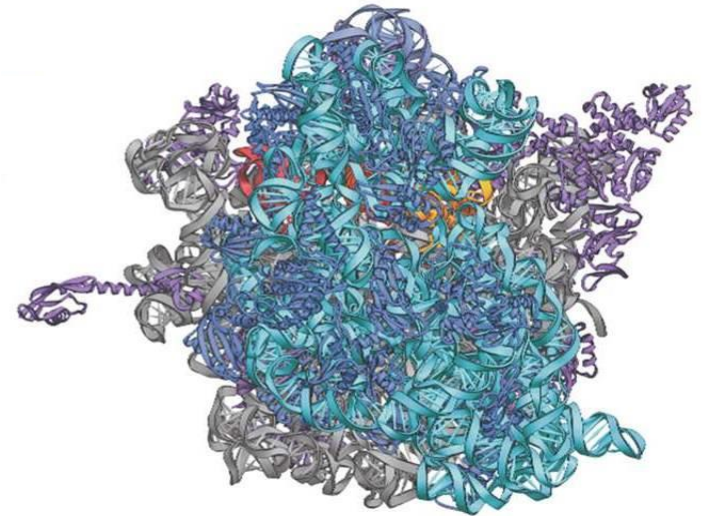
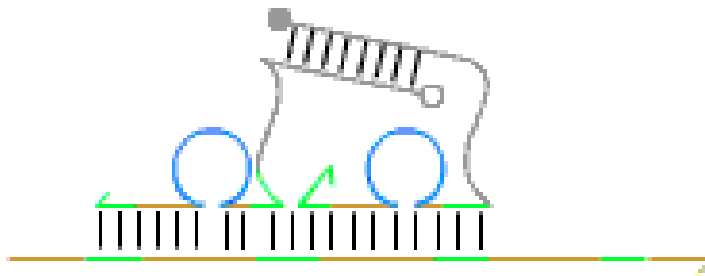


Programming Dynamic DNA Nanosystems

Andrew Turberfield
Department of Physics
University of Oxford



Building with biomolecules: synthetic biology from the bottom up

Given the ability to manufacture 3D structures with nm precision, and to create molecular systems that integrate sensing, computation and actuation -

what should we make?

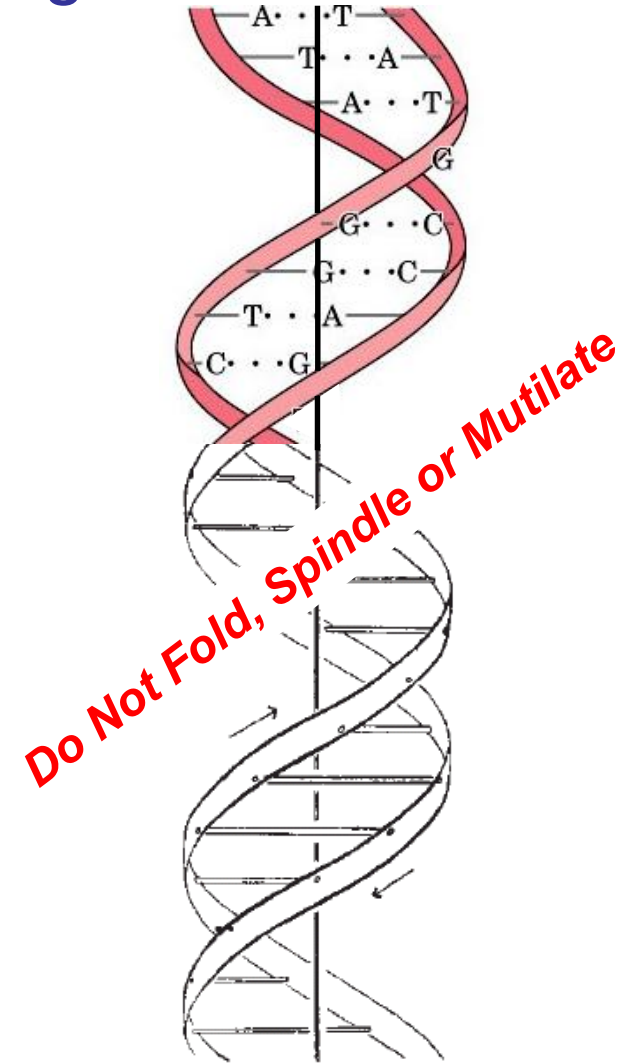
Introduction

**DNA Nanostructures:
building and computing with
DNA helices and junctions**

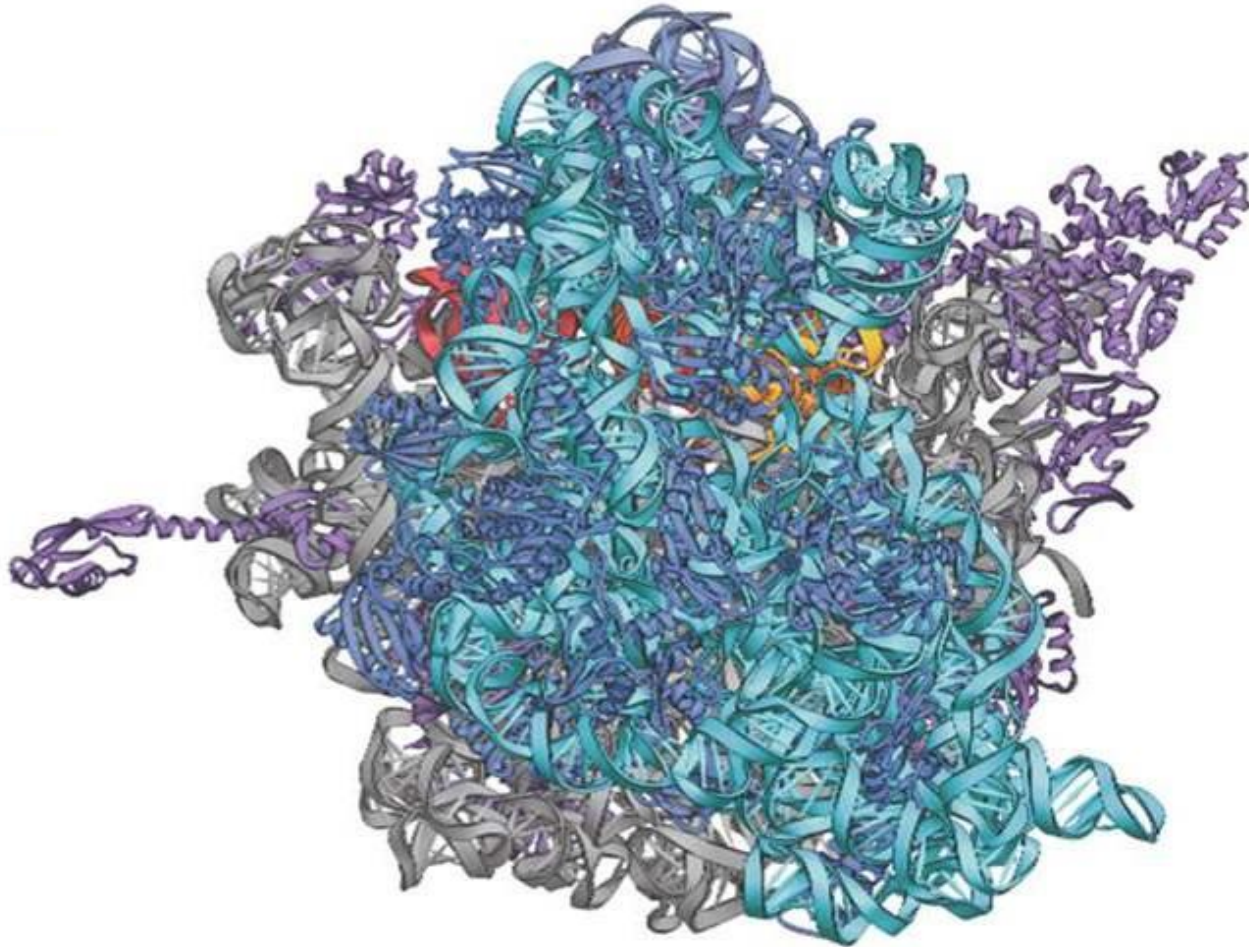
DNA: an unlikely material for building devices and executing programs?



J. D. Watson and F. H. C. Crick, *Nature* **171**, 737 (1953)



Not so unlikely: all life depends on
nucleic acid structures and machines



X-ray structure of *T. thermophilus* ribozyme



EPSRC

Engineering and Physical Sciences
Research Council



OXFORD
MARTIN
SCHOOL



Turberfield Group – Current Members

Jonathan Bath
Joakim Bohlin
Rafael Carrascosa Marzo
Antonio Garcia Guerra
Seham Helmi
Juan Jin
Behnam Najafi
Emma Silvester
Joel Spratt
Sam Tusk
Katie Young

Former Members

Florence Benn
Michael Boemo
Helen Carstairs
Frits Dannenberg
Katherine Dunn
Aiman Entwistle
Anthony Genot
Russell Goodman
Simon Green
Natalie Haley
Céline Journot
Parminder Lally
Le Liang

Alex Lucas
James Mitchell
Robert Machinek
Mireya McKee **Richard
Muscat**
Carlos Sanchez
Daniele Selmi
Ibon Santiago Gonzales
Thomas Sharp
Anthony Walsh
Wenjing Meng
Shelley Wickham
Adam Wollman

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Allen Mills

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Marta Kwiatkowska
Tom Ouldrige

Hiroshi Sugiyama
Masayuki Endo

Rachel O'Reilly
Phillip Milnes
Tom Wilks

Rob Cross

Bell Labs/Boise State
Bell Labs/UC Riverside

iCeMS,
Kyoto University

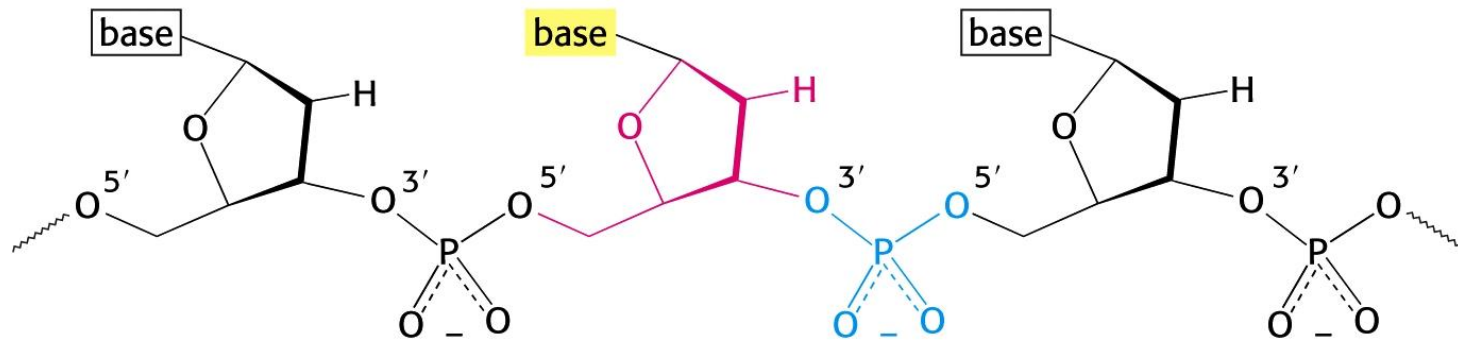
Computer Science, Oxford
Imperial College London

iCeMS,
Kyoto University

Chemistry, Warwick University

Warwick Medical School

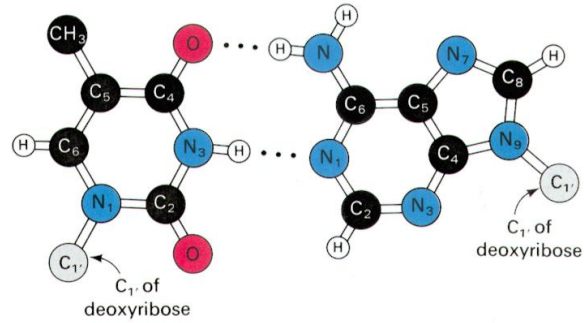
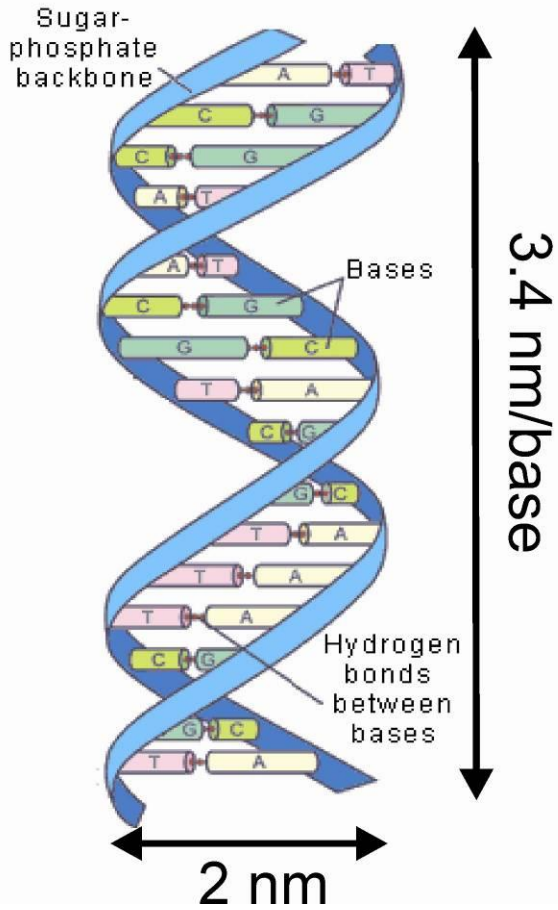
DNA



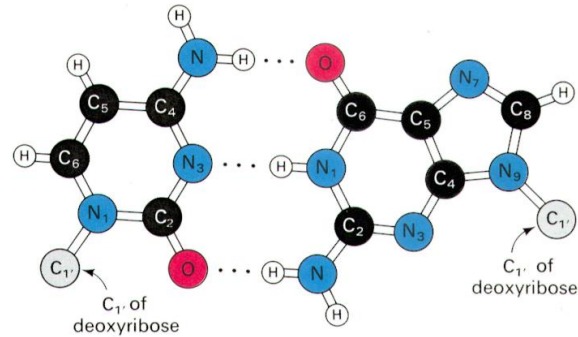
Information storage with an alphabet of four characters:

base = A, C, G or T

DNA



T ——— A



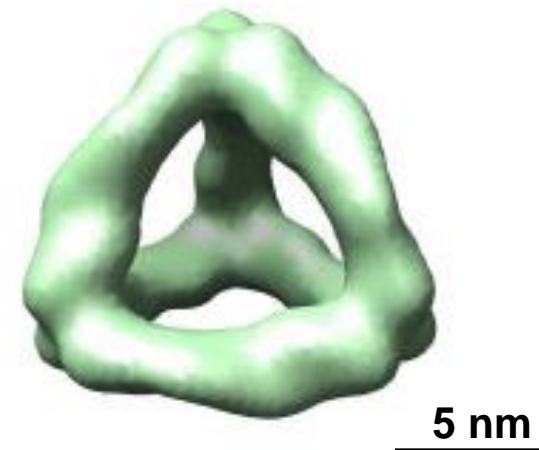
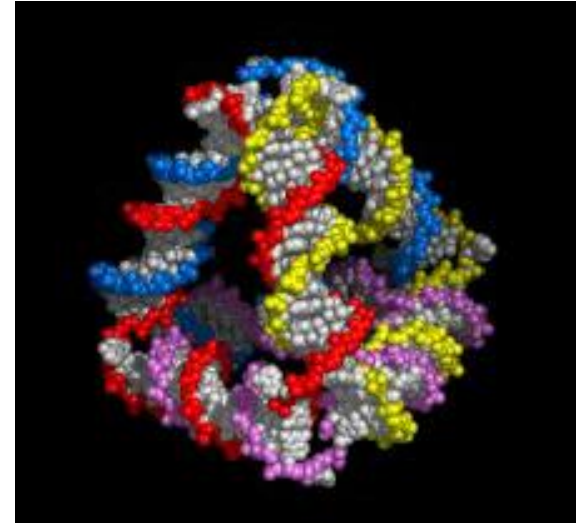
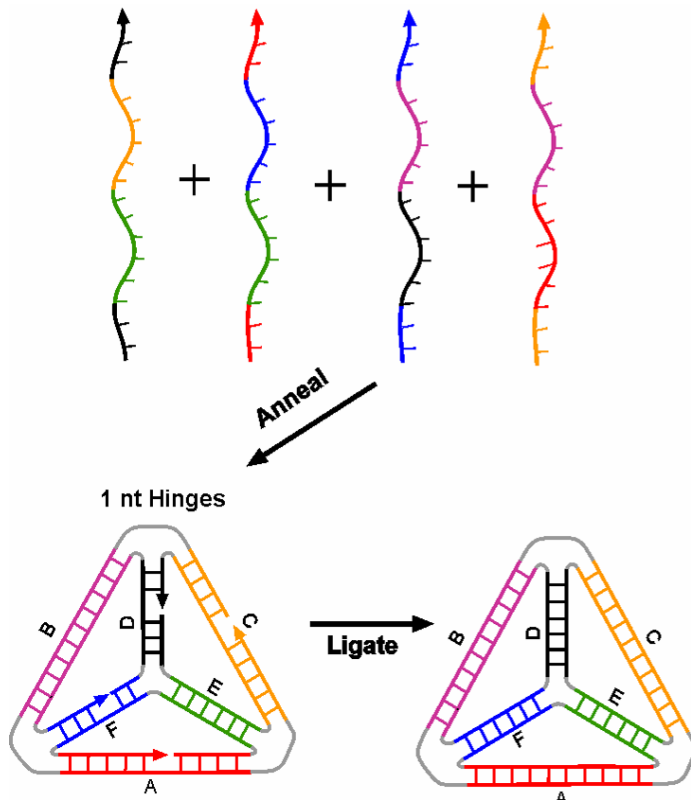
C ——— G



Rapid Chiral Assembly of Rigid DNA Building Blocks for Molecular Nanofabrication

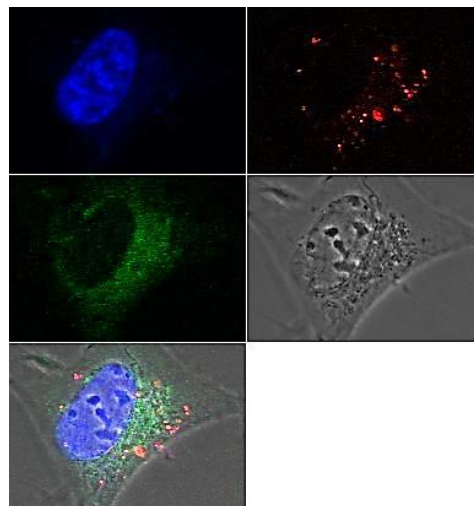
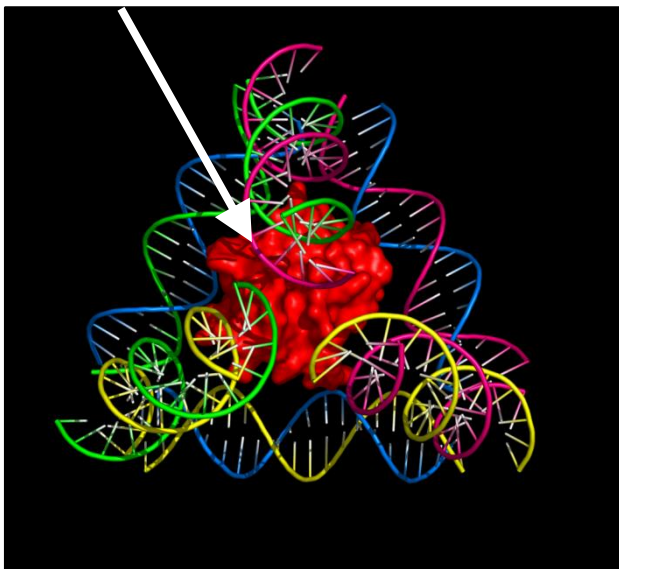
R. P. Goodman,¹ I. A. T. Schaap,² C. F. Tardin,² C. M. Erben,¹
R. M. Berry,¹ C. F. Schmidt,² A. J. Turberfield^{1*}

Science **310**, 1661-1665 (2005)



A molecular cage

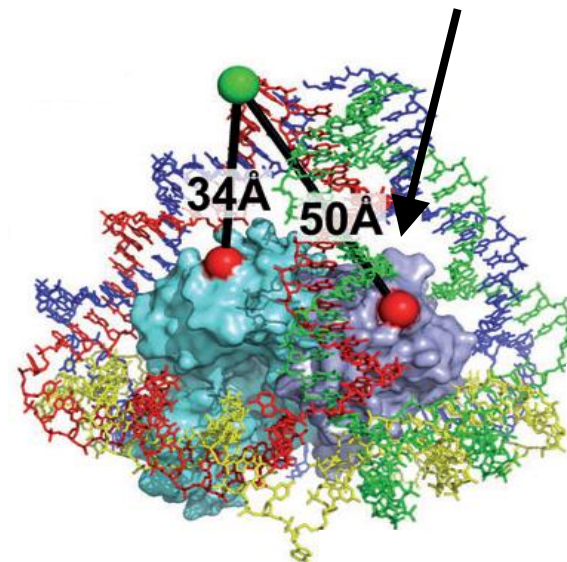
Cytochrome c



Red: Cy5 (tetrahedron)
Blue: nuclear stain
Green: LysoSensorTM (lysosomes)
Grey: phase contrast.

