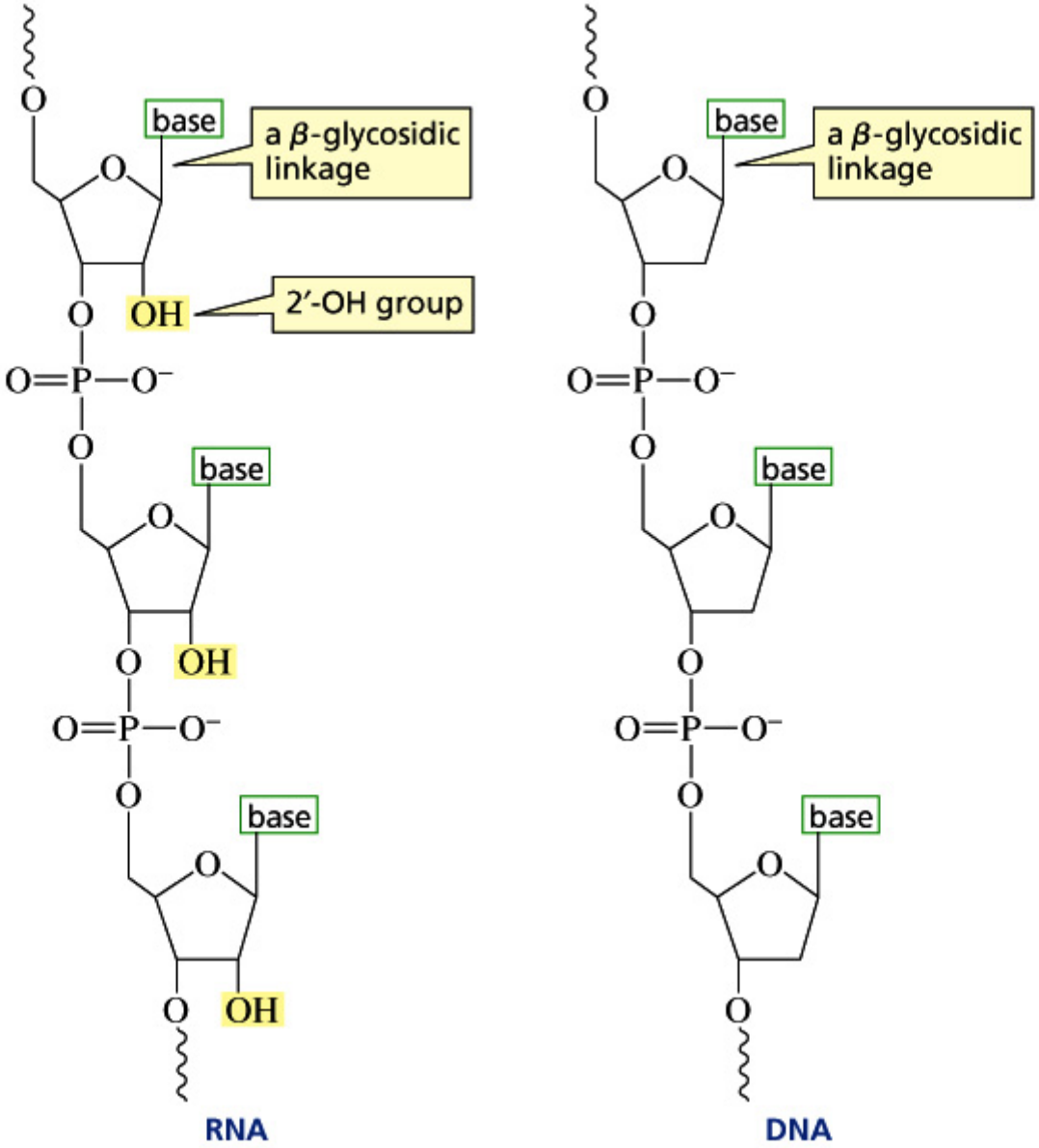
DNA nanostructures

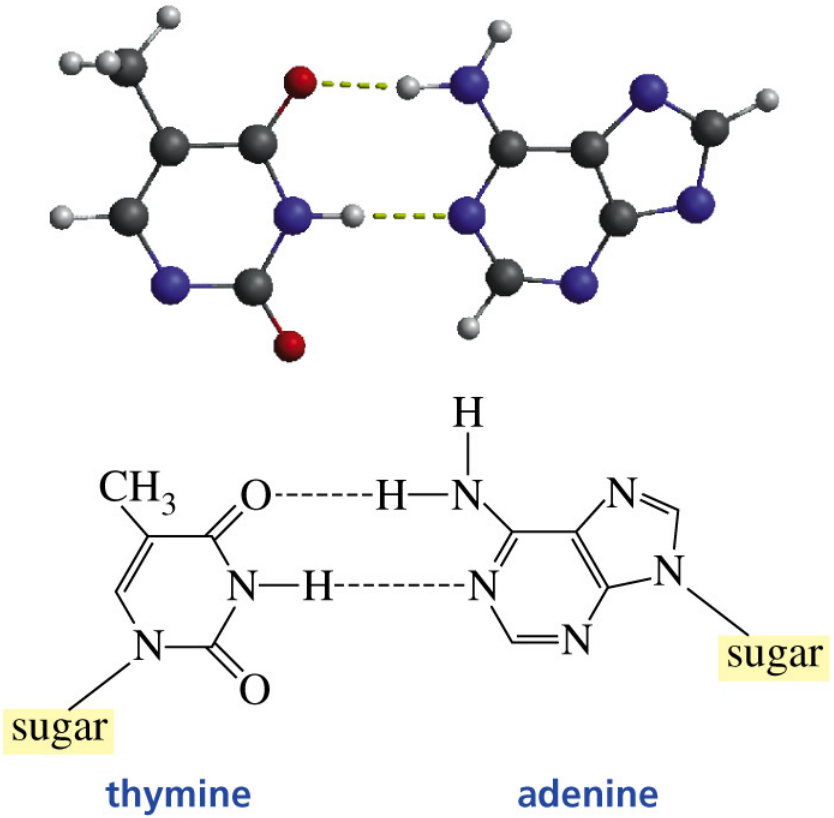


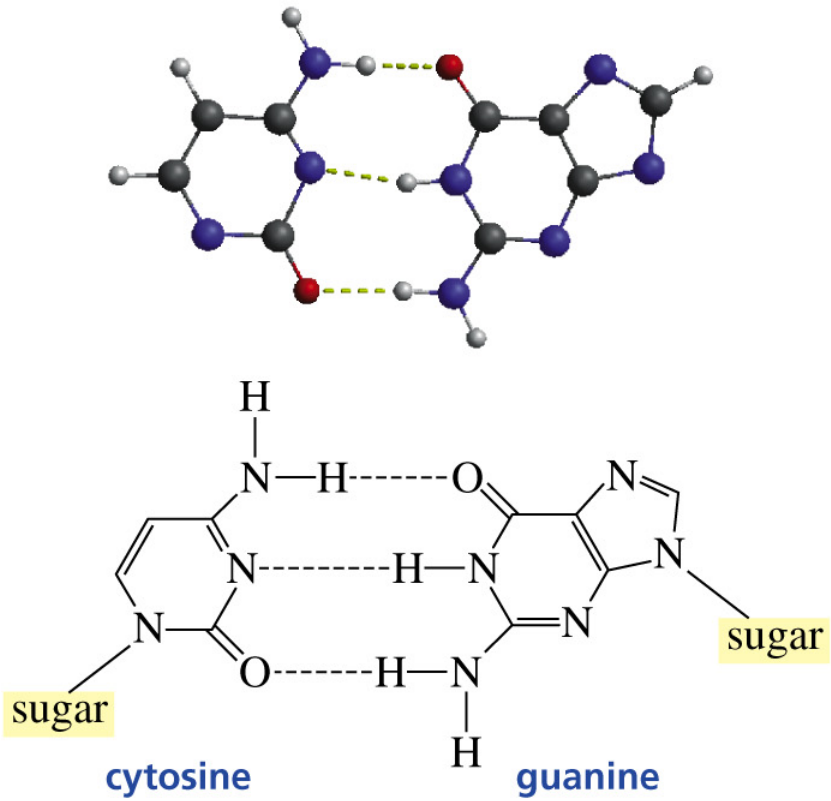
From a chemical point of view, DNA and RNA are nucleotides copolymers.

When have complementary sequences, DNA polymers are able to self recognize.

DNA not only encodes the genetic information but also the chemical information allowing for many different structural and recognition motifs.

