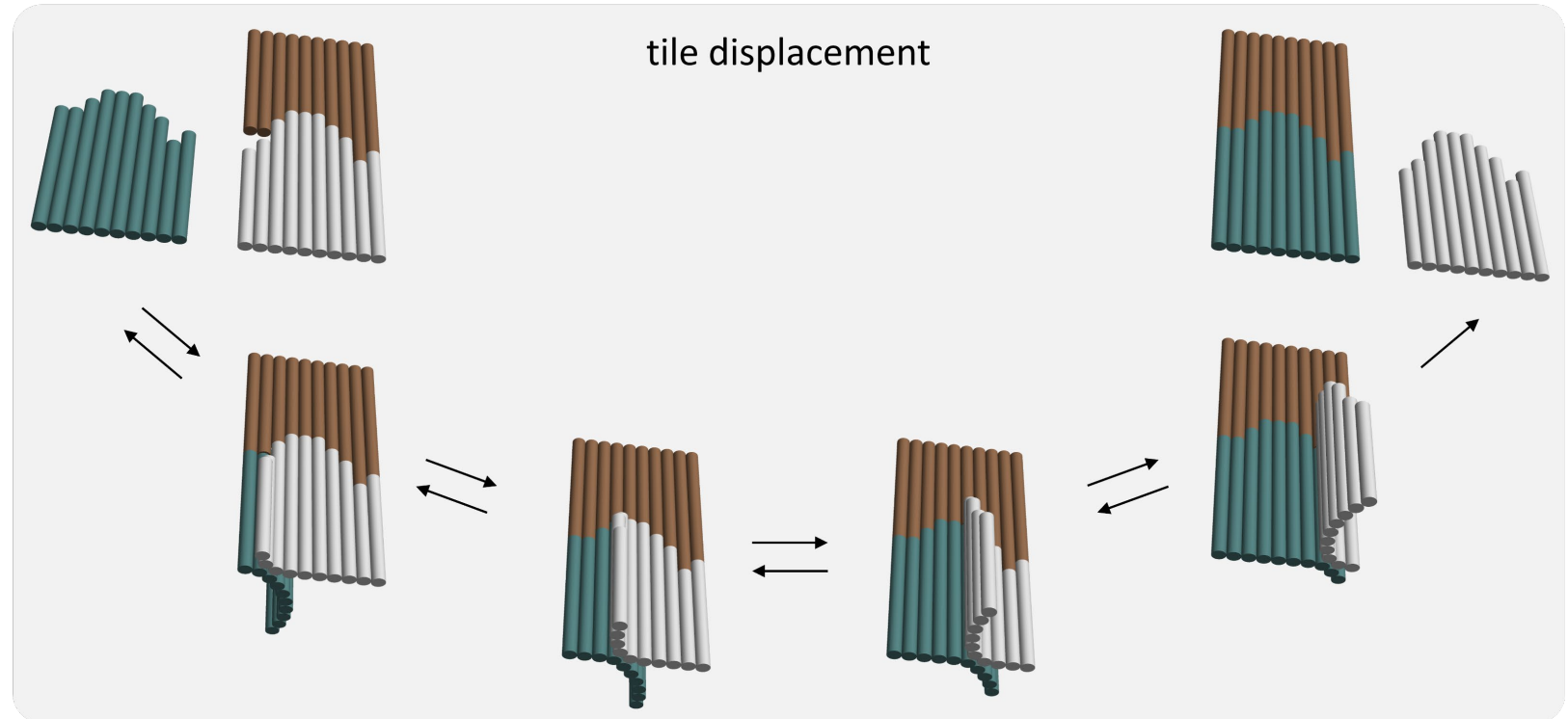
Binding between DNA tiles has limited specificity, and thus tile assembly systems must operate near melting temperature.