Scale bar 20 μ m

Catabolite Activator Protein

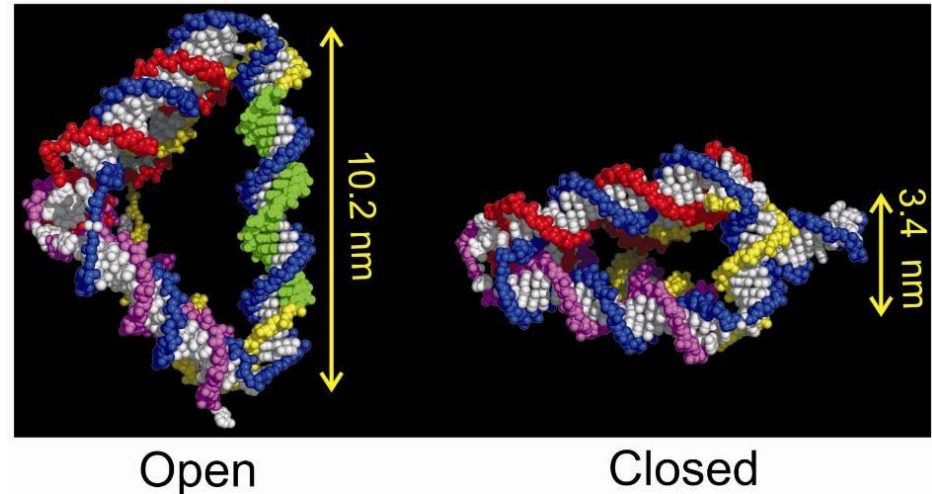
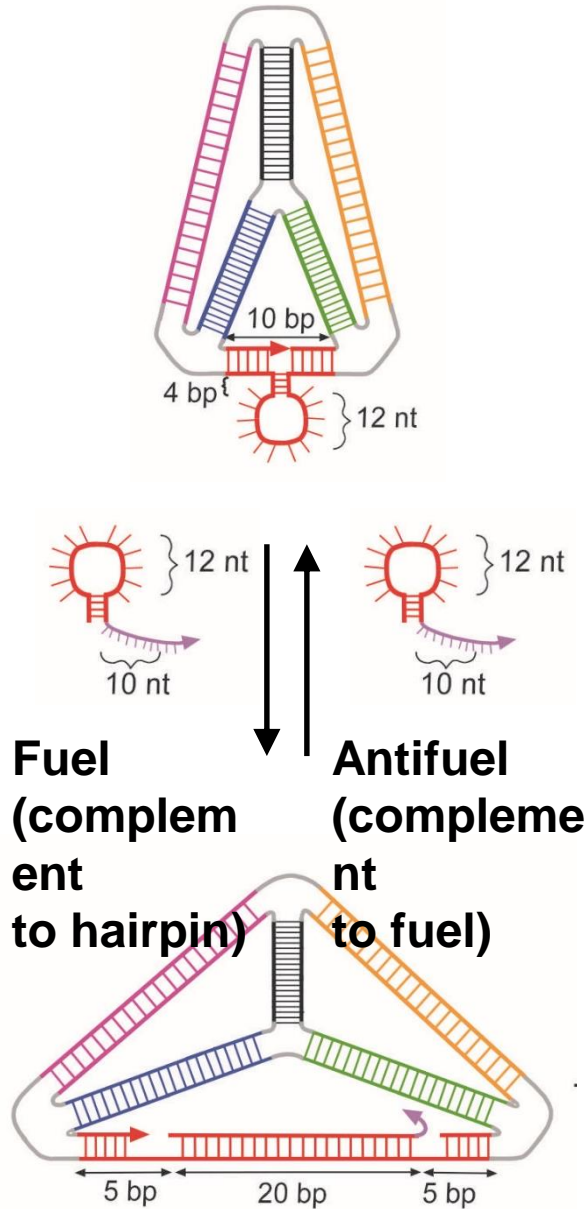


Single-Molecule Protein Encapsulation in a Rigid DNA Cage
C. M. Erben, R. P. Goodman, A. J. Turberfield
Angew. Chem. Int. Ed. **45**, 7414-7417 (2006).

DNA cage delivery to mammalian cells
A.S. Walsh, H.F. Yin, C.M. Erben, M.J.A. Wood, A.J. Turberfield
ACS Nano **5**, 5427-5432 (2011)

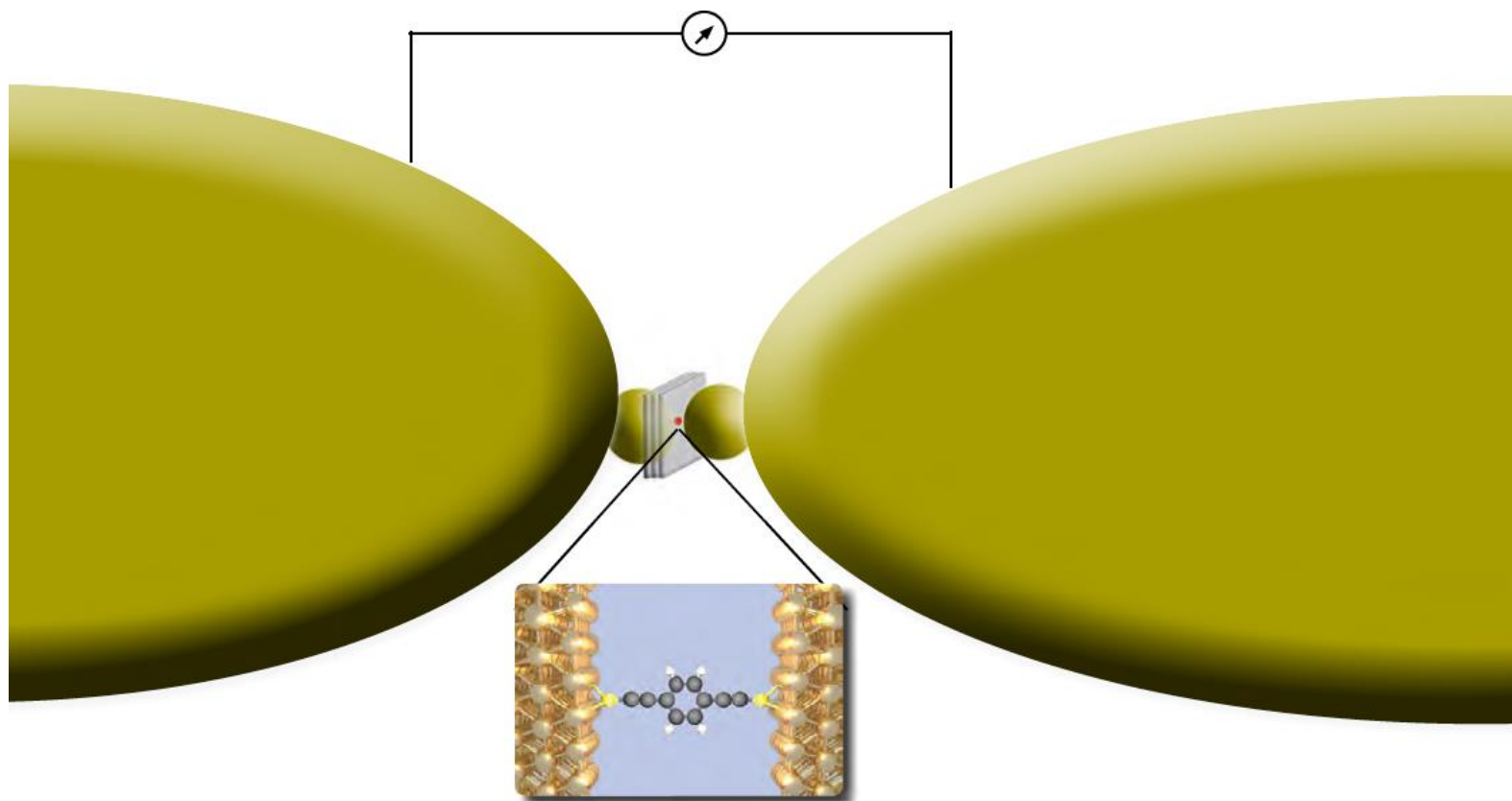
Non-covalent single transcription factor encapsulation inside a DNA cage
R. Crawford, C. M. Erben, J. Periz, L. M. Hall, T. Brown, A. J. Turberfield, A. N. Kapanidis
Angew. Chem. Int. Ed. **52**, 2284-2288 (2013)

Controlled cage opening



R. P. Goodman, M. Heilemann, S. Doose, C.M. Erben, A.N. Kapanidis, A. J Turberfield
Nature Nanotech. **3**, 93-96 (2008)

Molecular electronics?

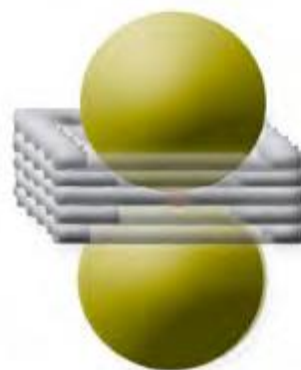
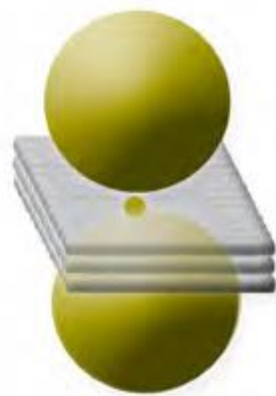
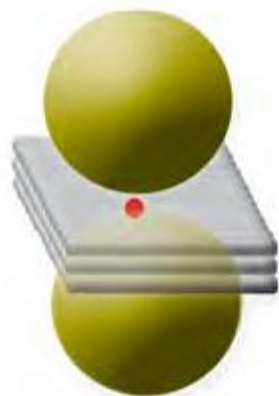


Gap size

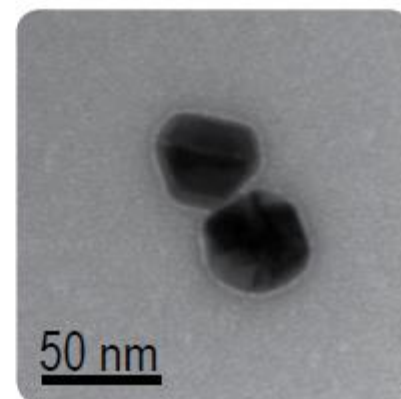
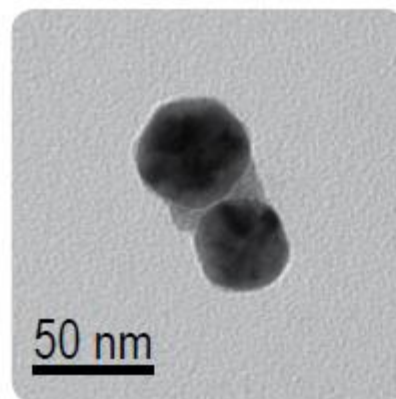
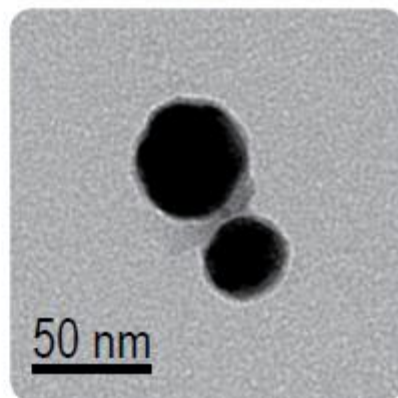
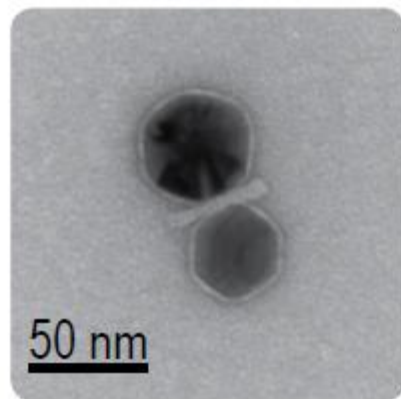
three-layer structure
 5.2 ± 0.5 nm

one-layer frame
 1.7 ± 0.4 nm

Schematic



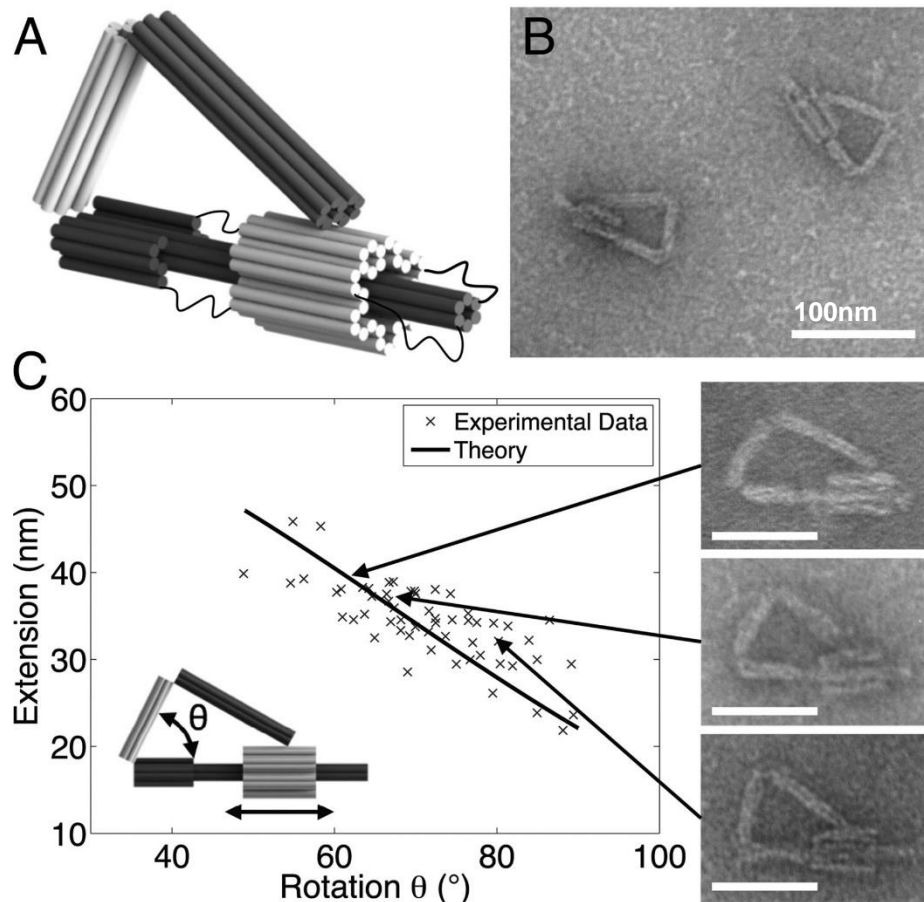
TEM image



Programmable motion of DNA origami mechanisms

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

Proc. Natl Acad. Sci. USA **112**, 713-718 (2015)



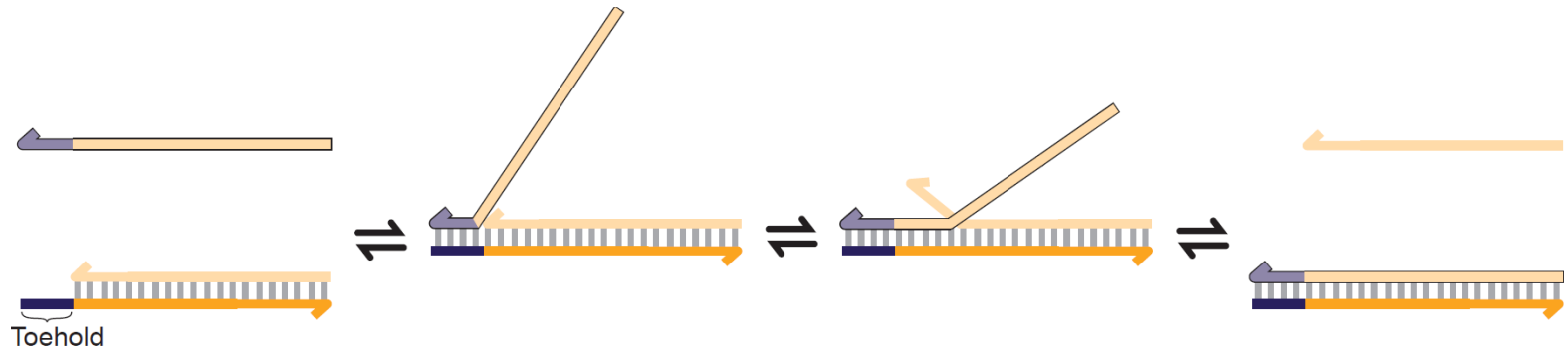
So far –

- sequence-specific hybridization can be used to program the self-assembly of DNA and RNA nanostructures.
- nucleic acid nanostructures can act as atomically precise scaffolds

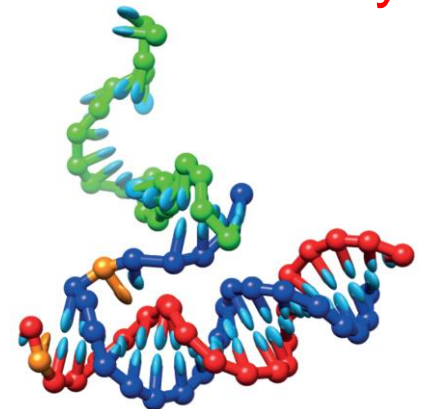
Next –

- dynamics ...