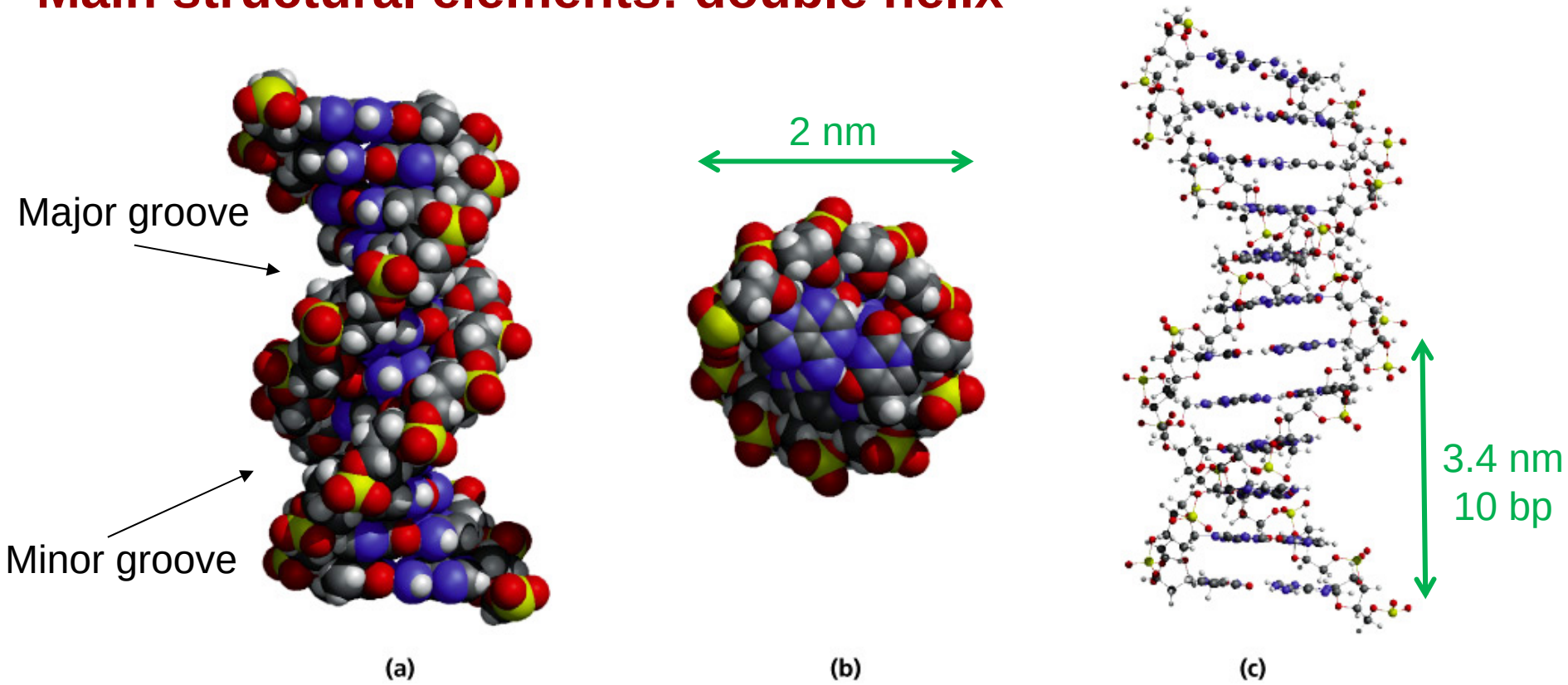
Main structural elements: base pairs





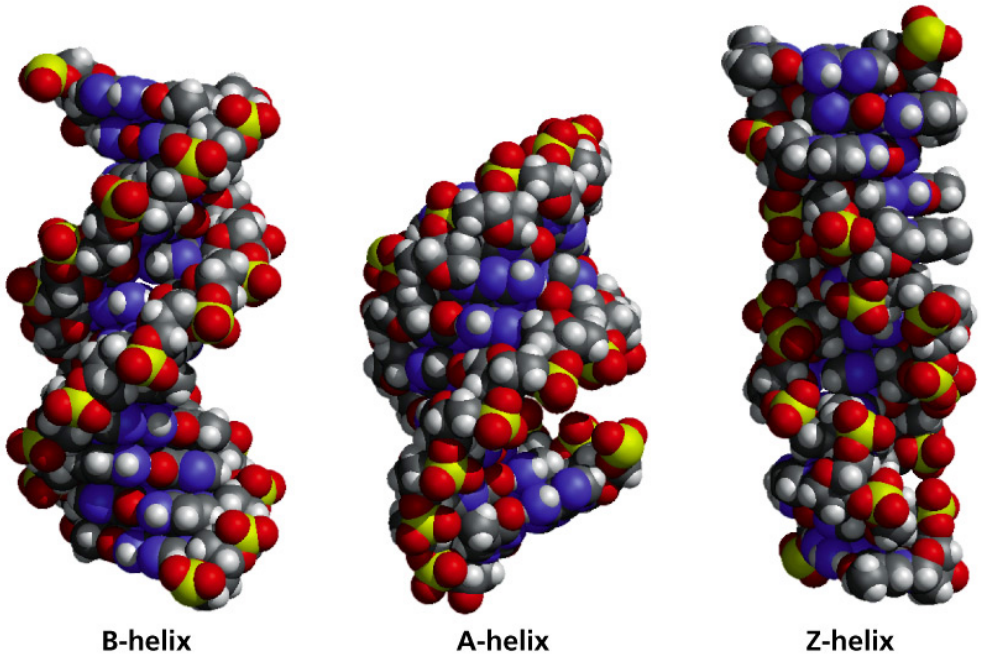
Watson and Crick base pairs

Main structural elements: double helix

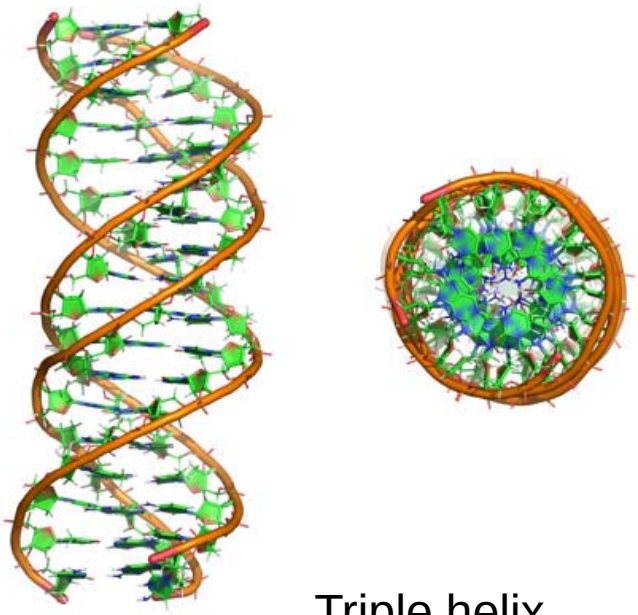


In the double helix form, DNA is relatively rigid and with a defined shape, the dimensions of the DNA double helix are in the nanoscale range

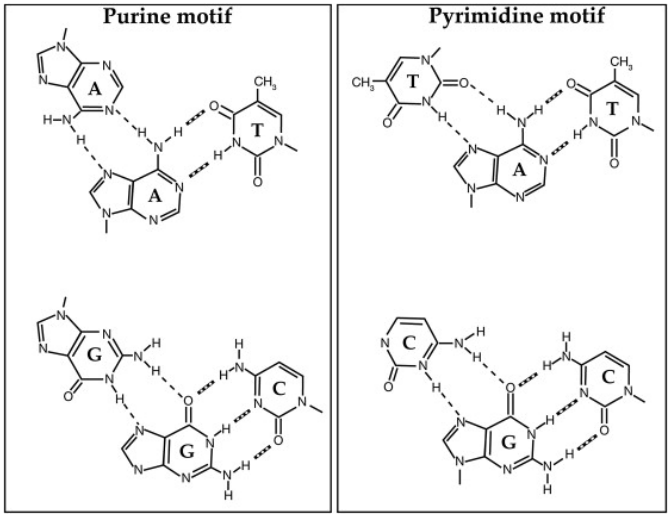
Many structures from the same molecule



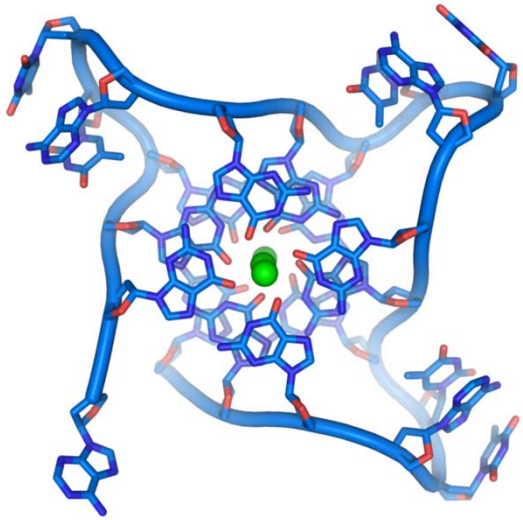
Double helices



Triple helix

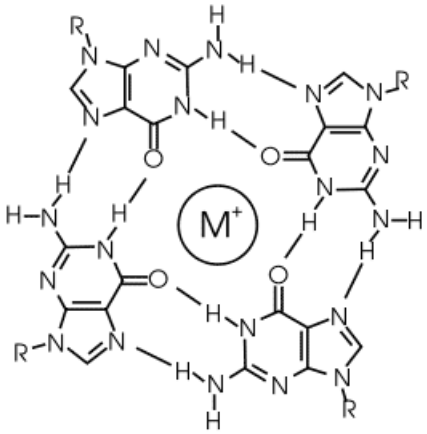


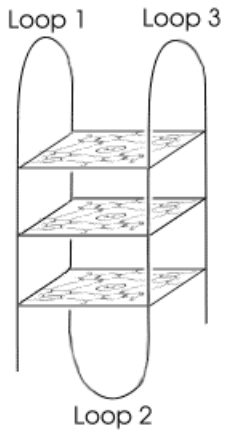
Many structures from the same molecule

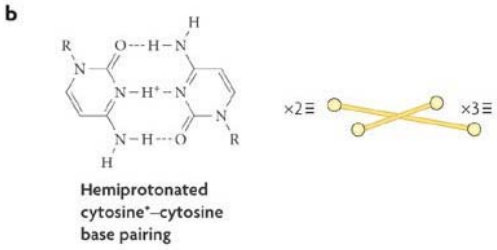


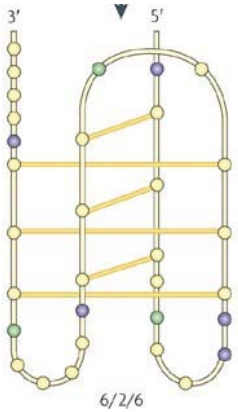
G-quadruplex

I-motif









Many structures from the same molecule

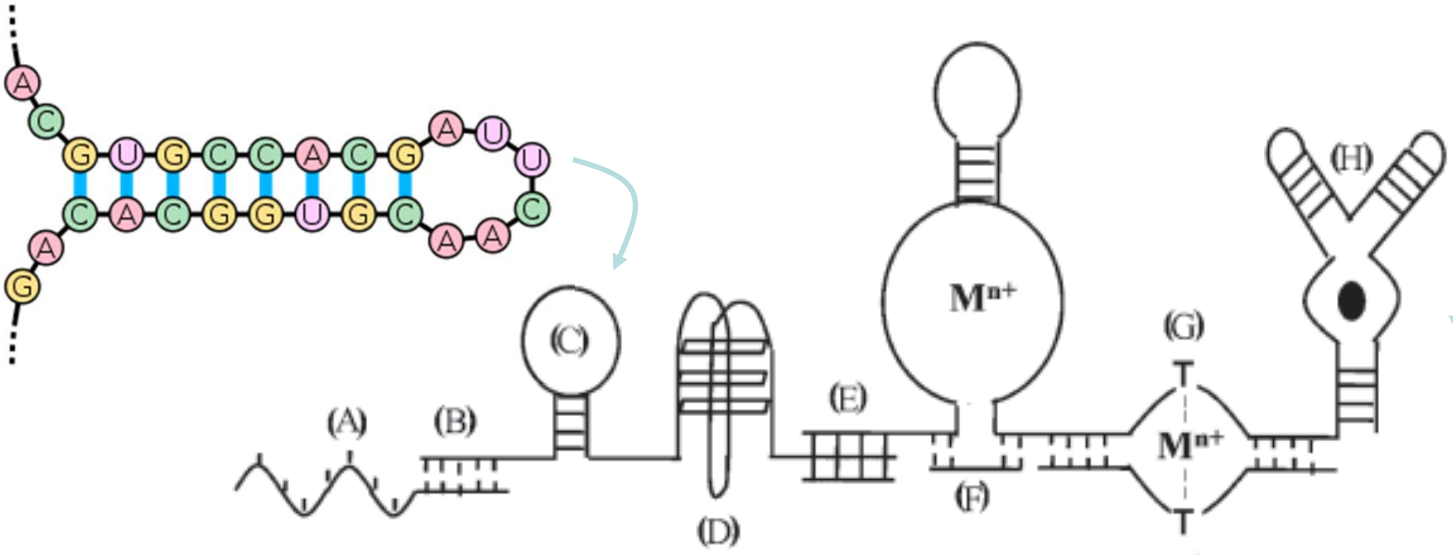
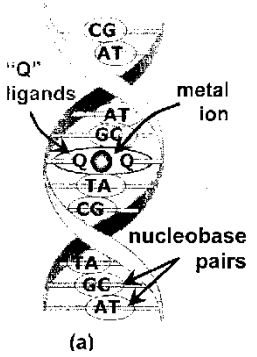
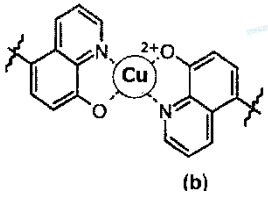
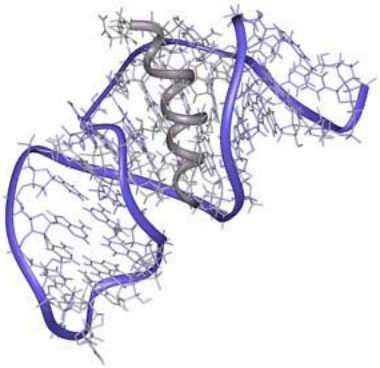


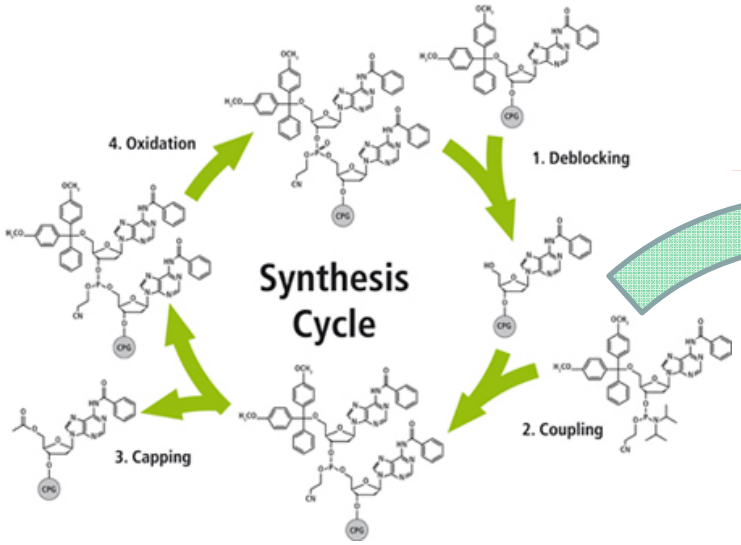
Figure 1. Schematic structural and functional features of nucleic acids: (A) single-stranded sticky end; (B) duplex hybridization; (C) hairpin nanostructure; (D) G-quadruplex; (E) triplex hybrid; (F) DNAzyme structure; (G) metal-bridged duplex; (H) aptamer nanostructure.