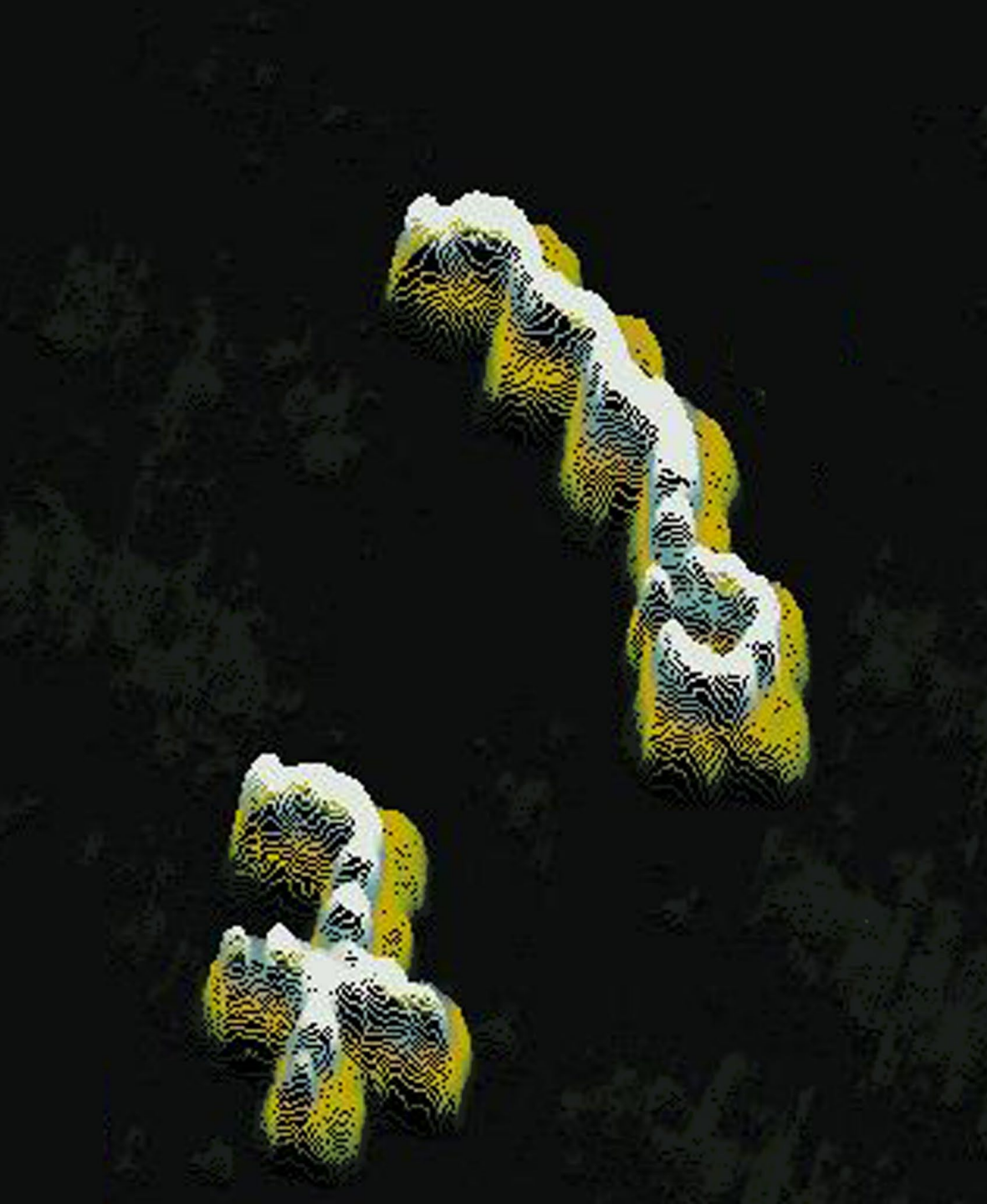


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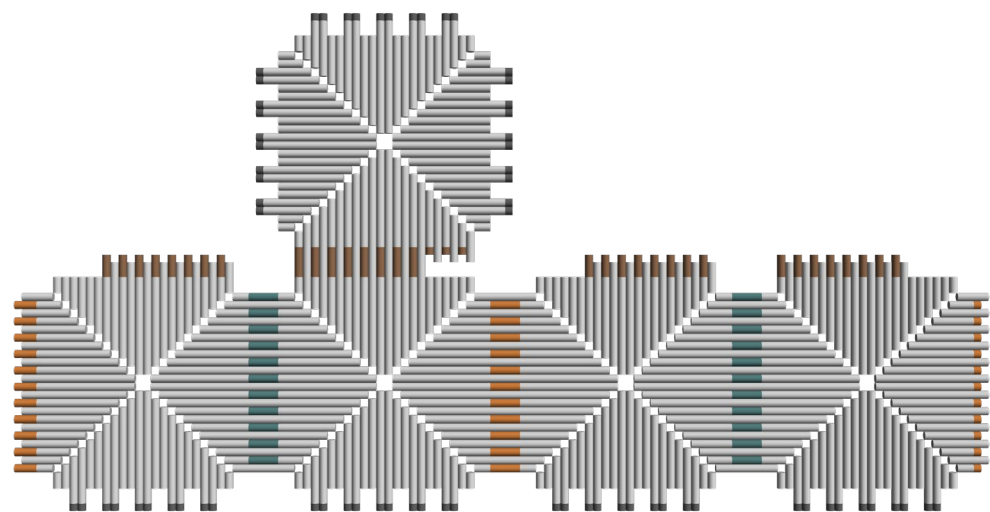


Tile displacement systems operate at room temperature with little crosstalk between distinct reactions, serving as a mechanism for modular reconfiguration robust to temperature and tile concentration.

