Functional DNA Nanomaterials

by

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ABSTRACT

The discovery of DNA helical structure opened the door of modern molecular biology. Ned Seeman utilized DNA as building block to construct different nanoscale materials, and introduced a new field, know as DNA nanotechnology. After several decades of development, different DNA structures had been created, with different dimension, different morphology and even with complex curvatures. In addition, after construction of enough amounts DNA structure candidates, DNA structure template, with excellent spatial addressability, had been used to direct the assembly of different nanomaterials, including nanoparticles and proteins, to produce different functional nanomaterials. However there are still many challenges to fabricate functional DNA nanostructures. The first difficulty is that the present finite sized template dimension is still very small, usually smaller than 100nm, which will limit the application for large amount of nanomaterials assembly or large sized nanomaterials assembly. Here we tried to solve this problem through developing a new method, superorigami, to construct finite sized DNA structure with much larger dimension, which can be as large as 500nm. The second problem will be explored the ability of DNA structure to assemble inorganic nanomaterials for novel photonic or electronic properties. Here we tried to utilize DNA Origami method to assemble AuNPs with controlled 3D spacial position for possible chiral photonic complex. We also tried to assemble SWNT with discrete length for possible field effect transistor device. In addition, we tried to mimic in vivo compartment with DNA structure to study internalized enzyme behavior. From our results, constructed DNA cage origami can protect encapsulated enzyme from degradation, and internalized enzyme activity can be boosted for up to 10 folds. In summary, DNA structure can serve

as an ideal template for construction of functional nanomaterials with lots of possibilities to be explored.

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DEDICATION

This thesis is dedicated to my most beloved ones:

To my parents for raising me up and for their unconditional support in the past twenty-five years. Without their love and guidance, I would not reach my dream.

And to my lovely wife for her love and support.

TABLE OF CONTENTS

Page

CHAPTER Page

CHAPTER Page

CHAPTER Page

LIST OF FIGURES

Figure Page

Chapter 1

DNA Nanotechnology, Inorganic Material and Biomolecules

1.1. Introduction of DNA Nanotechnology

1.1.1. DNA Nanotechnology. DNA is one of three most important molecules that encoded with genetic information. To program information, DNA is composed with four different nucleotides, including guanine, adenine, thymine and cytosine, and different combination of the four nucleotides makes unique information sequence. In 1953, Watson and Crick published one paper to describe the double helical structure of DNA, [1] which opened the door of molecular biology. Inspired by nature's branched structure, such as replication junction and recombination junction, [2] Ned Seeman laid out the concept of building design shaped DNA nanostructure with branched unit (Holliday junction), [3] which initiated the field known as DNA nanotechnology. In the following part of this chapter, I will discuss the important concepts, progresses and the remaining challenges, opportunities for this field.

To construct 2D DNA structure, DNA helix, linear structures, must have branches. Inspired by three way junction and Holliday junction, Seeman produced the first designed DNA structure, immobilized Holliday junction (4-arm junction). To better control the formation of DNA structure, he also proposed three design principles to generate uniquely paired structure with non-migratory junctions. First, there should be no slides bases; Second, there should be no repeating DNA unit sequence (usually choose adjacent 4 bases as a unit); Third, to prevent G-quartets structure, the maximum number of G bases in one unit should be less than 4. [3, 4]

After the construction of 4-arm junction, Seeman also proposed to build large DNA arrays based on this unit. The end of each 4-arm junction unit was extended with extra ssDNA, known as sticky end, which can be hybridized with complimentary strand on other junctions. With the combination of 4-arm junction and sticky end, different large 2D array, even 3D array can be constructed. Furthermore, Seeman proposed to use the constructed 3D lattice to direct the assembly of protein, as shown in figure 1B, which could be applied to solve the protein crystallization problem.

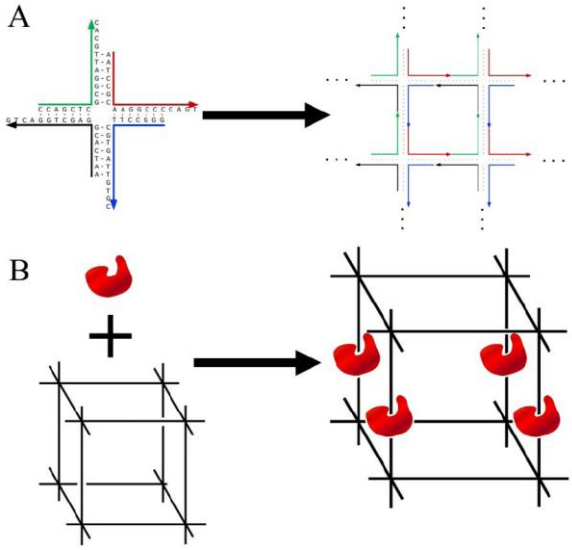

Figure 1.1. Ned Seeman's original proposal of construction of periodic DNA array. (A) Holliday junction tiles with sticky ends are connected together to form a 2D periodic array through self-assembly process. (B) A 3D DNA lattice templated protein array could be used for X-ray crystallography.

Ever since the invention of DNA nanotechnology field, it had attracted more and more attentions. There are several reasons to make DNA an ideal material as template for structural nanotechnology. First of all, DNA has identical structure; the helix diameter is

2nm, and 10.5 base pairs is one repeating turn in B-form DNA. Secondly, the hydrogen bond in between guanine and cytosine, adenine and thymine makes DNA hybridization predictable; Thirdly, DNA synthesis and chemical modification can be easily accomplished with low cost; All these great features provide DNA as a good candidate as nanostructure template.

1.1.2. 2D DNA Tiles. Fu and Seeman constructed several double-crossover structures, in which DNA molecules containing two crossover sites between helical domains. [5] Further study found that antiparallel structure (DX) showed best stability. After that, almost all the DNA nanostructures were constructed based on DX system. With the DX unit, different sized 2D tiles were constructed by connecting different numbers of helix together, such as 2HX, 3HX, 4HX, 8HX and 12HX.[6-8] With the same principle, tube shaped structures had also be created, such as 3HT, 6HT, 18HT.[9-12]

Another group of tiles is rigid arm junctions, in which DX structures are applied to arm junctions. Yan constructed a rigid 4-way junction, named 4×4 structure, based on 4-arm junction and one central strand was applied to link 4 arms together. [13] Mao built a three-point-star structure based on 3-arm junction with three DX designed arms and one long central connection strand. [14]

With appropriate designed sticky ends, 2D arrays could be constructed with above tiles. Mao reported the 2D array formation with 4-arm junction. [15] Winfree built micrometer sized 2D array with DX tiles. [16] Yan found that with proper control, lattice and ribbon structures could be constructed with 4×4 tile. [13]

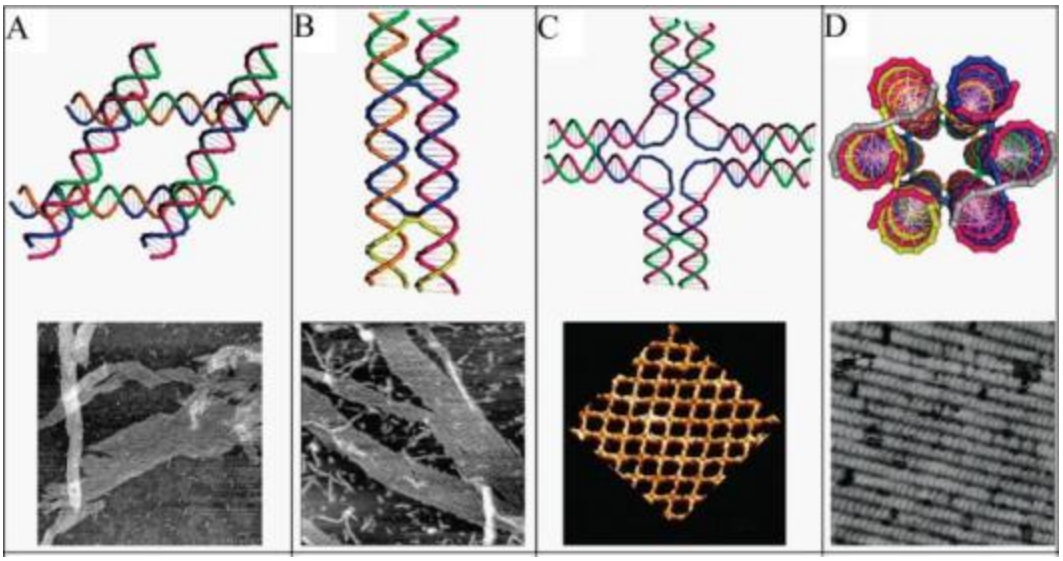

Figure 1.2. Small DNA tile and their extended structure through sticky ends hybridization.

1.1.3. 3D DNA Tiles. DNA nanostructure is an ideal template for nanomaterial assembly in 2D and 3D. Previous constructed 2D structures, including 2D arrays are good candidates to direct 2D assembly. However it is even more important to assemble nanomaterial in 3D: for example, metal NPs plasmonic field is mapped in 3D space, and protein protein interaction need good control in 3D direction. Ever since the invention of DNA nanotechnology field, researchers tried to build 3D DNA structures. Chen and Seeman constructed the first DNA 3D structure, DNA cube with 10 strands. [17] Zhang and Seeman built truncated octahedron with 4-arm junction unit. [18]

Goodman and Turberfield used 4 strands to construct a rigid DNA tetrahedron structure with each face covered by one DNA strand.[19, 20] AFM image can clearly prove the formation of tetrahedron. With fuel strands, DNA tetrahedron structure can be switch to open and close, which can be potentially used as a carrier for drug delivery.[21] Shih

used one long ssDNA to build octahedron, which can be used for in vivo cloning amplification.[22]

Yu and Mao employed three-point-star tile to construct different DNA polyhedron structures. With longer loop (5 bases) in the middle of tile and 75nM unit concentration, DNA tetrahedron could be constructed; with shorter loop (3 bases), low concentration (50nM) could produce dodecahedron and high concentration (500nM) could create buckyball structure, as shown in figure 3. [23]

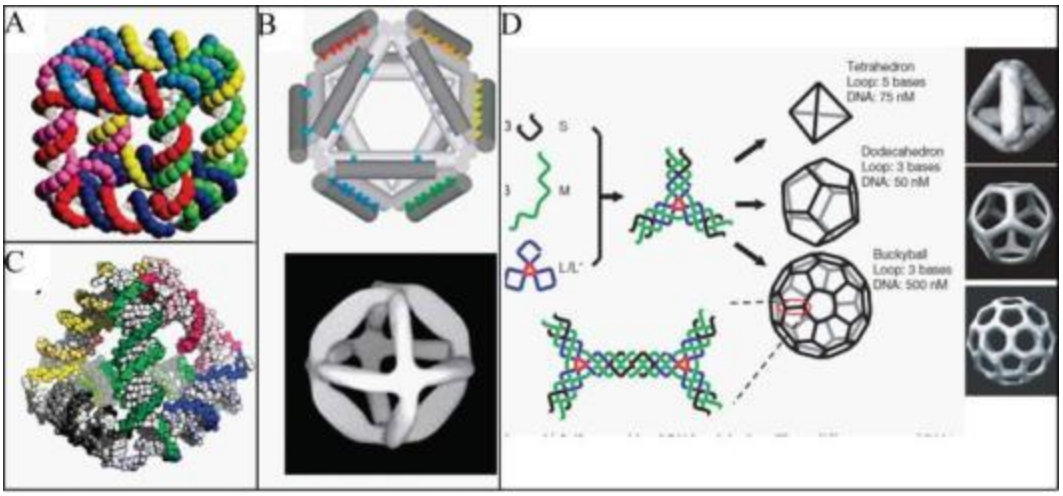

Figure 1.3. 3D DNA structures. A) DNA cubic; B) DNA Octahedron; C) DNA tetrahedron; D) DNA polyhedron formed with three-point-star.

1.1.4. DNA finite array and DNA Origami. Large 2D array produced large template for material assembly, however formed 2D array did not have controlled size and boundary, which would limit its application for site specific attachment. These limitations make construction of finite sized DNA arrays is desirable.

Park and LaBean constructed 16 different 4×4 tiles array specifically,[24] and with particular designed sticky ends, 80 nm × 80 nm finite sized structure had been assembled.

Yan and Reif utilized long ssDNA as scaffold to assemble DX tiles together, forming barcode patterned lattices, which can achieved high yield and specificity. [25]

In 2006, Paul Rothemund expanded the scaffold strategy further to introduce DNA origami technology, [26] which was a milestone for DNA nanotechnology field. DNA origami is a DNA structure constructed with long circular ssDNA, named M13, which has 7249 bases, and 200 short ssDNA, named staples, holding the scaffold in place. The resulted DNA structures were roughly 100 nm in diameter with desired shapes such as triangle, square, five-pointed star and smally faces, as shown in figure4. Furthermore, each staple could serve as a 6-nm pixel, which made the structure to be programmable, bearded with complex information. With proper designed staple linkers, DNA origami could be assembled together to form even larger structures with more information encoded. This achieved spatially addressable DNA origami structure with high complexity, revolutionarily changed the field. After the introduction of DNA origami to the field, many developments had been achieved.

Douglas and Shih expanded the concept to 3D space.[27] With developed software, named caDNAno, different 3D DNA origami could be constructed, including monolith, square nut, railed bridge, genie bottle, stacked cross, slotted cross, with precisely controlled dimension ranging from 10-100nm. After that, Dietz and Shih introduced twist and curve into DNA origami. [28] With targeted insertions and deletions of base pairs, DNA bundles could be developed with controllable twist or curve. Han and Yan expanded the curved DNA origami structure further to have intricate curved surfaces in 3D space.[29] Concentric rings of DNA were used to generate in-plane curvature, while

out-of-plane curvature was introduced by adjusting the particular position and pattern of crossovers between adjacent DNA double helices.

Recently, Wei and Peng developed single-stranded tile (SST), [30] a canvas strategy, to the field. SST was constructed with only ssDNA, and this scaffold free strategy had been used to construct 100 different structures. With the same strategy, Ke and Peng extended the cavas method to 3D space, named DNA bricks, [31] which had been used to construct 102 distinct structures.

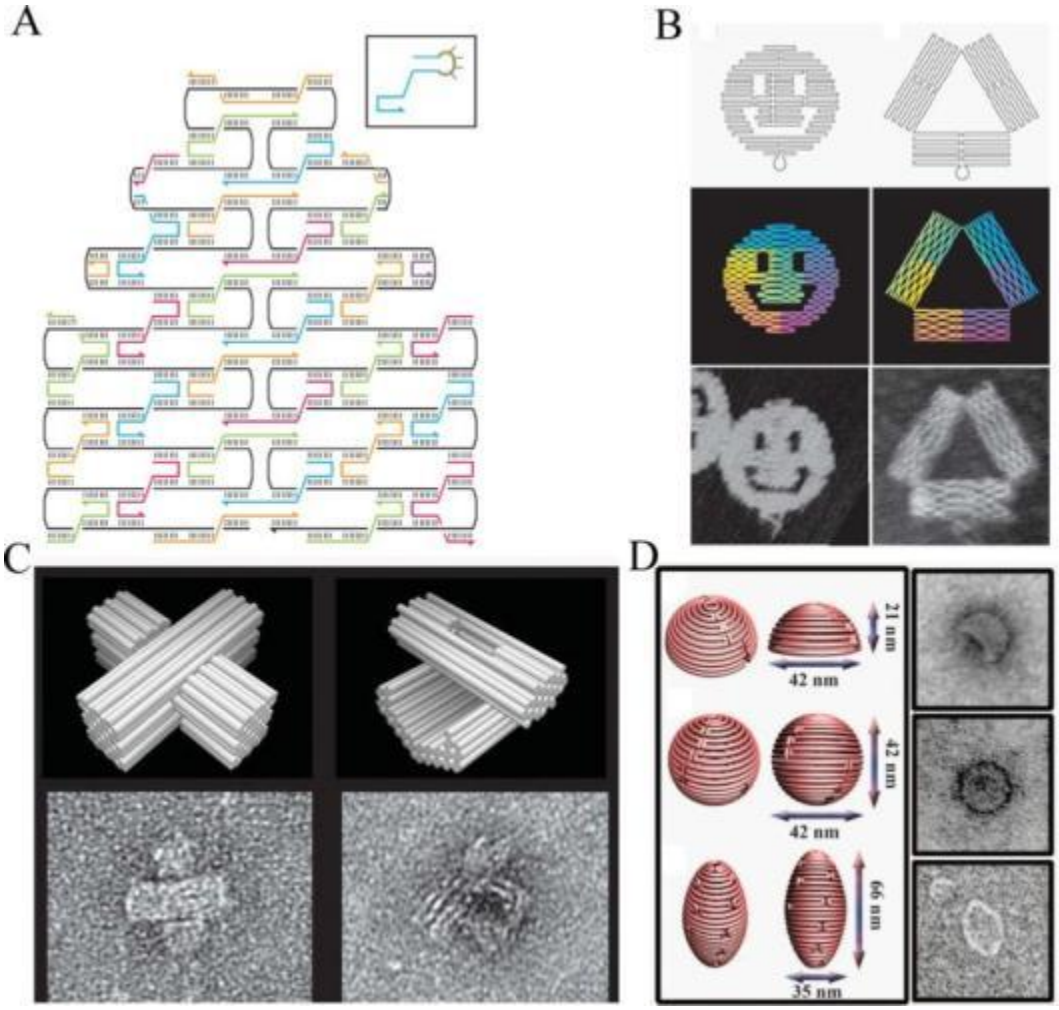

Figure 1.4. DNA Origami structures. A) DNA Origami design in detail; B) 2D DNA Origami structure; C) 3D DNA Origami structure; D) DNA Origami with curvature in 3D;

1.1.5. Interfacing with inorganic materials. The spatial addressability of DNA structures makes it an ideal template for nanomaterial assembly, and they had been used to direct the assembly of different materials, including inorganic materials and biomolecular for different purposes.

Le and Kiehl reported the first example to assembly inorganic materials on DNA template.[32] They employed DX tile assembled 2D arrays to assemble DNA functionalized AuNPs, creating controlled density AuNPs arrays, which could be used in nanoscale integrated circuits for logic, memory, sensing, and other applications. After that, Yan group expanded the concept of interfacing DNA structures with inorganic materials. Sharma and Yan assembled AuNPs onto DNA origami template with improved yield. [33, 34] Pal and Yan functionalized AgNPs [35] and Au nanorods [36] with DNA, and assembled them onto DNA triangle origami separately.

Kuzyk and Liedl assembled AuNPs on DNA Origami template in chiral pattern, [37] achieved plasmonic structure with strong circular dichroism signal, which proved that DNA structure has much more potential regarding the application with inorganic material.

Deng and Liu functionalized Quantum Dots with phosphorothiolated DNA, and assembled with DNA origami template with high yield, for futhre photonic study. [38]

Maune and Winfree arranged single-walled carbon nanotubes on DNA origami with controlled position and orientation, creating excellent field effect transistor device. [39]

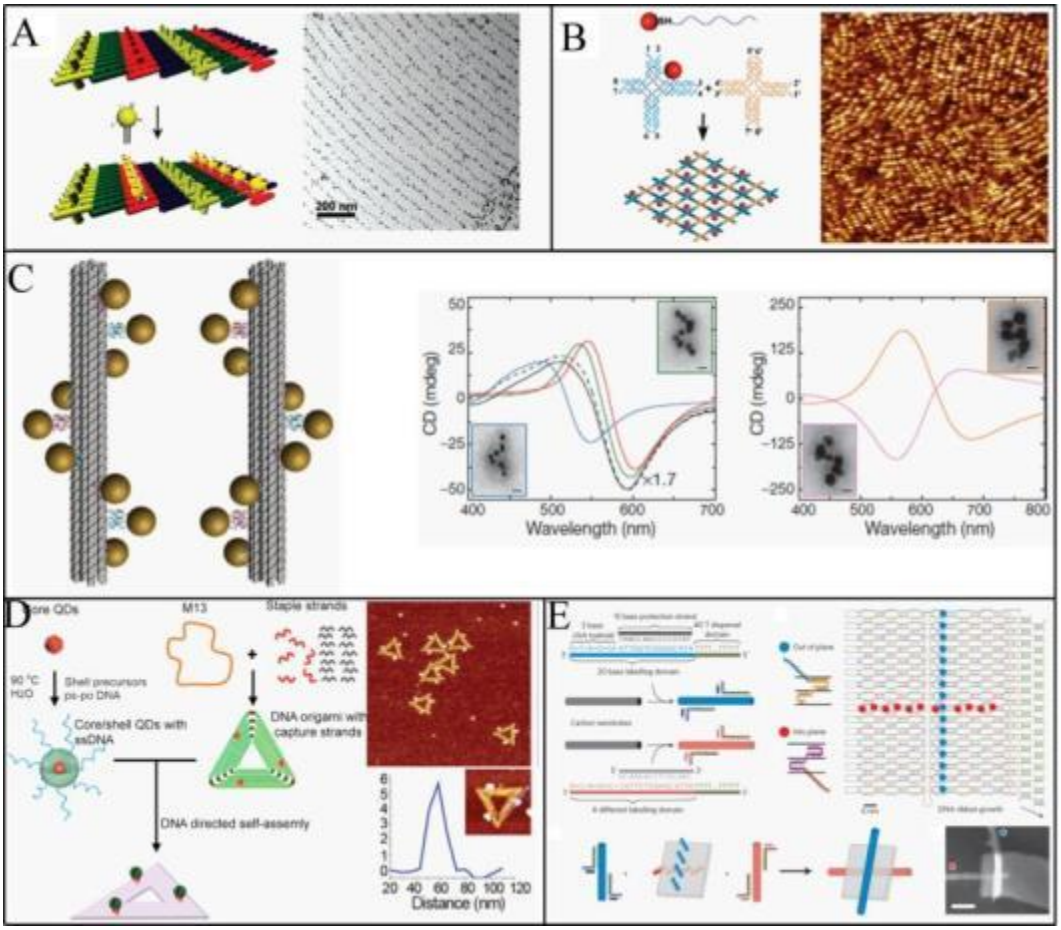

Figure 1.5. DNA structure template assembly of inorganic materials. A) DX tile array template assembly of AuNPs; B) AuNPs assembled on 4×4 structure with optimized protocol; C) AuNPs helical array formed with 3D DNA Origami with strong chiral property; D) Assemble QDs on DNA Origami template; E) Assembled SWNT array on DNA Origami;

1.1.6. Interfacing with biomolecules. Li and Yan was the first to report assembled protein on DNA scaffolds. [40] With biotin labeled DNA strands, streptavidin could be attached onto TX tiles through strong interaction between streptavidin and biotin. To attach protein on DNA structures, different strategies had been applied, including

aptamer method, a sequence of DNA, RNA or peptide that is selected to bind to a specific target through SELEX approach, and chemical modification method to link DNA with protein. Rinker and Yan utilized 5HX to study multivalent binding effect on aptamer protein binding. [41] With controlled distance between two aptamers on 5HT, the affinity between DNA structure and target protein thrombin was measured, which showed that bivalent interaction is much stronger than monovalent interaction. Fu and Yan used chemical method to link DNA with enzymes, and arranged two cascade enzymes, [42] Glucose oxidase (GOx) and horseradish peroxidase (HRP) together on DNA origami template to study distance dependent activity change.