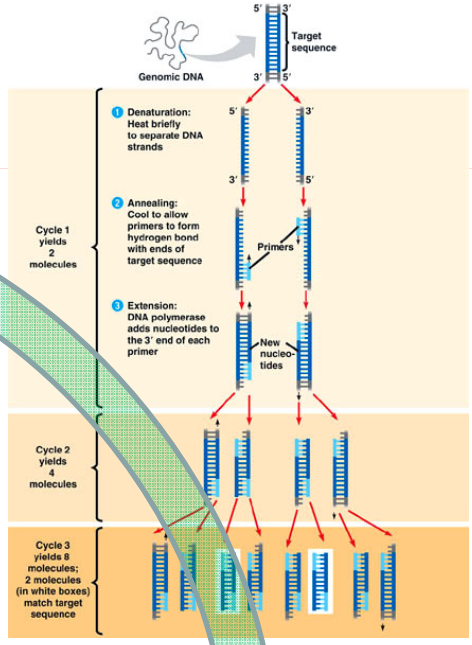


Synthesis and manipulation



Automated synthesis

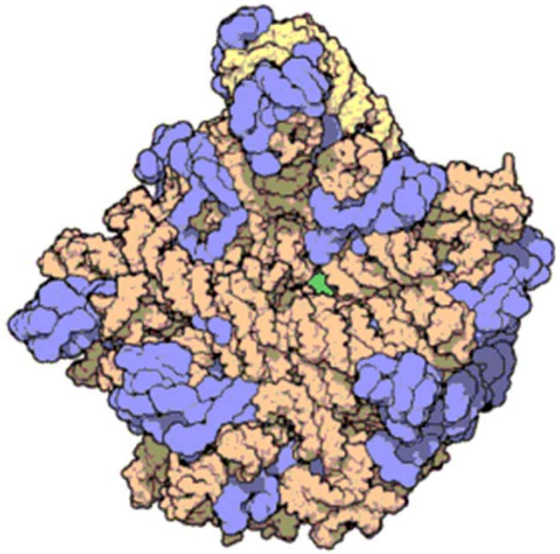
PCR amplification



Enzyme machinery

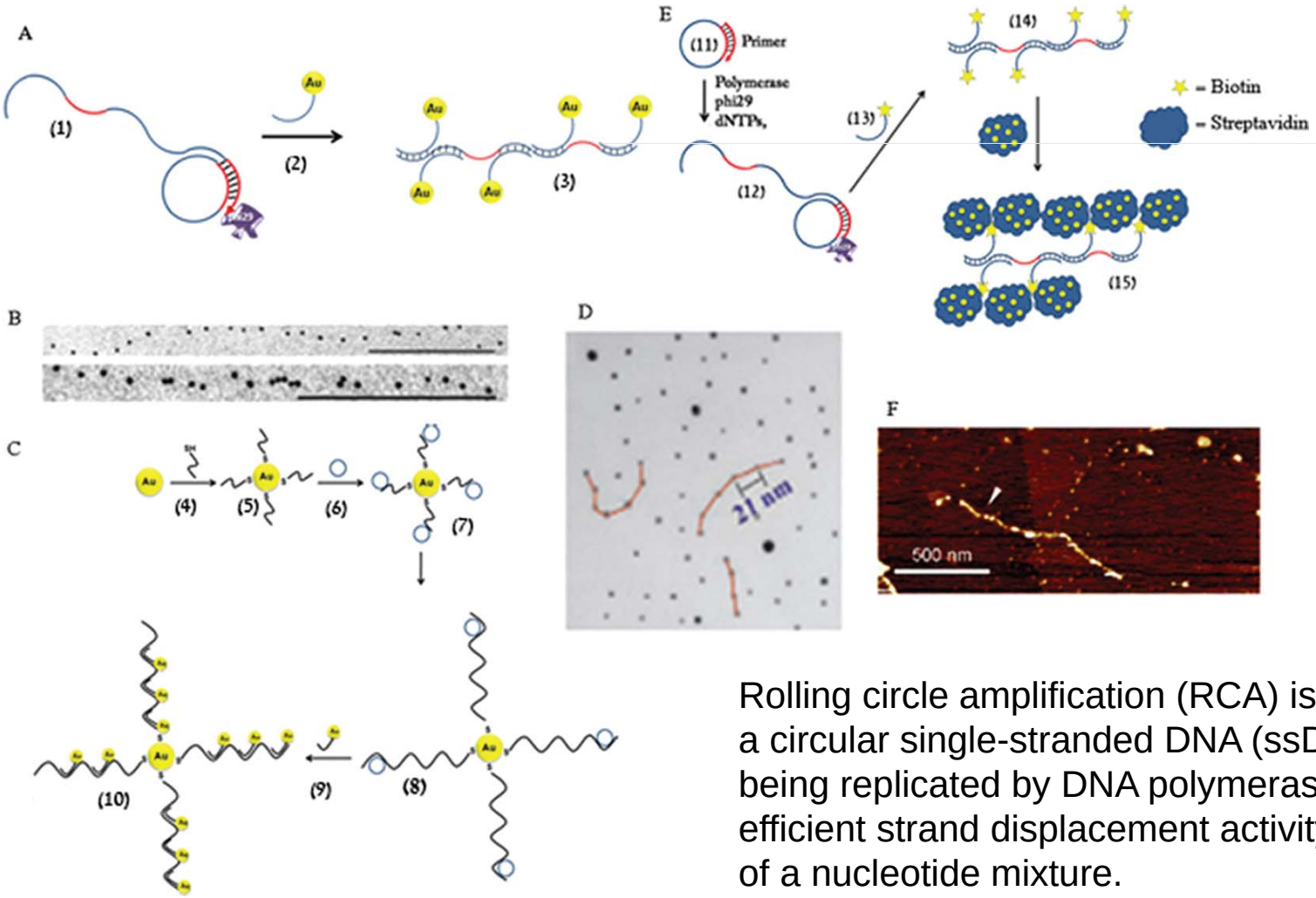
- Polymerases
- Transcriptases
- Telomerases
- Nucleases
- Nicking enzimes

DNA-protein self-organization



Ribosome: protein-DNA functional aggregate

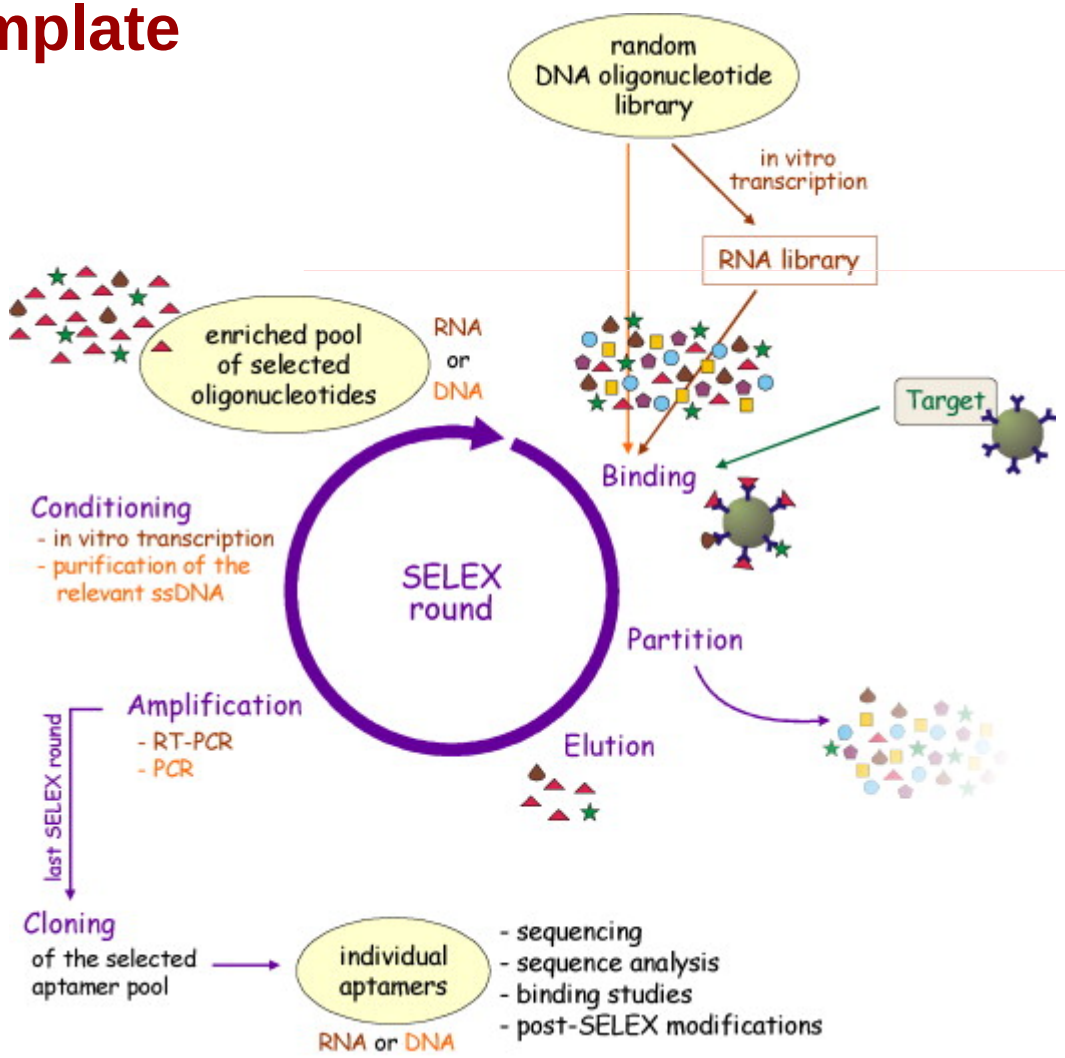
DNA as a template



Rolling circle amplification (RCA) is a process where a circular single-stranded DNA (ssDNA) template is being replicated by DNA polymerase, with an efficient strand displacement activity, in the presence of a nucleotide mixture.

This reaction can be applied to the preparation of gold nanoparticles chains (A-B), stars (C-D), and wires (E-F)

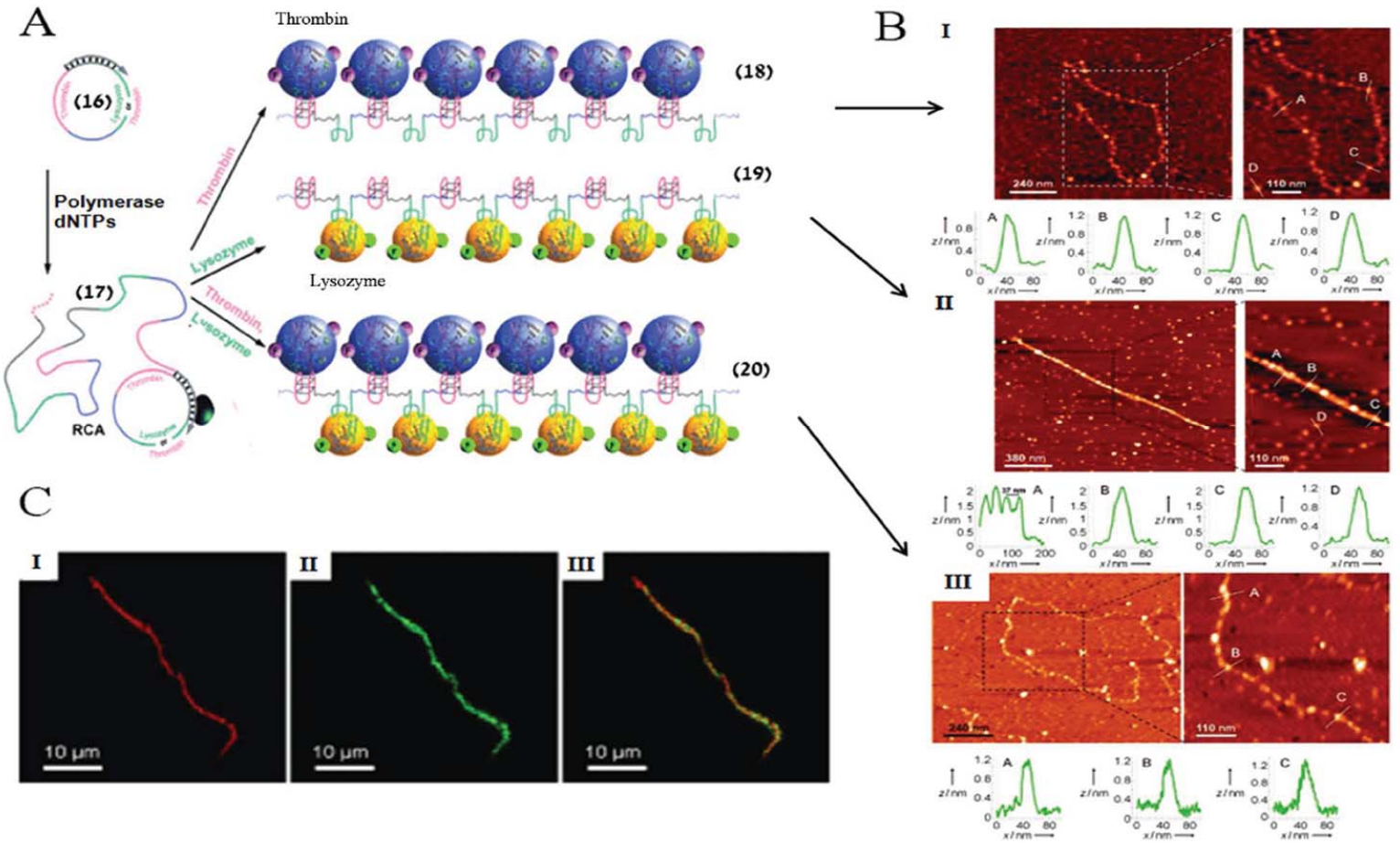
DNA as a template



Aptamers are nucleic acid sequences exhibiting specific recognition properties of low-molecular-weight substrates or macromolecules .