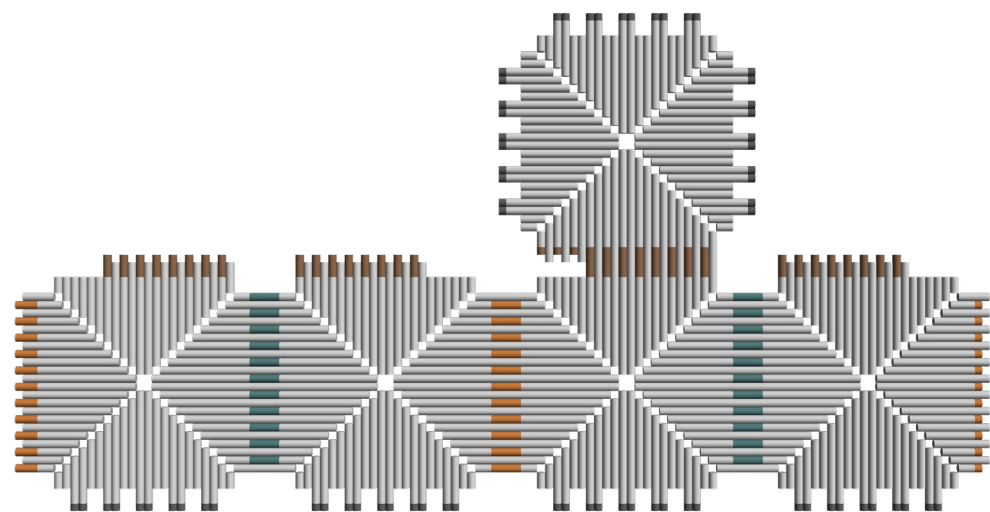


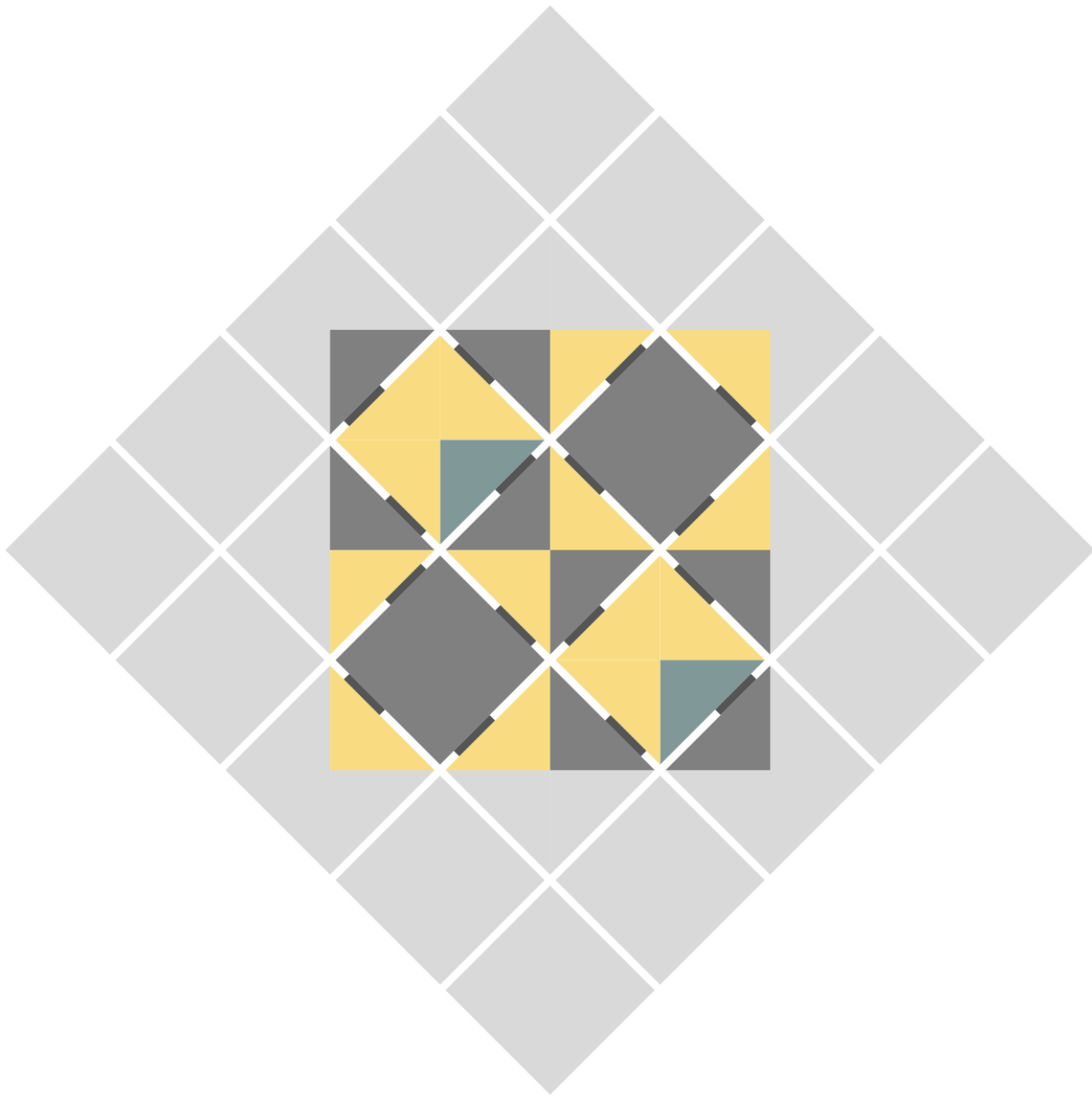


Future work: localized tile displacement



↕





Tile displacement cellular automata

Erik Winfree and Lulu Qian

Bioengineering
Computer Science
Computation & Neural Systems

Caltech

DNA29, September 14, 2023

The Qian lab @ Caltech



*Lulu
Qian*



*Greg
Tikhomirov*



*Wei
Li*



*Tianqi
Song*



*Dominic
Scalise*



*Boya
Wang*



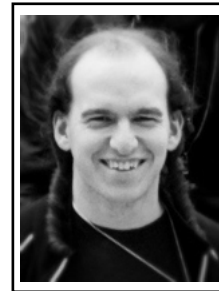