Toehold-mediated strand displacement



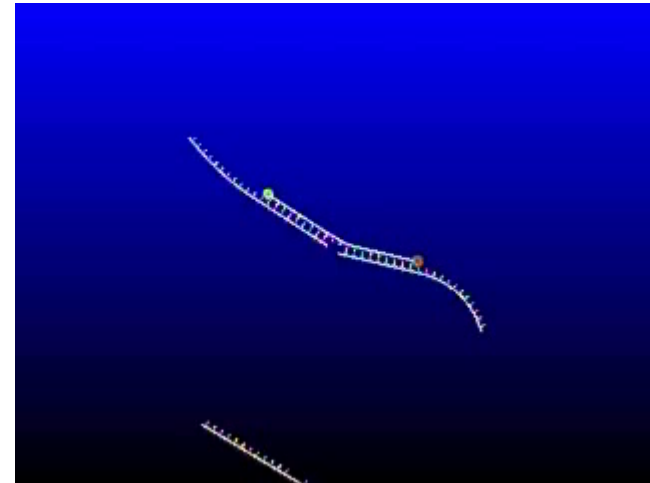
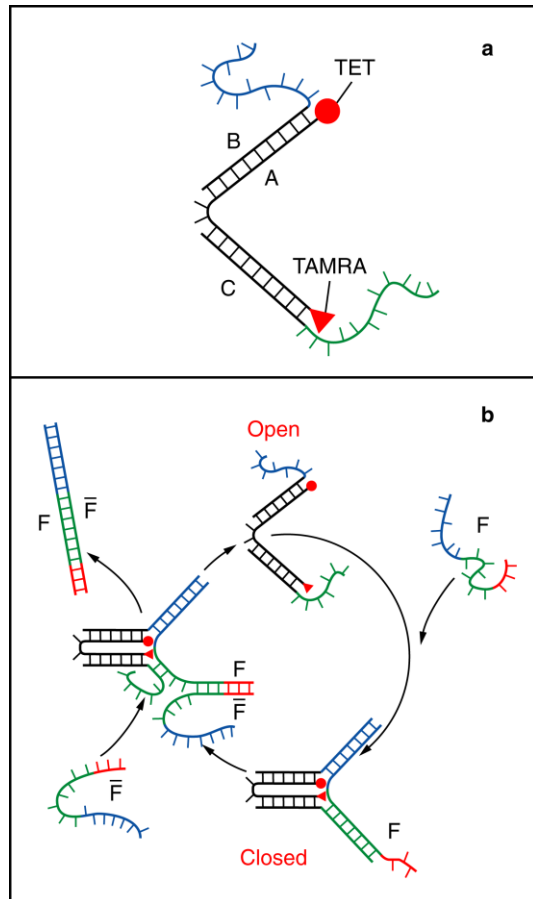
... underpins most current research in dynamic DNA nanotechnology, including synthetic molecular machinery and molecular computation



A DNA-fuelled molecular machine made of DNA

**Bernard Yurke^{*}, Andrew J. Turberfield^{*†}, Allen P. Mills Jr^{*},
Friedrich C. Simmel^{*} & Jennifer L. Neumann^{*}**

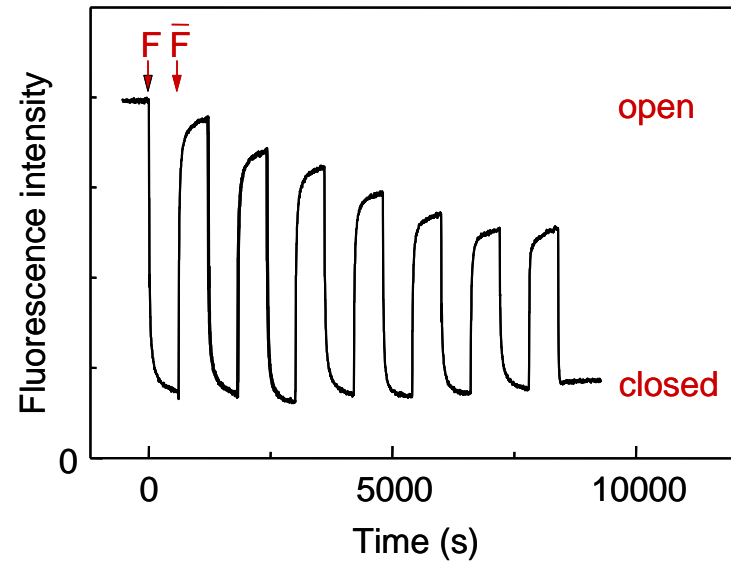
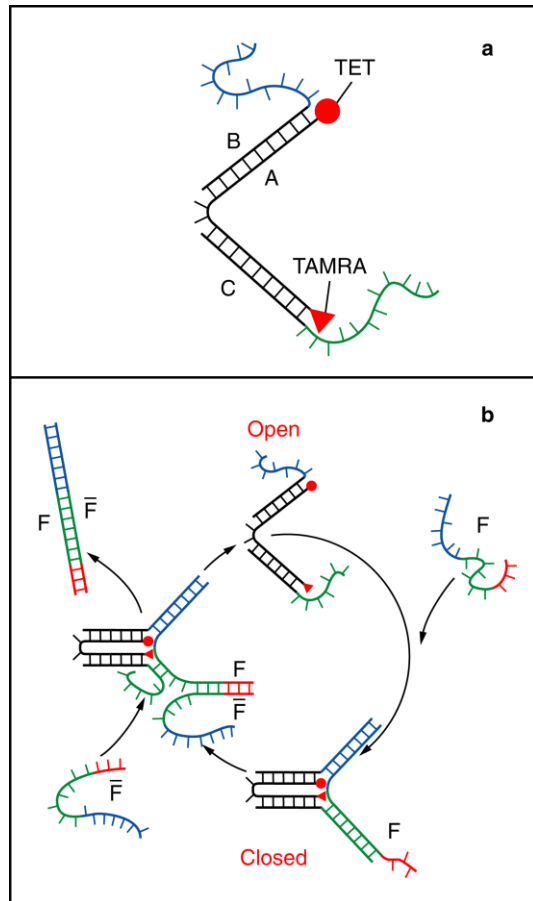
Nature **406**, 605-608 (2000)

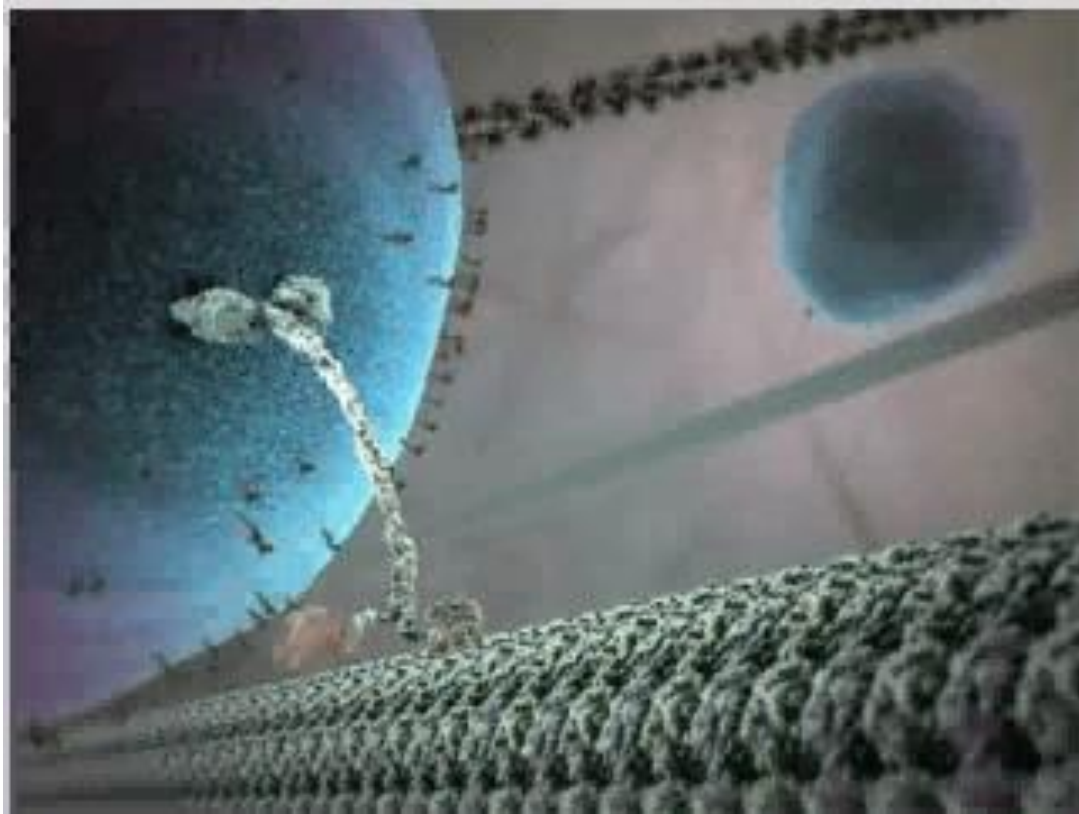


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Friedrich C. Simmel^{*} & Jennifer L. Neumann^{*}

Nature 406, 605-608 (2000)





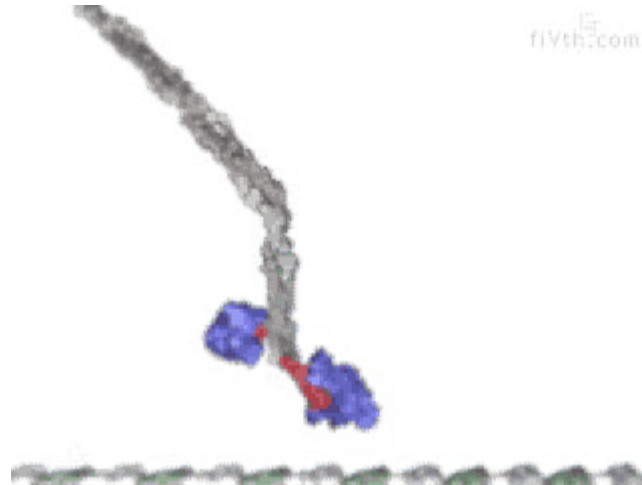
from The Inner Life of the Cell, Harvard

Aim: to build a synthetic molecular motor

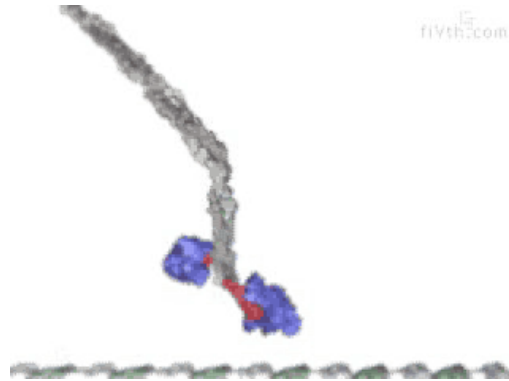
- capable of transporting a load along a track
- chemically fuelled
- autonomous

Inspiration: kinesin

R.D. Vale and R.A. Milligan,
Science **288**, 88 (2000)



- transport along microtubules: proteins, mRNA, organelles, DNA (cell division)
- powered by ATP: motor catalyzes hydrolysis $\Delta G \approx -12 \text{ kcal mol}^{-1}$
- fast ($1 \mu\text{m s}^{-1}$ in 8 nm steps)
- processive (hundreds of steps without falling off)
- essential that catalytic activities of the two identical feet are coordinated



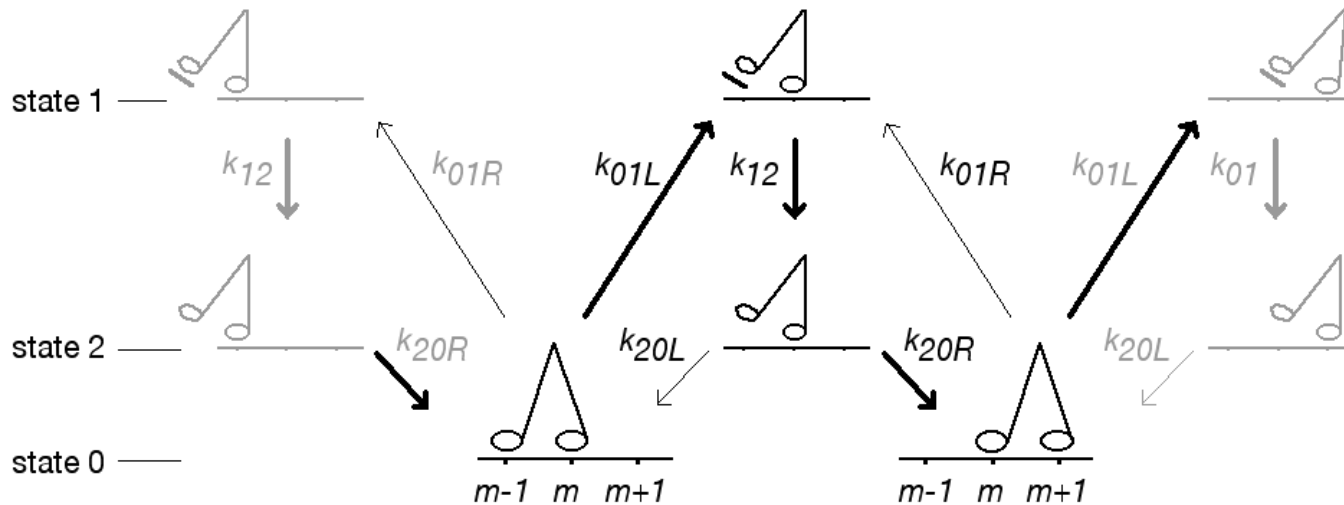
What do we need to make an autonomous, chemically powered motor?

- fuel
- motor catalyzes reaction of fuel
- reaction of fuel coupled to mechanical motion

and for a two-footed motor:

- coordinate chemomechanical cycles of feet to achieve directionality, processivity

Directionality through control of transition rates



$$\alpha = \frac{k_{01L}}{k_{01R}}$$

$$\beta = \frac{k_{20L}}{k_{20R}}$$

0→1 fuel lifts foot from track

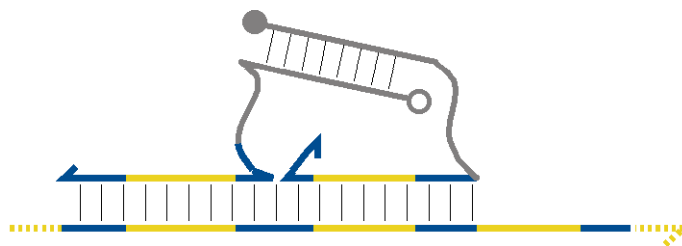
1→2 foot catalyzes reaction of fuel, fuel displaced

2→3 foot rebinds track

- each transition is thermodynamically downhill
- dissipation of free energy by reaction of fuel uncouples foot lifting and replacing

→ **possibility of directional bias by control of reaction rates** $\frac{\alpha}{\beta} \neq 1$

Coordinating two chemomechanical cycles

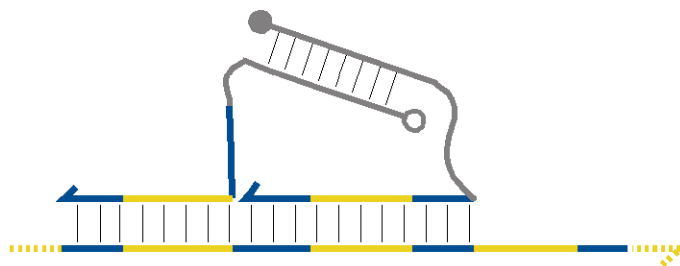


Mechanism for coordinated motion of a synthetic molecular motor

S.J. Green, J. Bath, A.J. Turberfield *Phys. Rev. Lett.* **101**, 238101 (2008)

J. Bath, S.J. Green, K.E. Allen, A.J. Turberfield *Small* **5**, 1513-1516 (2009)

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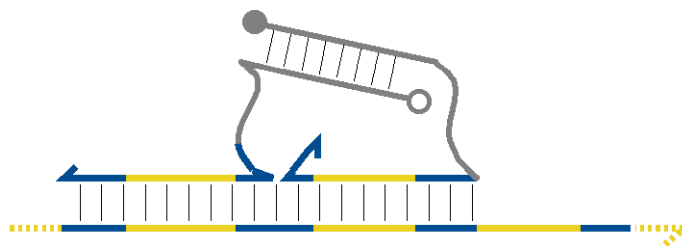


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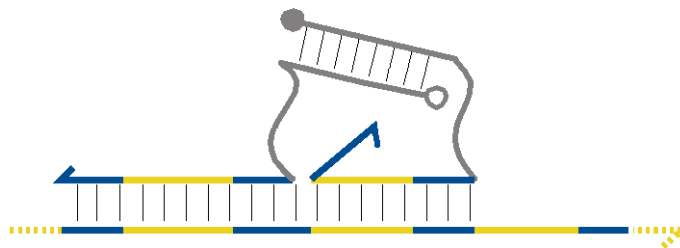


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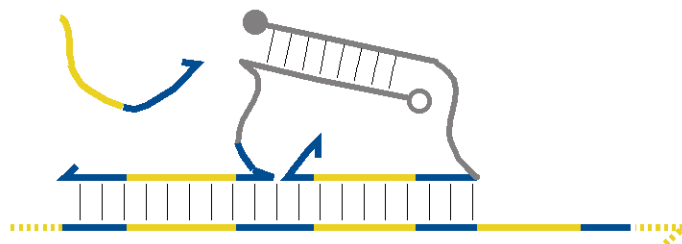


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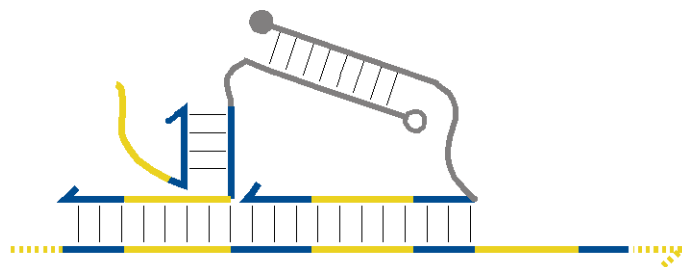


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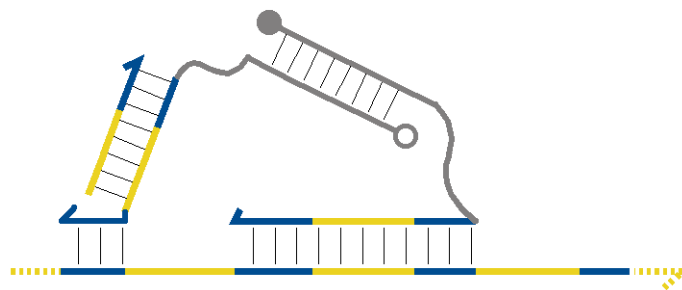


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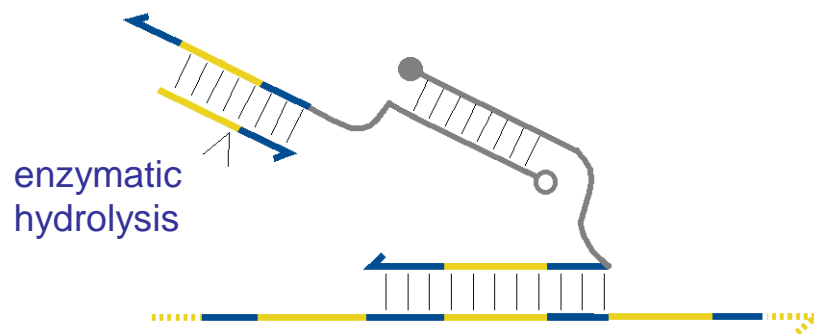