The aptamers are prepared by a selection process named “systematic evolution of ligands by exponential enrichment” (SELEX).

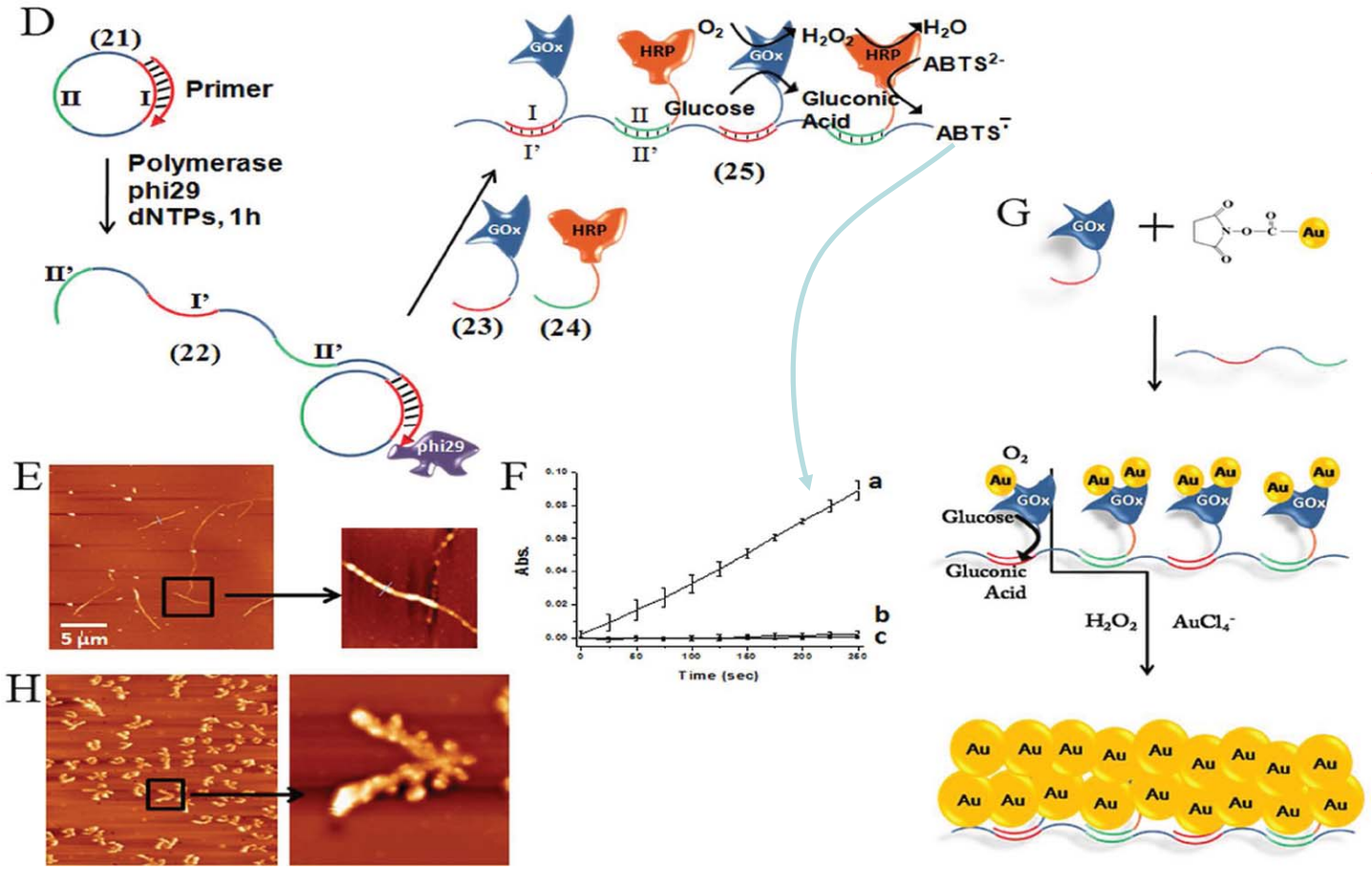
DNA as a template



A circular DNA (**16**) that includes two domains that are complementary to the thrombin-binding aptamer or the lysozymebinding aptamer was used as a template for the activation of an RCA process.

Micrometer-long RCA products (**17**) were generated, where each revolution of the RCA process generated two separated aptamer sequences against thrombin or lysozyme (dye labeled, C)

DNA as a template

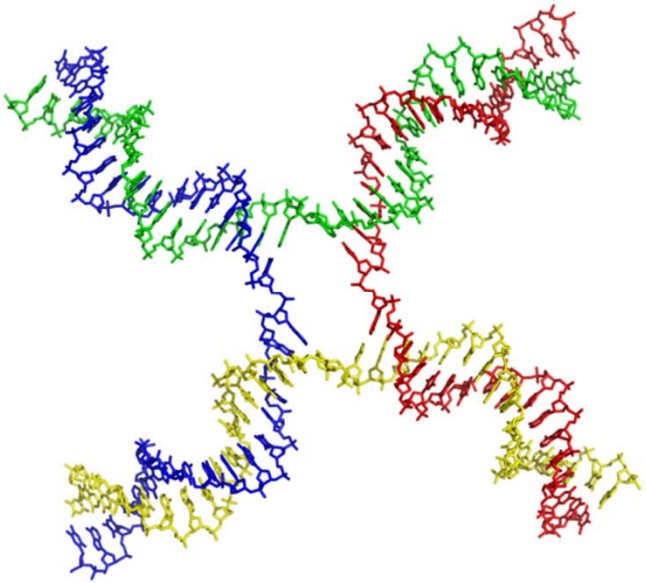


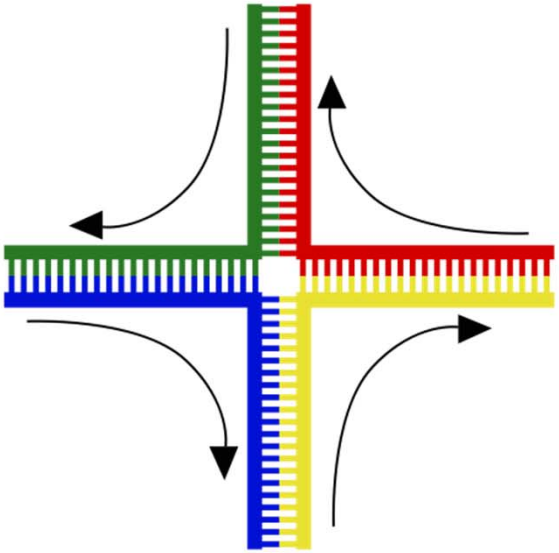
The enzymes glucose oxidase (GOx) and horseradish peroxidase (HRP) were modified with nucleic acid tethers (**23** and **24**) that are complementary to the domains of the RCA template.

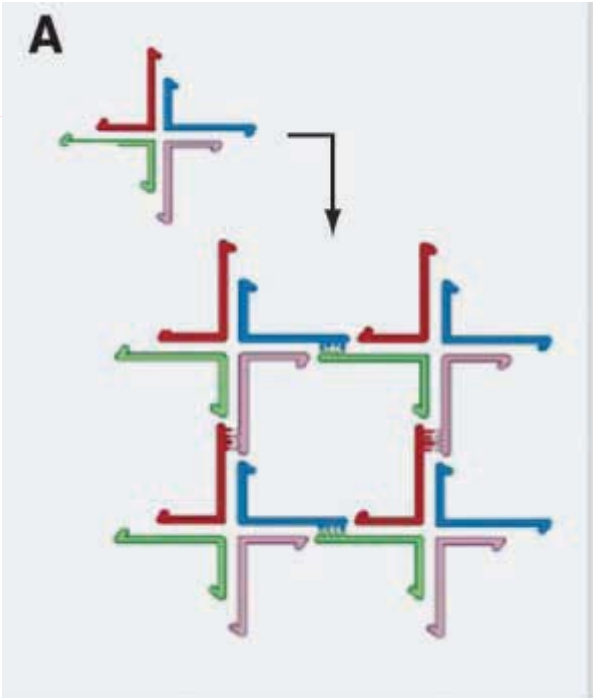
The spatial proximity between the two enzymes on the DNA template enabled the activation of the enzyme cascade, a process that was prohibited in the homogeneous phase.

The system can be modified for the biosynthesis of nanoparticles (G).