Zhang and Mao organized protein in 3D with self-assembled symmetric DNA polyhedral. [43] With spatially organized biotin strands, on polyhedron arm, streptavidin could be anchored inside DNA polyhedron structure. Crawford and Kapanidis applied the protein DNA noncovalent interaction to encapsulate a transcription factor inside DNA tetrahedron cage with controlled orientation. [44]

Derr and Reck-Peterson utilized DNA structure template to investigate the mechanisms of microtubule-based motors.[45] 3D DNA origami was used as synthetic cargo, carried with varying numbers of DNA oligonucleotide-linked motors, which allowed for control of motor type, number, spacing and orientation in vitro. After labeled motor molecule with dye, confocal microscopy could be used to visualize the motor movement.

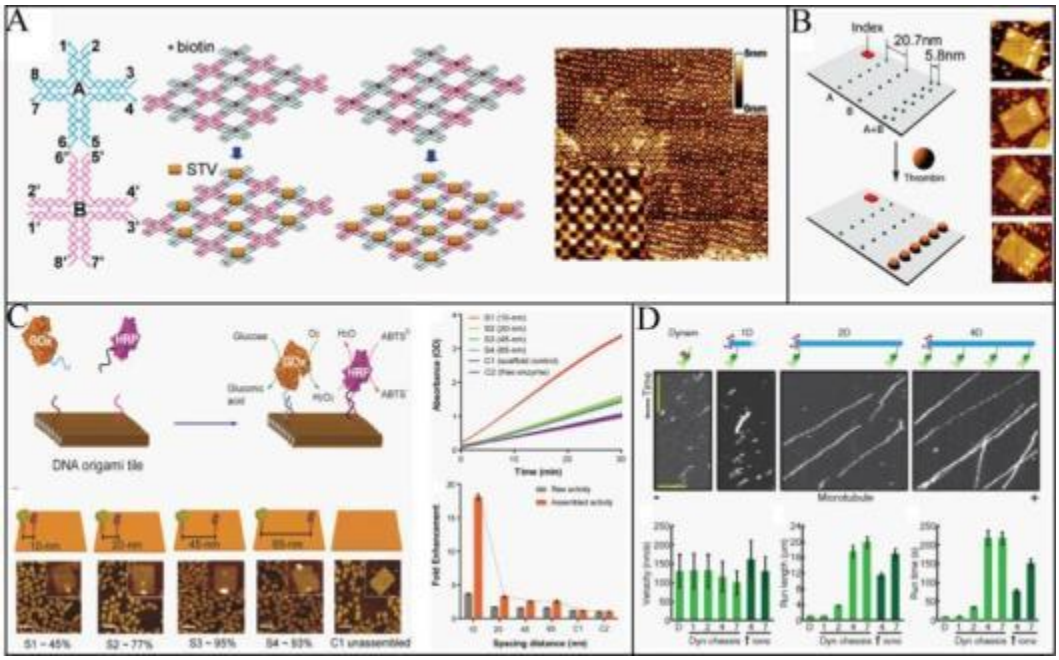

Figure 1.6. DNA structure template assembly of protein. A) Streptavidin assembled on 4×4 array; B) Assembled thrombin on DNA tile through bivalent aptamer interaction; C) Enzyme cascades assembled on DNA Origami with controlled distance; D) DNA Origami as carrier to study motor process.

1.1.7. DNA Structure Immobilized on Surface. To bridge DNA nanotechnology with top-down method together, approaches to place DNA structure placement on surface are in demand. Kershner and Wallraff [46, 47] described a method of using electron-beam lithography and dry oxidative etching to create DNA origami-shaped binding sites on technologically useful materials. In the buffer with 100mM $MgCl_2$, DNA origami could bind on surface with high selectivity and good orientation. Ding and Yan demonstrated fixed length DNA origami tubes, [48] modified with thiol groups, could be anchored in between gold islands.

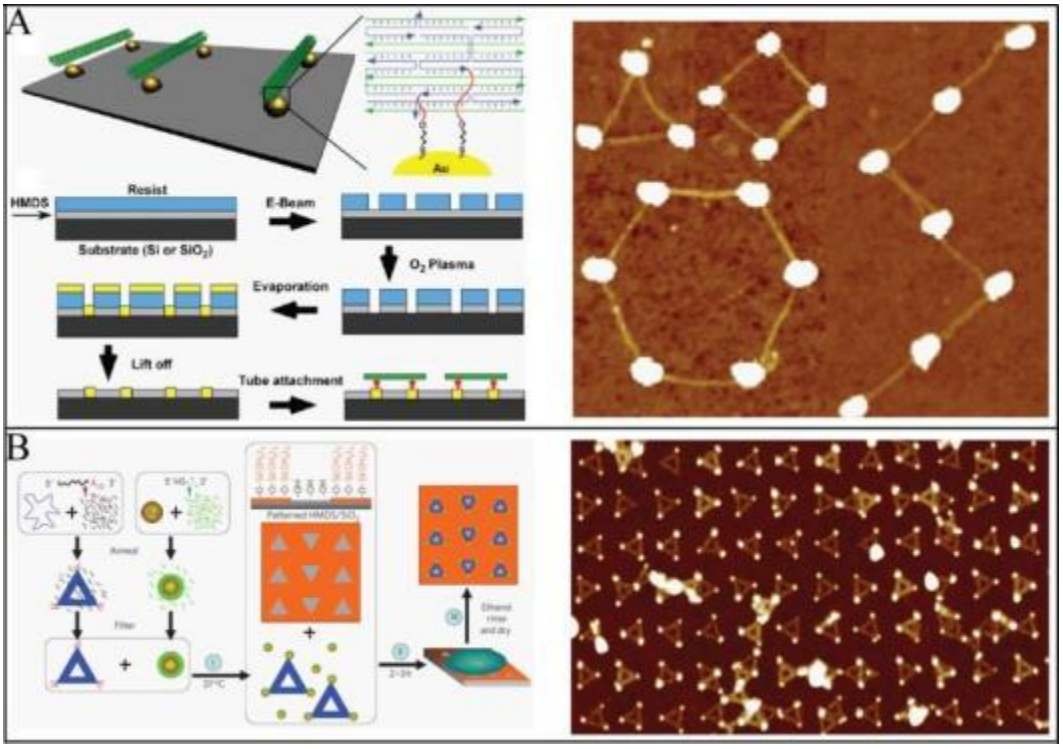

Figure 1.7. DNA structure placement on surface. A) Gold island directed immobilization of DNA tube on surface; B) EBL pattern placed DNA Origami, carried AuNPs, on surface.

1.1.8. DNA Structure Application in vivo. Delebecque and Silver [49] designed and assembled multidimensional RNA structures and used them as scaffolds for the spatial organization of bacterial metabolism. Engineered RNA modules were assembled into discrete, 1D, and 2D scaffolds with distinct protein-docking sites and used to control the spatial organization of a hydrogen-producing pathway, as shown in figure 8. Douglas and Church [50] described an autonomous DNA nanorobot capable of transporting molecular payloads to cells, sensing cell surface inputs for conditional, triggered activation, and reconfiguring its structure for payload delivery. Nanorobots loaded with

combinations of antibody fragments were used in two different types of cell-signaling stimulation in tissue culture.

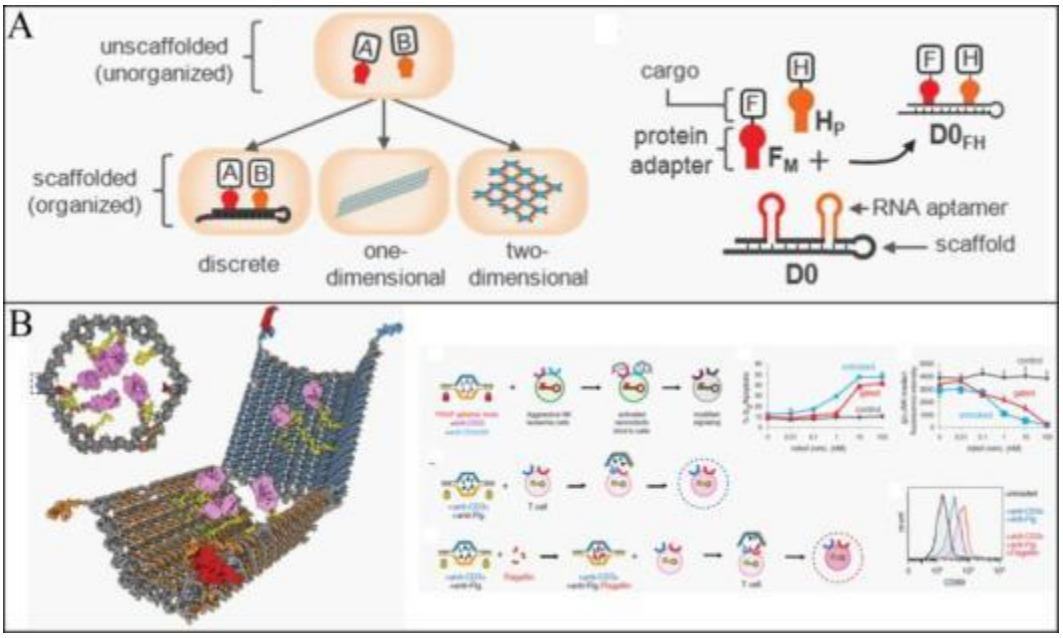

Figure 1.8. DNA structure in vivo application. A) Assembled RNA structure for developing artificial pathway; B) DNA cage nanorobot as logic gate;

1.2. Inorganic Materials

1.2.1. Inorganic Material Assembly. Ensembles of nanoparticles show properties that are quite different from those of discrete nanoparticles and corresponding bulk materials, because of quantum effect at nanoscale. Coupling of the surface plasmons, excitons or magnetic moments of individual nanoparticles or from a coherent state of collections of nanoparticles will result in new collective nanoparticle properties. [51]

When nanoparticles are placed sufficiently close to each other, near-field coupling between the surface plasmon of the neighbouring nanoparticles occurs owing to the transfer and confinement of electromagnetic energy. Plasmonic nanoantennase create

highly enhanced local fields when pumped resonantly, leading to increased Raman scattering and fluorescence signal. For example, Kinkhabwala and Moerner observed enhancement of a single molecule's fluorescence up to a factor of 1340 using gold bowties nanoantennas, as shown in figure 9. [52]

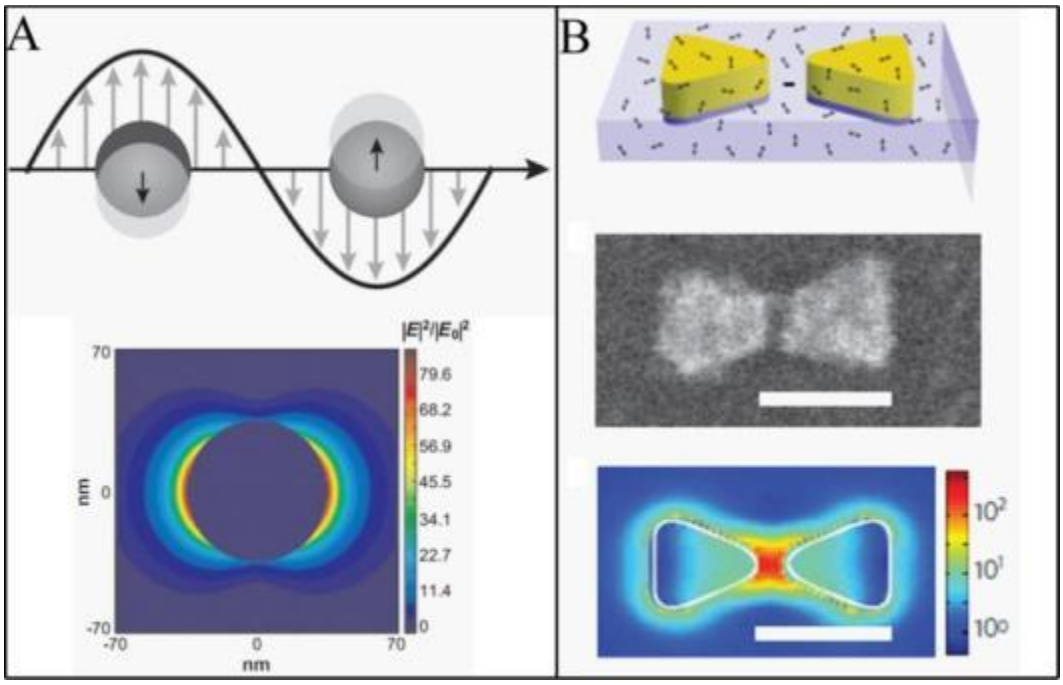

Figure 1.9. Coupling of plasmons and bowties nanoantennas. A) Metal NP plasmonic field; B) Bowties structure enhanced fluorescence signal for over thousands times; (Scale bar: 100nm)

1.2.2. Different Scaffolds.

Peptide scaffold. Peptide has 20 amino acid residues, and each one can be coded with different information, which makes peptide scaffold bear more information than DNA scaffold. However until now it is still a great challenge to construct design shaped peptide structure. Many inorganic nanoparticle superstructures, including nanoparticle

chains, nanoparticle sheets, nanoparticle spheres, and nanoparticle double helices, had been designed and synthesized using peptide-based method through different interactions, including electrostatic interaction and metal coordination interaction.[53] For example, Wang and co-workers demonstrated that T1 peptide self assembled nanofibers would assemble negatively charged AuNPs, created double-helical arrays, through electrostatic interaction.[54]

Polymer scaffold. Polymer scaffold technique has been developed for long time, and different shaped polymer structure has been constructed, including sphere, tube shaped structure with controlled parameters. However polymer structures are usually constituted with one or two units, which make polymer scaffold bear less information. Chen reported the measurement of the ensemble-averaged Surface Enhanced Raman Spectrum (SERS) enhancement factor from spatially isolated colloidal nanosclusters with polymer scaffolds. [55] They used polystyrene-block-poly(acrylic acid) (PSPAA) to enclose and protect Au@Ag core-shell NPs, and separated with enriched in dimer (85%) and trimers (70%) and found the enhanced SERS signal, as shown in figure 10.

Compared with DNA scaffold, peptide scaffold has more information encoded, because of 20 amino acid residues; however peptide structures can also be hard to control. For polymer scaffold, although they are easily accomplished, they do not have enough parameter to change for different organization. In conclusion, DNA scaffold has enough information to be coded and are easily to be designed, which makes it a better template for inorganic materials assembly.

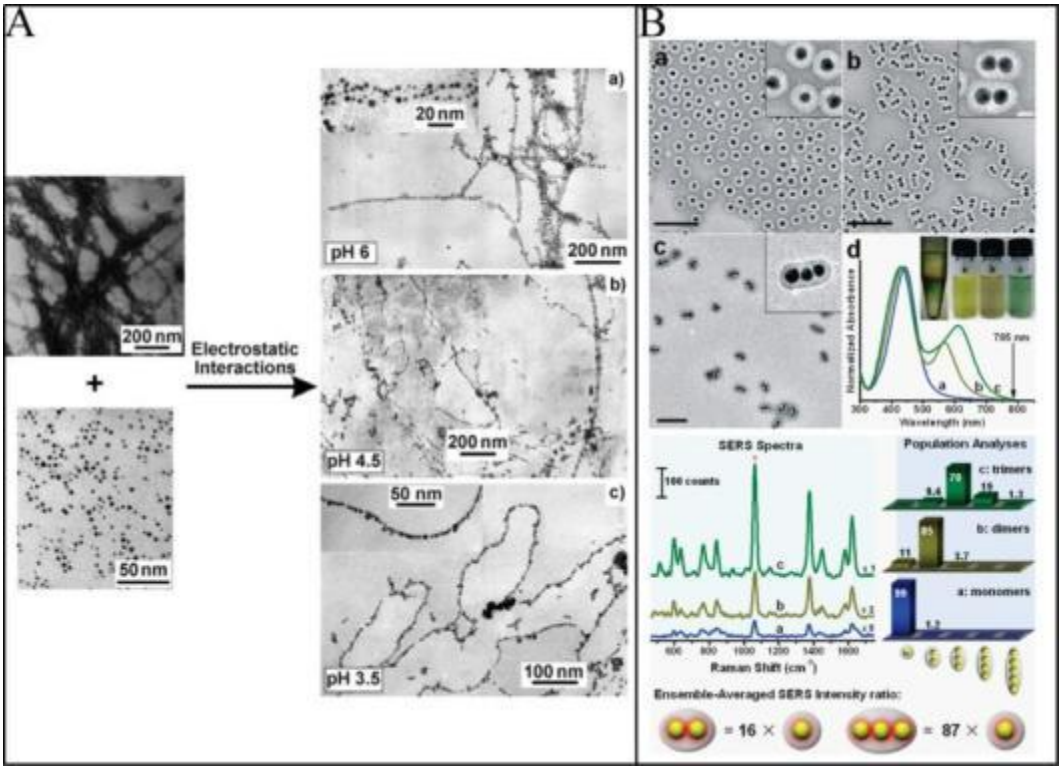

Figure 1.10. Peptide scaffold and polymer scaffold. A) Peptide scaffold directed assembly of AuNPs; B) Polymer directed formation of Au monomer, dimer and trimer and their SERS enhancement;

1.2.3. Nanomaterial Assembly in 3D. Plamonic field of metal NP is mapped in 3D space, which means controlled assembly of metal NPs in 3D is important for chemical sensing, nanophotonics and photocatalysis. [56, 57] One example is to assemble nanomaterial in 3D chiral pattern. [58, 59]

Chiral is defined as object lacks S_n symmetry elements. Although random structure can also have chirality from definition, people are usually interested structure with consistent chirality over long range, for example, helical spring and the rotational symmetry (C_n axis) in fans or propellers. Chirality in nanostructures could potentially be very useful. Chiral nanostructures could interact with chiral biomolecules; and chiral

springs, gears and propellers could potentially create a new dimension of mechanical applications in nanodevices. The physical properties of chiral nanostructures could be of interest, for example, chiral plasmonic nanostructures had been shown to have the ability to rotate the plane of the polarization of light. Moreover, the high sensitivity of plasmonic coupling to the interparticle distances in a chiral cluster could be explored for developing a 'plasmon ruler' that uses CD spectra. Moreover, chiral metal nanostructures of a few nm in size could provide a new platform for asymmetric catalysis with high surface area and stable metallic structure. In addition, according to the theory developed, chiral structure would have negative refractive index, which had never been observed. Self assembly of metal NPs with chiral properties would be the first experimental demonstration for negative refractive index, which will have wide range of applications in biology and physics, including the structural determination of proteins and DNA and further investigation on photonics. However, the synthesis of chiral material in nanometer scale is still a great challenge, because they are too big to be made by well-established molecular synthesis, and too small to be made individually by top-down methods. DNA nanostructure provided an ideal template to assemble metal NPs with chiral properties. Figure 11 showed several examples for chiral nanostructures; Wu et al. reported the construction of helical structures formed inside AAO nanochannels with different diameters. [60] Chen et al. demonstrated the arrangement of AuNPs in a double helix configuration on a helical polypeptide superstructure. [61] Guerrero-Martinez observed plasmonic circular dichroism in chiral 3D organizations of gold nanorods obtained by self-assembly of the nanoantennas onto a fiber template with a twisted morphology. [59]