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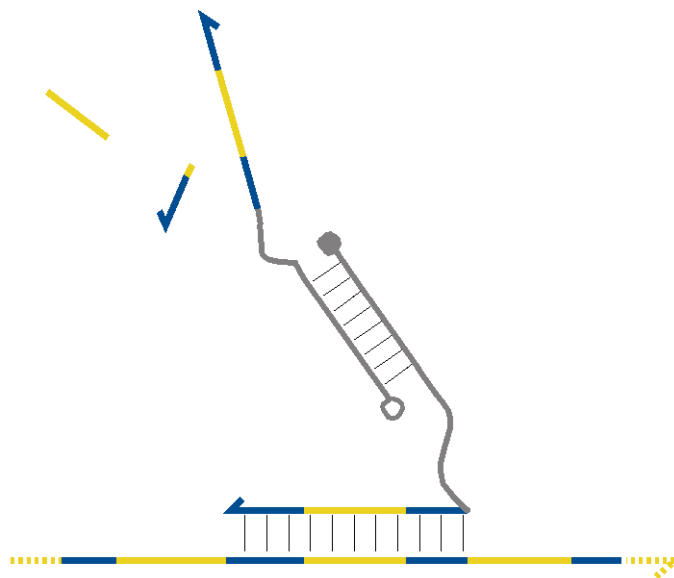


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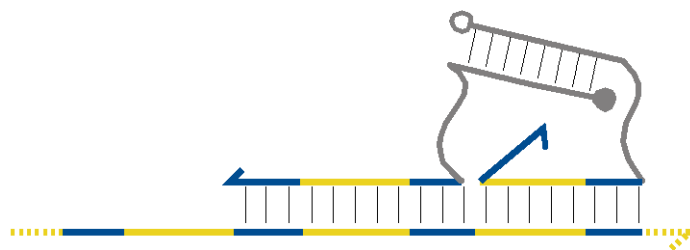


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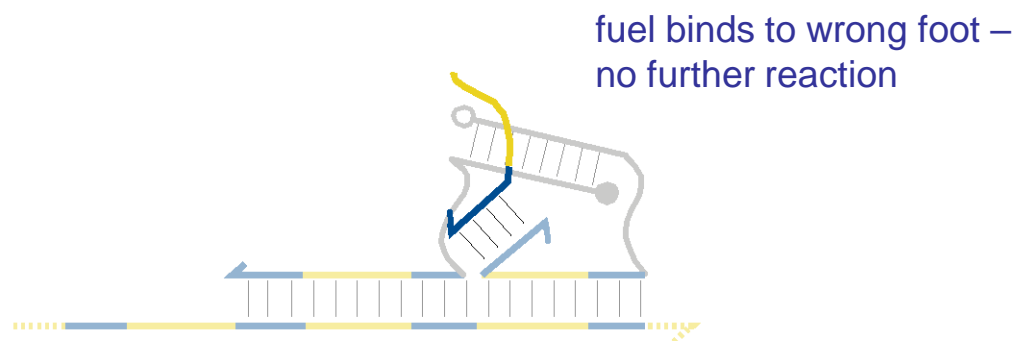


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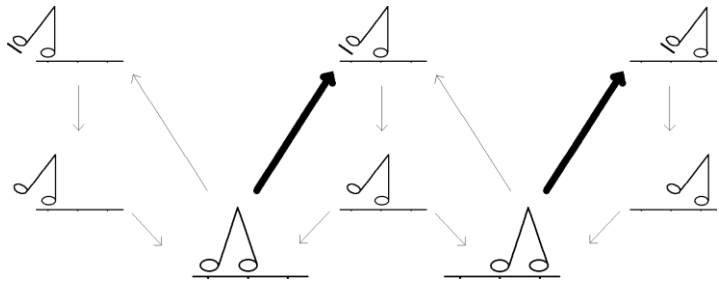


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J. Bath, S.J. Green, K.E. Allen, A.J. Turberfield *Small* **5**, 1513-1516 (2009)

the mechanism is both directional and processive

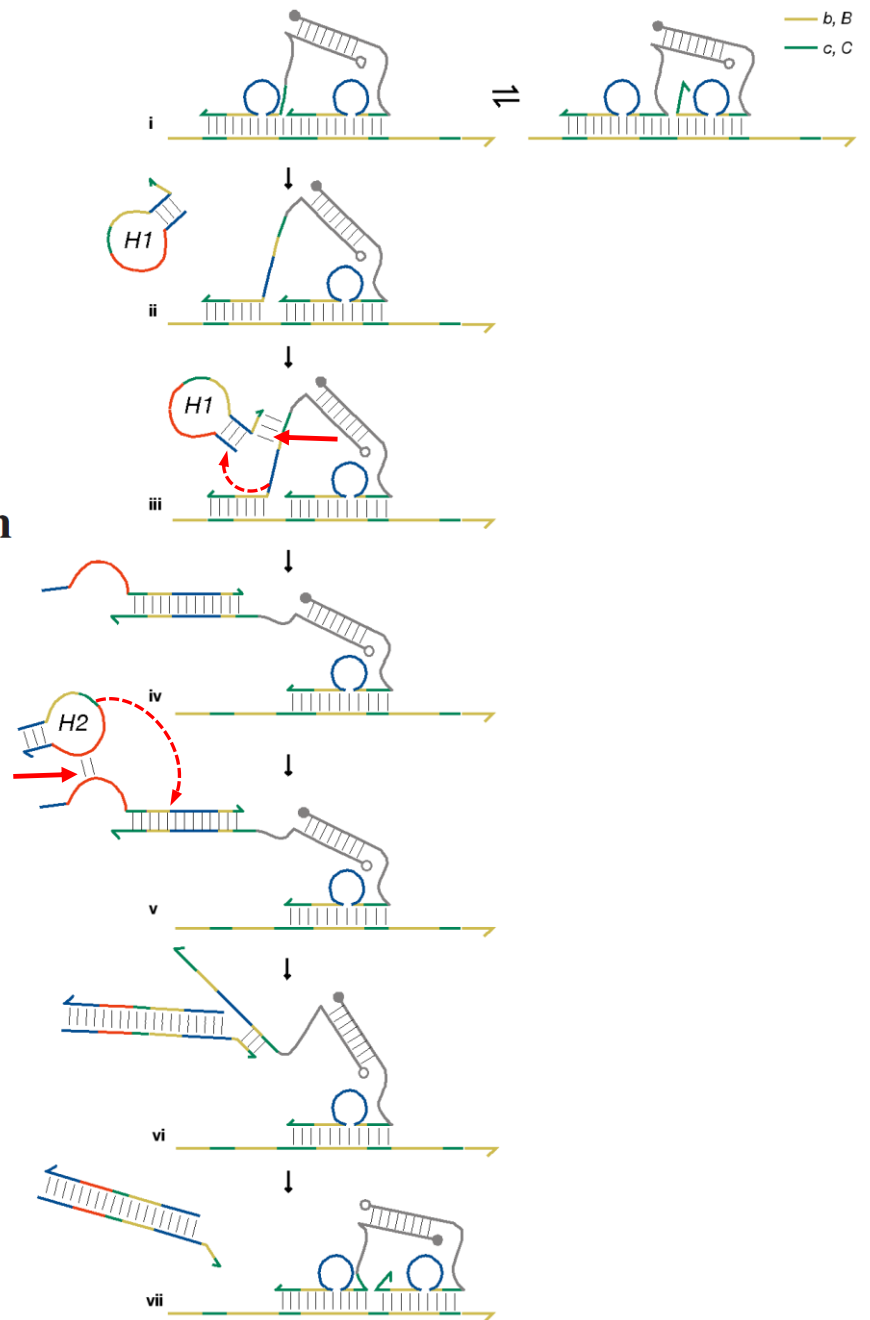


-
- engineered 30-fold bias toward lifting the left foot
 - once the left foot is lifted the standing foot is unlikely to be lifted from the track
 - there is no intrinsic bias in replacing a lifted foot either side of the standing foot
- **the mechanism works as designed**

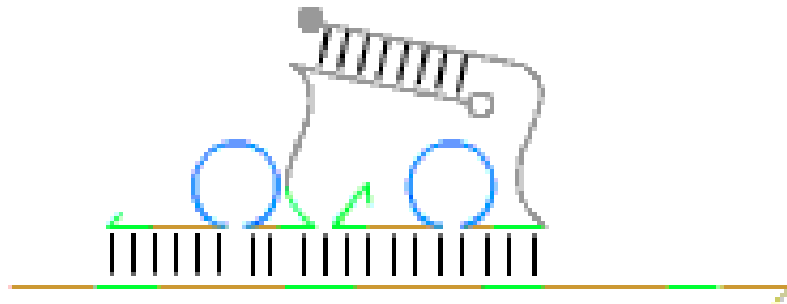
Coordinated Chemomechanical Cycles: A Mechanism for Autonomous Molecular Motion

S. J. Green, J. Bath, and A. J. Turberfield

Phys. Rev. Lett. **101**, 238101 (2008)



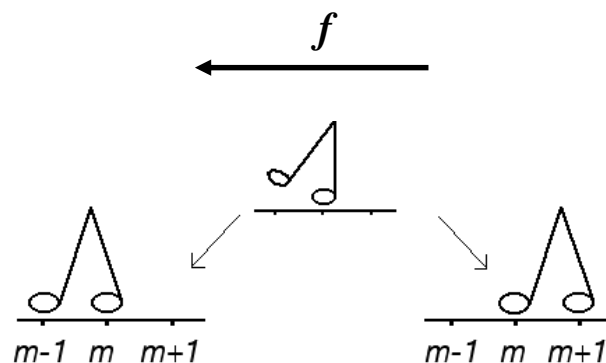
Coordinated chemomechanical cycles: a mechanism for autonomous molecular motion



S.J. Green, J. Bath and A.J. Turberfield
Phys. Rev. Lett. **101**, 238101 (2008)

These motors are **Brownian ratchets**: movement of the lifted foot is driven solely by thermal fluctuations; the fuel provides the energy necessary to rectify this motion by breaking the detailed balance between lifting and replacing front and back feet.

Model load f by favouring foot replacement in left (back) position by a factor $\exp(fx/k_B T)$ where x is the distance between transition states for forward and backward steps (set $x \approx$ step size d).



velocity
$$v = k_{eff} d \left(\frac{1}{1 + \alpha^{-1}} - \frac{1}{1 + \beta^{-1} e^{-fd/k_B T}} \right),$$

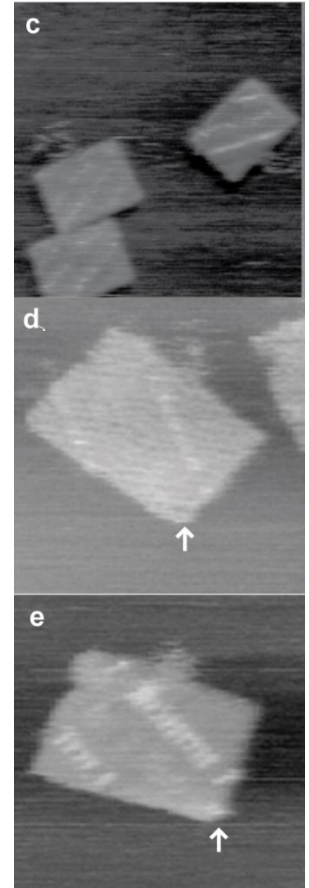
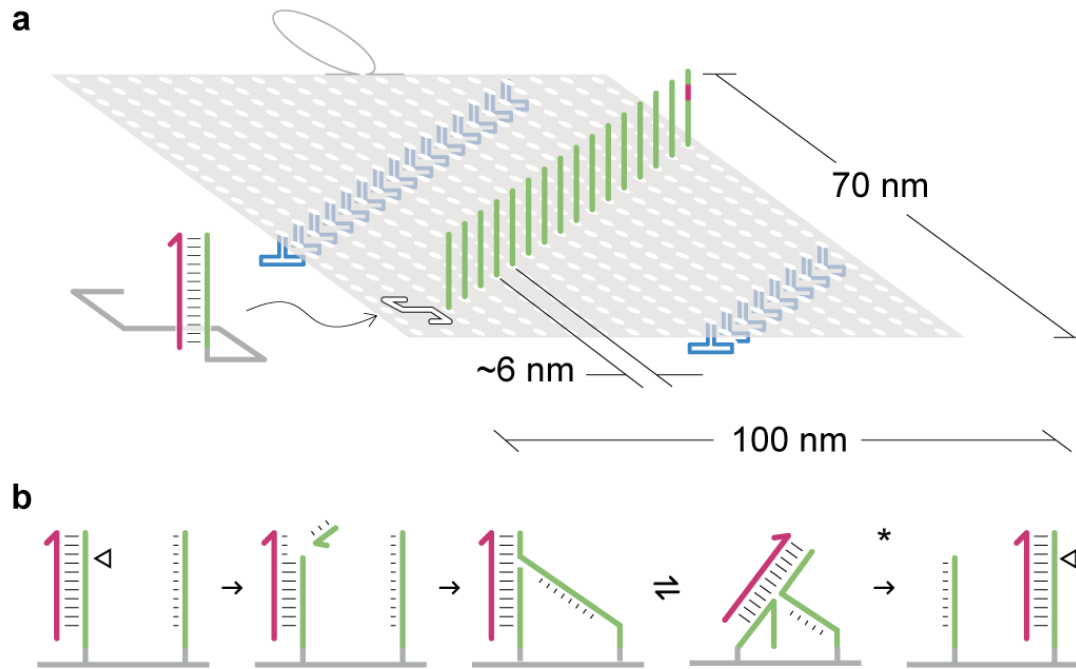
where

$$k_{eff}^{-1} = (k_{01L} + k_{01R})^{-1} + k_{12}^{-1} + \left(k_{20L} e^{fd/2k_B T} + k_{20R} e^{-fd/2k_B T} \right)^{-1}.$$

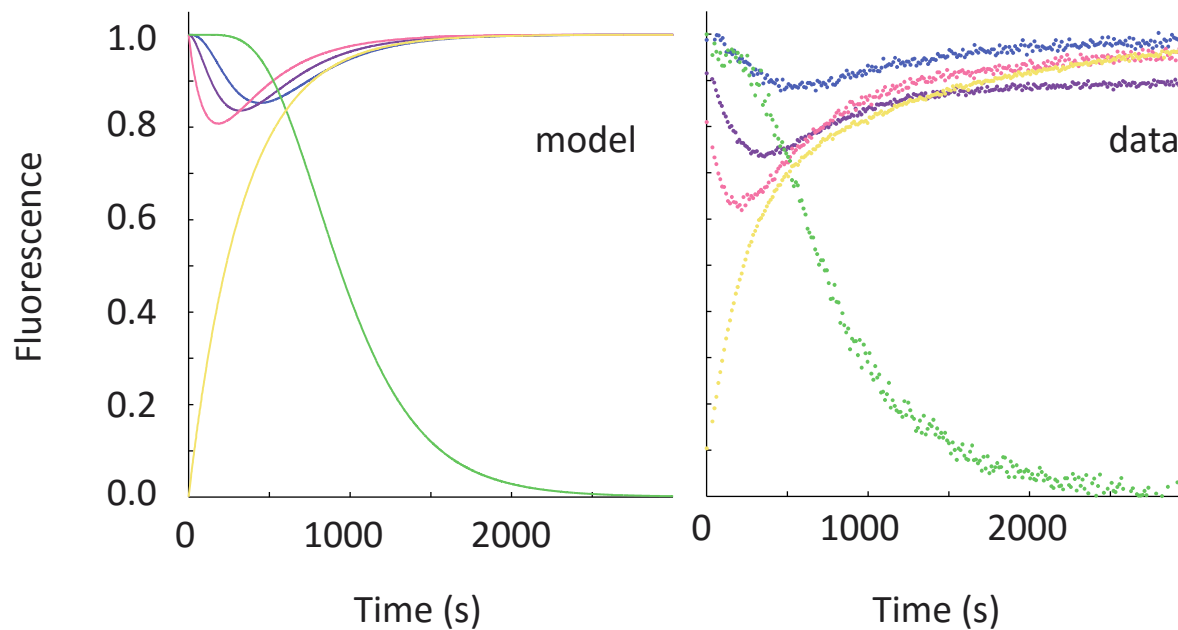
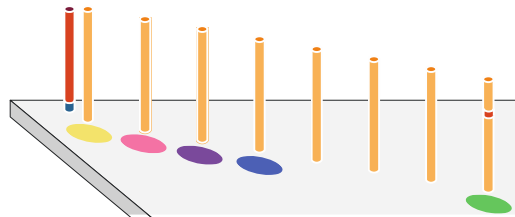
set $v = 0$:

$$f_{stall} = \frac{k_B T}{d} \ln \frac{\alpha}{\beta} \approx 3 \text{ pN}$$

DNA walker mechanism

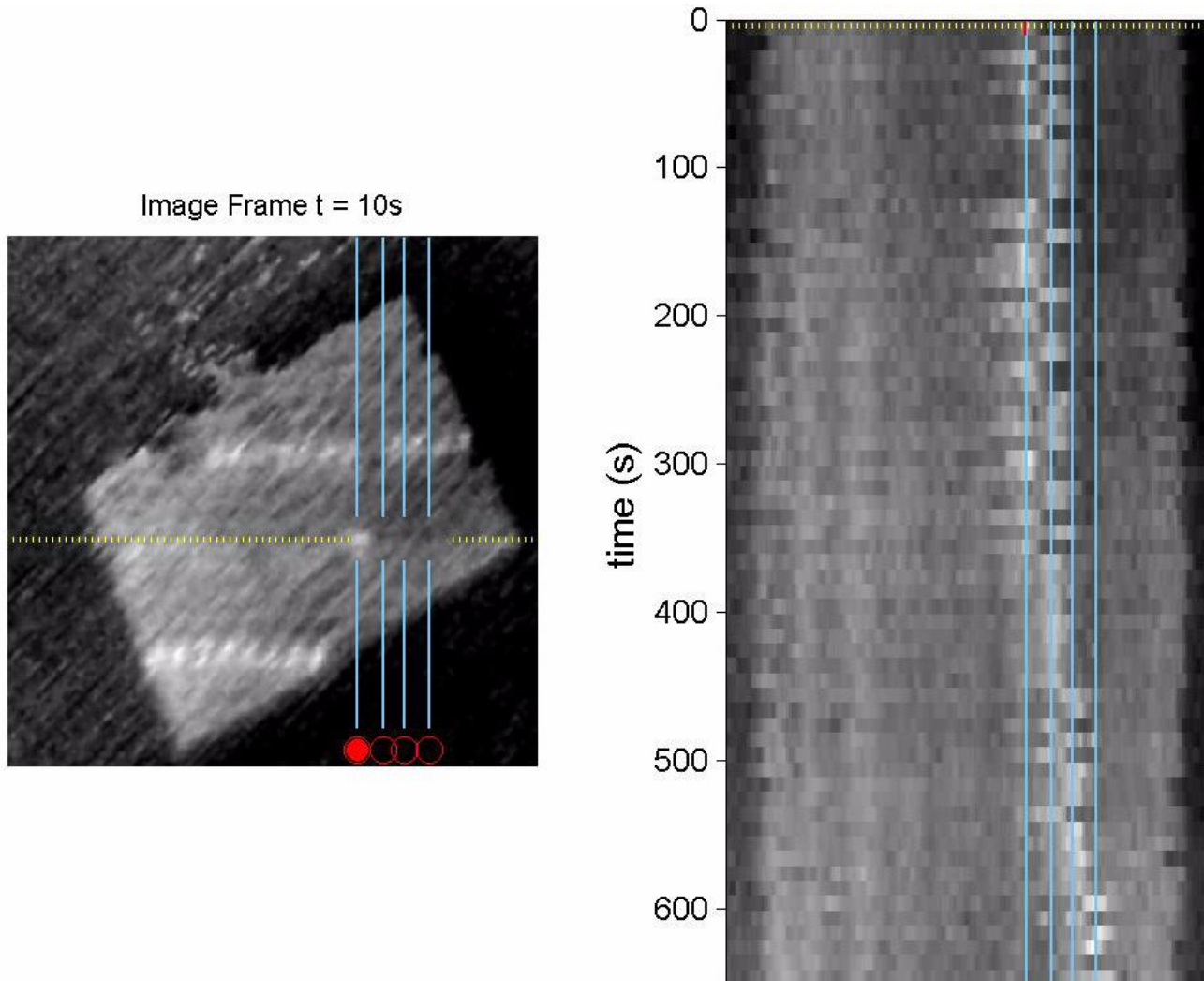


Direct observation of stepwise movement of a synthetic molecular transporter
S. F. J. Wickham, M. Endo, Y. Katsuda, K. Hidaka, J. Bath, H. Sugiyama and A. J. Turberfield
Nature Nanotechnol. **6**, 166 (2011)