DNA as a structural element

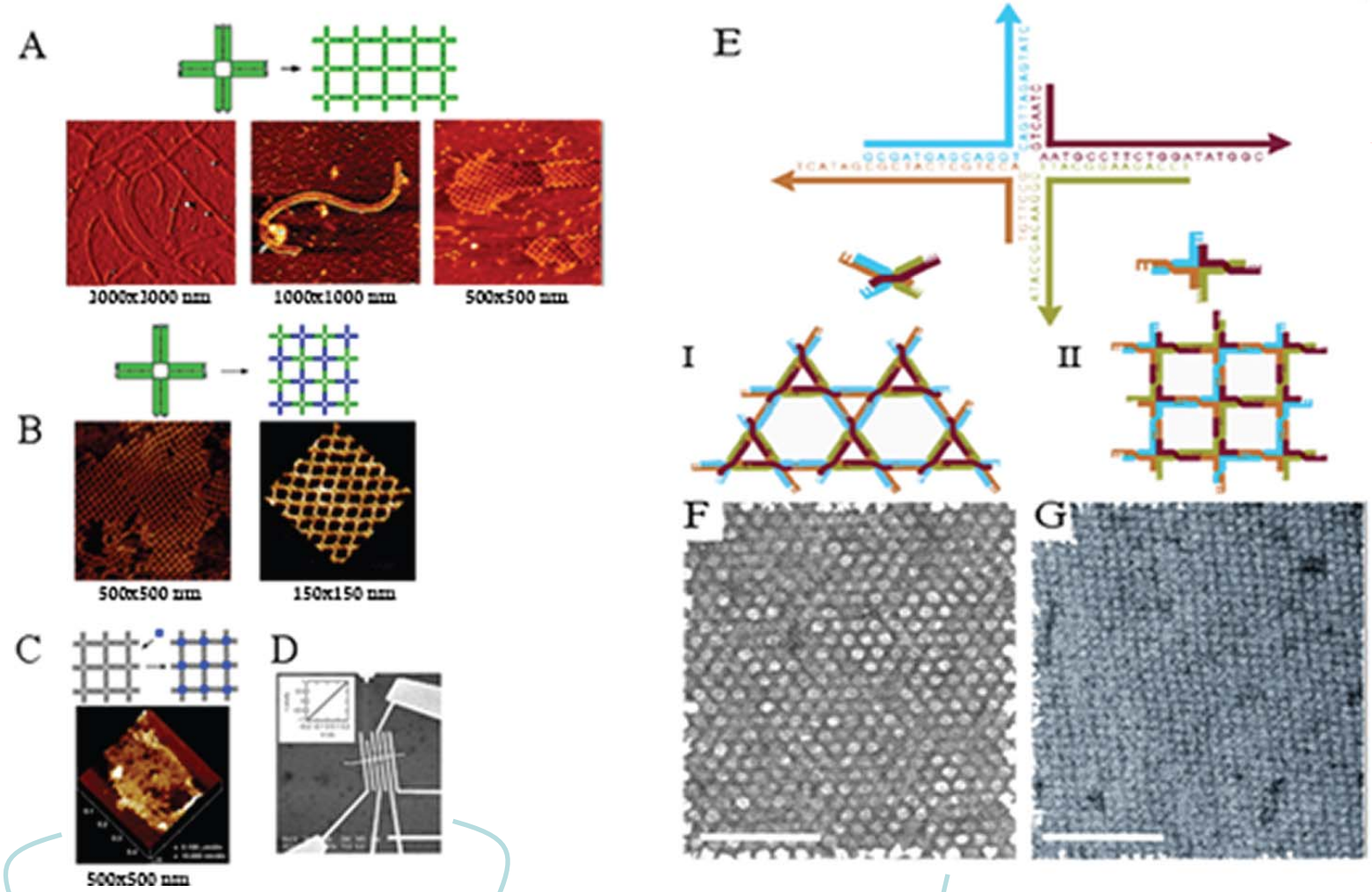






Holliday junctions are natural occurring branched DNA structure. By conjugating such structure with single strand ends suitable for hybrydization, the junction is converted into a “DNA tile” for the realization of 2D nanostructures.

2D surface patterning

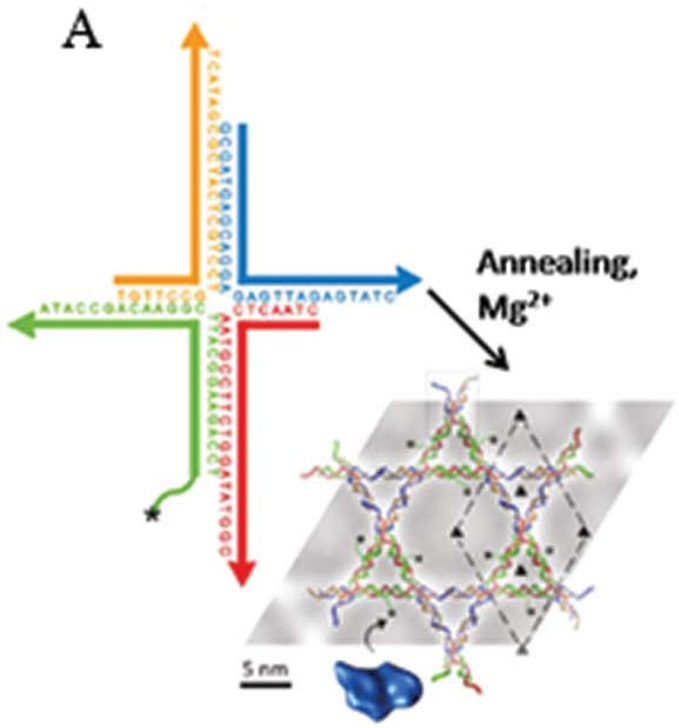


Avidin coating

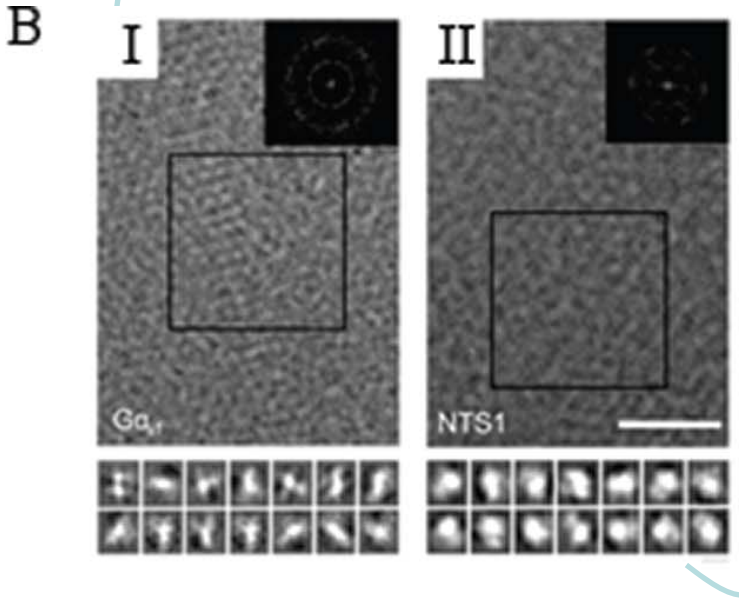
Ag nanowires after deposition

Without RuvA protein (Holliday junctions binding protein)

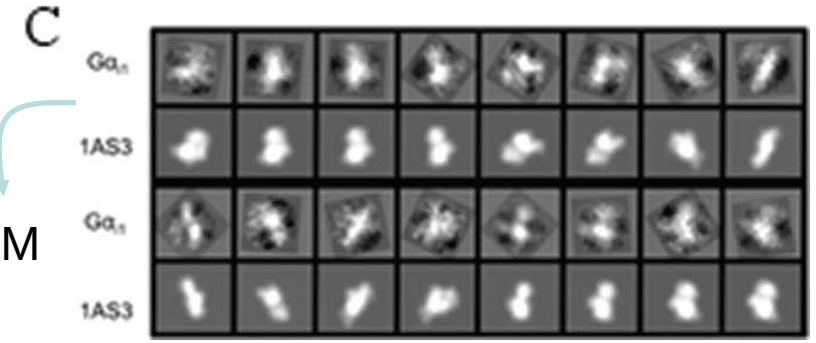
2D surface patterning



Trisnitrilotriacetic/ His-6 functionalized guanine nucleotide-binding protein (Gai1)



neurotensin peptide (NT)/ neurotensin receptor type 1 (NTS1)



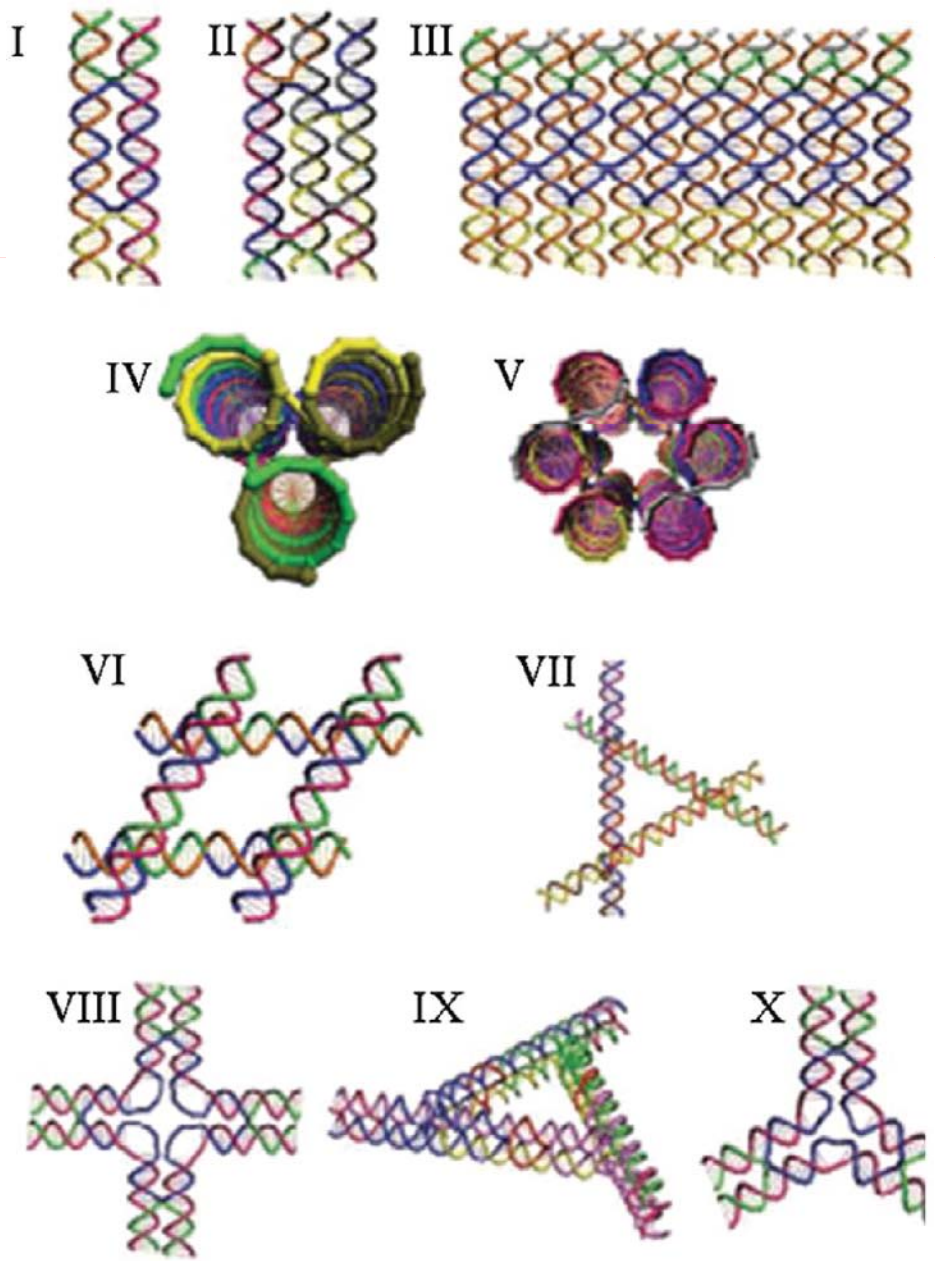
Single protein TEM

X-ray structure

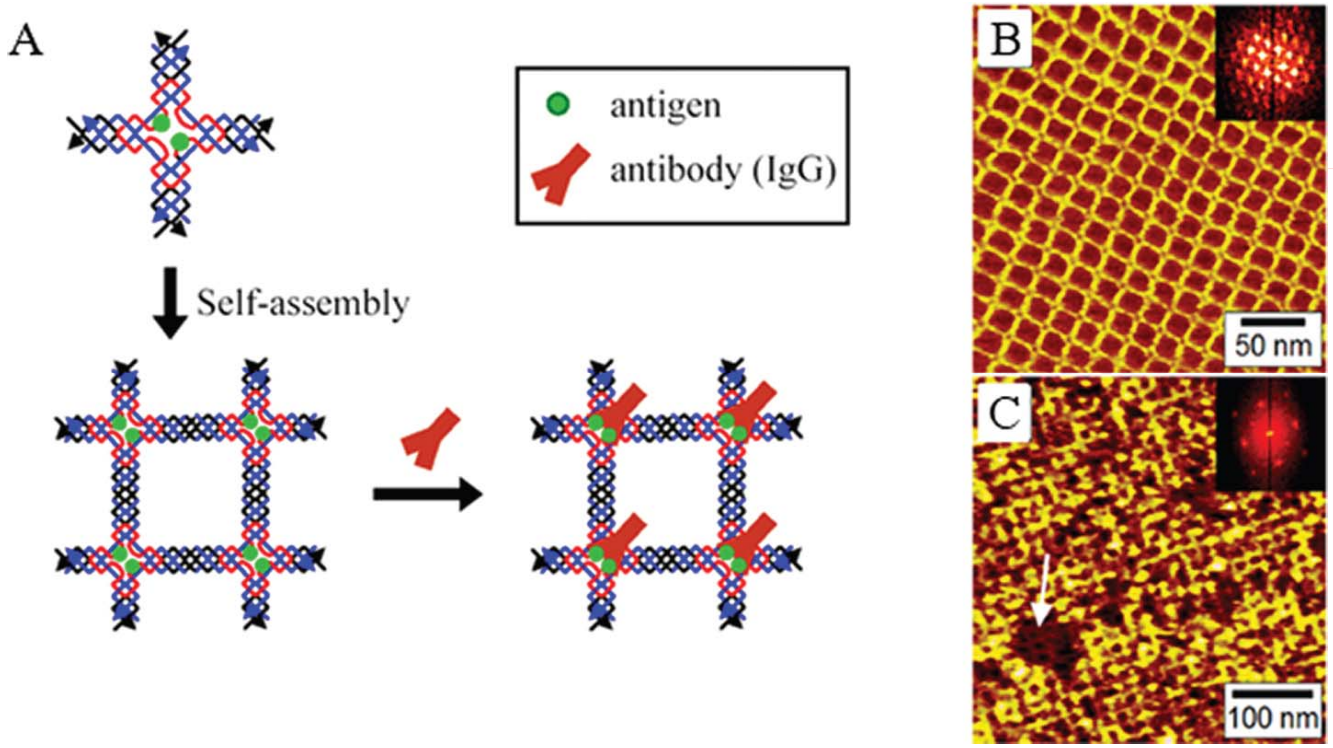
DNA as a structural element

By joining two DNA double helices with a single strand that begins on one helix and switches onto an adjacent helix, tiles that have “crossovers” and addressable sticky ends at their edges and are of greater rigidity are generated (I).