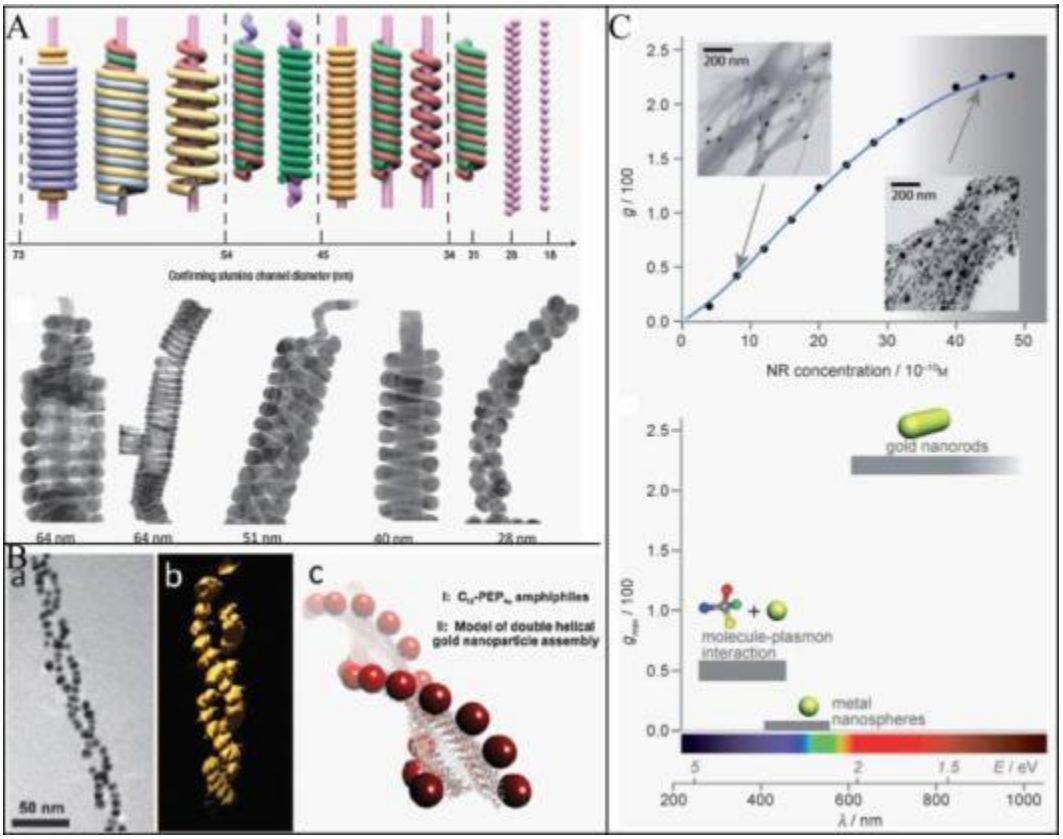

Figure 1.11. 3D chiral assembly examples.

1.2.4. Single-wall carbon nanotube (SWNT) field effect transistor (FET).

SWNT properties. In 1991, Sumio Iijima discovered carbon nanotubes in high-resolution electron microscopy, [62] with graphite-like materials closed in on itself to form cylinders with diameter from 1nm up to several nanometers. Single-walled carbon nanotube is a layer sidewall carbon nanotube structure, with extraordinary aspect ratio (cm in length and nm in diameter) strong local covalent structure, and long-range structure that is essentially free of defects. SWNT have some remarkable properties, such as extraordinary strong rigidity, and SWNT can be either metallic or semiconducting depending on their chirality. [63]

DNA wrapped SWNT. In 2003, Zheng [64, 65] discovered that ssDNA could be used to disperse SWNT solution, with DNA wrapped on SWNT sidewall through stacking interaction between SWNT sidewall and DNA bases, as shown in figure 12. After that, Zheng found with the help of size exclusive chromatography, SWNT-DNA complex could be separated with discrete length.[66] Furthermore, Zheng discovered that DNA sequence can selectively bind to SWNT with specific chirality, which could be used to separate 12 major single-chirality semiconducting species. [67]

SWNT FET device. Field effect transistor [68] is a transistor that uses electric field to control the shape and hence the conductivity of a channel of one type of charge carrier in a semiconductor material, and FET is one of the most important devices now. The excellent conductivity properties of SWNTs make them ideal wiring candidates for molecular-scale circuitry. Lieber reported [69] on a nanowire crossbar fabrication approach that employed microfluidics to align nanowires within lithographically defined channels, coupled with deposition onto a chemically patterned surface. Diehl and Heath described electric field assisted deposition and orientation of SWNT. [70] However all the above method cannot control precisely control the SWNT array distance and angles, and they could not be scaled up.

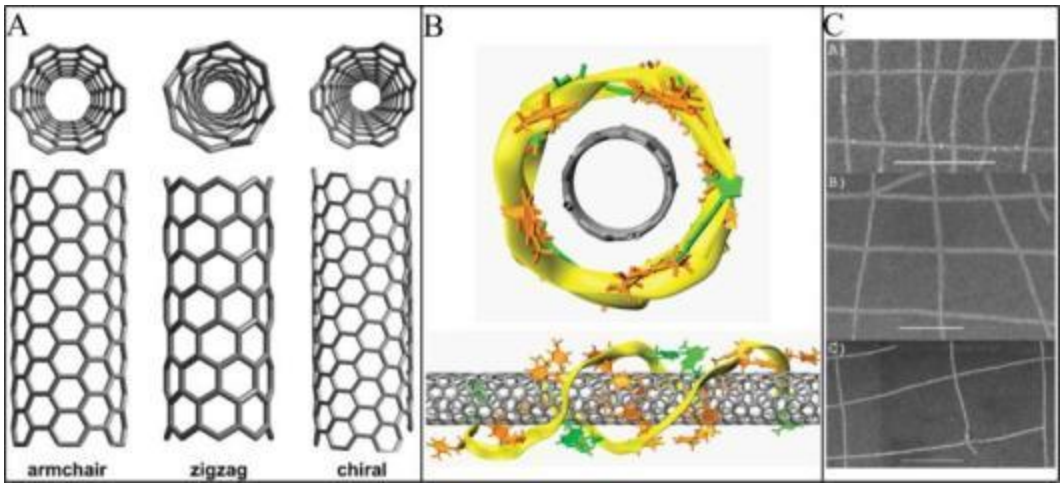

Figure 1.12. SWNT FET device. A) SWNT structure; B) DNA wrapped SWNT; C) eletrofield assisted deposition of SWNT FET array;

1.3. Interface with Biology

1.3.1. In vivo Compartment. Enzymes are large biological molecules responsible for the thousands of chemical inter-conversions that sustain life. They are highly selective catalysis, greatly accelerating both the rate and specificity of metabolic reactions. Enzymes are organized in three levels in vivo: [69] firstly, metabolism pathway enzymes are confined in compartment; secondly, protein scaffolds are applied to organize enzymes together with controlled order and ratio; thirdly, more precisely control of orientation will result in substrate tunneling to transfer intermediate more efficiently;

Cell faces many challenges regarding enzyme catalytic reactions. First, some enzymes suffer from slow turnover, which resulted in flux imbalances or bottlenecks in pathways. Second, diffusion of volatile intermediates through the cell membrane resulted in their loss from the cell. Third, biosynthetic pathways could generate toxic intermediates that inhibit growth. Finally, metabolites could participate in multiple competing reactions, reducing their availability for any single pathway. To deal with

these challenges, nature had evolved compartmentalization [70] strategies, such as large enzyme complexes and organelles, to spatially organize metabolism.

1.3.2. Compartment Examples. In some bacteria, carboxysomes encapsulate ribulose 1, 5-bisphosphate carboxylase oxygenase (RuBisCO) and carbonic anhydrase (CA), enzymes involved in the rate-limiting step of the Calvin cycle. [71] They are proposed to help overcome the slow turnover rate of RuBisCO by providing a high local concentration of carbon dioxide to the enzyme.

The ethanolamine utilization (Eut) microcompartment sequesters acetaldehyde, a volatile and toxic intermediate of the ethanolamine utilization pathway. [72]

1.3.3. Compartment Examples.

Liposome. Lipids, often in the form of membranes, are widely used to encapsulate reactions in nature. Lipid vesicles and oil emulsions have been used to perform a wide variety of reactions in vitro, such as gene expression, sequencing, and evolution of new enzymes. Graff and Meier reported [73] to study enzyme activity internalized inside liposome, which was incorporated with membrane channel protein, and found enzyme kinetic did not change compared with free enzyme.

Capsid. A capsid is the protein shell of a virus, which consists of several structural subunits made of protein called protomers. At low pH, protomers would assemble to form capsid, with small pore (<2nm) on surface, which will be ideal for substrate and product diffusion. Nolte [74] reported the incorporation of horseradish peroxidase (HRP) enzymes in the inner cavity of capsid, and found increased turnover numbers, with single molecule fluorescence technique. However, the encapsulation was

accomplished by random diffusion of enzyme inside cavity before the formation of capsid structure, so the encapsulation yield was still very low.

Polymer. Similar with polymer directed encapsulation with inorganic materials, polymers could also be used to encapsulate enzymes to mimic compartment. Liu and Lu [75] showed that two or more enzymes with complementary functions could be assembled and encapsulated within a thin polymer shell to form enzyme nanocomplexes, which exhibited improved catalytic efficiency and enhanced stability compared with free enzymes, as shown in figure13. Furthermore, the toxic intermediates generated by one enzyme can be promptly eliminated by another enzyme.

Inorganic tube. Inorganic materials had been used as enzymes support for enzyme catalytic reactions. Immoblization of enzymes on an appropriate inorganic material support could increase their stability and activity under a broader range of conditions. Sang and Coppens [76] systematically studies interaction of proteins with the surface of cylindrical nanopores to elucidate how surface curvature and surface chemistry affect the conformation and activity of confined proteins in an aqueous, buffered environment.

DNA tube. Spatially addressable DNA structure has been used to study distance dependent enzyme activity. Wilner [77] reported to attach enzyme cascades or cofactor-mediated biocatalysis to DNA strips, and observed enhanced enzyme activity. Fu and Yan applied planar DNA origami template to study the distance dependent activity of cascade enzymes.

Fu and Fan [78] reported to assemble cascade enzymes, GOx, HRP on planar and tube origami, and found the activity increased after roll the planar origami to tube morphology.

Rudiuk and Baigl [79] reported enzyme activity boost after conjugated with giant DNA. They conjugated several enzymes with lambda DNA, and found Kcat value increased 2-3 folds, which may resulted from negative charged DNA environment can stabilize internalized enzyme.

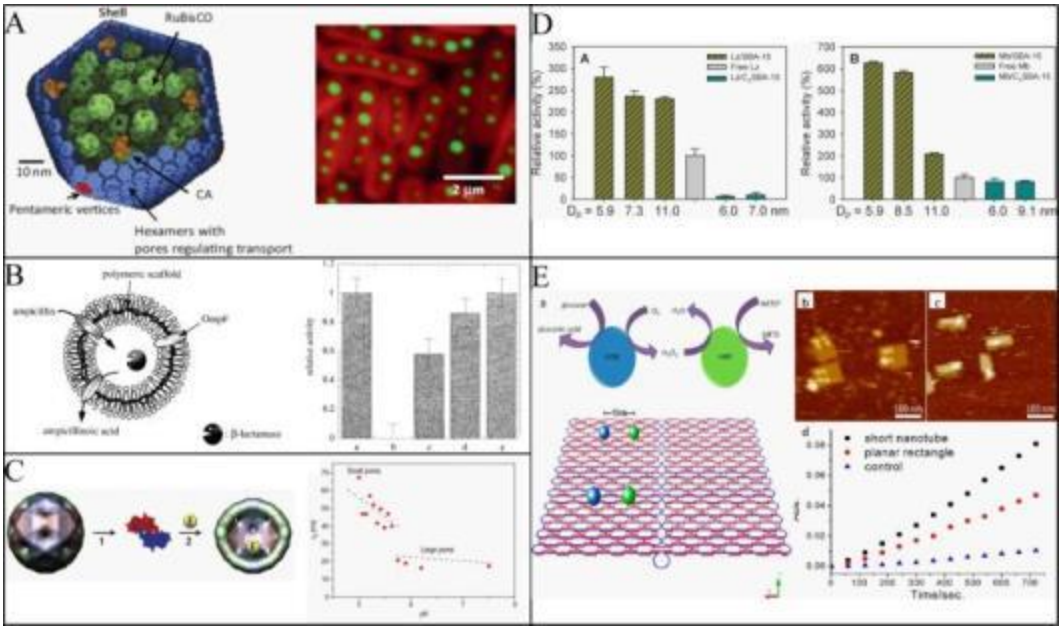

Figure 1.13. Microcompartment (carboxysome, capside and polymersome, inorganic tube and DNA tube).

1.4. Projects

1.4.1 A Route to Scale Up DNA Origami Using DNA Tiles as Folding Staples. A new strategy is presented to scale up DNA origami using multi-helical DNA tiles as folding staples. Atomic force microscopy images demonstrate the two-dimensional structures formed by using this strategy.

1.4.2. Organizing DNA Origami Tiles Into Larger Structures Using Pre-formed Scaffold Frames. Structural DNA nanotechnology utilizes DNA molecules as programmable information-coding polymers to create higher order structures at the nanometer scale. An important milestone in structural DNA nanotechnology was the development of scaffolded DNA origami in which a long single stranded viral genome (scaffold strand) is folded into arbitrary shapes by hundreds of short synthetic oligonucleotides (staple strands). The achievable dimensions of the DNA origami tile units are currently limited by the length of the scaffold strand. Here we demonstrate a strategy referred to as “superorigami” or “origami of origami” to scale up DNA origami technology. First, this method uses a collection of bridge strands to prefold a single stranded DNA scaffold into a loose framework. Subsequently, preformed individual DNA origami tiles are directed onto the loose framework so that each origami tile serves as a large staple. Using this strategy, we demonstrate the ability to organize DNA origami nanostructures into larger spatially addressable architectures, shown in chapter 3.

1.4.3. Encapsulation of Gold Nanoparticles in a DNA Origami Cage. A critical challenge in nanoparticle (NP) surface functionalization is to label the NP surface with a single copy of a functional group or to display multiple, unique molecules on the NP surface with control of the orientation and intermolecular distance. This challenge

was addressed with the construction of a spatially addressable, self-assembling DNA origami nanocage that encapsulates gold nanoparticles and interrupts its surface symmetry.

1.4.4. DNA Origami Templated Self-assembly of Discrete Length Single Wall Carbon Nanotubes. Constructing intricate geometric arrangements of components is one of the central challenges of nanotechnology. Here we report a convenient, versatile method to organize discrete length single-walled carbon nanotubes (SWNT) into complex geometries using 2D DNA origami structures. First, a size exclusion HPLC purification protocol was used to isolate uniform length, SWNTs labeled with single stranded DNA (ssDNA). The nanotube-bound ssDNA are composed of two domains: a SWNT binding domain and a linker binding domain. Although initially bound to the SWNTs, the linker domain is displaced from the surface by the addition of an external ssDNA linker strand. One portion of the linker strand is designed to form a double helix with the linker binding domain, compelling the DNA to project away from the SWNT surface. The remainder of the linker strand contains an ssDNA origami recognition sequence available for hybridization to a DNA origami nanostructure. Two different 2D DNA origami structures, a triangle and a rectangle, were used to organize the nanotubes. Several arrangements of nanotubes were constructed, with defined tube lengths and inter-tube angles. The uniform tube lengths and positional precision that this method affords may have applications in electronic device fabrication, shown in chapter 5.

1.4.5. DNA Origami Cage Trapping Enzyme: Protection and Boosting Enzyme Activity. Intracellular compartments are a key factor in cell metabolism.[1-4] These evolved confined compartments ensure efficient intermediate transfer for slow

turnover rates reaction, elimination competing metabolic reactions, and toxic intermediates. Construction of functional enzyme complexes that are confined in similar way remains challenging.[5-8] Here we utilize spatial addressable DNA Origami structure to encapsulate enzymes to mimic compartment phenomenal. Enzymes, which are chemically modified with ssDNA, can be assembled into DNA Origami cage with high yield. The DNA Origami 'shell' can protect internalized enzyme from degradation factors, such as protease, metal ions and BSA. Furthermore, internalized enzymes showed enhanced activity, which resulted from 5-10 folds increase of Vmax value, compared with fresh enzymes. With DNA Cage system, cascades enzymes can be assembled together to increase intermediate transfer efficiency.

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Chapter 2

A Route to Scale Up DNA Origami Using DNA Tiles as Folding Staples Adapted with permission from Zhao, Z.; Yan, H.; Liu, Y,: A Route to Scale Up DNA Origami Using DNA Tiles as Folding Staples, *Angew Chem Int Ed*, **2010**, 49, 1414–1417. Copyright 2010 Wiley-VCH.

2.1. Abstract

A new strategy is presented to scale up DNA origami using multi-helical DNA tiles as folding staples. Atomic force microscopy images demonstrate the two-dimensional structures formed by using this strategy.

2.2. Introduction

DNA-based molecular self-assembly offers an efficient route to fabricate nanostructures of increasing complexity. [1] Recently, progress in structural DNA nanotechnology has demonstrated that DNA tiles consisting of branched DNA junction motifs can be used as versatile building blocks for programmable construction of two- and three-dimensional structures with custom-designed surface patterns.[2–4] These nanostructures can be used as templates to organize proteins and nanoparticles into rationally designed patterns.[5–16] An important milestone for the advance of structural DNA nanotechnology was the development of a DNA nanostructure folding strategy, called scaffolded DNA origami, which was achieved by Rothemund.[17] In this technique, a long single-stranded viral genome (M13 phage) serving as a scaffold is arranged in a 2D plane following a designated folding path, and hundreds of short oligonucleotides, termed staple strands, hybridize with the scaffold strand through complementary base pairing to form many branched DNA junctions between adjacent helices. The staple

strands assist the folding of the scaffold strand into planar 2D arrays with custom-designed shapes defined by the initial scaffold folding path. Recently, the concept of DNA origami has been applied to engineer a series of 3D DNA nanostructures with a broad range of geometric complexities, [18–23] thus further showing that DNA is one of the most promising materials to achieve highly programmable self-assembling systems that mimic the complexity of nature.

One critical challenge facing the further development of DNA origami technology is to scale up the size of DNA origami structures. Herein we present a new strategy to construct 2D DNA origami of larger dimensions using rectangular-shaped DNA tiles as staple tiles rather than using traditional staple strands. A small portion of the M13 scaffold (about 1140 nucleotides) is shown in Figure 1 to illustrate the concept.

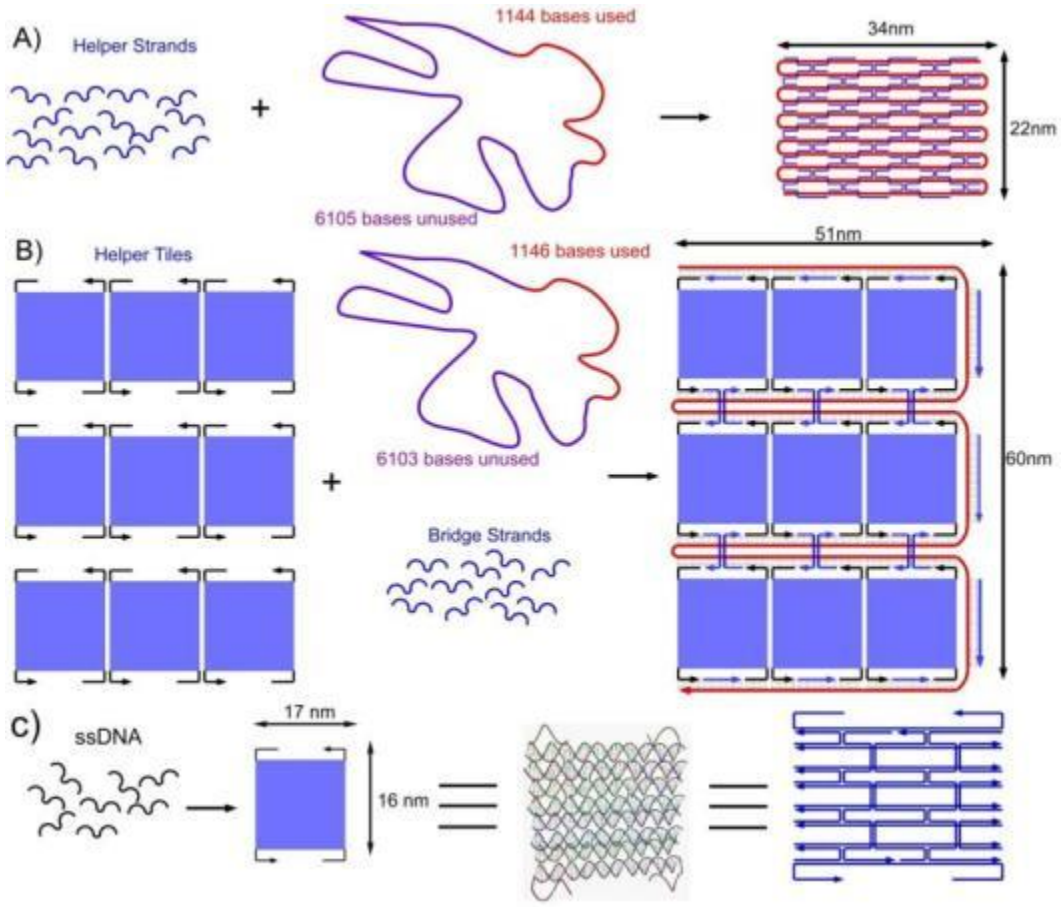

Figure 2.1. Experimental design. A) The formation of Rothemund's origami using many short staple strands to fold a single-stranded M13 DNA scaffold following a predetermined path into a closely packed 2D pattern. B) Formation of a larger-sized origami using a number of multihelical tiles, each containing single-stranded extensions at the four corners (short black lines; arrows indicate 3' ends) as staple tiles, together with a number of bridge strands (blue) to fold the M13 DNA scaffold into a predetermined 2D structure. C) Self-assembly of the staple tiles, each being an 8-helix tile, 5 full helical turns long of about 17 nm×16 nm. Each 8HX tile contains 18 strands of varying length, of which 16 strands remain unchanged, with two strands (one on the top and one on the

bottom) extended with different sequences of single stranded overhangs to base-pair with different parts of the M13strands.