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Nature Nanotechnol. **6**, 166 (2011)

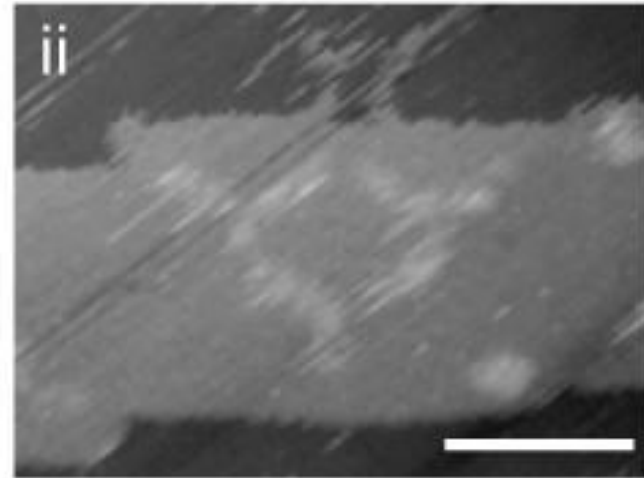
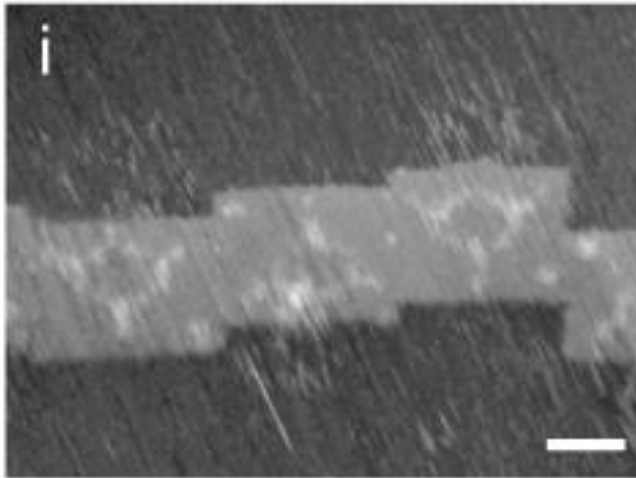
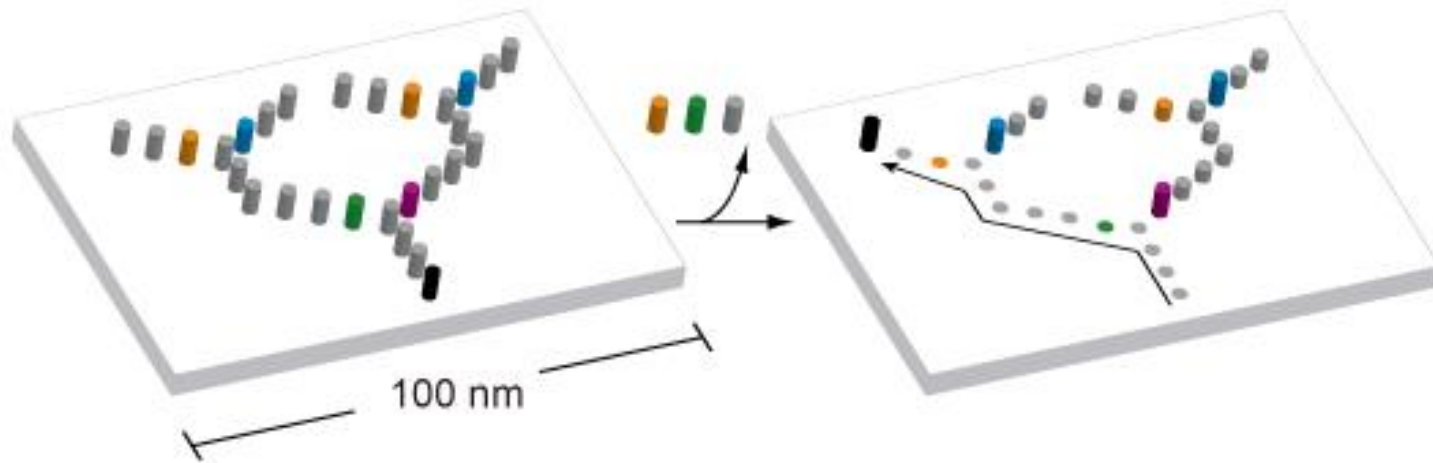
Individual steps resolved by real-time AFM



Direct observation of stepwise movement of a synthetic molecular transporter

S. F. J. Wickham, M. Endo, Y. Katsuda, K. Hidaka, J. Bath, H. Sugiyama and A. J. Turberfield
Nature Nanotechnol. **6**, 166 (2011)

Navigating a network of tracks

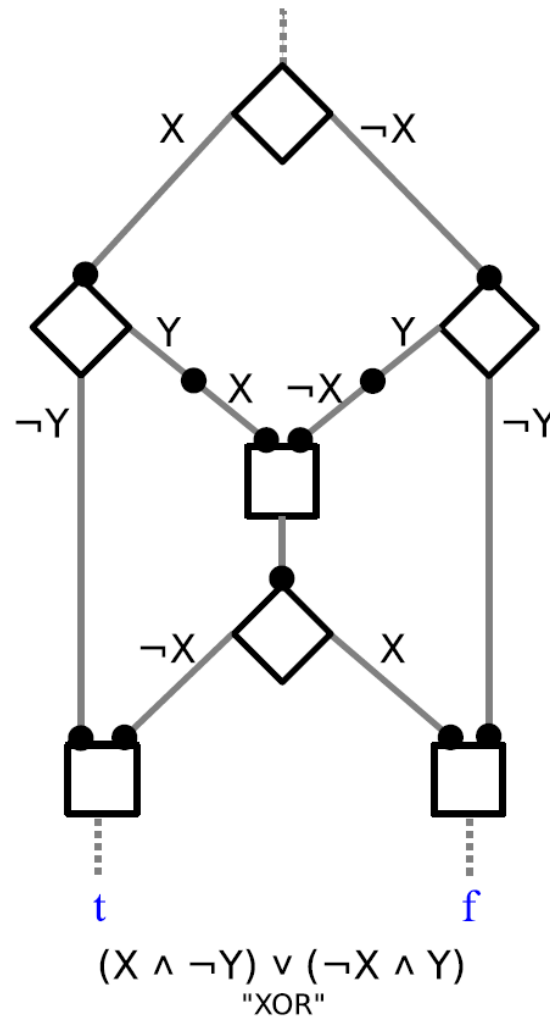


Molecules that navigate a network of tracks

S. F. J. Wickham, J. Bath, Y. Katsuda, M. Endo, K. Hidaka, H. Sugiyama and A. J. Turberfield, *Nature Nanotechnol.* **6**, 166 (2011)

Localized computing by selectively blocking DNA walkers

Composable
XOR circuit



Computing with interacting DNA walkers

NOR (x,y)



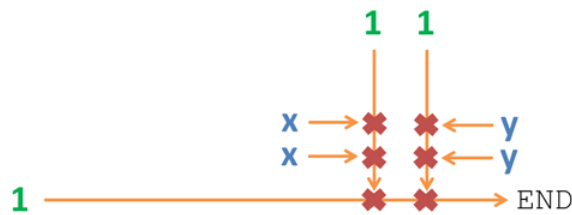
NOT (x)



AND (x,y)



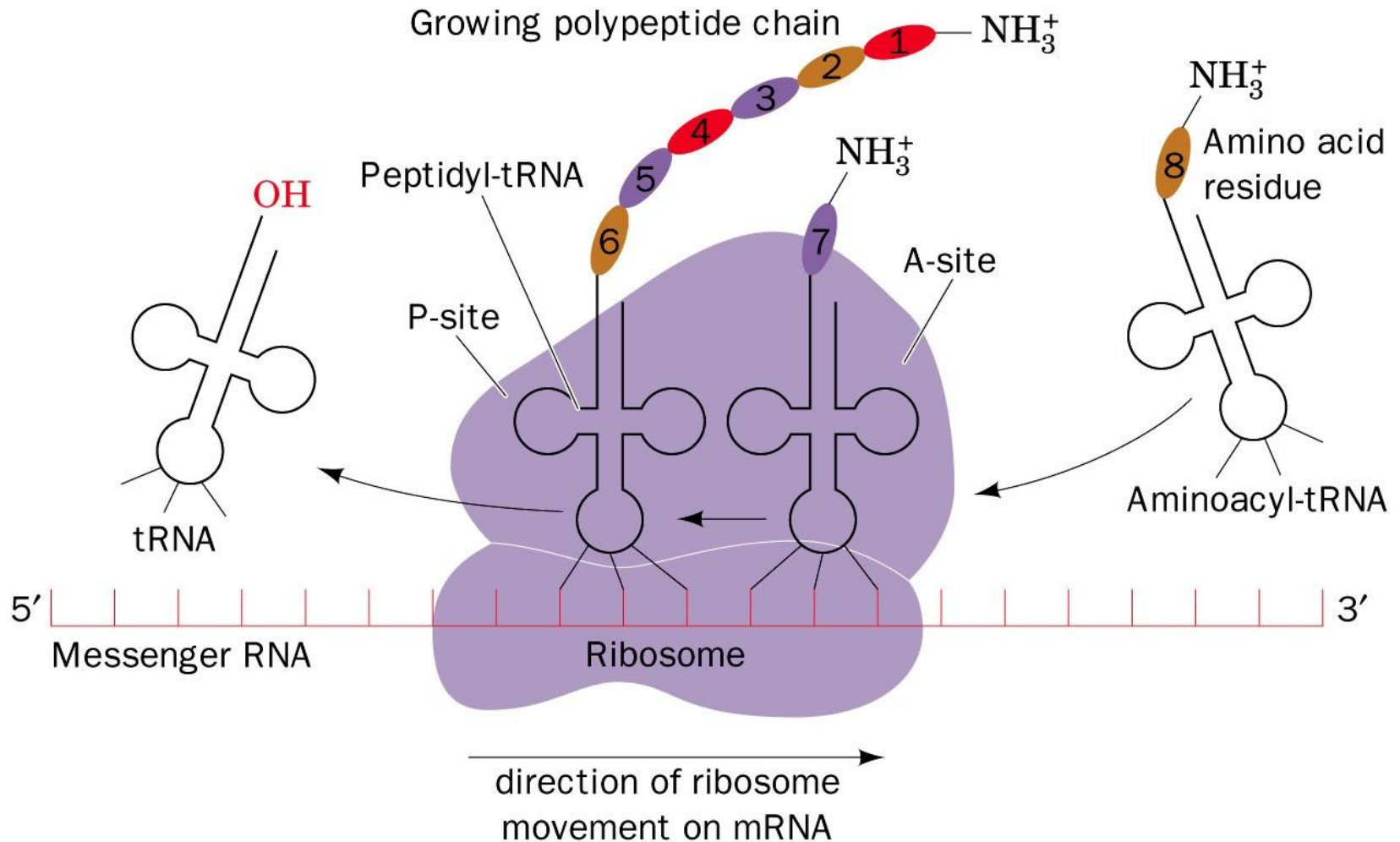
AND (x,y) = NOR(NOR(x,x),NOR(y,y))



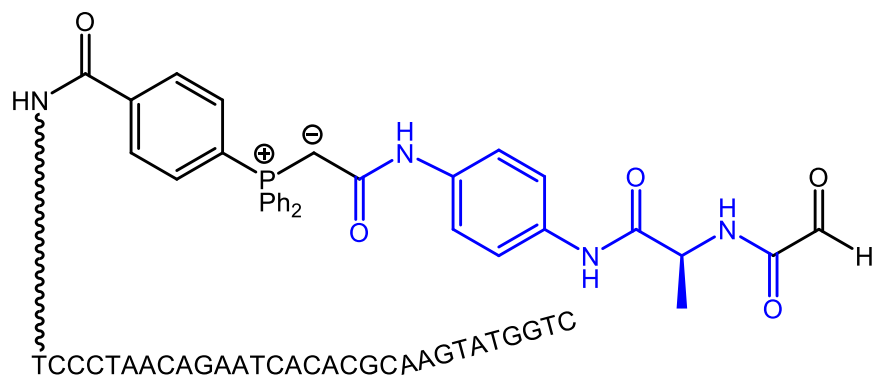
OR (x,y)



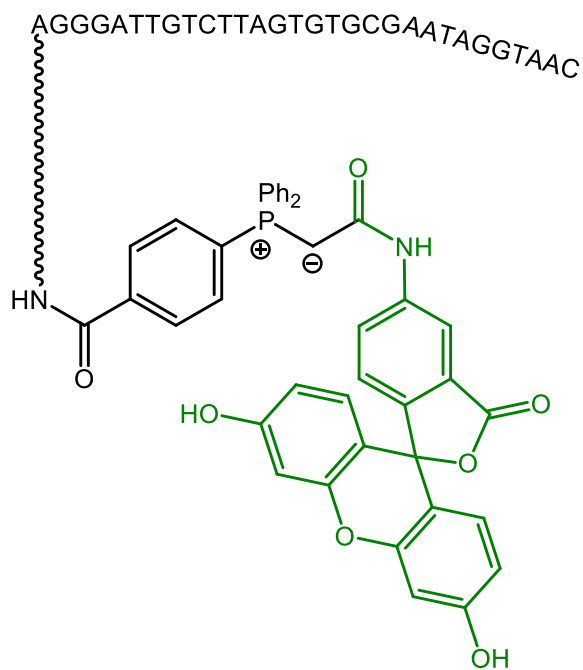
DNA-templated chemistry – towards a synthetic ribosome



DNA-templated chemistry – towards a synthetic ribosome



Strand2-Phos-Ala-Ald

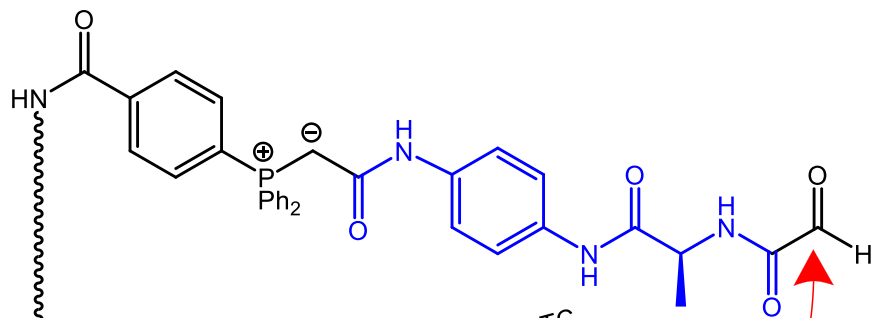


Strand1-Phos-FAM

Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

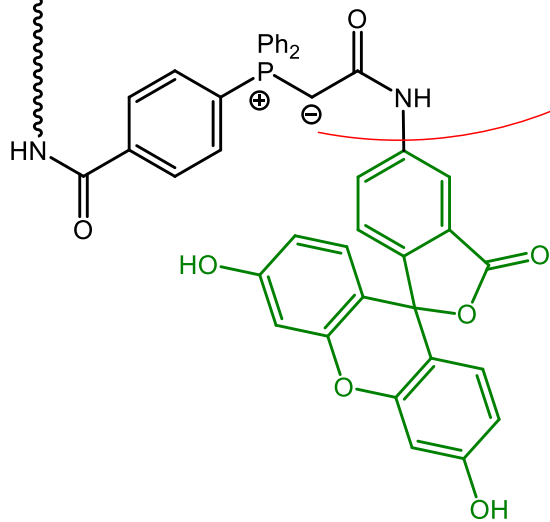
Angew. Chem. Int. Ed. **49**, 7948 (2010)