More compex structures include: (II) a triple crossover tile; (III) a 12-helix DNA tile; (IV) a 3-helix bundle tile; (V) a 6-helix bundle tile; (VI) a DNA tile consisting of four 4-arm junctions; (VII) a triangular motif consisting of three 4-arm junctions; (VIII) a cross-shaped tile; (IX) a triangular tile composed of three double-crossover DNA units; (X) a 3-point “star” DNA tile.

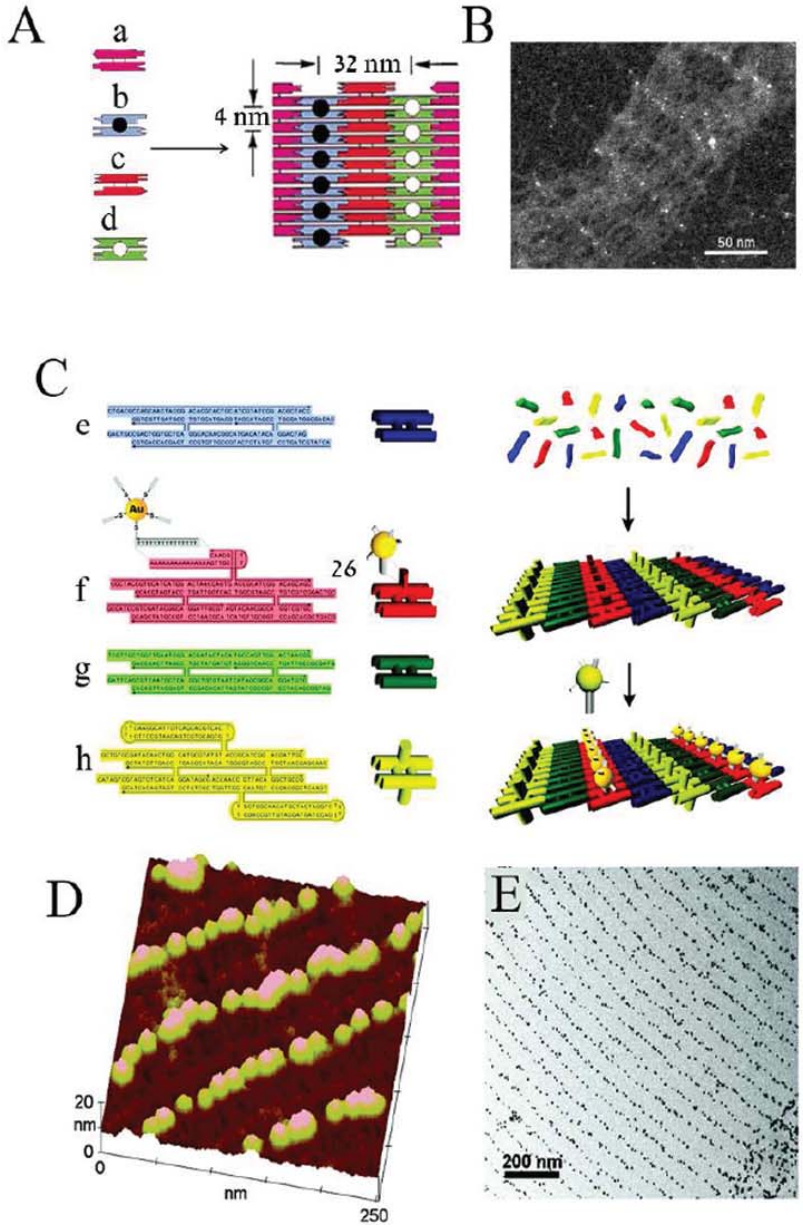


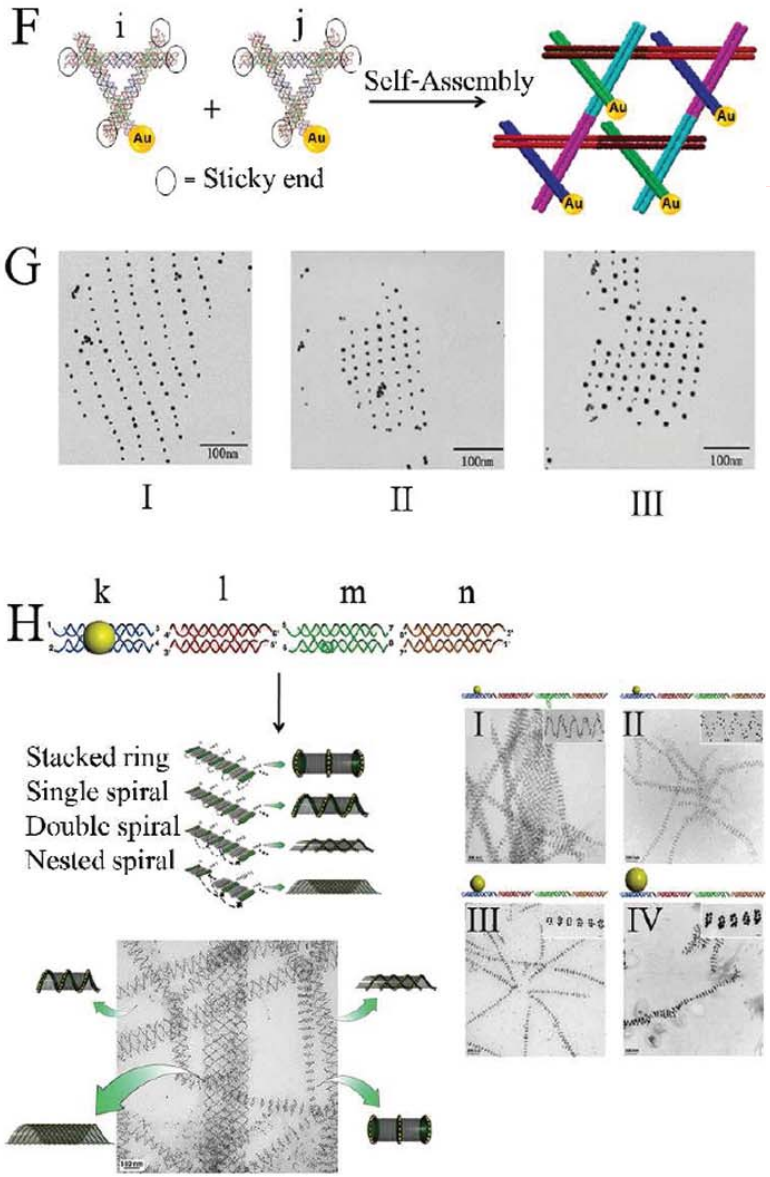
2D surface patterning



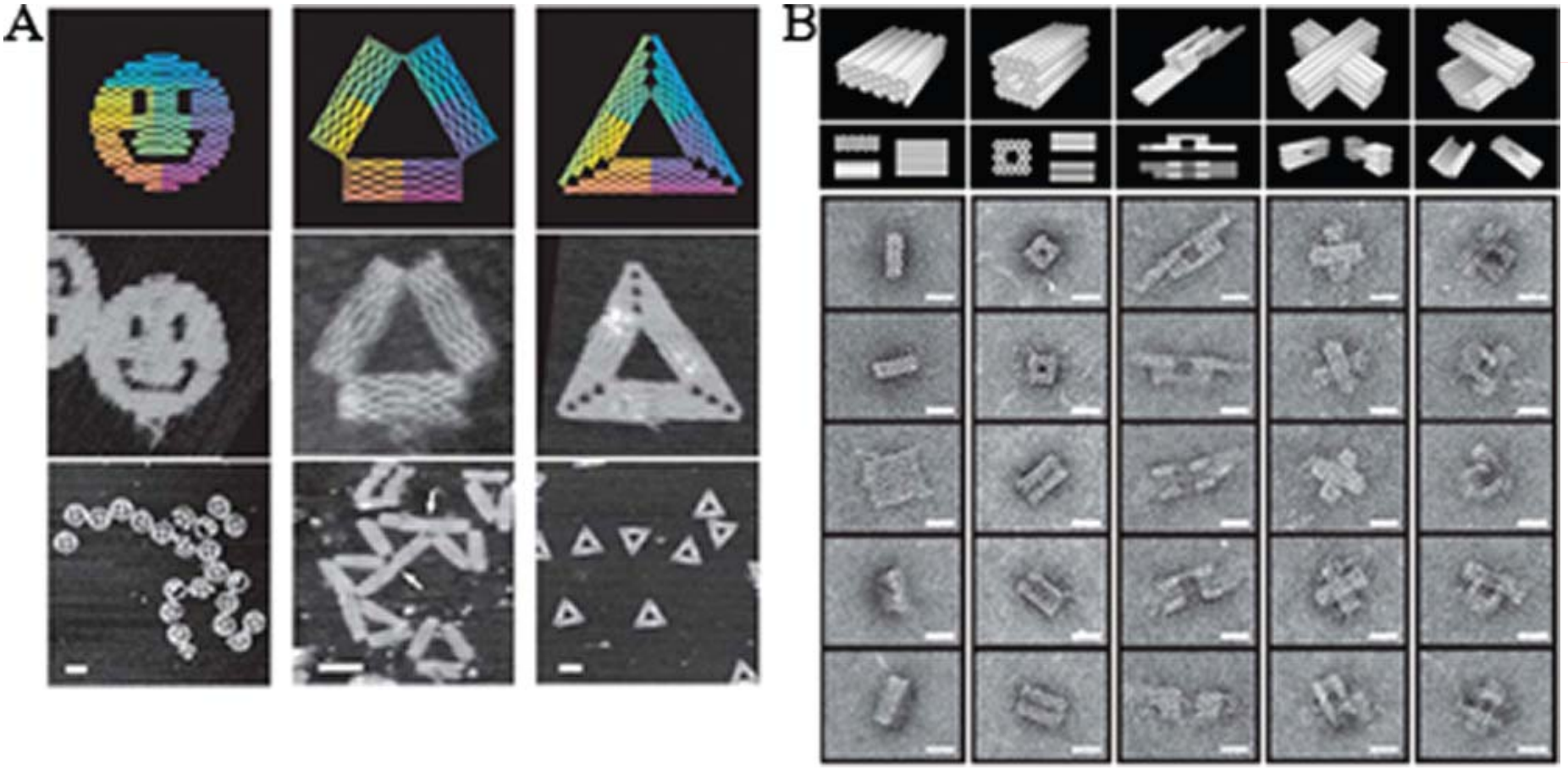
Antibody surface patterning.