Using Rothemund's original strategy, a segment of M13 can be folded by many short DNA staple strands into a rectangular shaped 2D origami of about 34 nm× 22 nm in dimension (Figure 1A). In our new strategy (Figure 1B), we use nine staple tiles, each of which is an eight-helix tile [24] (Figure 1C) with protruding single-stranded overhangs at the four corners that base-pair with the M13 scaffold. Together with additional bridge strands, a segment of M13 of the same length can be folded into a fully packed 2D origami of circa 70 nm×54 nm in two dimensions, which is more than quadruple the size of the structure shown in Figure 1A. In principle, it is possible to use the staple-tile strategy to scale-up 2D DNA origami using the full-length M13 scaffold. This strategy may be further scaled up using larger staple tiles, such as a single tile of origami, to fold a longer scaffold strand (e.g. origami of origami).

As a proof-of-concept demonstration, we tested the construction of three fully packed 2D origami structures using altered numbers of staple tiles. The total numbers of tiles used in the three constructs are 5×5=25 (90 nm×110 nm), 7×8=56 (140 nm×200 nm), and 5×11=55 (100 nm×280 nm). Additionally, a number of short bridge strands were used to guide the folding of the M13 scaffold into a flexible framework with correctly spaced cavities to facilitate access of the individual helper tiles to the scaffold. Single-stranded thymine, T2, was added at the ends of each helix to reduce inter-tile end-to-end base stacking. To minimize the cost of DNA synthesis, the core sequences of each individual eight-helix tile were kept the same, and only the DNA oligomers containing the overhangs that hybridize with the scaffold were modified. The scaffold used in the

study was the single-stranded M13 mp18, (7249 nucleotides (nt) in length), same as that used in Rothemund_s original origami experiments.[17] The final structures were designed so that 41%, 88%, or 90% of the scaffold strand were basepaired with the overhangs of the staple tiles and the bridge strands. The remaining scaffold was left as an unpaired loop at one side of the helices.

2.3. Materials and Methods

The formation of the three DNA origami structures using the staple-tile folding strategy were carried out in a two-step annealing procedure: 1) individual eight-helix staple tiles with unique overhangs at the four corners were annealed from 90°C to 4°C in 1xTAE-Mg buffer (pH 8.0), containing 20 mm Tris acetate, 1 mm EDTA, and 12.5 mm $Mg(OAc)_2$; in a separate tube, M13 scaffold strands and all of the bridge strands were annealed together in the same buffer conditions from 90°C to 4°C. 2) The above two solutions were mixed together and further annealed from 45 °C to 4°C using various lengths of time to form the final structures. The molar ratio of the bridge strands to staple tiles to M13 scaffold was 10:2:1 for each assembly. The individual eight-helix tile has a melting temperature circa 65°C, [24] so it should be stable at 45°C. In our design, each individual eight-helix staple tile shares the same core sequence, so it is necessary to form the eight-helix tile first to prevent them from forming mismatched pairs with the M13 scaffold strand. The pre-annealing of the M13 scaffold strand with the bridge strands prepares the scaffold strand to pre-fold with a defined path, so that in the second annealing step, each individual staple tile can efficiently fill in the correctly spaced cavities along the scaffold to form the final target structure.

Folding of the 5×5 structure was quick and efficient. Complete 5×5 structures were observed with a 12 h thermal annealing from 45°C to 4°C. The formation of the 7×8 structure took a longer time. The correct folding was observed with annealing over the course of 60 h. The formation of the 5×11 structure was the least efficient process, with a limited yield even after 100 h of annealing.

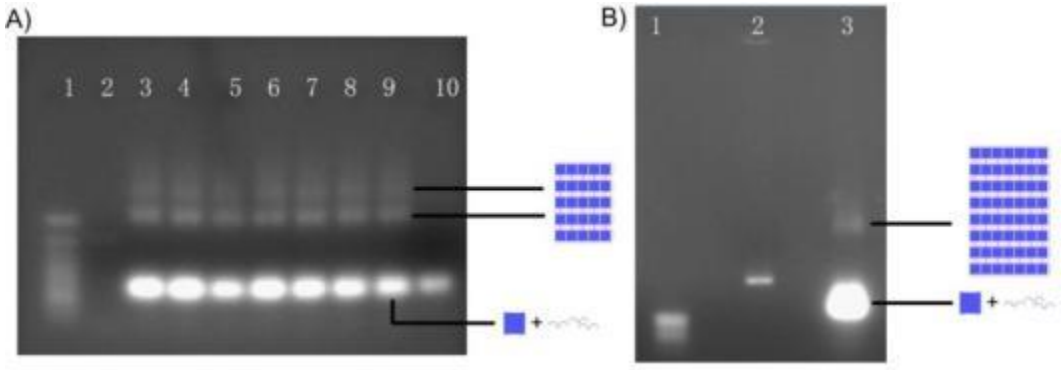

Figure 2.2. Agarose gel images that confirm the formation of the 5×5 and 7×8 structures. A) 5×5 structure. Lane 1: 100 bp marker ladder with a maximum marker size of 3000 bp; lane 2: single-stranded M13; lanes 3–9: annealed 5×5 structures at different Mg^{2+} concentrations (12.5 mm to 20 mm); lane 10: 8HX scaffold tiles. 0.7% agarose gel was used. B) 7×8 structure. Lane 1: 100 bp marker with a maximum marker size of 1000 bp; lane 2: single-stranded M13; lane 3: annealed mixture of 7×8 structure in 1.2xTAE-Mg buffer (15 mm Mg). 0.3% agarose gel was used. The gels were stained with ethidium bromide.

The annealed mixtures were subjected to non-denaturing agarose gel electrophoresis (Figure 2, and Supporting Information, Figure S8) to check the yield of the target structures and purification. For the 5×5 structure, two distinct bands appeared

that migrated more slowly than the M13 single strand. The relative intensities of these two bands showed no significant variation with an increase of the Mg^{2+} concentration from 12.5 mm to 20 mm with circa 1 mm increments. For the 7×8 and 5×11 structures, the agarose gel images (Figure 2B, and Supporting Information, Figure S8) showed one distinct slower migrating band. These two structures showed a higher yield with a moderately higher Mg^{2+} concentration (15 mm). It seems that this particular concentration of divalent cations aids the folding of the larger origami structures. From Figure 2 it appears that the M13 scaffold is fully consumed to form lower mobility structures. By measuring the relative intensity ratio of the target bands from the corresponding lane, excluding the faster migrating excessive helper tiles and bridge strands, the estimated yields are about 70% for the 5×5 structure (the lane used for AFM imaging) and circa 48% for the 7×8 structure. The bands (or smears) appeared above the target structures may come from misfolded products, as single stranded M13 scaffold may still contain some secondary structures at the initial temperature used (45°C) in the second annealing step.

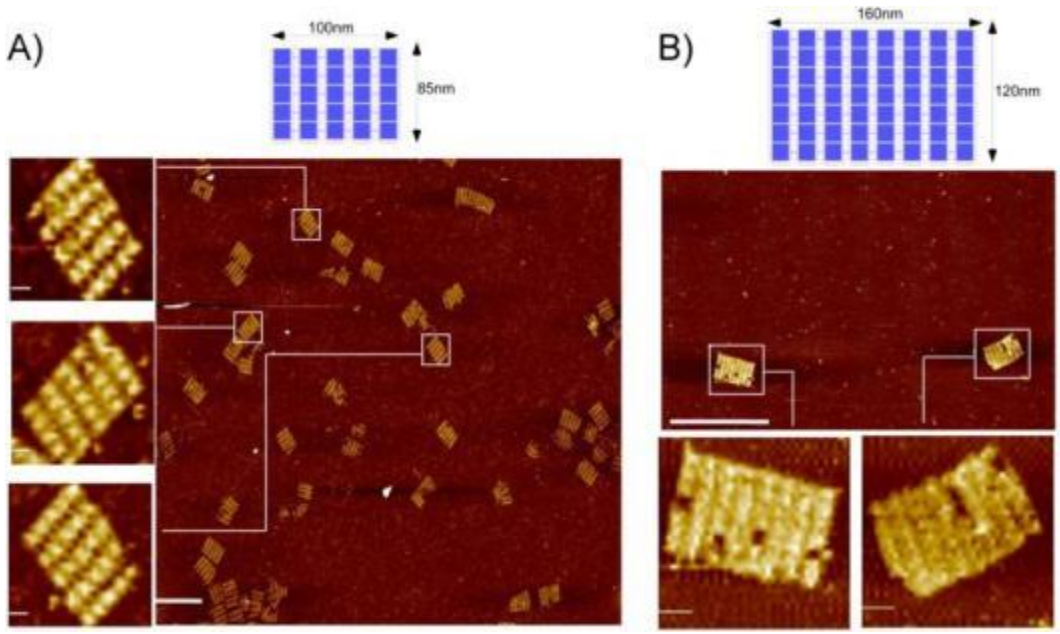

Figure 2.3. A) AFM images of the 5×5 structure. Scale bars in the insets are 20 nm. B) AFM pictures for the 7×8 structures. Scale bars in the insets are 40 nm. The yield of the desired structure is high, although the absence of one to three tiles at random positions is observed.

Both of the prominent slower migration bands for the 5×5 structure were excised from the gel and gently extracted using Freeze-N-Squeeze columns. The purified structures were then deposited on mica and imaged in liquid by tapping mode atomic force microscopy (AFM). The AFM images (Figure 3A, see also the Supporting Information for more images) show that both the higher and lower bands contain complete or nearly complete assembly of the desired structure with no obvious differences. For this 5×5 structure, nearly 60% of the M13 sequence remains as a large flexible loop out of the structure. The two distinct bands might have resulted from a part of the M13 strand in the loop region breaking into a linear strand, thereby causing significant differences in the migration speeds of the structures in the gel.

2.4. Results and Discussion

AFM images (Figure 3) for the 5×5 and 7×8 structures reveal the correct folding of the designed structures using the staple tiles. Individual tiles of the correct dimension can be clearly distinguished in the images. The measured dimensions of the structures match the designed parameters. Both gel and AFM images demonstrate that the yield (or degree of completeness) of the final structure has a trend of 5×5>7×8. It is logical that in a reaction with more components, a lower overall yield would be expected.We also noted that the 7×8 structure had a higher yield than the complete 5×11 structure, although they contain similar number of tiles in the assembly (56 tiles versus 55 tiles). This lower yield of the complete 5×11 structure (estimated to be about 30%; see the Supporting Information, Figure S8) may be explained by the larger aspect ratio of the final 5×11 structures (greater than 2:1, or even close to 3:1 when the stretching effect between the layers is considered), which resulted in unbalanced growth rates of the staple tiles in the vertical and lateral directions during the tile annealing. We tested the partial assembly of the 5×11 structure with various number of layers (8 to 11), and confirmed that fewer number of layers indeed gave better yields (see additional AFM images in the Supporting Information).

The 7×8 structure prepared here contains a single copy of the M13 strand, with a molecular weight of about 20 million Daltons, and circa 30000 base pairs. This is about four times the size of Rothemund_s origami structure using the same length scaffold.[17] Because the core of the 8HX staple tiles was kept constant, the 16 strands were purified and used repeatedly in the assembly. The total number of DNA strands with a unique sequence remained a manageable size: 248, which is only a marginal increase from the

original design of 226 strands used in the Rothemund's rectangular DNA origami.[17] As we used a two-step annealing strategy, it is foreseeable that we can selectively modify strands in each tile at particular positions and use them to create addressable binding sites to direct the assembly of other materials.

2.5. Conclusion

In summary, we have demonstrated a new strategy to scale up DNA origami using multihelical DNA tiles as folding staples. This strategy currently works more efficiently in creating 2D structures with roughly equal dimension in the 2D plane. The yield may be further improved by designing DNA staple tiles of different aspect ratios and optimizing the annealing procedures based on thermodynamic parameters of the helper tiles. In principle this method could be applied to create large DNA origami nanostructures reaching the size domain of conventional photolithography techniques (1 um), which may become a viable approach to bridge bottom up self-assembly with top-down lithography. For example, if the individual Rothemund rectangular 2D origami of 60×90 nm[17] were used as the staple tiles to fold a DNA scaffold of the size of l DNA (45 000 nucleotides, if a single strand of DNA of such length can be generated), it is possible to create super-origami of circa 10×8 of such tiles with an overall size of 1 um×0.5 um. Such super-origami should be easier to be patterned onto lithographically generated substrates. We anticipate the strategy demonstrated here could be combined together with other scale up techniques, such as hierarchical DNA assembly[18, 19, 25, 26] or surface mediated self-assembly,[27, 28] to realize the great potential of structural DNA nanotechnology.

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Chapter 3

Organizing DNA Origami Tiles Into Larger Structures Using Pre-formed Scaffold Frames

Adapted with permission from Zhao, Z.; Yan, H.; Liu, Y.: Organizing DNA Origami Tiles Into Larger Structures Using Pre-formed Scaffold Frames, *Nano Letters,* **2011,** 11, 2997–3002.

3.1. Abstract

Structural DNA nanotechnology utilizes DNA molecules as programmable information-coding polymers to create higher order structures at the nanometer scale. An important milestone in structural DNA nanotechnology was the development of scaffolded DNA origami in which a long single stranded viral genome (scaffold strand) is folded into arbitrary shapes by hundreds of short synthetic oligonucleotides (staple strands). The achievable dimensions of the DNA origami tile units are currently limited by the length of the scaffold strand. Here we demonstrate a strategy referred to as "superorigami" or "origami of origami" to scale up DNA origami technology. First, this method uses a collection of bridge strands to prefold a single stranded DNA scaffold into a loose framework. Subsequently, preformed individual DNA origami tiles are directed onto the loose framework so that each origami tile serves as a large staple. Using this strategy, we demonstrate the ability to organize DNA origami nanostructures into larger spatially addressable architectures.

3.2. Introduction

Since the introduction of scaffolded DNA origami[1] the technology has been extensively applied to engineer a variety of two-dimensional (2D)[1-4] and three-

dimensional (3D)[5-14] nanostructures with a broad range of geometric complexities. One of the challenges to the functional development of DNA origami technology is to expand and adjust the size of the assemblies. Thus far the size has been restricted by the limited lengths of available single stranded DNA (ssDNA) scaffolds, where a 7 kilobase single stranded genome from the bacteriophage M13mp18 has become the standard. Two methods have recently been developed to address this problem. In the first approach, Shih and co-workers[15] utilized a one-pot assembly strategy to produce two different origami structures from a single double stranded scaffold (7560 bps). To achieve this, the initial double stranded DNA scaffold was denatured by a combination of heat and formamide to get complete separation of the forward and reverse scaffold strands. While denatured, the mixture was quickly cooled to room temperature to promote the faster hybridization of the staple strands and kinetically trap the scaffold-staple complexes. The remaining formation of the structures was achieved by gradually removing the formamide by dialysis. In the second method Woolley and co-workers[4] used biotinylated primers in a PCR reaction to obtain single stranded DNA (ssDNA) products to be used as scaffolds for the assembly of origami structures. Using this approach they generated several different DNA origamis with sizes ranging from 756 to 4808 bps. Although large double stranded genomes are a promising source for longer DNA origami scaffolds, it is still not known how to optimize the assembly of larger structures. As the scaffold strand gets significantly longer the number of staple strands required to fold the scaffold will also drastically increase, which may result in considerable sequence mismatches. Furthermore, shear forces applied to longer scaffolds may lead to DNA breaks and only partial assembly of the target structures.

Another strategy to create large DNA origami superstructures is to connect individual origami tiles through sticky end associations. Recently, a periodic 2D lattice of DNA origami tiles was achieved by Seeman and co-workers[16]. They used a symmetric cross-like design with the helical axes of the component DNA propagating in two perpendicular directions to avoid nonspecific polymerization. This design strategy led to large periodic DNA origami lattices with dimensions up to 2 μm × 3 μm. This design has not been applied to create large discrete architectures with multiple units. In another effort, Sugiyama and coworkers[17] employed a 'JigSaw puzzle strategy' which relied on shape complementarity and sticky end association to create a large, discrete DNA origami structure composed of 9 different DNA origami tiles with overall assembly efficiency of ~35%.

An alternative way to assemble larger DNA origami structures is to use more complex staples. We recently reported the use of 8-helix tiles (20 nm x 20 nm x 2nm), rather than single stranded oligonucleotides, as staples and demonstrated that DNA origami assemblies of more than 30000 bps can be constructed.[18] Herein, we aim to determine whether the 'tile staple' concept can be applied to large DNA origami tiles (e.g. equilateral triangle shaped DNA origami tiles with 120 nm edges and 2 nm thickness) to create 'origami of origami' and, if successful, what are the key factors to achieve high assembly efficiency.

As illustrated in Figure 1, a multi-step folding procedure is necessary to implement the 'origami of origami' strategy. First a series of DNA origami tiles, each with a unique set of single stranded extensions (probes) is assembled in separate tubes. Concurrently, a loose framework is constructed by folding a different single stranded

DNA scaffold with a separate group of bridge strands. Finally, the loose framework is folded further by the large, pre-formed origami tile staples through hybridization between the probes of the staple origami and the complementary sites within the loose framework. We demonstrated that very high assembly efficiencies (up to 85%) can be achieved by optimizing the formation of the loose framework and that the 'origami of origami' approach is a highly programmable approach to organize DNA origami tiles into larger complexes. The scaffold frames with three different design strategies was imaged (Figure S4), which showed that scaffolds formed flexible structure with bridges.

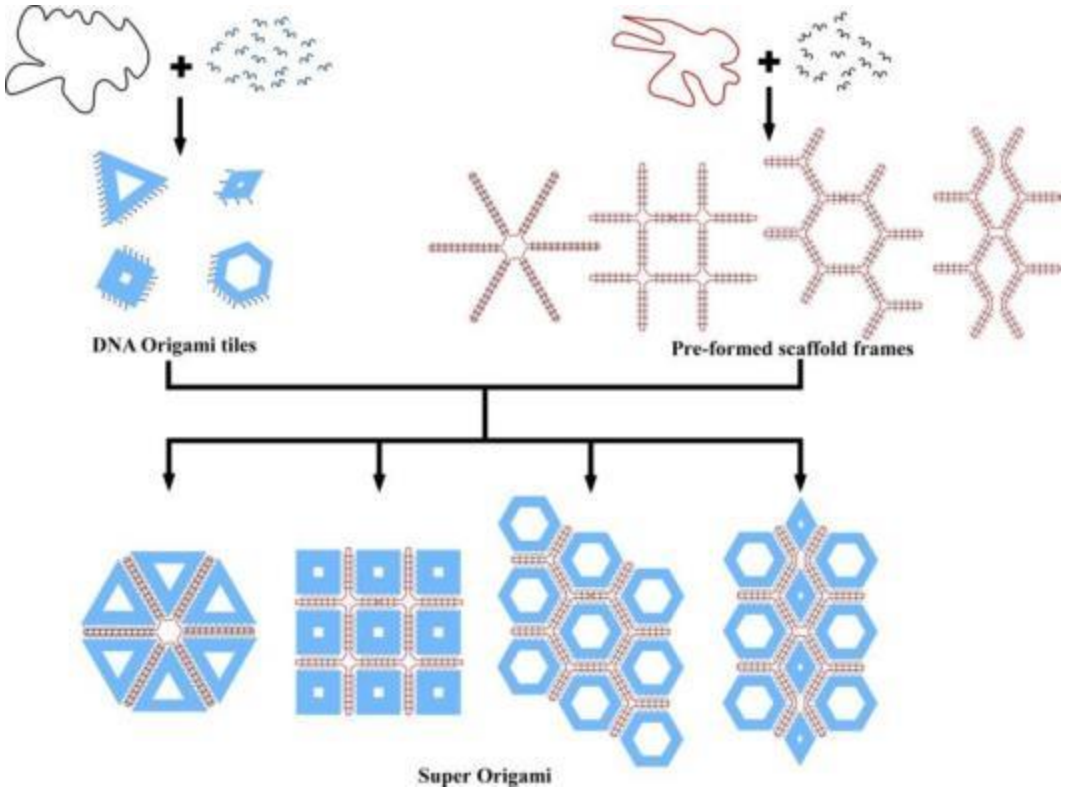

Figure 3.1. Schematic illustrating the 'origami of origami'. Top left: An M13 scaffold (black circular strand) is folded by a set of short DNA staples (blue strands) to form various individual DNA origami tiles. Each individual origami tile displays a group of

single stranded extensions that are subsequently used as sticky-points to interact with the pre-formed scaffold frames shown on the right. Top right: A PhiX174 scaffold (red circular strand) is folded by a set of bridge strands (black strands) to form the loose frameworks that interact with the individual pre-formed origami tiles to create the various super-origami structures shown at the bottom.