Strand2-Phos-Ala-Ald

TCCCTAACAGAATCACACGCAAGTATGGTC

AGGGATTGTCTTAGTGTGCGAATAGGTAAC

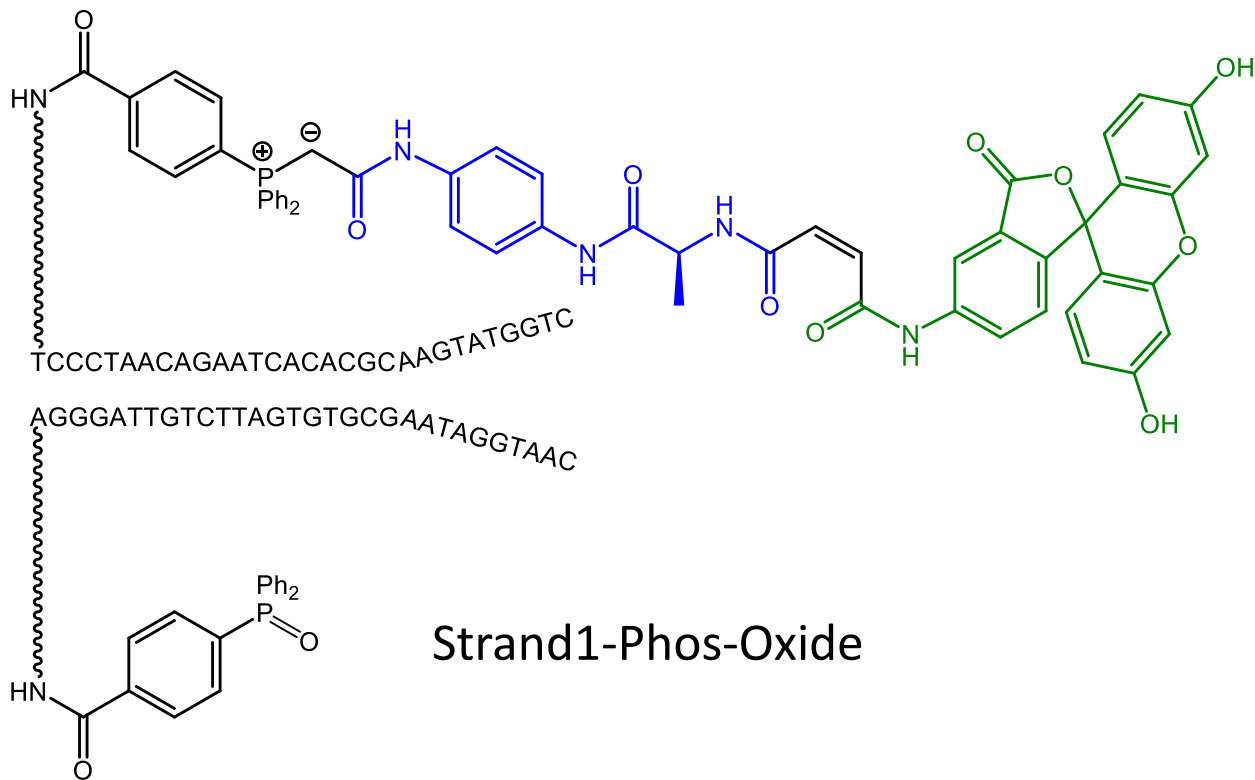


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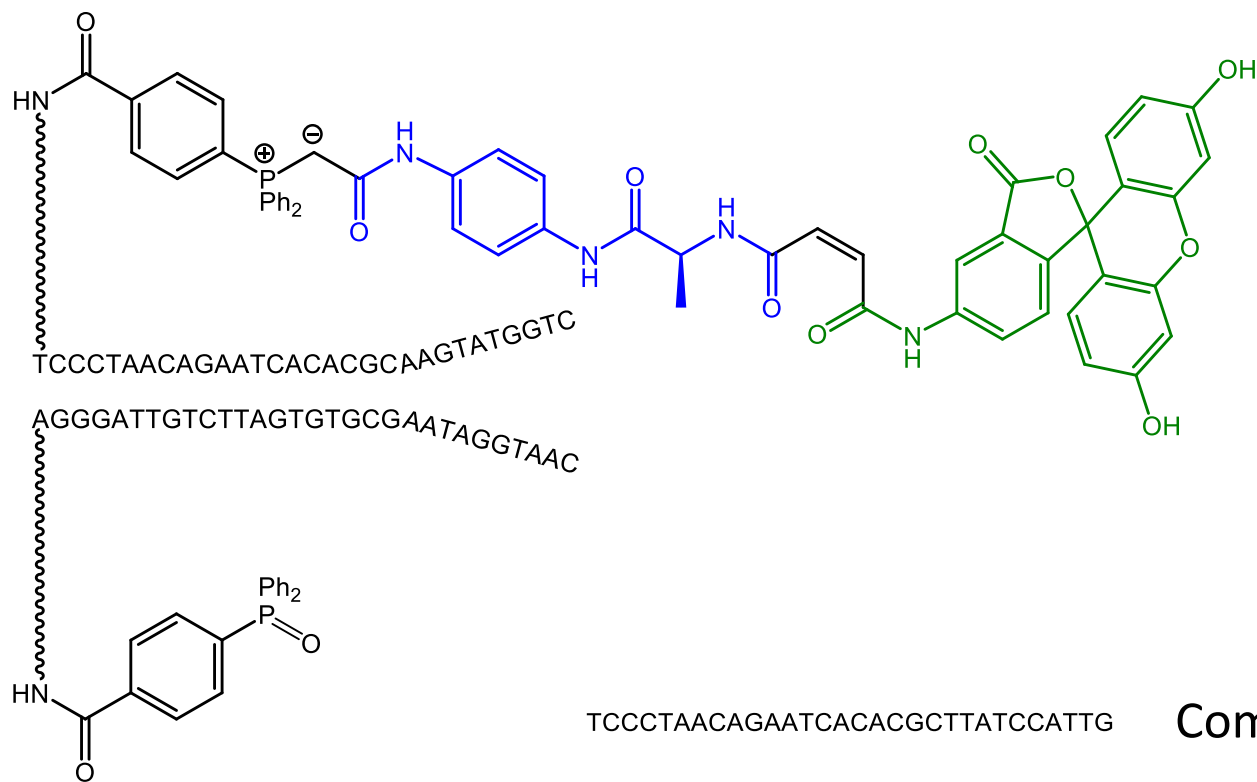
Strand2-Phos-Ala-FAM

Strand1-Phos-Oxide

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M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

Angew. Chem. Int. Ed. **49**, 7948 (2010)



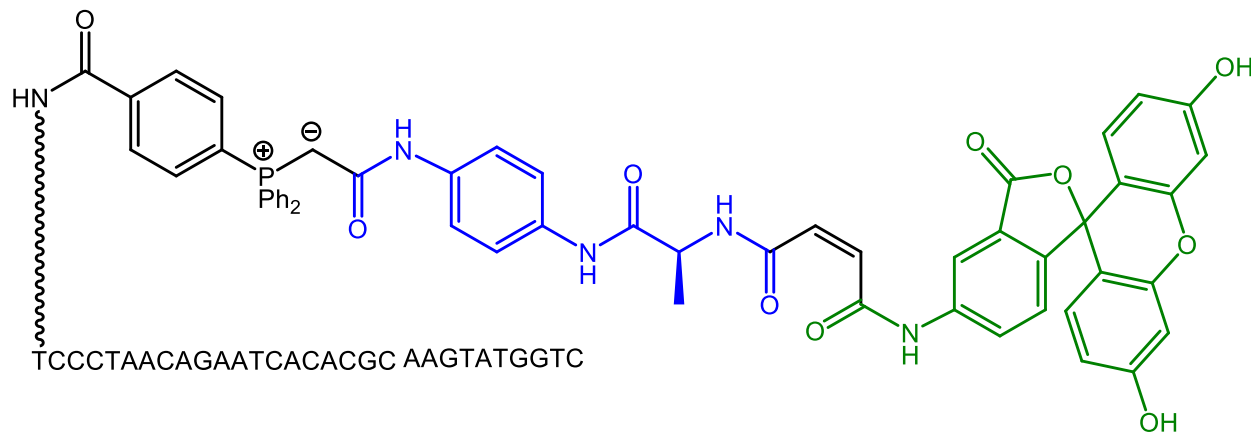
Strand2-Phos-Ala-FAM

Complementary1

Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

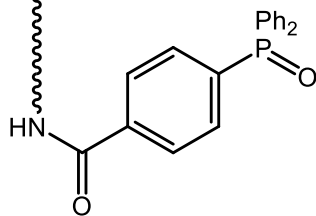
M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

Angew. Chem. Int. Ed. **49**, 7948 (2010)



Strand2-Phos-Ala-FAM

TCCCTAACAGAATCACACGCTTATCCATTG
 AGGGATTGTCTTAGTGTGCGAATAGGTAAC

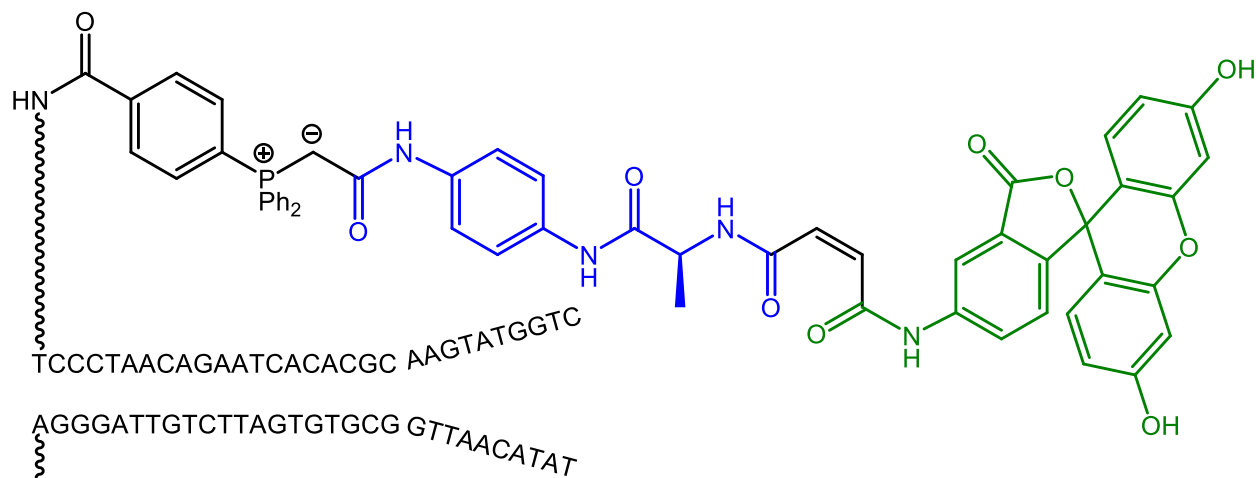


Complementary1
 Strand1-Phos-Oxide

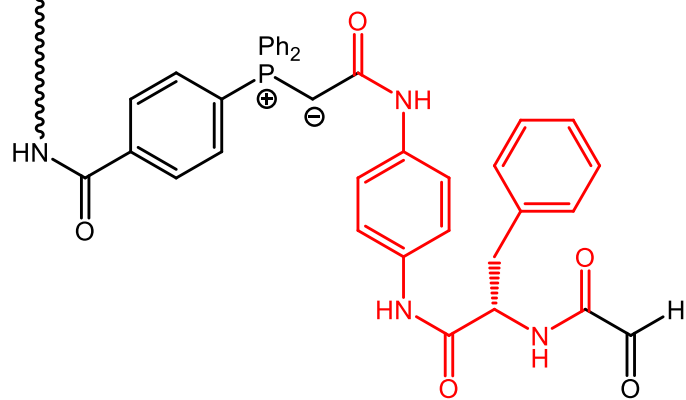
Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

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Angew. Chem. Int. Ed. **49**, 7948 (2010)



Strand2-Phos-Ala-FAM

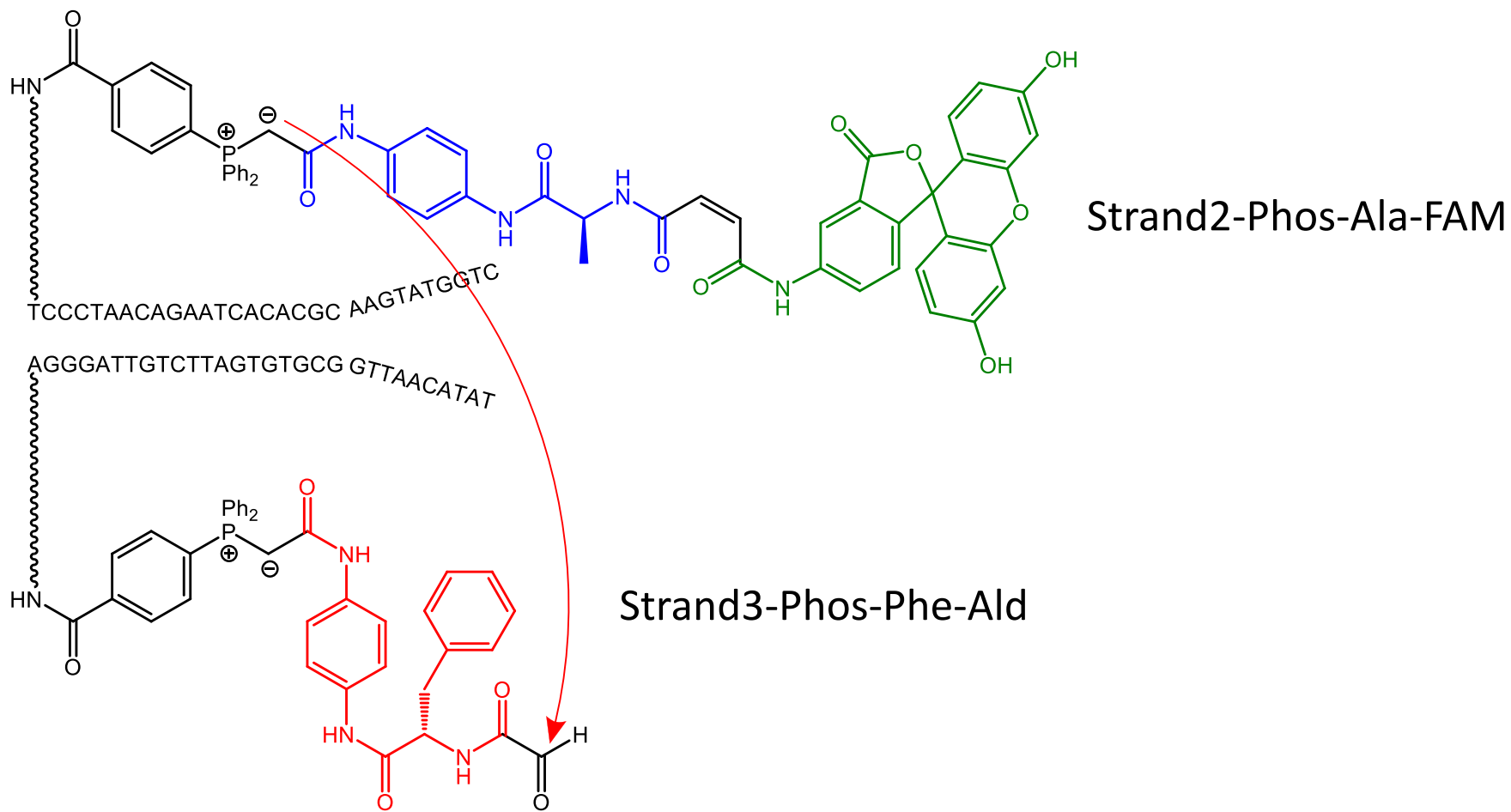


Strand3-Phos-Phe-Ald

Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

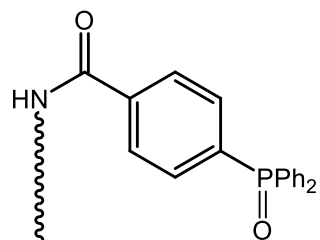
Angew. Chem. Int. Ed. **49**, 7948 (2010)



Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

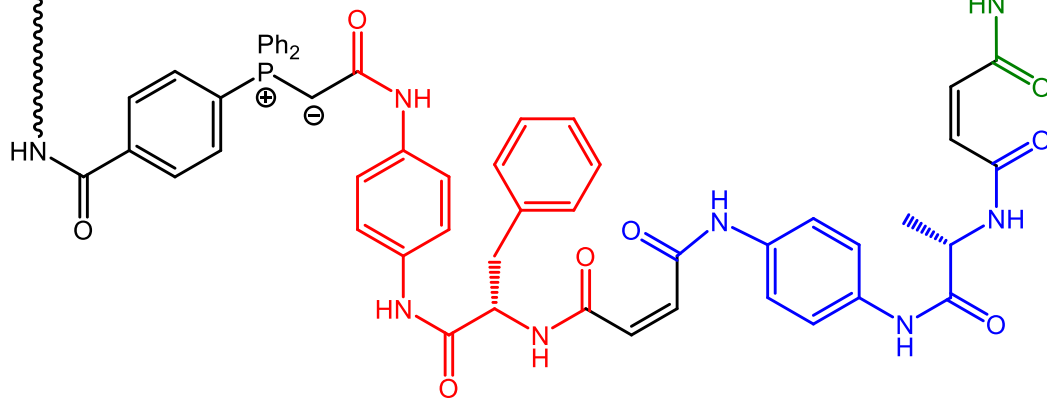
Angew. Chem. Int. Ed. **49**, 7948 (2010)



Strand2-Phos-Oxide

TCCCTAACAGAATCACACGC AAGTATGGTC

AGGGATTGTCTTAGTGTGCG GTTAACATAT



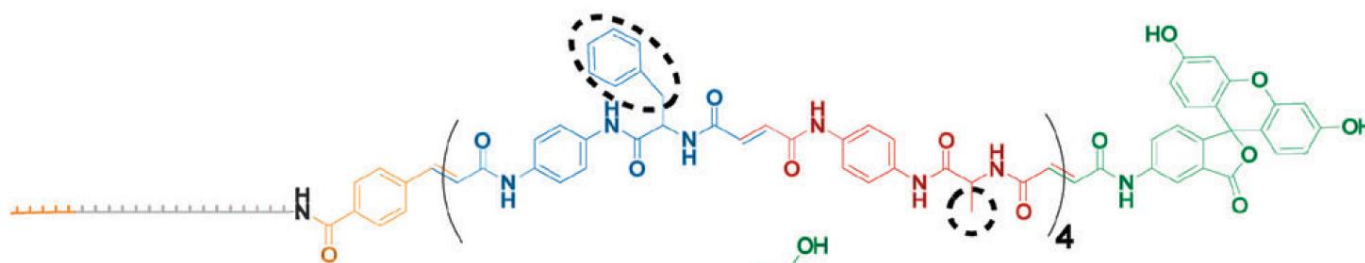
Strand3-Phos-Phe-Ala-FAM

Multistep DNA-templated reactions for the synthesis of functional sequence controlled oligomers.

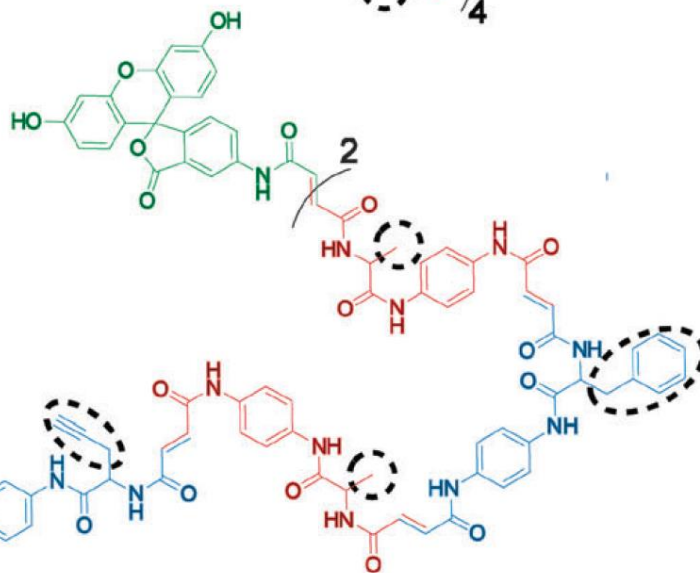
M.L. McKee, P.J. Milnes, J. Bath, E. Stulz, A.J. Turberfield, R.K. O'Reilly

Angew. Chem. Int. Ed. **49**, 7948 (2010)

DNA-templated chemistry – 10-mers!