*Anu
Thubagere*



*Philip
Petersen*



*Kevin
Cherry*



*Hope
Johnson*



*Namita
Sarraf*



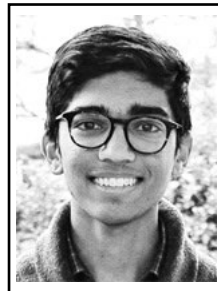
*Sam
Davidson*



*Olivia
Zou*



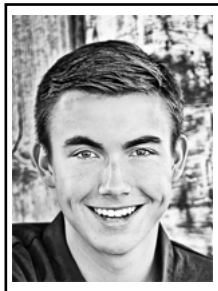
*Matthew
Plazola*



*Gokul
Gowri*



*Dallas
Taylor*



*Kellen
Rodriguez*



*Allison
Glynn*



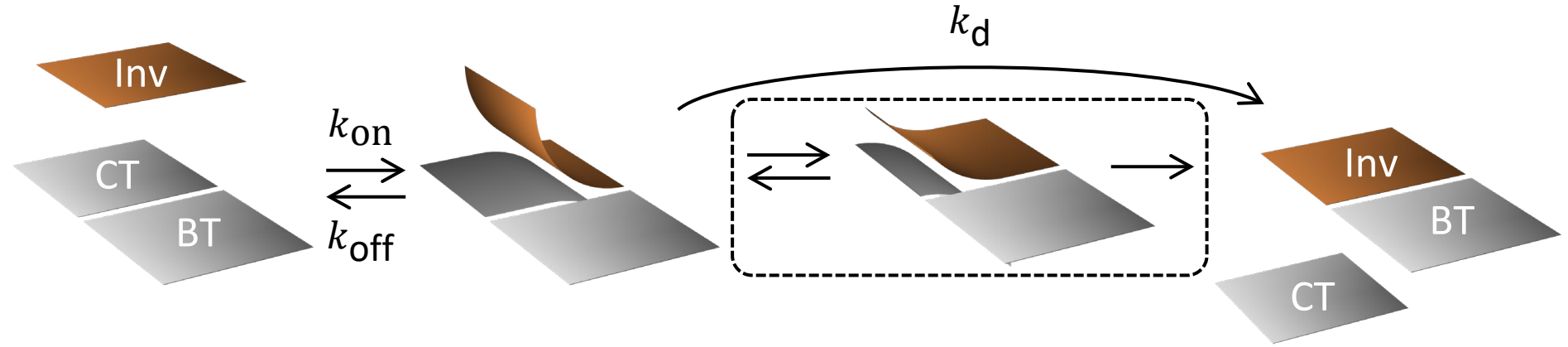
*Spencer
Winter*



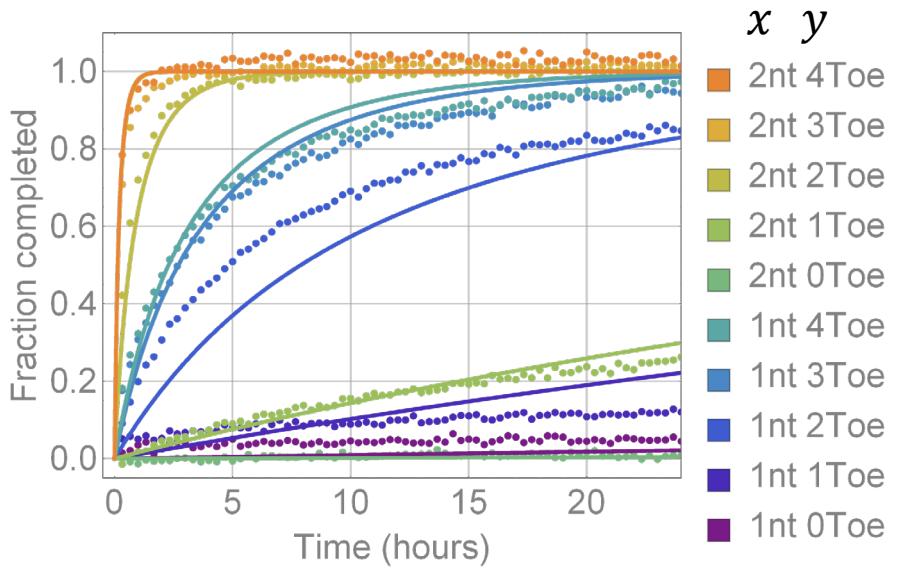
*Martin
Holmes*



Kinetics of DNA tile displacement



••• experiments — simulations



	Tile displacement		Strand displacement
binding rate (k_{on})	$x = 1$	$2.5 \times 10^4 / \text{M/s}$	$2 \times 10^6 / \text{M/s}$
	$x = 2$	$4.5 \times 10^5 / \text{M/s}$	
dissociation rate (k_{off})	$x = 1$	$10^{1-1.1y} / \text{s}$	$10^{6-L} / \text{s}$
	$x = 2$	$10^{3-2y} / \text{s}$	
displacement rate (k_d)	0.025/s		1/s

Petersen, Tikhomirov, and Qian, *Nature Communications* (2018)