For our initial design (Figure 2) we used six triangular origami tiles (M13 scaffold; 120 nm x 120 nm x 120 nm) as the preassembled staple tiles (shown in blue) and single stranded PhiX174 as the scaffold forming the loose framework (shown in red) to assemble hexagonally shaped super-origami structures. The PhiX174 scaffold was partitioned into six equivalent loops; half of each loop was designed to interact with probes from a specific side of the triangular origami and the other half with a different side. The final side of the triangular origami tile remained unmodified. Three different strategies of association between the staple tiles and the framework scaffold were investigated with various yields of the final hexagonal super-structure. It should be noted that the single stranded PhiX174 scaffold shares little sequence similarity with the M13 scaffold so that any sequence overlap is minimal and can be neglected.

For strategy 1 (Figure 2, left), 22 probes were extended from two sides of the triangular origami staple tiles. Each ssDNA probe consisted of 8-nucleotides (shown in blue) that were designed to hybridize directly to the PhiX174 scaffold at the corresponding positions. Bridge strands (~ 16 nts long, shown in black) were designed to hybridize to the remaining portions of the scaffold framework, holding the framework in place and maintaining the correct spacing. Each crossover point (junction) between the individual triangular origami and the scaffold framework is formed from the participation

of two probe strands. The distance between the neighboring crossovers of adjacent helices was kept at 32 bp, approximately three full turns.

For strategy 2, in contrast to strategy 1, only 12 probes were extended from the sides of the triangular origami tiles. In this design only the 12 probes corresponding to positions farthest from the center (with respect to the hexagonal super-structure) were kept, while the 10 probes nearest the center were deleted. The bridge strands (32 nt each) were extended to include the deleted positions and designed to hybridize to the available portions of scaffold strand at those locations. In this way, the potential twisting and structural tension in the super-structure that might occur due to inclusion of non B-form DNA conformations could be partially relaxed.

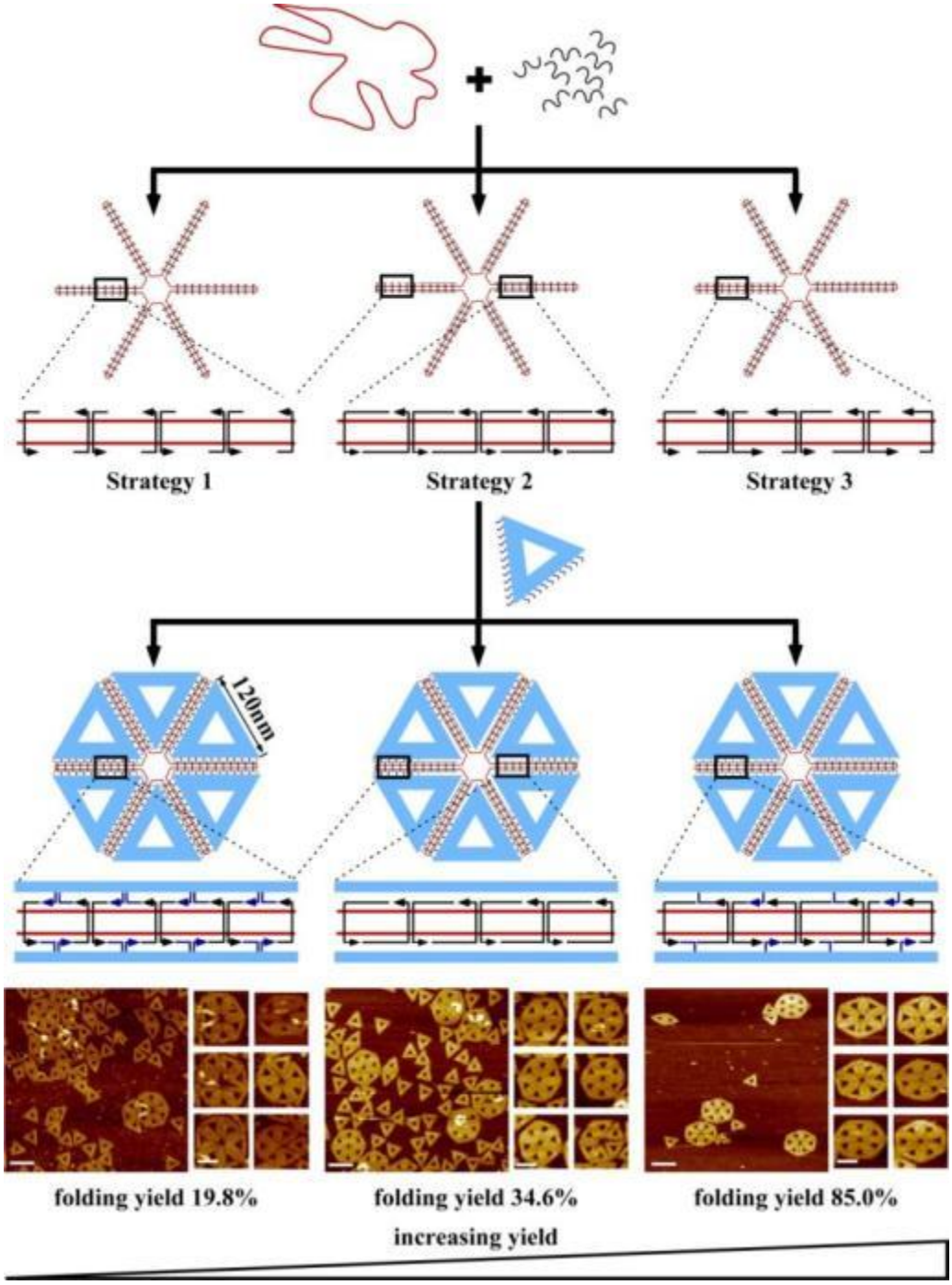

Figure 3.2. Hexagonal shaped super-origami assembled from six individual triangular origami tiles. Three different strategies for the association between the origami tiles (blue) and the framework scaffold strand (red) are shown. Probe strands (dark blue, arrow

points to 3‘ end) were extended from two sides of each of the individual origami tile and were designed to hybridize to specific positions within the framework scaffold strand. Periodic bridge strands (black) were also designed to assist the folding of the framework scaffold. AFM images of the final super-structures reveal varying efficiency among the designs, increasing from strategy 1 to strategy 3 (scale bar: 200 nm for zoom out images and 100 nm for zoom in images).

Strategy 3 involved the use of 11 probes spaced evenly along two arms of the triangular origami tiles. Unlike the first two strategies which contain reciprocal crossovers at the junctions between the individual triangular origami and the scaffold framework, each crossover point for strategy 3 is formed by a single probe strand. This design can more effectively relax any structural tension.

3.3. Materials and Methods

For all three design strategies, the formation of the hexagonal shaped super-origami was carried out in a two-step annealing procedure: 1) six individual triangular DNA origami tiles, with unique single stranded probes extended from two arms at selected positions, were annealed in separate tubes from 90 °C to 4 °C over 10 h in 1×TAE-Mg^{2+} buffer (pH 8.0, 20 mM Tris acetate, 1 mM EDTA, and 12.5 mM $Mg(OAc)_2$), with a 1:10 molar ratio of the M13 scaffold strand to the staple strands. The annealed structures were purified with 100 KD MWCO Microcon centrifugal filters to remove any excess staple strands. Concurrently, the PhiX174 framework scaffold strand and the entire set of bridge strands were mixed, with a 1:10 molar ratio of the PhiX174 scaffold strand to the bridge strands, in a separate tube and annealed from 90 °C to 4 °C in 1×TAE-Mg^{2+} buffer.) The two solutions were subsequently mixed together (with a

1.5:1 or 2:1 molar ratio of individual origami tiles to framework scaffold) and annealed from 45 °C to 4 °C with a temperature gradient of 2°C per hour. The annealing program was repeated 10 times and in each consecutive cycle the starting temperature of the program was decreased by 0.5 °C. The entire annealing process lasted approximately 100 hrs.

3.4 Results and Discussion

In this design strategy each individual triangular DNA origami tile contains the same scaffold and most of the same staple strands, differing only in the locations and sequences of the probes; thus, it is necessary to form each of the individual origami tiles separately in the first step. This prevents the individual origami tiles from forming incorrect associations with the PhiX174 scaffold strand. Assembly of the PhiX174 scaffold with the bridge strands pre-folds the scaffold framework into approximately the desired shape so that the subsequent addition of the pre-formed individual tiles will proceed efficiently, with each individual origami tile fitting into the evenly spaced cavities along the scaffold. This process is analogous to protein folding in which stepwise folding provides fast, pre-determined kinetic pathways to efficiently achieve the most thermodynamically stable folded structure.

The AFM images shown in Figure 2 reveal that strategy 3 has the best assembly efficiency, with approximately 85.0% complete (all six individual tiles) super-origami formation. The efficiency is calculated by multiplying the number of the complete hexagons by 6 and dividing the result by the total number of origami tiles. Strategy 2, which relieved some of the structural tension at the core of the hexagonal super-structure, resulted in ~ 34.6% assembly efficiency. Meanwhile, strategy 1 achieved only ~19.8%

assembly efficiency. Agarose gel was also used to characterize these super Origami structures, however the molecular weight of them (more than 30 MD) were too large that they cannot run into gel. Furthermore, from the AFM images it is evident that the super-structure assembled by strategy 1 does not always form correctly; occasionally the individual origami tiles do not fit perfectly within the framework and the hexagonal superstructure often appears twisted or partially broken. The super-structures assembled by strategy 2 displayed improved morphology and those assembled by strategy 3 appear nearly perfect. These results indicate that relaxing the structural tension within the superstructure, either by deliberate probe placement or through single stranded crossovers (rather than reciprocal crossovers) between the individual tiles and the scaffold, can significantly improve the efficiency of super-structure assembly. In Rothemund's original DNA origami report he attempted to utilize complementary sticky end association to organize six triangular DNA origami tiles into the same hexagonal structure.[1] However, the reported assembly efficiency was only ~2%, lower than the efficiency achieved using all three strategies reported here, and much lower than what was achieved by strategy 3.

To test the versatility of our super-origami method we designed several other unique DNA origami staple tiles including square, hexagonal and diamond shaped tiles. For each of the additional staple tile systems we assembled the super-origami structures using the optimized folding strategy 3.

The square shaped staple tile[14] has four equivalent sides, with each side consisting of nine parallel helices decreasing in length from the outermost to innermost layer (Figure 3). The longest helix is 224 base-pairs (bps), or 73 nm, in length. To form perfect

90 degree angles at each of the four corners, the length of helix n is designed to be 16 bps greater than the immediate neighboring helix n-1 (n corresponds the relative outer helical layer). This is based on the consideration that an 8 bp DNA duplex has a length of ~ 2.5 nm; 2.5 nm is equal to the diameter of a single DNA double helix (2.0 nm) plus the estimated gap between two neighboring parallel double helices (0.5 nm). Nondenaturing gel electrophoresis (Figure S10) and AFM analysis (Figure S9) revealed that the square origami tiles formed properly with very high yield (>95%).

PhiX174 scaffold framework was pre-formed to accommodate nine square origami tiles, ultimately arranged in a 3x3 pattern within the super-structure. The super-structure was assembled following the same annealing procedure as described above, with 1:10:2 molar ratios between the PhiX174 scaffold strand, the bridges strands, and the pre-assembled square tiles. AFM images (Figure 3b) reveal that the super-structure is assembled with ~ 49% efficiency, somewhat lower than the folding efficiency for the triangle staple tile system.

The lower efficiency may have several causes: 1) 9 origami tiles were used in the square staple tile super-structure, while only 6 tiles were used in the triangle staple tile super-structure. It is possible that as the final assembly grows larger there is a requirement for more units to simultaneously associate with the correct stoichiometry resulting in a less favorable kinetic situation. 2) Although the total number of probe-scaffold framework connections is slightly more in the square staple tile super-structure than the triangle staple tile super-structure, 144 vs. 132, the number of probes per origami unit (on average) is fewer, 16 vs. 22. This is especially relevant to the 4 square tiles located in the corners of the square super-structure which are only linked to the scaffold

framework by 12 probes, far fewer than the 22 probes per triangular origami in the hexagonal super-structure. Thus, the total enthalpy gain per origami unit tile is lower for the square tile than the triangular tile.

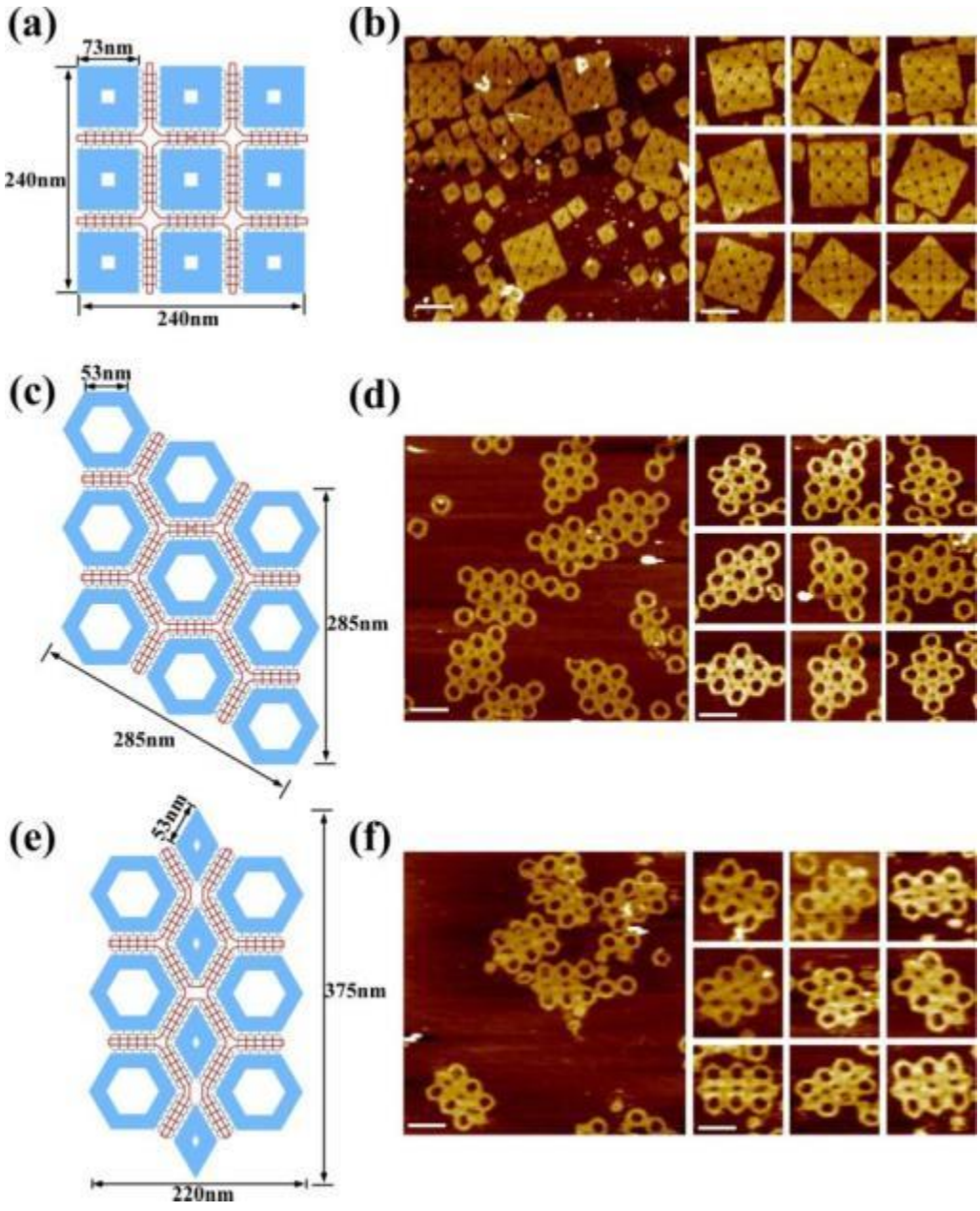

Figure 3.3. Illustration Square, hexagonal and diamond shaped DNA origami staple tiles assembled into super-structures using the design strategy depicted in Figure 2. (a), (b)

Design and AFM images, respectively, of 3 x 3 square staple tiles assembled into a super-structure. The length of each side of the individual square tiles is 73 nm; the length of each side of the super- structure is 240 nm. (c), (d) Design and AFM images, respectively, of 3 x 3 hexagonal staple tiles assembled into a super-structure. The length of each side of the hexagonal tiles is 53 nm; the length of each side of the super-structure is 285 nm. (e), (f) Design and AFM images, respectively, for mixed hexagonal and diamond staple tiles assembled into a super-structure. The length of each side of the diamond tiles is 53 nm; the dimensions of the super-structure are 220 nm × 375 nm. (scale bars: 200 nm).

The hexagonal shaped staple tile (Figure S12) was designed with similar principles as the square staple tile. Each side contains nine parallel helices decreasing in length from the outermost (160 bps, or ~52 nm) to the innermost layer. To achieve the 120 degree angle at each corner, the length of helix n is designed to be 8 bps greater than the immediate neighboring helix n-1 (n corresponds the relative outer helical layer). Non-denaturing gel electrophoresis (Figure S14) and AFM analysis (Figure S13) confirm that the hexagonal tiles form as designed with >95% yield. PhiX174 scaffold framework was pre-formed to accommodate nine hexagonal origami tiles assemble in the same manner as described above, with 1:10:1.5 molar ratios between the PhiX174 scaffold, the bridge strands, and the individual origami tiles. AFM images (Figure 3d) reveal that this super-structure forms with efficiency ~55%, similar to the square staple tile system. The total number of probe-scaffold framework connections is ~ 160 and the average number of probe strands per hexagonal origami unit is 17.8, both of which are similar to the square super-origami structure.

The square and hexagonal staple tile super-structure assemblies demonstrate that nine individual origami unit tiles can be co-assembled with a PhiX174 scaffold framework with relatively high efficiency. Furthermore, each of the staple tile units share the same core strands, differing only in the sequences of the probe extensions which keeps the cost of super-structure assembly relatively low. Even when you consider the need for a second scaffold strand (PhiX174 to form the scaffold framework, the cost to assemble a large super-structure increases by less than 1 fold compared to an individual tile.

Finally, we designed a diamond shaped staple tile (Figure S16) and assembled it with the hexagonal staple tile and PhiX174 scaffold framework to form a super-structure with mixed staple tiles. The pattern of the final structure is similar to a tessellation pattern; the gaps between the hexagonal tiles are filled in by the smaller diamond shaped tiles (Figure 3e).

The diamond shaped staple tile was also designed with similar principles as the hexagon and square staple tiles. Each side is composed of 9 parallel helices and the length of the outermost helix is 160 bps, or 53 nm, the same length as in the hexagonal tile. One end of each side forms a 120 angle with the adjacent side, and the other end forms a 60 degree angle with the other adjacent side. The same strategy employed for the hexagonal staple tiles was used to create the 120 degree angles, i.e. 4 bps were deleted from each helix n-1 compared to the outer neighboring helix (n); 13 bps were deleted to make the 60 degree angles. The formation of the diamond shaped staple tiles was confirmed by non-denaturing gel electrophoresis (Figure S18) and AFM analysis (Figure S17). The entire M13 scaffold strand was not utilized to assemble the individual staple

tiles; the unused portion was left as an unpaired loop in the inner cavity of the diamond. The single stranded loops can be observed in the background behind the super-structures in the AFM images.