DNA as a structural element

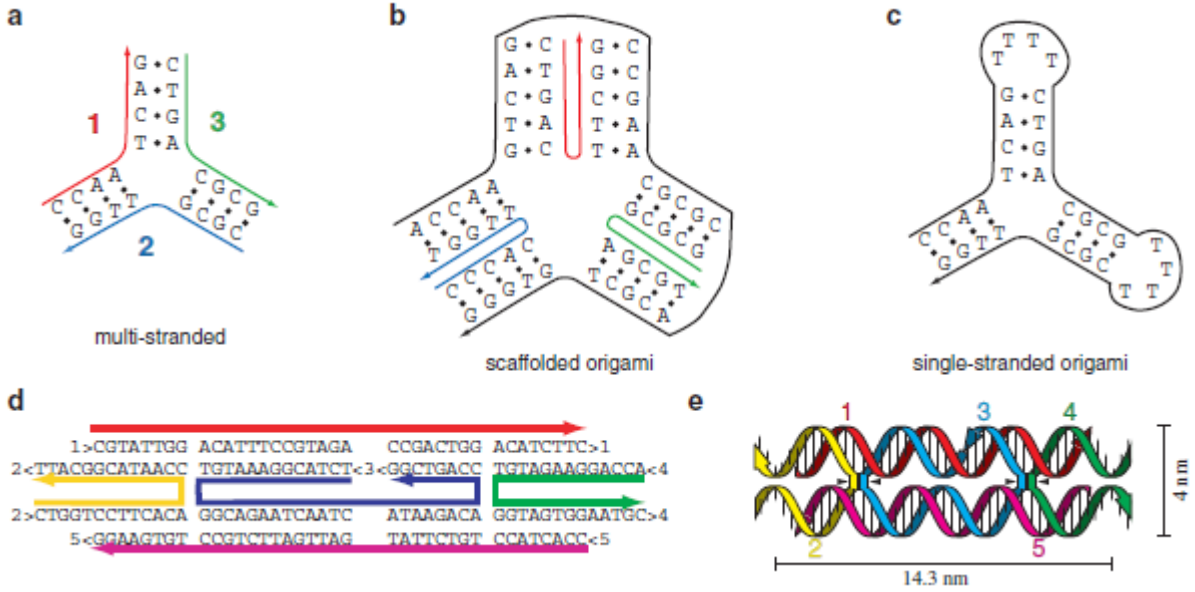




DNA origami

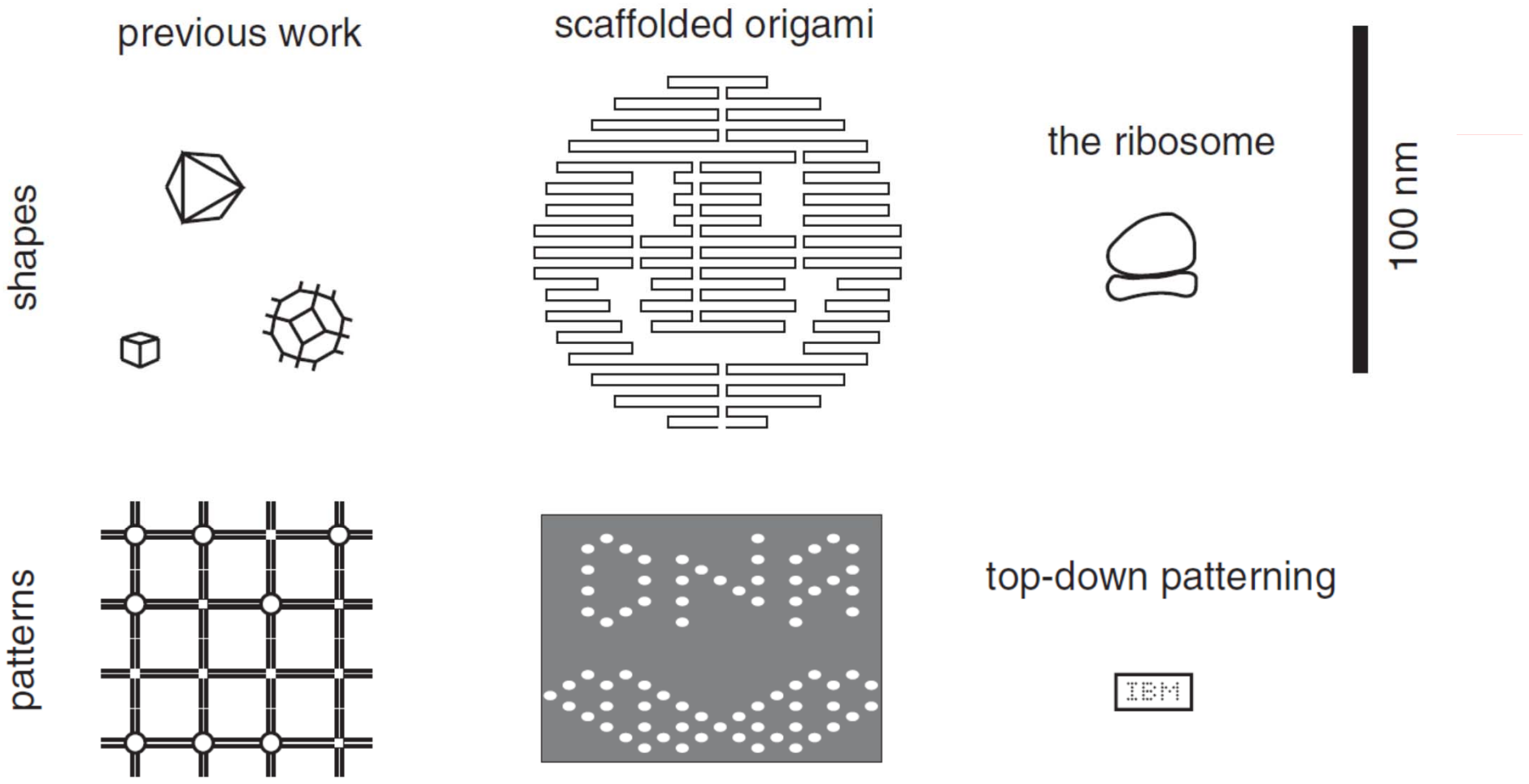


DNA origami

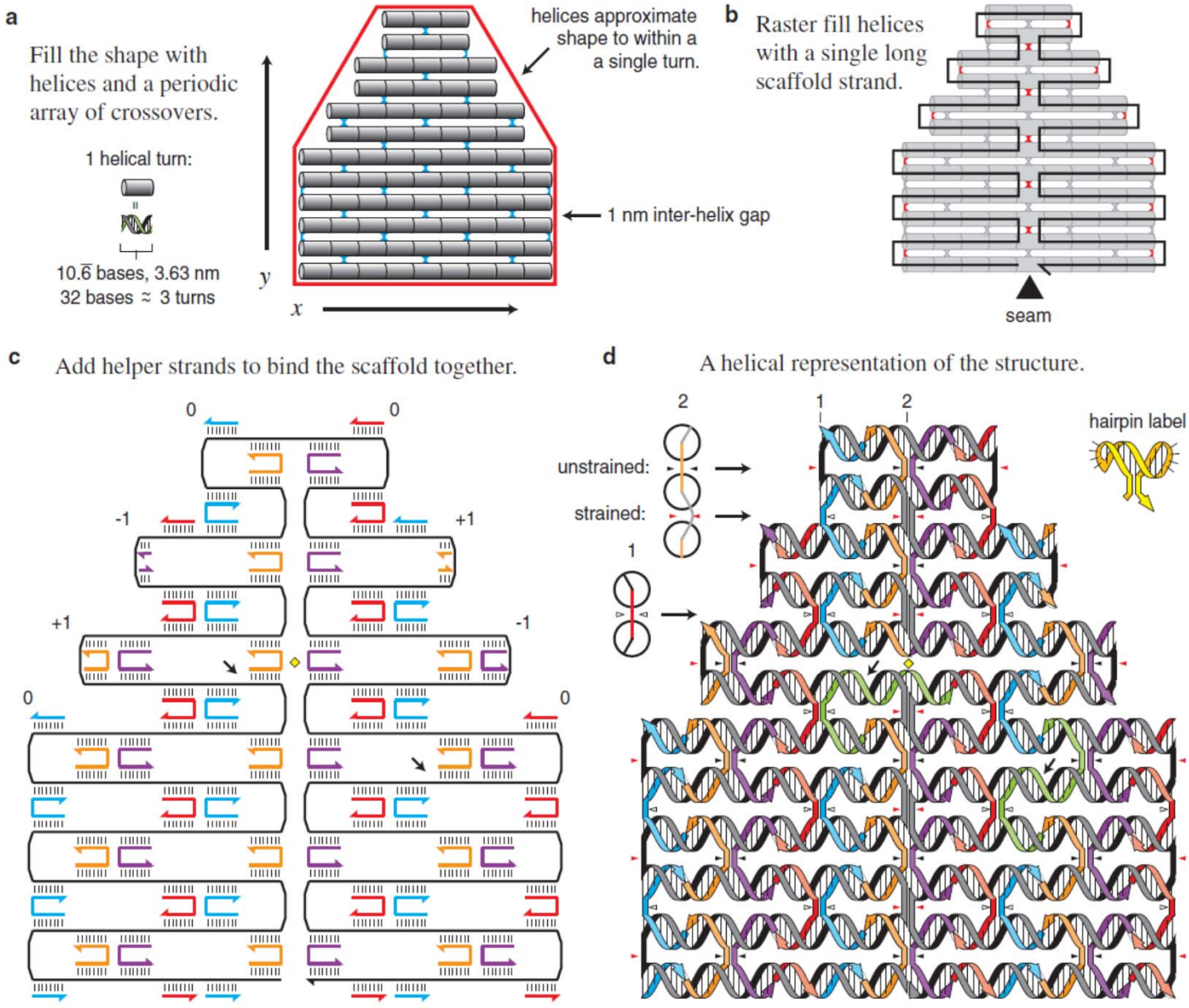


It is a method for folding long single strands of DNA into arbitrary two-dimensional shapes using a raster fill technique.
Shapes up to 100 nanometers in diameter can be approximated with a resolution of 6 nanometers and decorated with patterns of roughly 200 binary pixels at the same resolution.

DNA origami


previous work
scaffolded origami
shapes
the ribosome
100 nm
patterns
top-down patterning
IBM

DNA origami


a
Fill the shape with helices and a periodic array of crossovers.
1 helical turn:
10.6 bases, 3.63 nm
32 bases ≈ 3 turns
helices approximate shape to within a single turn.
1 nm inter-helix gap
y
x
b
Raster fill helices with a single long scaffold strand.
seam
c
Add helper strands to bind the scaffold together.
0
-1
+1
d
A helical representation of the structure.
unstrained:
strained:
hairpin label
1
2

DNA origami

Pick a pattern of nicks and merge short helper strands to form longer helper strands.