88% yield
per step



85% yield
per step

An Autonomous Molecular Assembler for Programmable Chemical Synthesis

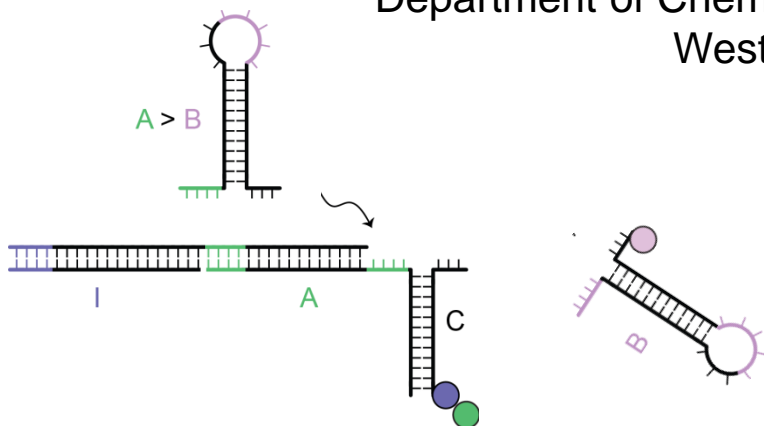
Nature Chem. **8**, 542-8 (2016)

Wenjing Meng, Richard Muscat, Mireya McKee,
Jonathan Bath, Andrew Turberfield

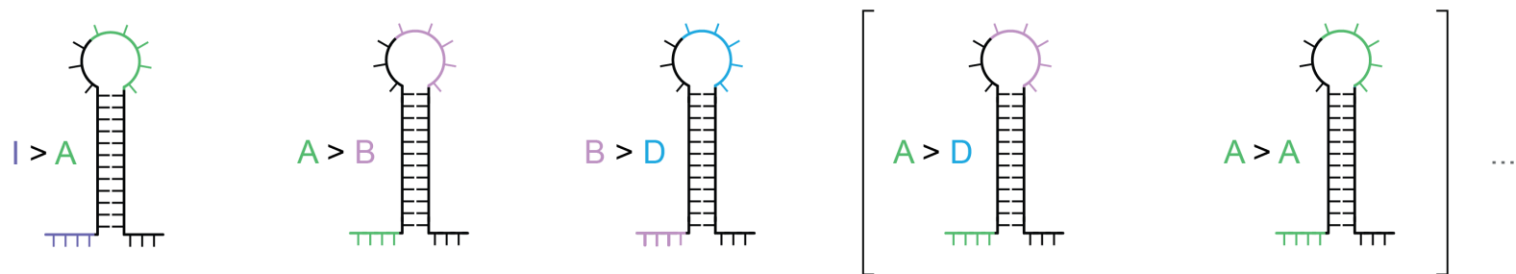
Department of Physics, University of Oxford, Clarendon Laboratory,
Parks Road, Oxford, OX1 3PU, UK

Phillip Milnes, Rachel O'Reilly

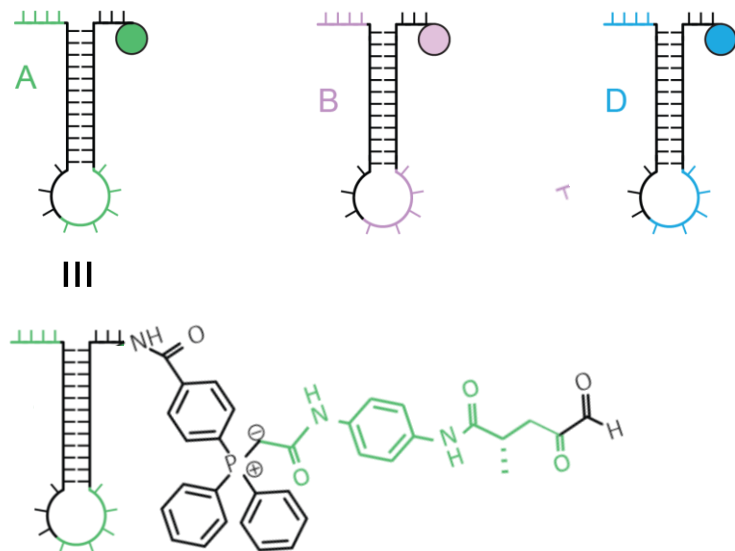
Department of Chemistry, University of Warwick, Coventry,
West Midlands CV4 7AL, UK



Instruction hairpins

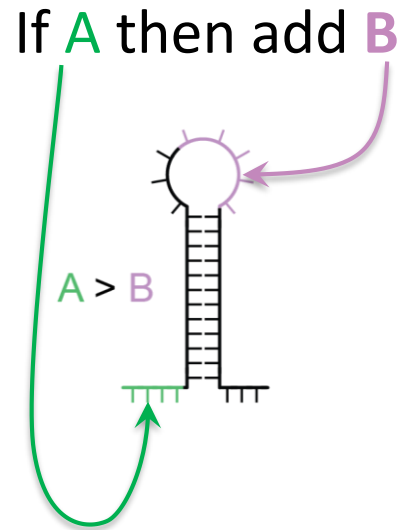


Chemistry hairpins

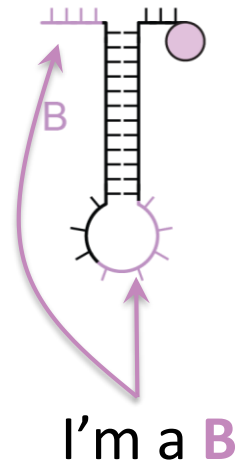


An Autonomous Molecular Assembler for Programmable Chemical Synthesis.
R.A. Muscat, M.L. McKee, P.J. Milnes, J. Bath, R.K. O'Reilly³ A.J. Turberfield
Nature Chem. **8**, 542-548 (2016)

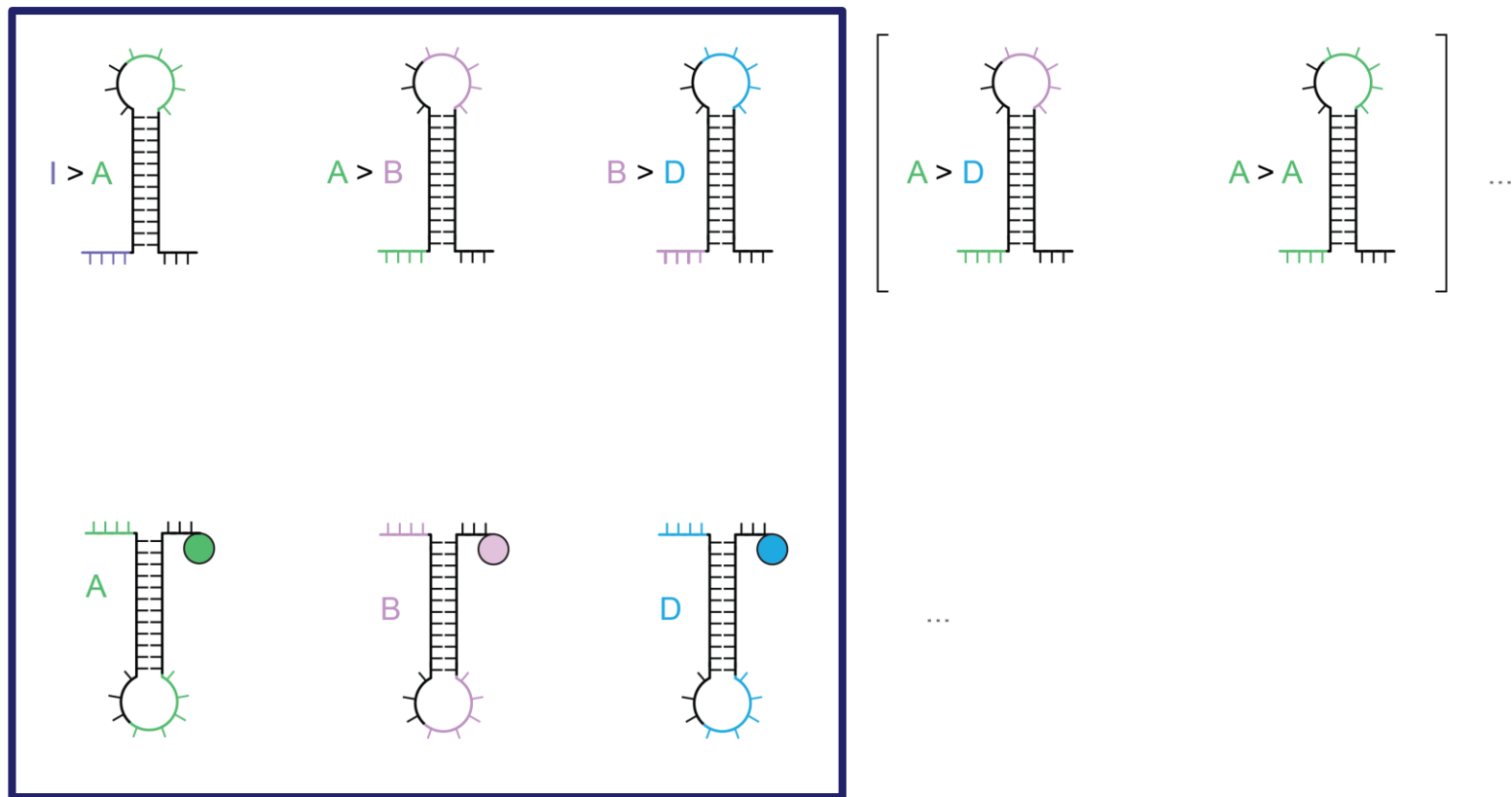
Instruction strand



Chemistry strand

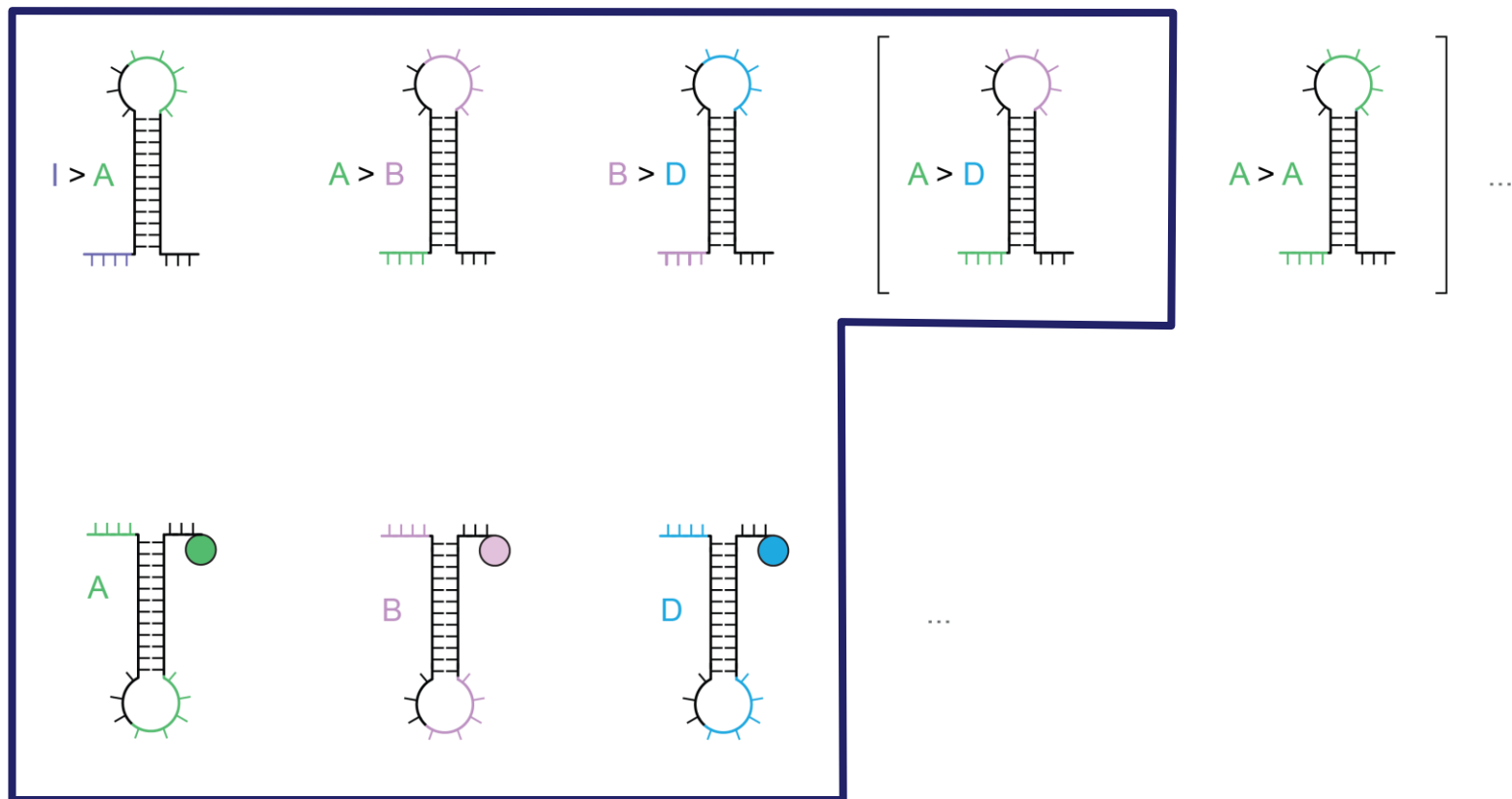


Simple program



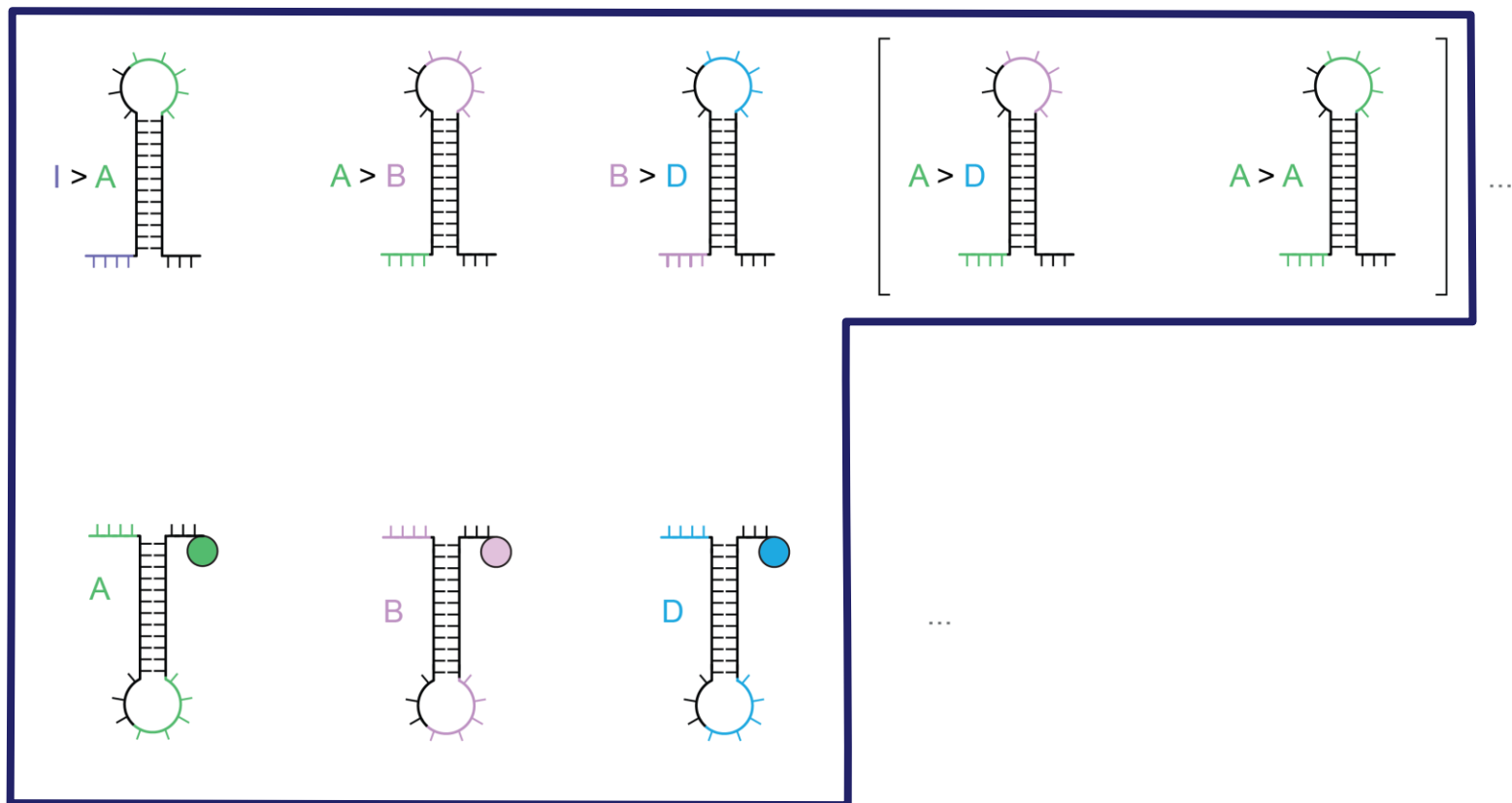
Make polymer **A B D** (● ● ●)

Non-deterministic program (branchpoint)



Make polymer **A B D** (● ● ●) or **A D** (● ●)

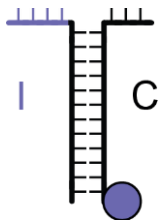
Non-deterministic program (branchpoint, indefinite loop)



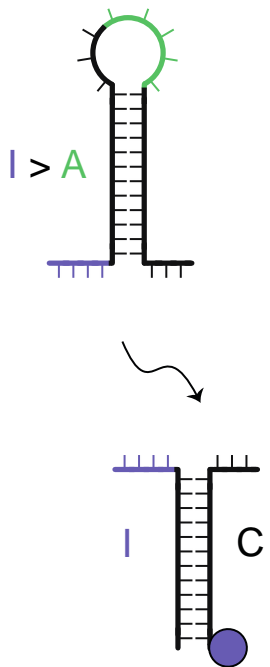
Make polymer $A_n B D$ or $A_n D$

Reaction starts with an initiator **I** bound to the cargo **C**

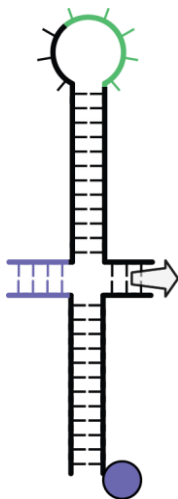
The growing polymer chain is built on the cargo strand **C**



The instruction $I > A$ binds to $I \bullet C$

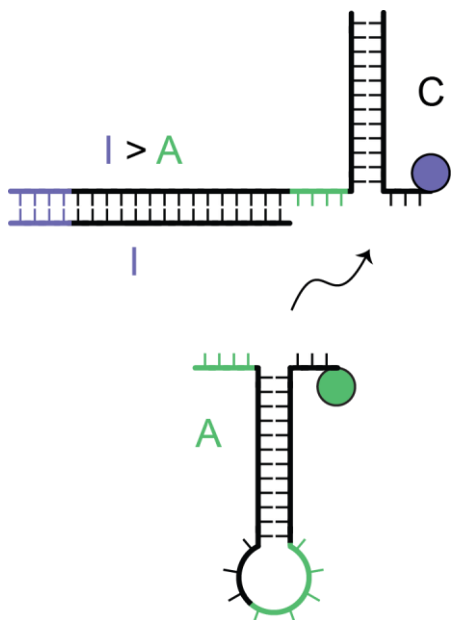


The hairpin **I** > **A** is opened by branch migration, **C** is transferred onto **I** > **A**



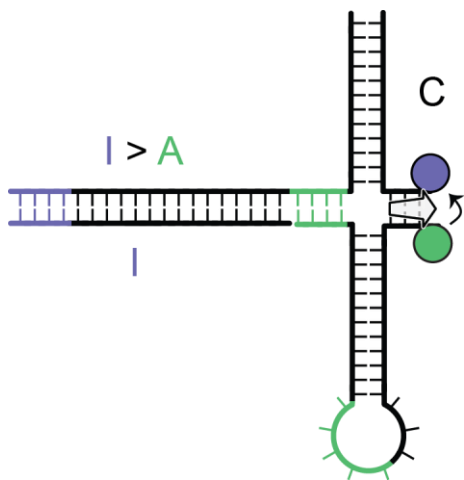
The hairpin **I** > **A** is opened by branch migration, **C** is transferred onto **I** > **A**

The chemistry hairpin **A** can bind to the open instruction hairpin

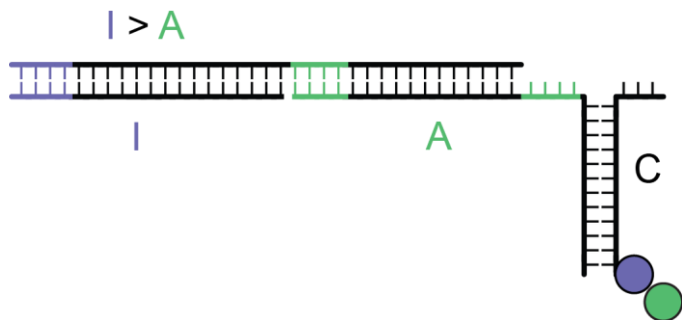


Once bound, the functional group **A** (●) is held close to **C** (●) and can react