Again the PhiX174 scaffold framework was pre-formed to accommodate the hexagonal and diamond shaped origami staple tiles and assembled in the same manner as described above, with 1:10:2:1.5 molar ratios between the PhiX174 scaffold, the bridge strands, the diamond shaped staple tiles and the hexagonal tiles. AFM results showed that the corresponding super-structure forms with ~ 41% efficiency. The lower efficiency may be related to the unique size and shape of the two origami staple tiles; notably, the diffusion and rotational dynamics of each of the tiles is expected to differ. In addition, the closely-packed design of the super-structure may impose considerable structural strain with the unit tiles experiencing increased steric hindrance. The unpaired region of the M13 scaffold within each staple tile may also interfere with the super-structure formation, ultimately reducing the overall yield.

3.5. Conclusions

In summary, we have improved and expanded upon the super-origami method that connects pre-assembled DNA origami tiles together to generate complex DNA super-structures. Uniquely shaped, geometric origami structures were designed and used as unit tiles to further assemble into large super-structures demonstrating the versatility of the method described here. The super-structures were assembled with high efficiency and exhibit an order of magnitude increase in size compared to the individual origami tile units. Super origami architectures formed from the triangular, square, hexagonal, hexagonal plus diamond origami unit tiles have molecular weights of 31.8 MD (96430

nt), 44.5 MD (134745 nt), 45.6 MD (138204 nt), 45.5 MD (137962 nt), respectively. The dimensions of the origami super-structures are close to the size domain of patterns generated by top-down photolithography, thus it may provide a viable approach to bridge bottom-up self-assembly with top-down methods and open up opportunities to build functional nanodevices.

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Chapter 4

Encapsulation of Gold Nanoparticles in a DNA Origami Cage

Used with permission from Zhao, Z; Jacovetty E. L.; Liu, Y.; Yan, H.: Encapsulation of Gold Nanoparticles in a DNA Origami Cage, *Angew Chem Int Ed*, **2011**, 50, 2041–2044.

4.1. Abstract

A critical challenge in nanoparticle (NP) surface functionalization is to label the NP surface with a single copy of a functional group or to display multiple, unique molecules on the NP surface with control of the orientation and intermolecular distance. This challenge was addressed with the construction of a spatially addressable, self-assembling DNA origami nanocage that encapsulates gold nanoparticles and interrupts its surface symmetry.

4.2. Introduction

A critical challenge in nanoparticle (NP) surface functionalization is to label the NP surface with a single copy of a functional group or to display multiple, unique molecules on the NP surface with control of the orientation and inter-molecular distance. Recently, a few elegant strategies have been developed to obtain nanoparticles with stoichiometric control of the number of attached ligands. These methods include the use of gel electrophoresis to isolate gold nanoparticles bearing discrete numbers of DNA oligonucleotides,[1,2] micron-sized beads with a large surface area to minimize the contacts between small nanoparticles to create monofunctional DNA-nanoparticle conjugates,[3,4] an ordered monolayer coating to create polar singularities on the nanoparticle surface,[5] and a stepwise surface-encoding protocol to assemble symmetric

and asymmetric nanoclusters.[6] Nevertheless, the challenge of achieving a single NP with multiple molecules arranged at spatially addressable locations on the particle surface still remains. By transforming the symmetric surface of a spherical nanoparticle into an asymmetric surface, control over the functionalization can be achieved.

Here we demonstrate the application of spatially addressable, self-assembling DNA origami nanocages to encapsulate gold nanoparticles and interrupt the symmetry of their surface (Figure 1). DNA origami is a technique in which a long, single strand of genomic DNA is folded into a variety of predesigned shapes through the direction of approximately 250 short, staple strands.[8-17] Due to the unique sequence of each staple strand, DNA origami structures possess addressable binding sites with ~ 6 nm resolution and have been utilized as templates to direct the assembly of metal nanoparticles, carbon nanotubes and biological materials.[18-29] Figure 1B and C illustrate the design and dimensions of the DNA origami cage. The structure is based on the honeycomb lattice design demonstrated by Shih and co-workers[9], with modifications that result in a 10 nm x 10 nm (cross section) inner cavity, an ideal size for the encapsulation of nanoparticles. Specifically, the cage contains 124 parallel helices; the length of each is ~6 full helical turns with two crossovers connecting adjacent helices. The outer dimensions of the cage are 41 nm × 24 nm × 21 nm, with inner cavity dimensions of 10 nm × 10 nm × 21 nm. (see supporting information for details of the design, strand sequences and experimental methods). To prevent end-to-end stacking, two thymine nucleotides were added to staples strands located at outer extremities of the helices. The DNA origami cage was annealed and subsequently purified using agarose gel electrophoresis (a typical gel image is shown in Fig. S1) and after using uranyl formate for negative-staining, transmission electron

microscopy (TEM) was used to visualize the purified DNA origami cage. TEM images (Fig. 1D) confirm the formation of DNA origami cages with nearly 100% yield, and reveal that the structures adopt one of two possible orientations when deposited onto the TEM grid (Fig. 1E).

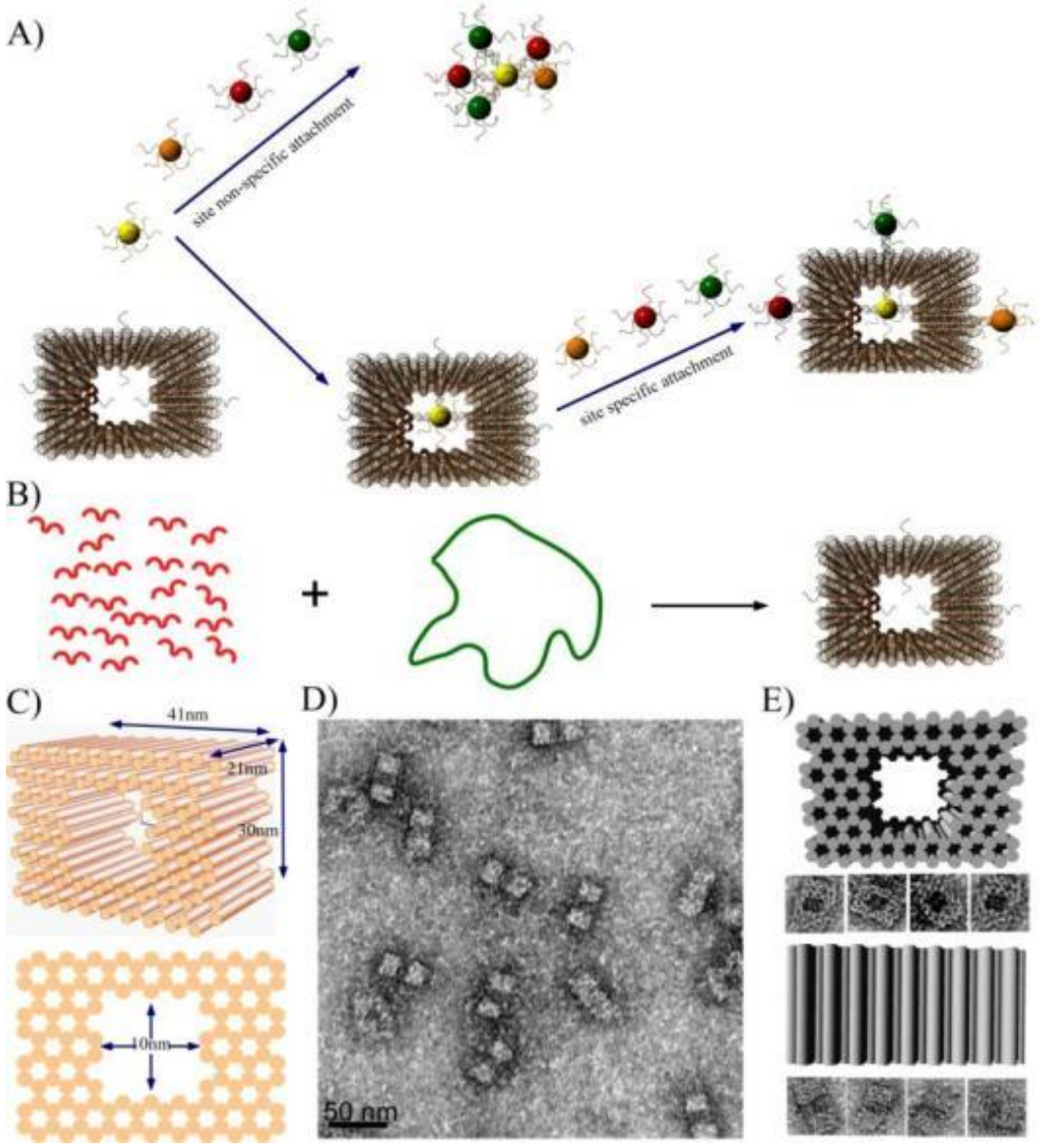


Figure 4.1. Diagrams and TEM images of DNA origami cages. A) Illustration of the challenge of assembling discrete nanoparticle architectures with site-selective functionalization of the spherical nanoparticle surface. B) The formation of a DNA origami cage using short staple strands (red) to direct the folding of single stranded M13 DNA (green loop). Single-stranded capture strands extend in or out of the DNA cage at specific positions. C) 3D and side view of the DNA origami cage with 41 nm×30 nm×21 nm outer dimensions and 10 nm×10 nm×21 inner dimensions. D) Low-magnification TEM image of a DNA origami cage (scale bar: 50 nm). E) High-magnification TEM images of DNA origami cages displaying two different orientations.

4.3 Results and Discussion

After verifying the nanocage had formed, the encapsulation ability of the cage was tested using 5 nm, spherical AuNP. The surfaces of AuNPs were covered with ssDNA (15 nucleotides in length) that was designed to hybridize with complementary probes displayed on the inner surface of the origami cage cavity. To compare the capture efficiency of 5 nm AuNP inside and outside of the cage, a single capture strand (15-nt ssDNA: 5'-AAAAAAAAAAAAAAA-3') was projected from both surfaces (Fig. 2A and Fig. S11). DNA cages (containing capture probes) were prepared by mixing the capture strand (purified by PAGE) with the M13 scaffold and unpurified staples strands with a 1:1:10 ratio, and subsequently annealing the mixture (see SI for experimental methods). 5 nm AuNPs (covered with ssDNA complementary, see SI for detailed information) were mixed with the preassembled cages with a ratio of 1:2.5, and slowly annealed from 40℃. DNA cages with captured NPs were then purified by agarose gel electrophoresis and imaged by TEM (Figure 2A, S4, and S14).

Analysis of TEM images reveals that AuNPs are captured by single probes located on the outside cage surface with a much higher efficiency (> 90%) than probes placed on the inside of cages (~36%). The lower efficiency of inner encapsulation may be due to the increased steric hindrance and limited space within the cavity. A strong, electrostatic repulsion between the DNA-AuNP conjugate and the inside walls of the DNA cage will also affect the efficiency of AuNP loading. The images show that a single probe does not hold the AuNP exactly in the center of the cavity and most of the AuNPs can be seen close to the opening of the channel, especially when viewed from the side (see additional images in Fig. S4).

To improve the encapsulation efficiency of the inner cavity, several (2-4) capture probes were added to the inner surface. When two capture strands were added to opposing, inner cavity walls, the loading efficiency increased dramatically to ~98% and nanoparticles were fixed in the center of the cage more often (Fig. 2B). When three or four capture strands were extended from various inner faces, 5 nm AuNPs were firmly anchored in the center of the cavity with loading efficiencies reaching nearly 100% (Fig. 2C and 2D). Based on these results, three inner capture probes were utilized for all subsequent experiments described below. Cryo-EM imaging (without negative staining) was used to reconstruct a 3D tomogram of the DNA cage containing a 5 nm AuNP. Figure 2E shows an example of the cryo-EM image and Figure 2F shows Z projections of the completely reconstructed tomogram from two different views of the structure, further verifying its 3D geometry.

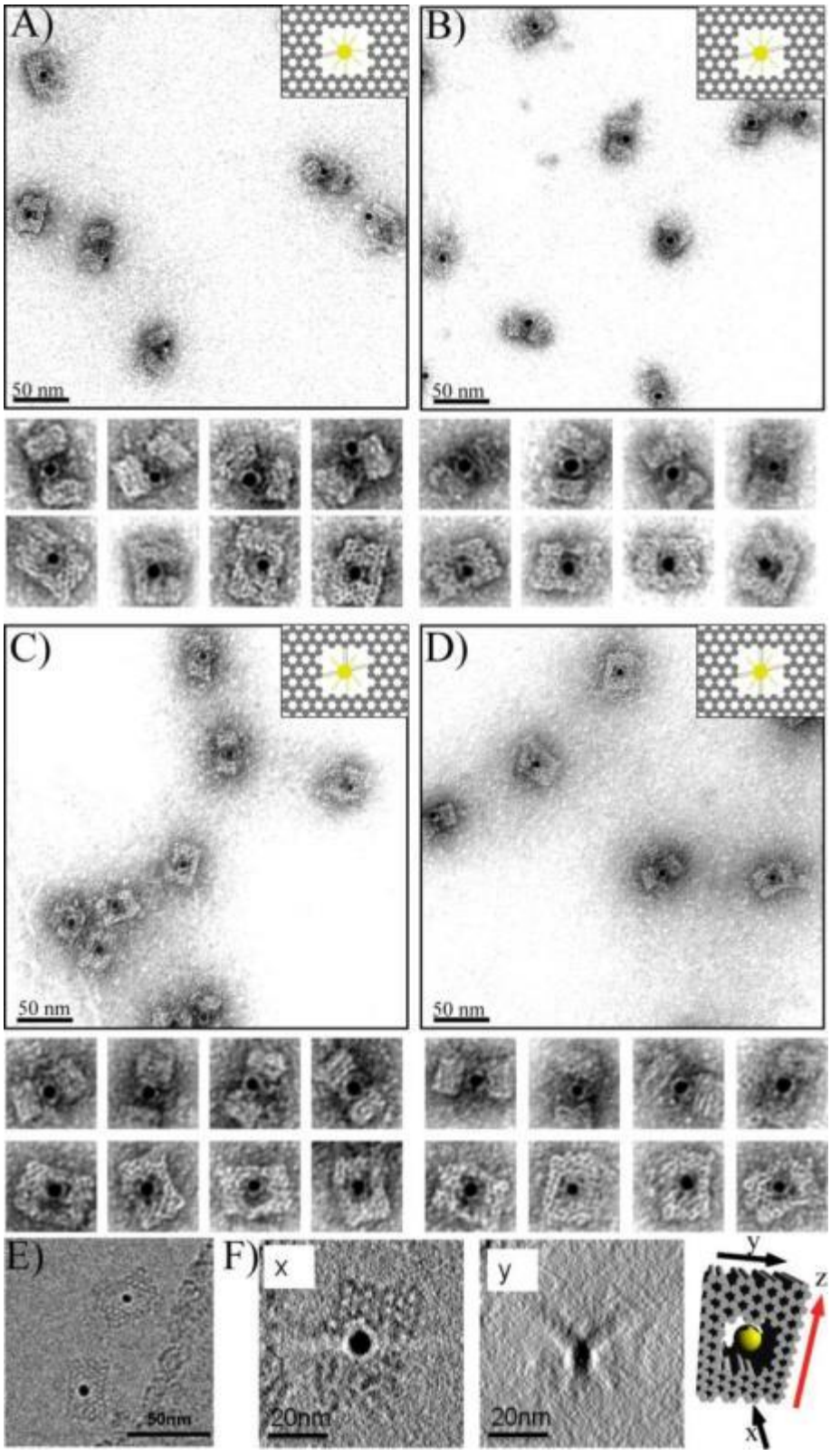

A)
50 nm
B)
50 nm
C)
50 nm
D)
50 nm
E)
50nm
F)
x
20nm
y
20nm
y
z
x

Figure 4.2. Schematic A–D) TEM images of DNA cages with 5 nm AuNPs inside, encapsulated using different numbers of capture strands: A) one, B) two, C) three, and D) four capture strands. The samples were negatively stained with uranyl formate to improve the imaging contrast. E) A typical cryo-EM image without negative stain showing the DNA cage with a 5 nm AuNP encapsulated inside. F) The Z projections of the complete reconstructed cryo-EM tomogram from two different views. Planes x and y correspond to the black arrows shown on the model to the right; x corresponds to the top view easily seen in the untilted micrograph, whereas y is the face coming into view as the sample is tilted. The bold red arrow shown on the model indicates the rotation axis.

The ability of the nanocage to discriminate between nanoparticles of various sizes was tested; 10 and 15 nm AuNPs with the same ssDNA on their surface were synthesized and used for study. We anticipated that the 10 nm AuNP would encounter some degree of steric hindrance, but would ultimately be encapsulated, and the 15 nm AuNP would be too large to fit within the cavity. The 10 nm AuNPs were successfully encapsulated by the cage with ~93% efficiency (slightly lower than for 5 nm AuNPs) and most particles were fixed in the center of the cavity (Fig 3A and S8). The lower yield is reasonable because 10 nm AuNPs that are covered with 15 nucleotide long ssDNA have an expected hydrodynamic diameter > 10 nm, resulting in a significantly crowded inner cavity. TEM images also show that for 10 nm nanoparticles, the cage is subject to a certain degree of deformation as a result of the relative dimensions of the cavity and the particle, especially when viewed from the side. However, the DNA cage structure possesses enough mechanical flexibility to accommodate a foreign object with slightly larger dimensions than the inner cavity.

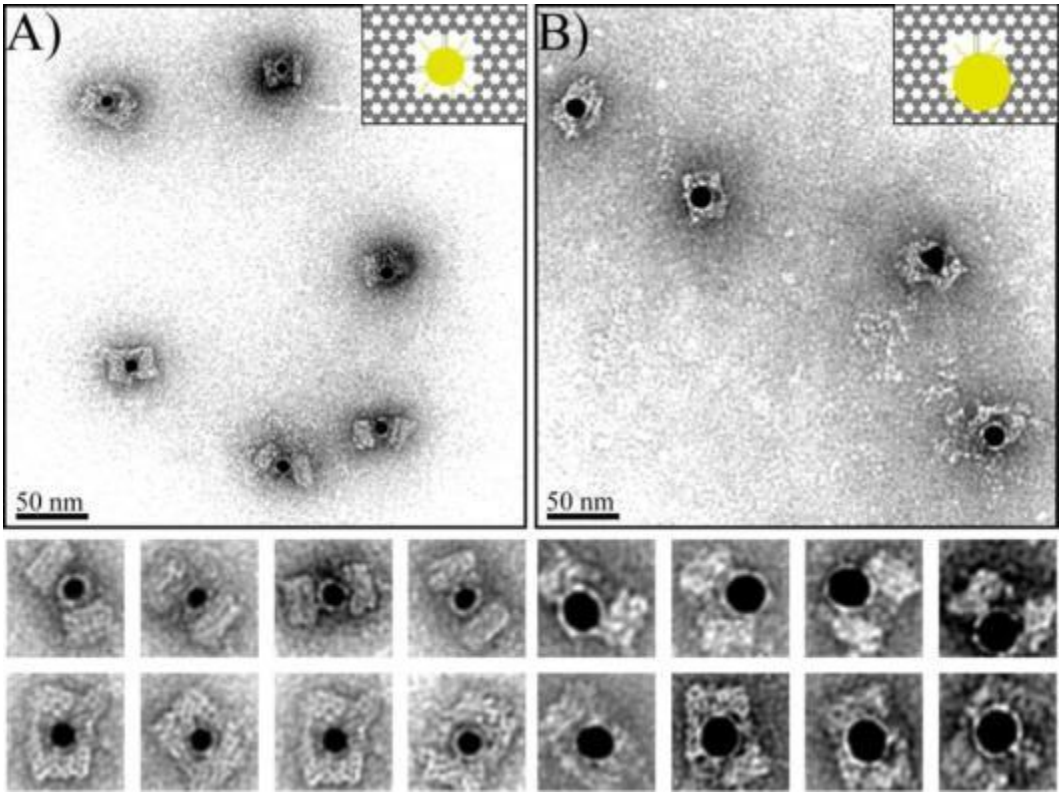


Figure 4.3. TEM images of DNA cages encapsulating 10 nm and 15 nm AuNPs using three capture DNA strands. A) 10 nm AuNP; B) 15 nm AuNP. The samples were negatively stained with uranyl formate before imaging.

When the cage was loaded with 15 nm AuNPs, the encapsulation efficiency was reduced to 68% (Fig. 3B and S9). To accommodate the larger size AuNPs, the DNA cage had to undergo severe deformation and the TEM images illustrate how 15 nm particles are generally located at one end of the cage with most of the particle surface still exposed to the outside. Although 15 nm particles are too big to fit within the cavity, the relatively high yield of attachment is probably a result of displaying three capture strands inside the cage, providing a strong enough binding force to hold the AuNP and DNA cage together. TEM images reveal the intrinsic flexibility of DNA nanostructures that allows the cage to

bend and make room for the large NP, responding to the external, enthalpic requirement to maximize the DNA hybridization.