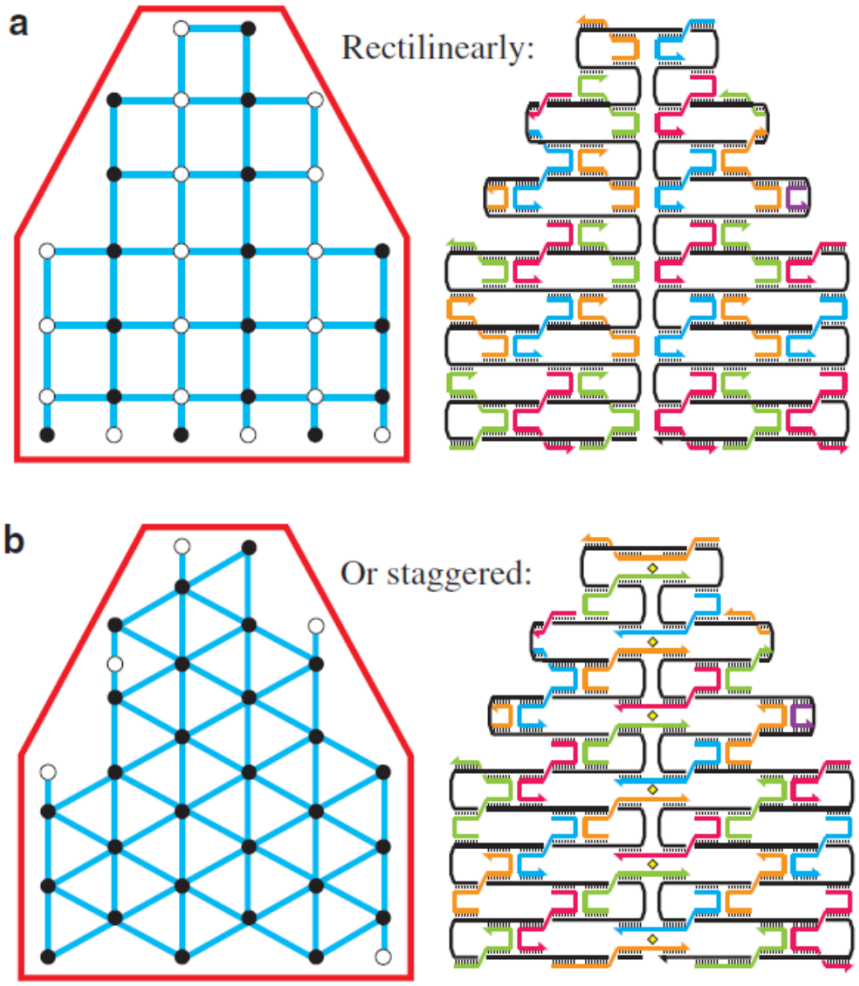
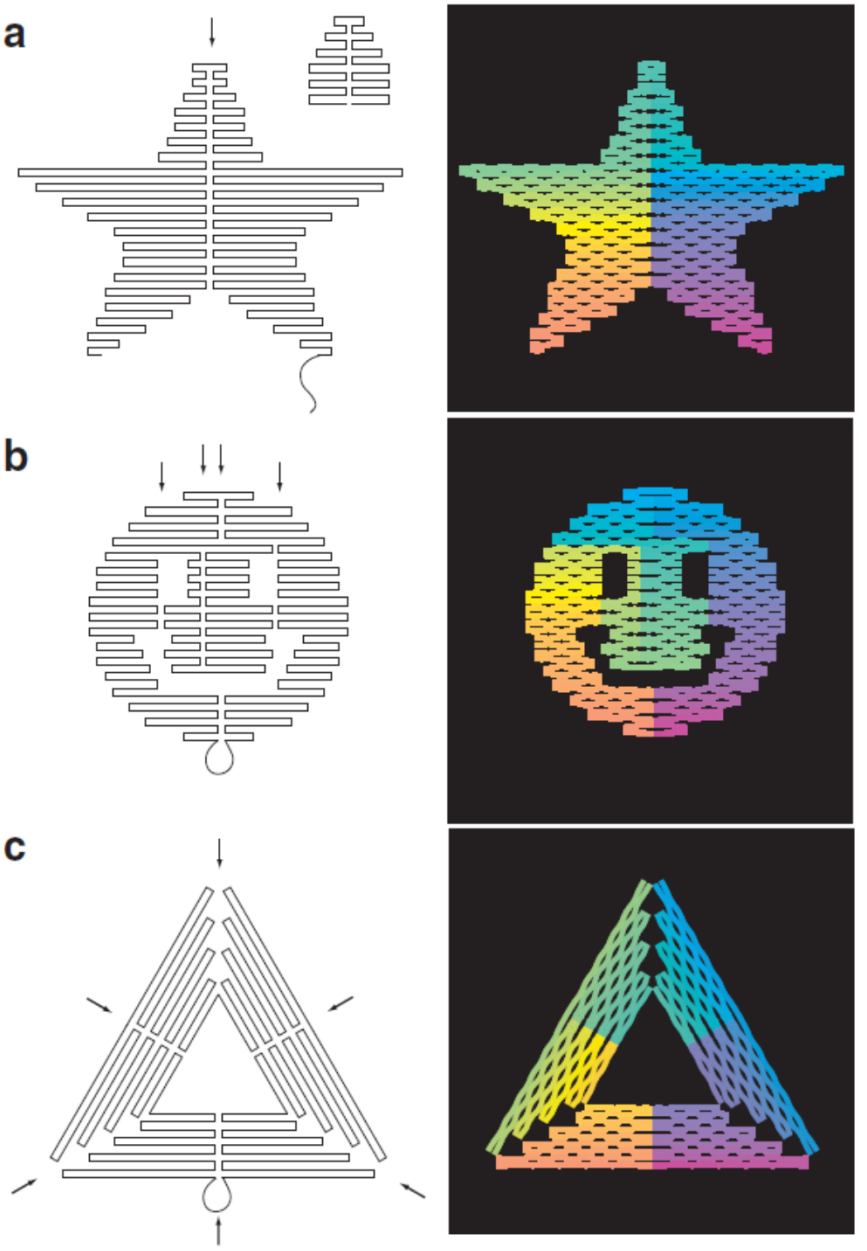
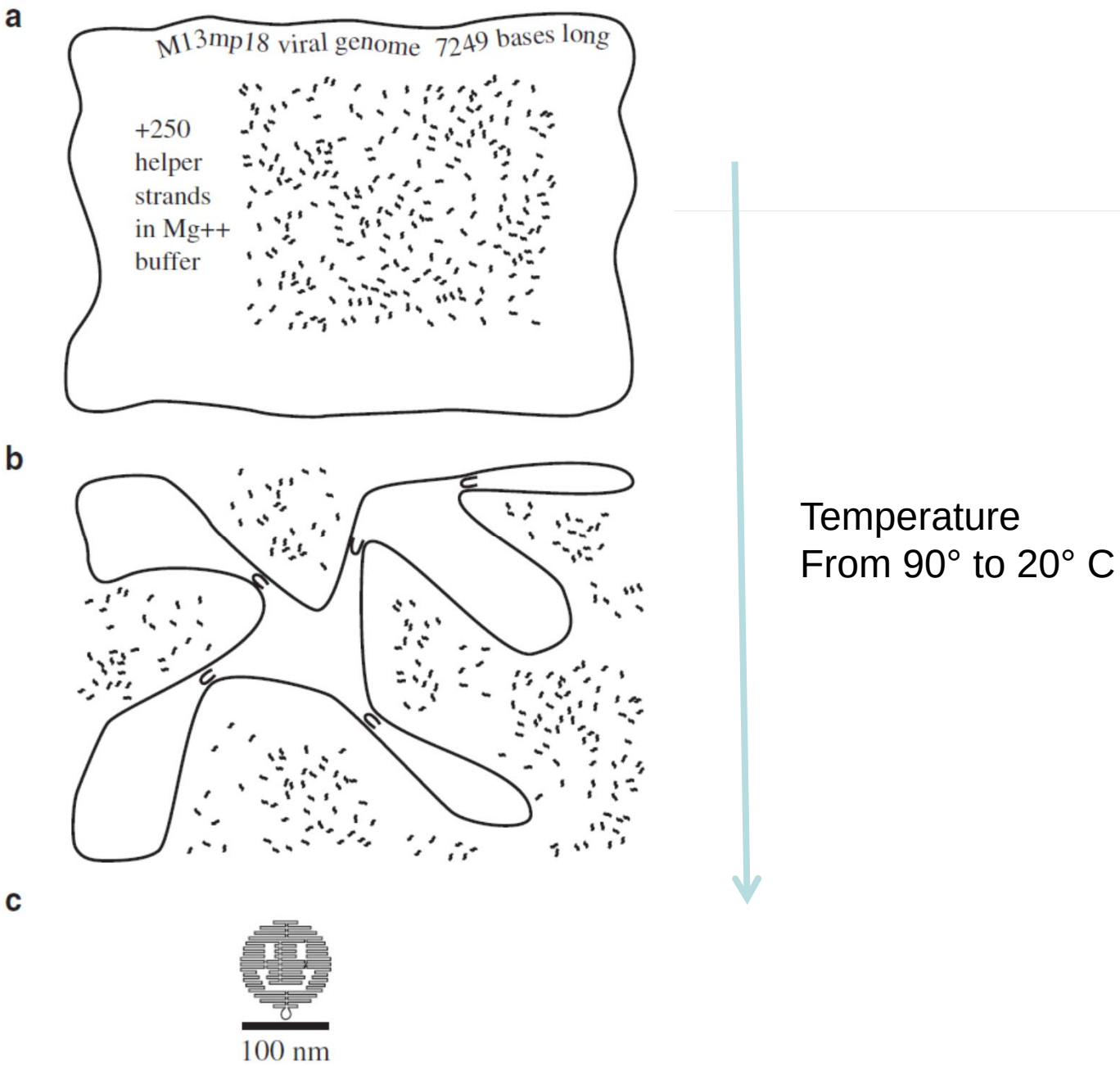


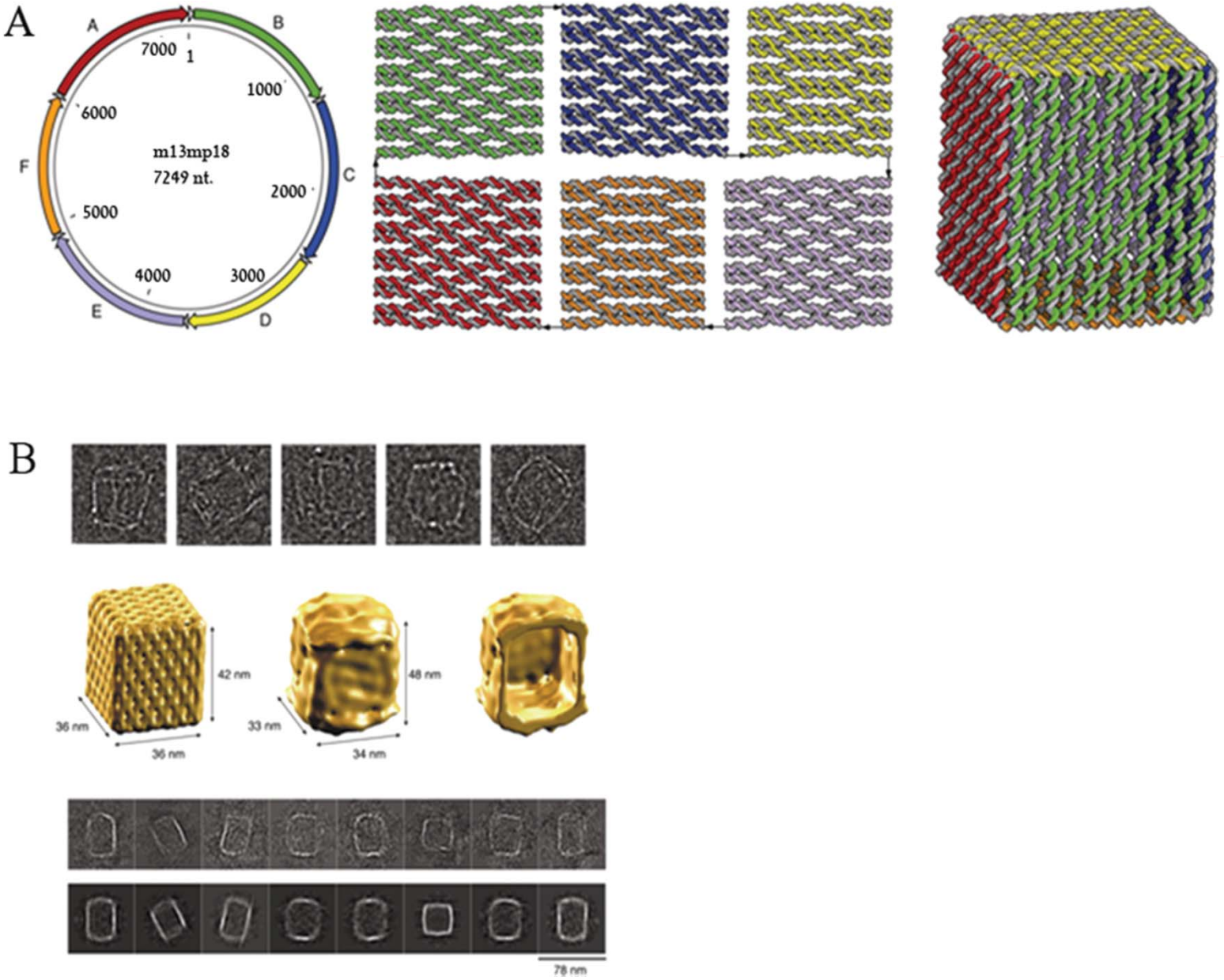
Fig. 4. Two different merge patterns and the structures that result.



DNA origami


a
M13mp18 viral genome 7249 bases long
+250
helper
strands
in Mg++
buffer
b
c
100 nm
Temperature
From 90° to 20° C

DNA origami


A
A
B
C
D
E
F
7000
1
1000
2000
3000
4000
5000
6000
m13mp18
7249 nt.
B
42 nm
36 nm
36 nm
48 nm
33 nm
34 nm
78 nm