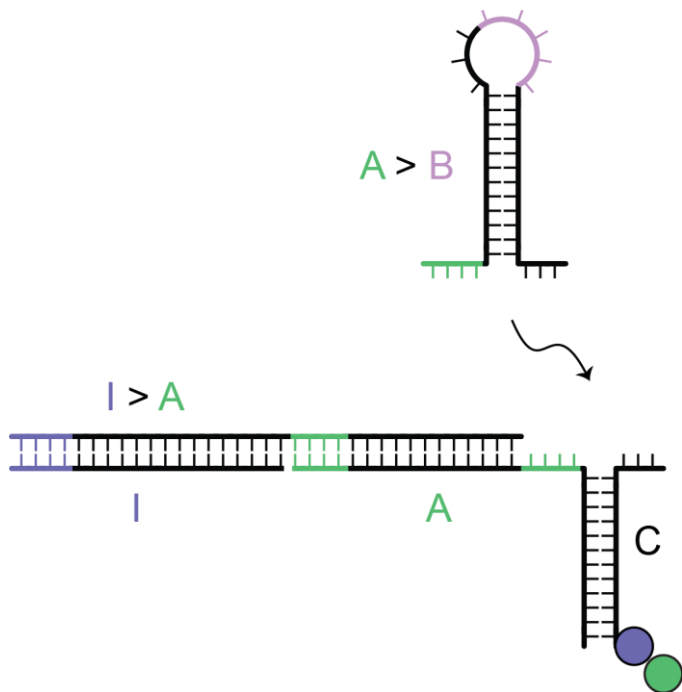
At the same time, **A** is opened by branch migration and **C** is transferred onto **A**



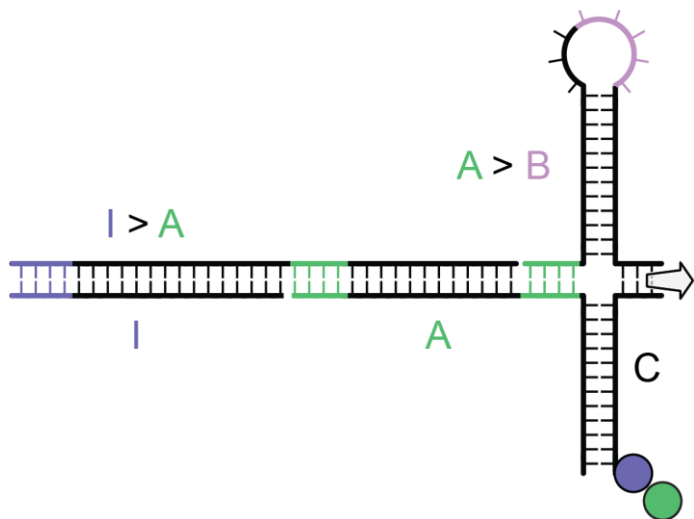
Building block **A** (●) is transferred to C (●)



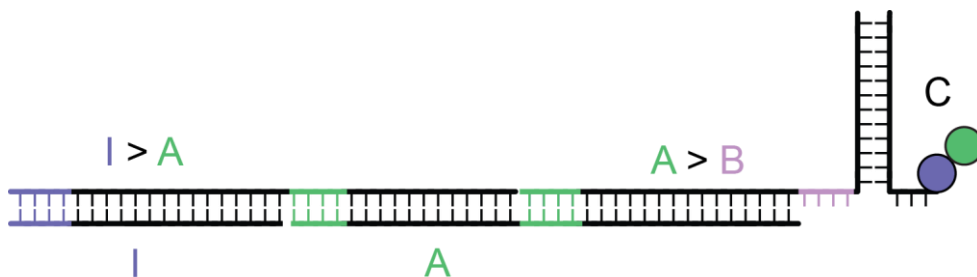
The next instruction, **A > B** binds



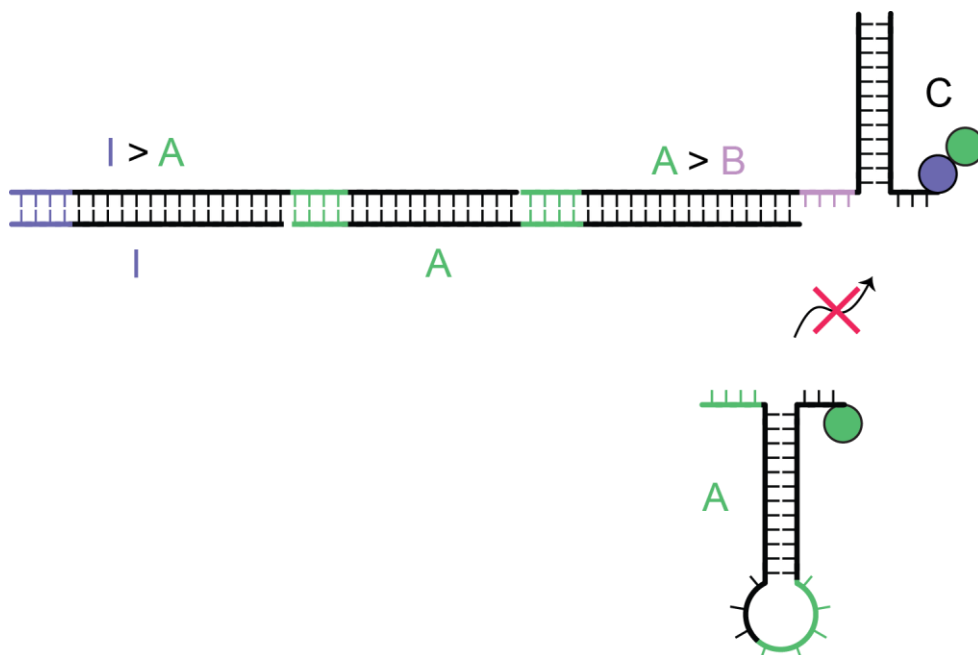
The next instruction, **A > B** binds



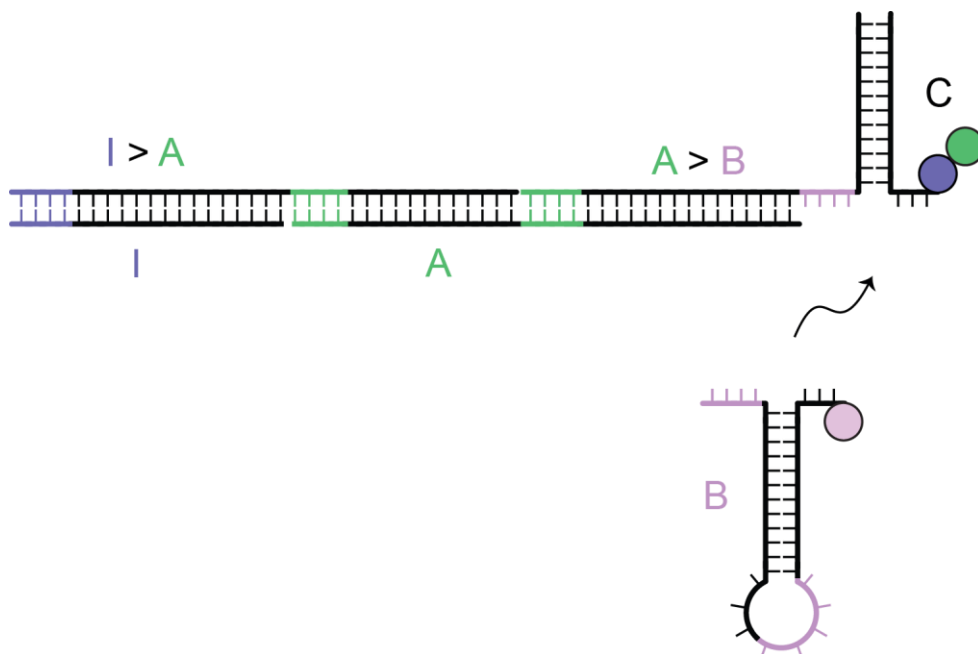
A > B is opened by branch migration



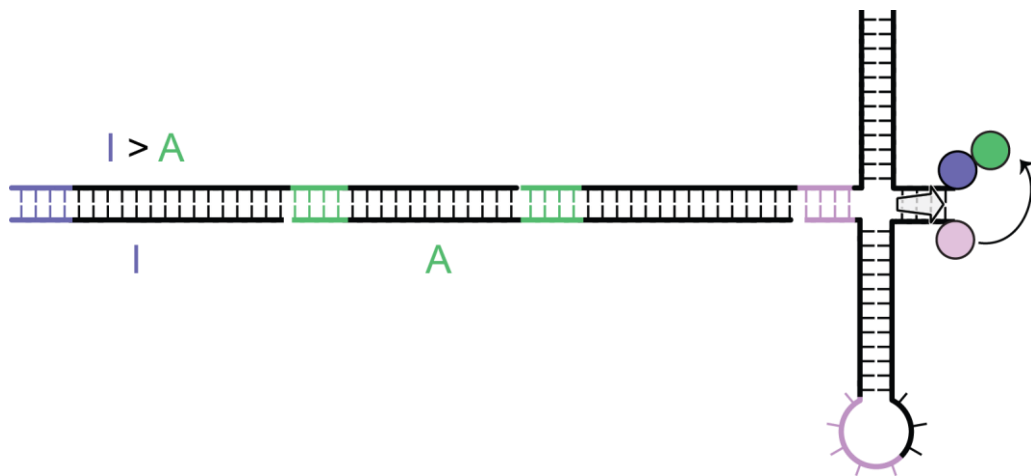
The chemistry strand **A**, although present in solution, doesn't bind (toeholds don't match)



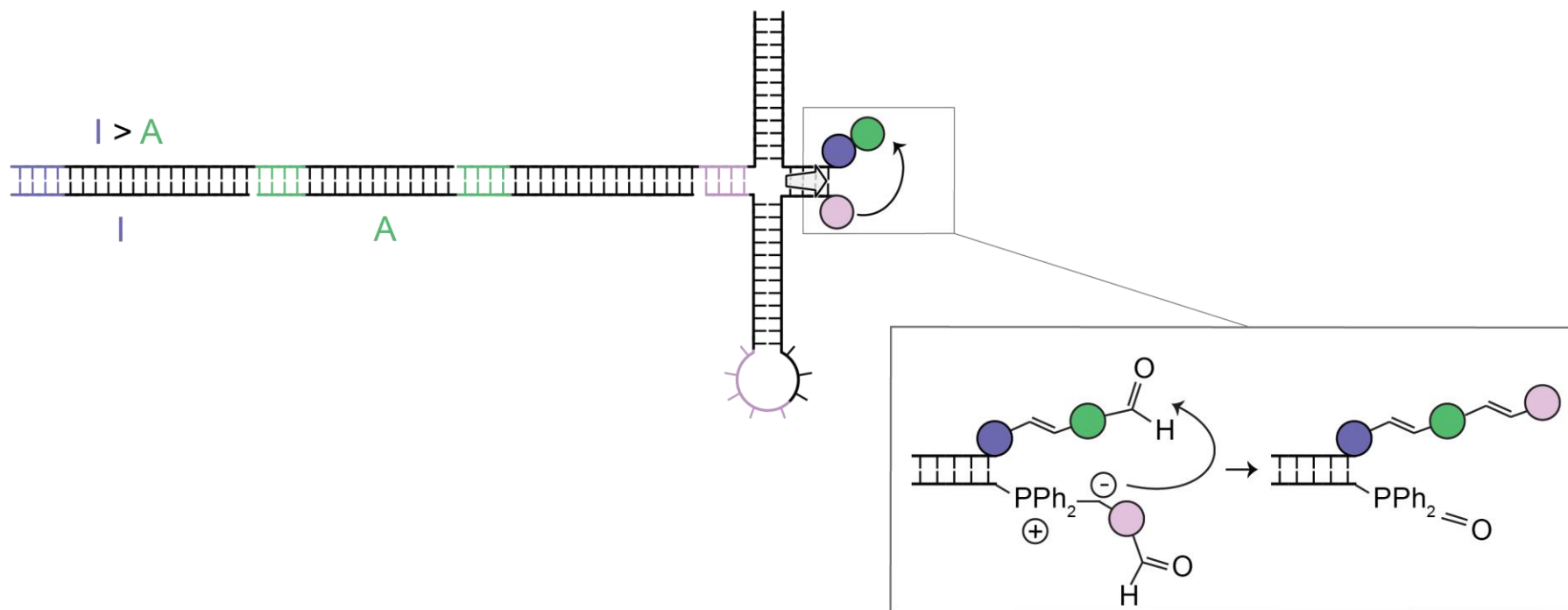
The chemistry strand **B** binds (toeholds match)



Building block B (●) is transferred to A (●)



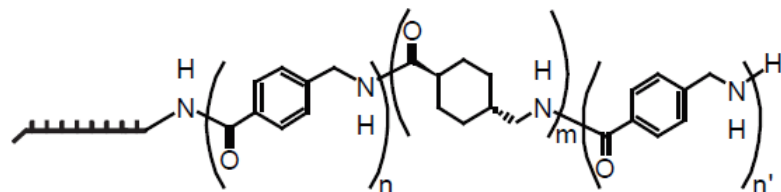
Building block B (●) is transferred to A (●)



An Autonomous Molecular Assembler for Programmable Chemical Synthesis.

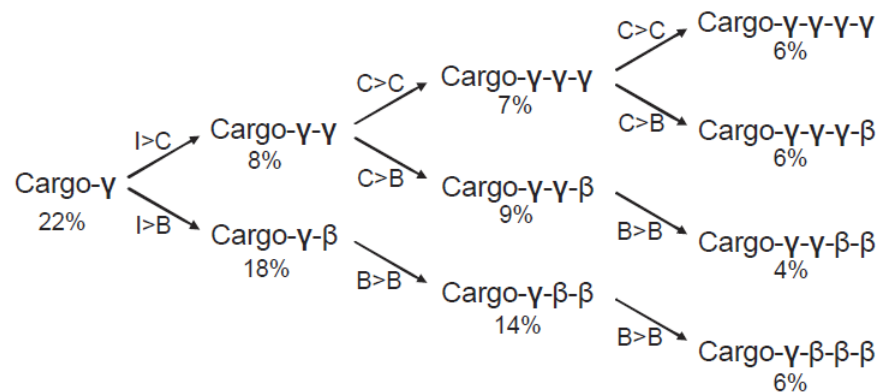
W. Meng, R.A. Muscat, M.L. McKee, P.J. Milnes, J. Bath, R.K. O'Reilly³ A.J. Turberfield
Nature Chem. **8**, 542-548 (2016)

Autonomous combinatorial synthesis of a polypeptide

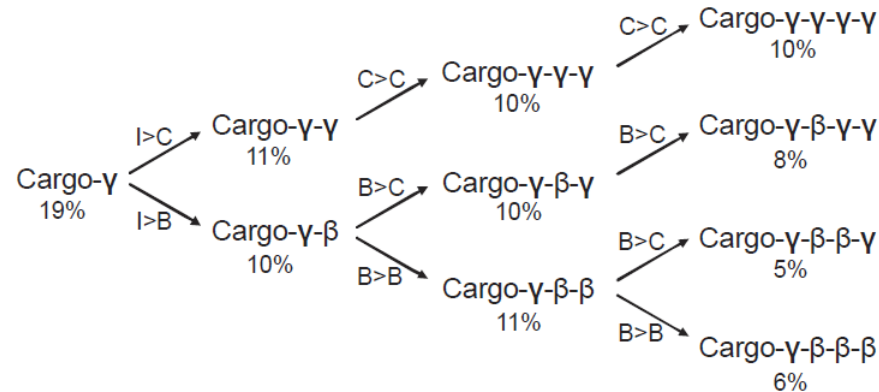


Cargo- $\gamma_n\beta_m\gamma_{n'}$ ($n = 1-4, m = 0-3, n' = 0-2$)

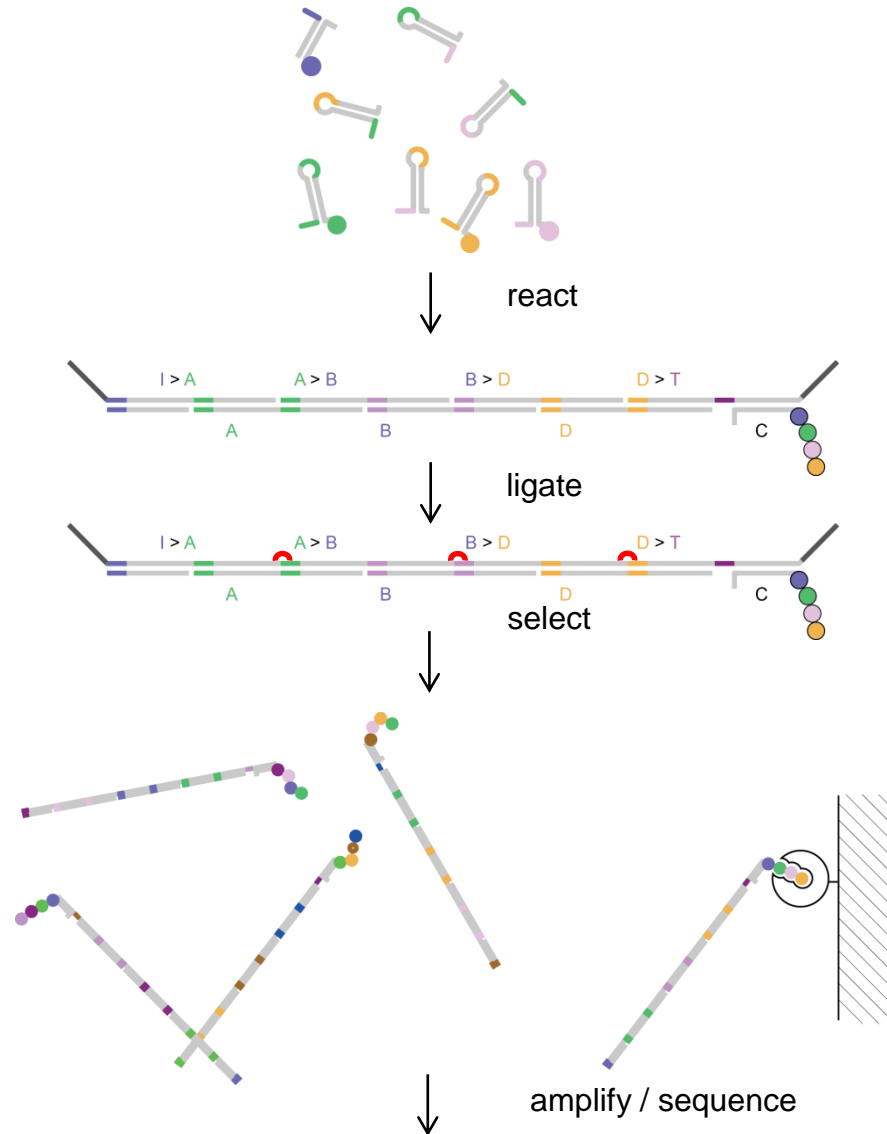
Reaction 1: I>B, B>B, C>C,
I>C, C>B



Reaction 2: I>B, B>B, C>C,
I>C, B>C




Ligation of one strand of the HCR duplex creates a permanent record



DNA-templated chemistry: selection and evolution

Use a DNA program to control oligomer synthesis; program determines reaction sequence (program is *gene*):

- Generate library of programs** random insertions
cut and shuffle
 - Synthesize product library** ensure product remains bound
to program (*ribosome display*)
 - Select fittest products** usually by binding or cleaving
 - Amplify selected programs** polymerase chain reaction
transform bacteria
 - Mutate**
- 

So far –

- sequence-specific hybridization can be used to program the self-assembly of DNA and RNA nanostructures.

nucleic acid nanostructures can ...

- act as atomically precise scaffolds
- exhibit programmed dynamic behaviour
- control chemical reactions
- compute
- function *in vivo* (or fixed cells)

Given the ability to manufacture 3D structures with nm precision, and to create molecular systems that integrate sensing, computation and actuation –

what should we make?