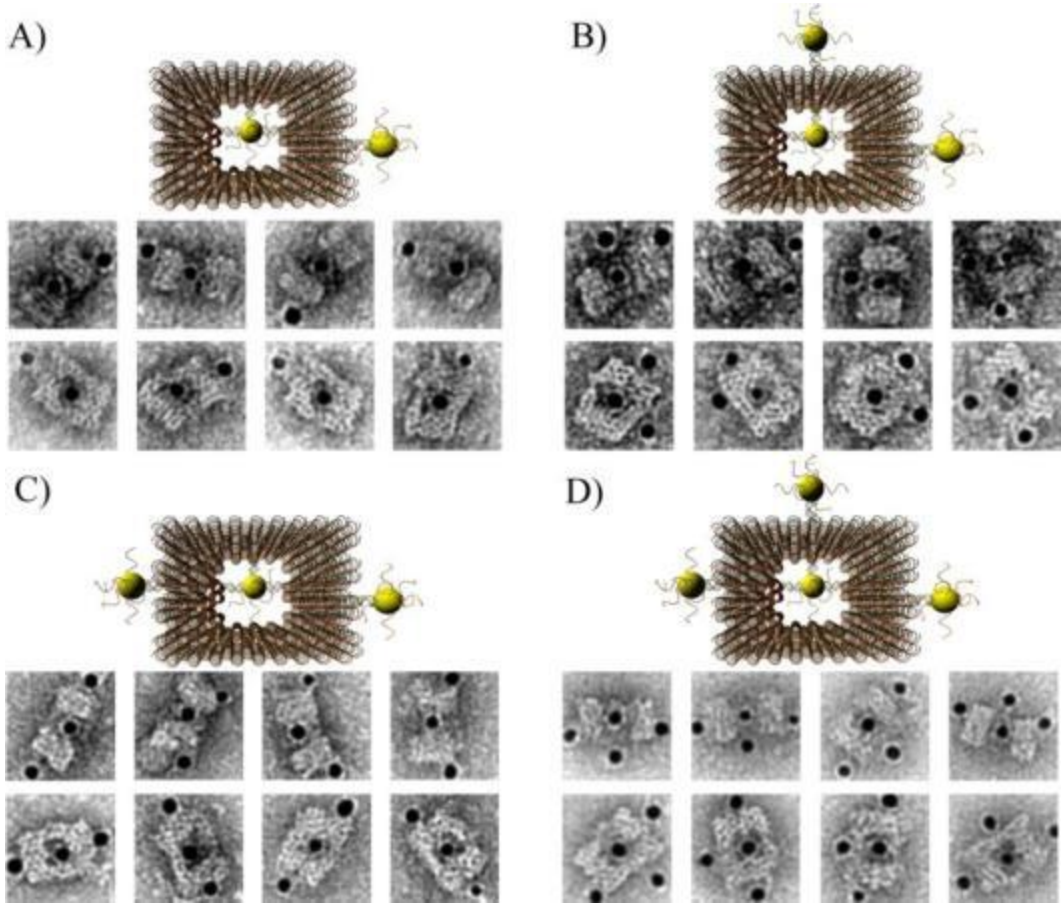


Figure 4.4. TEM images of DNA cages with one 5 nm AuNPs inside, and various numbers of 5 nm AuNPs outside. The samples were negatively stained with uranyl formate before imaging.

The outer surface of the DNA origami cage was modified with probes at addressable locations to capture other particles. We utilized this modification to demonstrate how the symmetry of a spherical nanoparticle surface can be broken; a 5 nm AuNP was encapsulated inside the DNA origami cage and a discrete number of 5 nm

AuNPs were attached to defined positions on the outside surface of the cage. To achieve this, single stranded capture probes were incorporated at unique sites on the outer surface of the cage and 5 nm AuNPs, functionalized with sequences complementary to the capture strands, were recruited. The molar ratio between the origami cage containing the particle inside and the external particle is 1:3. The assembled structures were purified by gel and imaged using TEM. Figure 4A shows a DNA cage containing a 5 nm AuNP inside, and a separate 5 nm AuNP outside. The yield of fully assembled structures with AuNPs inside and outside is ~85%. Additional AuNP structures with unique geometries were produced when cage structures with 5 nm AuNPs encapsulated inside were modified at various positions on the outside surface with two or three 5 nm AuNPs. The TEM images shown in Fig. 4B, C and D demonstrated designs with 90° and 180° between the particles, with formation efficiencies of ~80%, ~84% and ~35% respectively. Table 1 summarizes the AuNP loading efficiency for all the constructs described here.

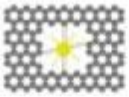
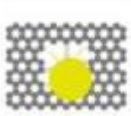
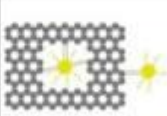
structure					
loading efficiency	36.2%	97.9%	96.9%	99.5%	92.7%
structure					
loading efficiency	67.8%	85.1%	80.0%	84.3%	36.7%

Figure 4.5. Efficiency of DNA cage–AuNP structure assemblies.

4.4. Materials and Methods

See APPENDIX C

4.5. Conclusions

In conclusion, we have demonstrated the ability of a DNA origami nanocage to encapsulate gold nanoparticles of various sizes. The spatially addressable surface of the DNA origami capsule presents an opportunity to interrupt the symmetry of spherical nanoparticles and provides a platform for further functionalization. Recently, Sleiman and co-workers constructed a DNA nanotube with alternating larger and smaller capsules for the size-specific encapsulation of gold nanoparticles (AuNPs), with selective release of the particles in response to externally supplied DNA. [30] By integrating the above strategies, the programmability of DNA cages and tube constructs can be utilized for a wide variety molecular encapsulation and release tasks, such as site specific protein bioconjugation, which may lead to an artificial structural platform for engineering novel bio-inspired, biomimetic and biokleptic materials.

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Chapter 5

DNA Origami Templated Self-assembly of Discrete Length Single Wall Carbon Nanotubes

Used with permission from Zhao, Z; Liu, Y.; Yan, H.: DNA Origami Templated Self-assembly of Discrete Length Single Wall Carbon Nanotubes, *Org. Biomol. Chem.*, **2013**, 11, 596–598.

5.1. Abstract

Constructing intricate geometric arrangements of components is one of the central challenges of nanotechnology. Here we report a convenient, versatile method to organize discrete length single-walled carbon nanotubes (SWNT) into complex geometries using 2D DNA origami structures. First, a size exclusion HPLC purification protocol was used to isolate uniform length, SWNTs labeled with single stranded DNA (ssDNA). The nanotube-bound ssDNA are composed of two domains: a SWNT binding domain and a linker binding domain. Although initially bound to the SWNTs, the linker domain is displaced from the surface by the addition of an external ssDNA linker strand. One portion of the linker strand is designed to form a double helix with the linker binding domain, compelling the DNA to project away from the SWNT surface. The remainder of the linker strand contains an ssDNA origami recognition sequence available for hybridization to a DNA origami nanostructure. Two different 2D DNA origami structures, a triangle and a rectangle, were used to organize the nanotubes. Several arrangements of nanotubes were constructed, with defined tube lengths and inter-tube angles. The uniform tube lengths and positional precision that this method affords may have applications in electronic device fabrication.

5.2 Introduction

Single-walled carbon nanotubes are among the most promising nanomaterials with projected uses in electronic, sensor, and biomedical applications.[1-2]

Compared to conventional semiconductor materials, they exhibit superior properties such as higher conductance, greater mobility, and chemical inertness, making them ideal components of field-effect transistor devices (FETs).[3-4] There have been many advances in the fabrication of 1D SWNT FET devices, and recently there were several reports of 2D SWNT assemblies.[5-6] Winfree and coworkers used LNA linkers to assemble SWNT cross junctions on rectangular DNA origami, where one device exhibited stable field effect transition behavior.[5] Törmä and coworkers used biotin-streptavidin interactions to create similar SWNT cross junctions on rectangular DNA origami.[6] However, neither method takes advantage of the convenience and versatility of unmodified DNA-DNA hybridization for nanotube organization. In addition, different lengths of SWNTs exhibit unique physical and electrical properties including absorbance, fluorescence and electric conductivity,[7-9] thus, for FET device applications it was imperative to develop protocols to separate heterogeneous populations of nanotubes.

With agitation, single stranded DNA will attach to SWNTs resulting in nanotube dispersion.[10-11] The strong Pi-Pi interaction between the bases within the DNA strand and the sidewall of the SWNT causes the DNA to wrap around the nanotube, forming the SWNT-DNA complex. It has been shown that certain DNA sequences can be used to separate different types of SWNTs,[12] and several methods have been used to separate the tubes based on length, including gel electrophoresis,[13] centrifugation[14] and size exclusion HPLC.[15] Zheng et al. reported a size exclusion HPLC protocol, with 200 nm,

100 nm, and 30 nm pore size columns arranged in series to separate DNA labeled SWNTs with lengths ranging from 500 nm to 1000 nm. Here we use a similar protocol to separate the DNA labeled nanotubes into different populations for subsequent organization by DNA origami structures.

DNA nanotechnology represents a massively parallel platform to assemble and organize heterogeneous nanoscale components.[16] Designing and constructing DNA nanostructure scaffolds is quite simple because of the reliability of DNA base pair interactions, the predictable structure of DNA double helices, and the self-assembling properties of single stranded DNA. The development of the DNA origami method has allowed the construction of arbitrary 2D and 3D nanoscale shapes that can be chemically modified at hundreds of addressable positions.[17-19] Towards electronic device applications, DNA origami structures have been used to pattern metal nanoparticles, semiconductor nanoparticles, and carbon nanotubes.[20-21] Here, 2D DNA origami triangles and rectangles were used to capture 150 nm, HPLC purified, DNA labeled SWNTs . The uniform length nanotubes were organized into several patterns, with control over the inter-tube angles.

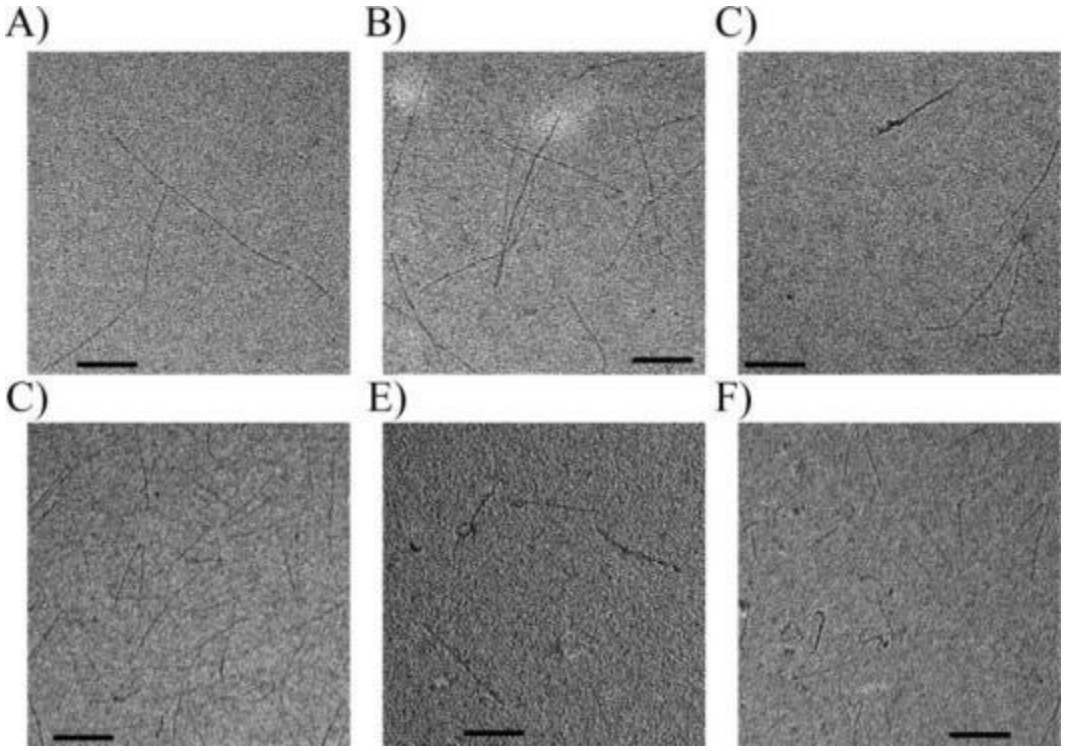

Figure 5.1. DNA labeled SWNTs separated by HPLC. A), B), C), D), E), F) are TEM images of HPLC separated fractions with length 450, 300, 200, 170, 150 and 100nm. (scale bar:100nm).

5.3 Results and Discussion

5.3.1 HPLC separation of SWNTs

The single stranded DNA label is composed of two domains, a nanotube binding domain with a repeating GT sequence that exhibits strong binding with the SWNT sidewalls, and a capture domain with a sequence selected for recognition by an external, ssDNA linker strand. The ssDNA label was mixed with an aqueous solution of SWNTs and sonicated for 2h at 9W. The solution mixture was subsequently centrifuged to remove aggregated bundles, and supernatant was injected into an HPLC system that was configured with three size exclusion columns connected in series (0.2mL/min, 1×TBS

buffer, UV-Vis detection at 260nm). A typical HPLC profile is shown in Figure S1; several fractions were collected and examined with a transmission electron microscope. The TEM results (Figure 1) revealed that the SWNTs were clearly separated by length, with each fraction containing a single SWNT population of uniform length (ranging from 100 nm to 500 nm).

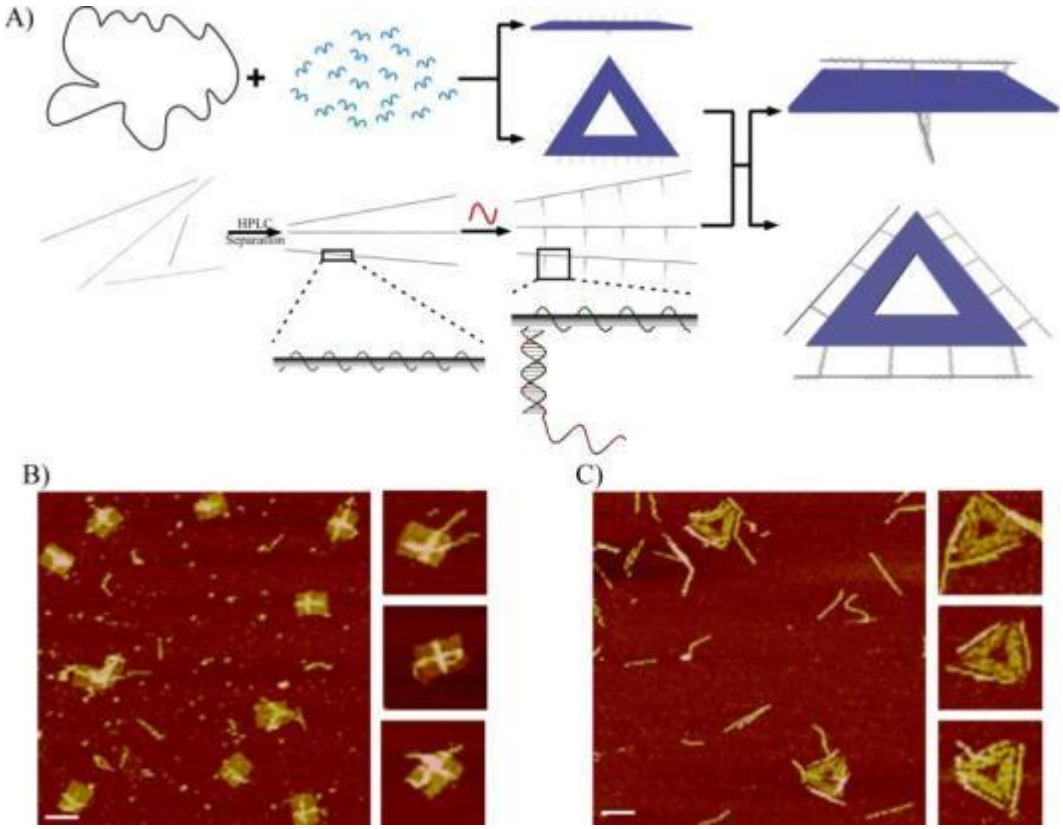

Figure 5.2. A) DNA origami-SWNT co-assembly schematic B), C) AFM images of SWNTs organized by rectangular origami and triangular origami, respectively. (scale bar: 100nm)

5.3.2 DNA origami organization of uniform length SWNTs

In principle, SWNTs could be labeled with ssDNA that contains a domain for direct hybridization to a DNA origami structure. However, this would require that single

stranded overhangs (probes) from the DNA origami structure could efficiently displace the corresponding DNA from the surface of the nanotube sidewall. Although desorption of ssDNA from SWNTs has been reported, the process is prohibitively slow.[5] A more plausible alternative, and the one employed here, is to use an intermediate single stranded DNA linker molecule. One domain of the linker has a sequence complementary to part of the ssDNA label (bound to the nanotube surface), and the other contains a sequence that will hybridize to a DNA origami probe. The addition of excess single stranded linker to a solution of ssDNA labeled SWNTs displaces part of the ssDNA label from the nanotube surface, forming a DNA double helix with the linker strand. Compared to the first scenario, this process is expected to be more kinetically favorable. After purification, the unbound single stranded region of the linker strand is captured by DNA origami probes and secured in a fixed position.

We selected 150 nm long SWNTs (shown in Figure 1E) for subsequent experiments. The HPLC isolated SWNTs were incubated with a ten-fold excess of linker strand for 48 hours so that the linker binding domain of the ssDNA label would be displaced from the surface of the nanotube. A microcon centrifugal filter was used to remove excess linker strand from the solution.

Meanwhile, the triangular and rectangular DNA origami structures, with several linker probes displayed from their surfaces, were prepared. Initially, several different probe sequences were evaluated including a poly T and several random sequences, and the results show that the poly T probe resulted in a much higher capture yield (shown in Figures S2 and S3). Rectangular origami with two perpendicular rows of poly T linker probes were prepared and incubated with the purified, DNA labeled, 150nm length

SWNTs for 30 minutes at room temperature. The atomic force microscope (AFM) images shown in Figures 2B and S4 confirm 50% yield of origami bound nanotubes. Longer incubation times induced aggregation, possibly because the length of the SWNTs is longer than the DNA origami structures and may increase the potential to crosslink different origami. To further evaluate this, 200 nm, 350 nm and 450 nm SWNTs were also considered. The results show (Figures S5-7) that the longer tubes tend to form aggregated structures. With the extra linker strands displayed from the surface of the tubes, the chance to cross link origami is increased. Finally, triangular origami structures with one row of poly T probes along each arm (3 rows total) were prepared and incubated with the purified DNA labeled SWNTs for 15 minutes at room temperature. The AFM images shown in Figures 2C and S8 reveal approximately 40% yield of origami bound nanotubes. Despite the reasonable yield, it is obvious from the AFM images that many free SWNTs remained and further purification is needed.

5.4. Materials and Methods

See APPENDIX D

5.5. Conclusions

In summary, we demonstrated that DNA origami nanostructures can be used to arrange SWNT of fixed length into complex, 2D patterns. In addition to dispersing SWNTs in aqueous solution, we developed a strategy in which ssDNA molecules can serve as efficient labels of SWNTs, for subsequent recognition by DNA origami probes. Our method of recognition is based on DNA-DNA hybridization, a very convenient interaction to employ. Several arrangements of nanotubes were constructed, with defined

tube lengths and inter-tube angles. The uniform tube lengths and positional precision that this method affords may have applications in electronic device fabrication.

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Chapter 6

DNA Origami Cage Trapping Enzyme: Protection and Boosting Enzyme Activity

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6.1. Abstract

Intracellular compartments are a key factor in cell metabolism.[1-4] These evolved confined compartments ensure efficient intermediate transfer for slow turnover rates reaction, elimination competing metabolic reactions, and toxic intermediates. Construction of functional enzyme complexes that are confined in similar way remains challenging.[5-8] Here we utilize spatial addressable DNA Origami structure to encapsulate enzymes to mimic compartment phenomenal. Enzymes, which are chemically modified with ssDNA, can be assembled into DNA Origami cage with high yield. The DNA Origami 'shell' can protect internalized enzyme from degradation factors, such as protease, metal ions and BSA. Furthermore, internalized enzymes showed enhanced activity, which resulted from 5-10 folds increase of Vmax value, compared with fresh enzymes. With DNA Cage system, cascades enzymes can be assembled together to increase intermediate transfer efficiency.

6.2. Introduction

Biological complexity requires varying degrees of organization. One example is that enzymes are spatially organized to perform catalytic reactions.[1-4] To achieve this, metabolism pathway enzymes are confined inside compartment, including membrane bound organelles, bacterial microcompartments, multi-enzyme complexes, and others.[9-

[10] Nature evolved microcompartments strategies brings several advantages. First of all, the confined environment will enrich the intermediate concentration for cascades enzyme system, which will significantly increase the overall reaction rate. Secondly, intermediate produced in metabolism pathways can participate in many competition reactions, confined environment can reduce the possibility for any other reactions. Thirdly, metabolism pathway may generate toxic intermediate, which will affect the biology behavior without compartment.

Inspired by nature's compartment system, researchers tried to mimic confined environment in vitro with liposome, capsid and polymer shell, to study enzyme activity.[5-8] Liposome is lipid molecule closely compacted structure, and molecules cannot free diffuse inside. To connect inside with outside environment, channel membrane proteins were used, and after encapsulate enzymes inside, there is almost no change for the internalized enzyme activity; Capsid is protein shell for virus, composed with subunit proteins. Different from liposome, capsid structure has many small pores in between subunits, which makes them a good candidate for mimicking microenvironment. Comellas-Aragones et al.[6] tried to encapsulate HRP inside capsid and found the HRP turnover number increased two folds. However capsid encapsulate enzyme inside through random diffusion before capsid formation, which makes the system cannot control the number and ratio of encapsulated enzymes. Rudiuk et al.[13] tried to wrap Lambda DNA on enzyme surface, which results in several folds increase for Kat value. Liu et al.[7] tried to encapsulate cascades enzymes inside polymer cavity and also found several folds enhancement for the enzyme activity.

Since its invention, DNA origami has attracted more and more attentions.[14-20] With spatially addressability, DNA Origami has been used for arrangement of nanoparticles, nanowires and biomolecular. [21-23] Fu et al. [23] showed that cascades enzymes can be assembled on planar DNA Origami with controlled distance, which resulted in different cascades activity. Here we constructed DNA Origami cage, mimicking of compartment, to encapsulate enzymes inside and study their activity and used DNA Origami cage to serve as protection shell for internalized enzyme against protease and BSA.

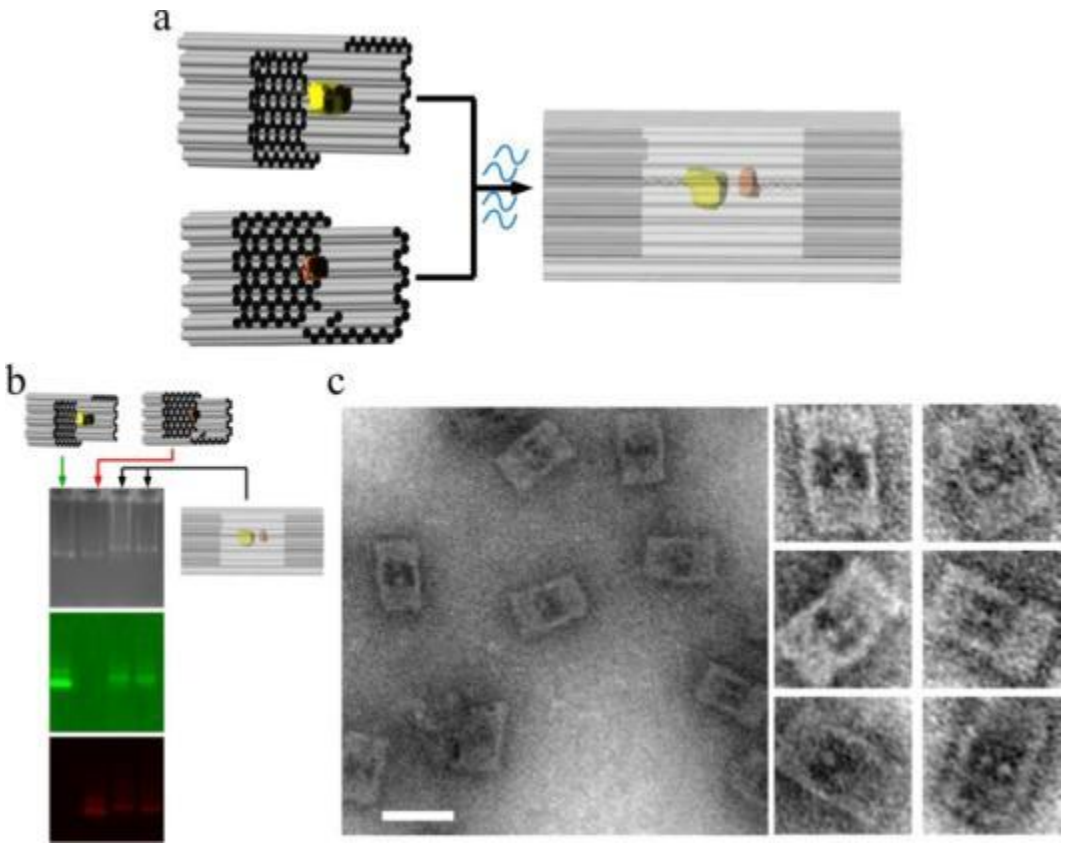

Figure 6.1. Cascades enzyme internalization inside DNA Origami cage. a) Schematic showing assembly of enzyme cascades, GOx and HRP inside DNA Cage; b)

Fluorescence agarose gel characterization (GOx labeled with Cy3 and HRP labeled with Cy5); c) Negative stained TEM image (zoom in and zoom out) for enzyme complex inside DNA cage (Scale bar: 50nm);

To achieve high assembly yield, two half DNA Origami Cage were designed to assemble with two different cascades enzyme, Glucose Oxidase (GOx) and Horseradish Peroxidase (HRP), then linker was used to link two half cage structure to form DNA cage structure with cascades enzyme inside cavity, as shown in figure 1a. SPDP method was applied to conjugate ssDNA on enzyme surface, as reported before. We also tried to optimize the assembly yield by optimize enzyme DNA conjugation process and purification process with high concentration of salt to wash off free ssDNA. Two different types of DNA half cage, opened side wall and closed side wall, had been designed and assembled with single GOx enzyme, as shown in SI. Transimittion Electron Microscopy (TEM) resulted showed that closed side wall design could achieve higher assembly yield, 77%. The overall dimension of the whole cage structure is 54 nm × 27 nm × 20 nm, while the cavity dimension is 20 nm × 20 nm × 20 nm. Agarose gel electrophoresis (AGE) and TEM had been applied to characterize the formed DNA Origami structure with internalized cascade enzyme as shown in figure 1b) c). GOx and HRP were labeled with Cy5 and Cy3 respectively, and AGE image showed that after the formation of dimer, the origami band mobility is slow compared with monomer, and dimer band showed two types of fluorescence signal, which proved that two enzymes are inside DNA cage structure. Negatively stained TEM showed high assembly yield, as shown in figure 1c) with both zoom in and zoom out image.

6.3 Results and Discussion

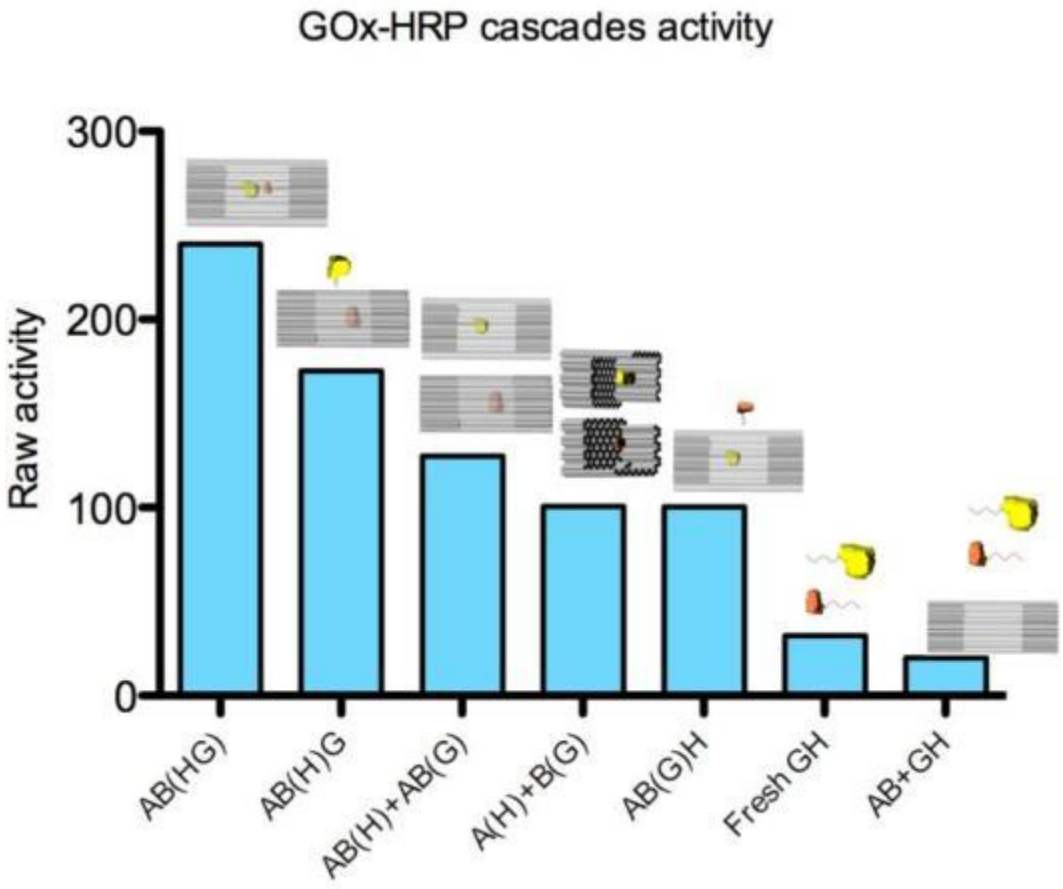

Figure 6.2. Different GOx-HRP cascades enzyme system raw activity.

Cascade enzyme assembled by DNA Cage with different arrangement had been tested as shown in Figure 2. Firstly, with the same annealing process, the two enzymes lost their activity, while with the incubation of DNA cage, there was half activity retained compared with fresh enzyme, which resulted from DNA cage structure can stabilize enzyme structure. Secondly, we observed 10 folds enhancement after encapsulate both enzymes inside cage structure, compared with fresh free enzymes. At the same time, if two enzyme were assembled separately inside and outside of cage structure, the activity for the cascade decreased, especially arranged HRP outside of cage, which means the

high activity for cascade inside cage may resulted from two factors, the close distance after encapsulation, and inside DNA cage environment could enhance enzyme activity, especially for HRP enzyme. Thirdly, we also observe high activity for mixture of full cage or half cage encapsulated with single enzymes, which is 5 folds increasing compared with fresh free enzymes. This result demonstrated that DNA cage structure can enhance internalized enzyme activity. To test our hypothesis, we measured the enzyme catalytic kinetics for 5 different single enzymes internalized inside DNA cage, shown in figure 6.3.

	Enzyme	GOx	G6pD		LDH	HRP		MDH
	Substrate	Glucose	NAD+	G6p	NADH	H2O2	ABTS	NADH
Vmax	Free enzyme	1	1	1	1	1	1	1
	Cage enzyme	5.4	4.8	3.6	4.2	9.1	6.8	7.5
Km	Free enzyme	1	1	1	1	1	1	1
	Cage enzyme	0.5	1.2	1.4	2.4	1.9	0.9	1.1

Figure 6.3. Single enzyme kinetic data for enzyme encapsulated inside DNA Cage, normalized with fresh free enzyme.

DNA cage structure was applied to assemble with five single enzymes, and their Km, Vmax value was calculated through titrating their substrate concentration. After normalized with their fresh free enzyme, Km value did not change too much, all in the range 0.5-2, which demonstrated DNA cage environment cannot affect substrate diffusion too much, which usually reduce the substrate diffusion. However, in the case of Vmax value, they all increased from 5-10 folds. For GOx, Glucose 6-phosphate dehydrogenase (G6pD) and Lactate dehydrogenase (LDH), which had pI value less than 8, their Kcat value increased around 5 folds, and in the case of HRP and Malate dehydrogenase (MDH), which had pI value higher than 8.5, their Kcat value increased around 10 folds. We proposed DNA cage structure has high mass of phosphate and charge density, which may result in the increasing of Kcat value. To test our hypothesis, we designed three different DNA cage structures with different DNA density to investigate inside enzyme behavior.

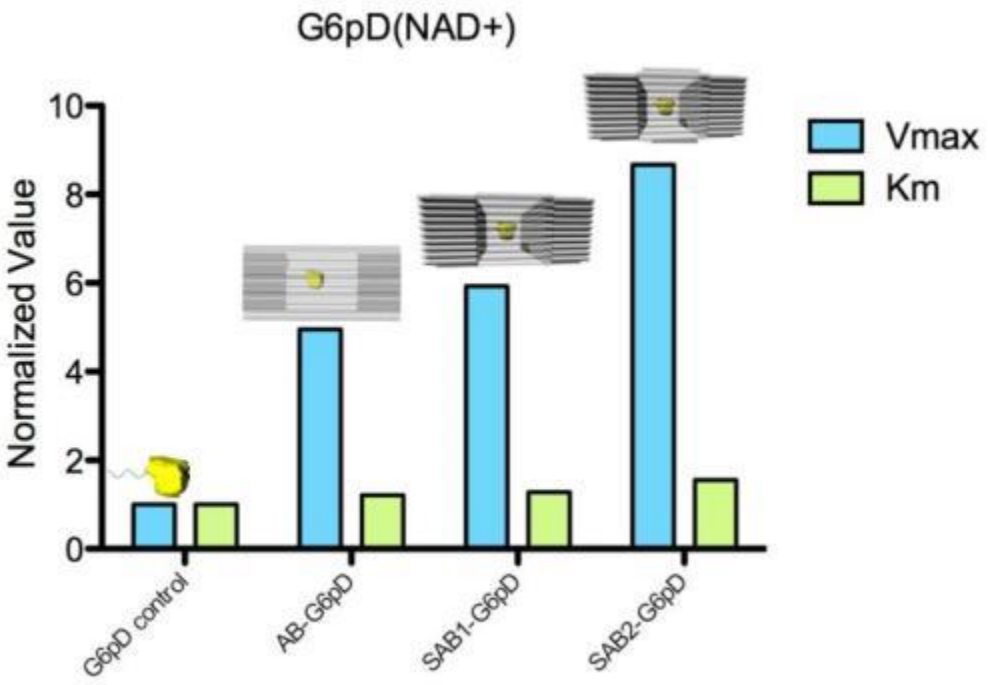

Figure 6.4. Single enzyme kinetic data (Vmax and Km, measured with different concentration of NAD+) for G6pD encapsulated inside different DNA Origami Cage.

As shown in figure 3, three different DNA cage structures were designed. The first origami designed with honeycomb unit and one DNA layer as side wall, the second origami designed with square lattice unit and one DNA layer as side wall and the third origami designed with square lattice unit and two DNA layers as side wall. The first structure had many large pores in z direction, 2.5nm in diameter, and small pores, 0.5-1nm size, in between DNA helix. The second and third structures only had small pores in between DNA helix, while the third structure had smaller pore with two layers for the sidewall. From the first structure to the third structure, the DNA density increased, and the pore size decreased. Three DNA cage were assembled with G6pD, after normalized enzyme kinetic data with fresh free G6pD, the Km value increased with the DNA density

increasing, which may result from decreasing of pore size could better prevent substrate diffusion. In the case of Vmax value, with increasing of DNA density, the Vmax value increased a lot, from 5 folds to 8 folds, which proved that the increasing of Vmax value resulted from the DNA environment. Previously, researchers found that crowded environment could change Kcat value for enzymes, through which enzymes can be stabilized inside crowded environment, while charged environment could also improve enzyme activity by increasing Kcat value. In addition, previous research proved that PO_4^{3-} was an ideal kosmotropic anion, [24-25] which could improve protein stability through accumulating high density water for protein. DNA cage structure had high density of PO_4^{3-} backbone and charge, in which 50 nm × 27 nm × 20 nm space has 28000 DNA nucleotides, which can be converted to 7M phosphate backbone negative charge and 250uM 6MD molecule crowed environment, which cannot be achieved with conventional method. To test our hypothesis, high concentration of glucose 6-phosphate had been used to incubate with free HRP, and its activity was enhanced up to 15 folds, as shown in SI. Furthermore, we believed that this high density of charge, PO_4^{3-} and mass can be supplied to mimic in vivo environment to study biomolecular behavior.

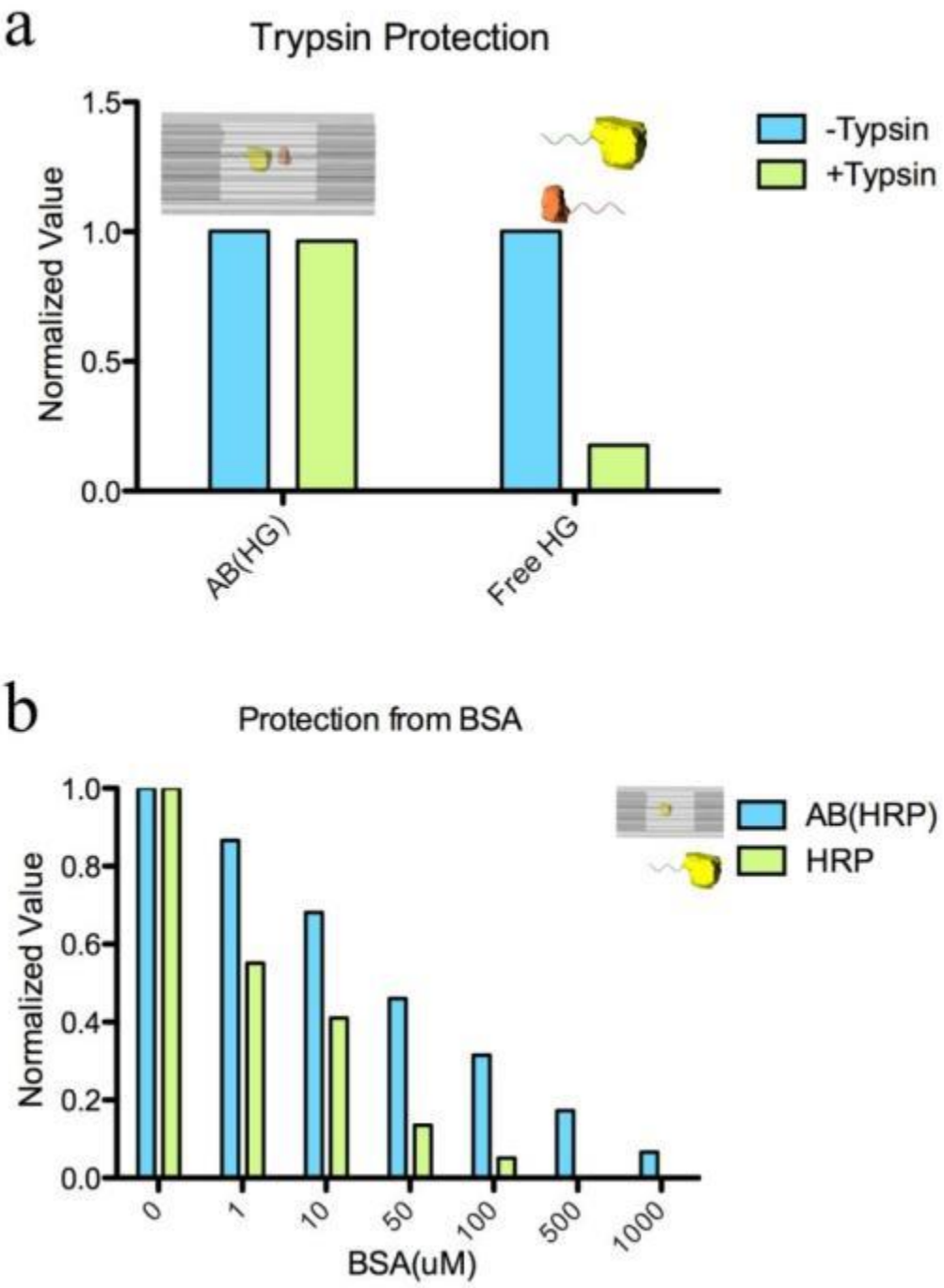

Figure 6.5. DNA Cage served as protection shell for internalized enzyme against a) Trypsin and b) BSA.

DNA cage structure could serve as protection shell for internalized enzymes to protect against many factors, including protease and BSA, [26] as shown in figure 4. After 24h incubation with 1000 times amount of Trypsin protease, DNA cage protected HRP enzyme activity did not change, while the free enzyme activity decreased around 80%. Bovine Serum Albumin (BSA) exists inside blood, served as cleaner, which can bind with almost everything, so BSA is a barrier for drug delivery. In figure 4b, we incubated enzyme with different concentration of BSA from 1uM to 1mM, and normalized enzyme activity with their BSA free group individually. Although DNA cage encapsulated HRP activity also decreased, but it can also withstand 50% activity at 50uM BSA concentration, which is close to the BSA concentration in blood, while the free enzyme group almost lost its activity. The decrease of DNA cage internalized enzyme group may result from the viscosity increase and the decrease of substrate, H_2O_2, which can be bind onto BSA surface strongly.

6.4. Materials and Methods

Materials: M13 was purchased from Biolab, and oligonucleotides were purchased from IDT. Chemicals and enzymes were purchased from Sigma, unless noted otherwise. Centricon separation devices were purchased from Millipore.

Enzyme DNA conjugation: Enzymes were firstly labeled with SPDP molecule in HEPES buffer, and purified with 30kD Amicon filter. Tcep treated thiolated DNA was incubate with SPDP modified enzyme with 1:10 ratio for 1h. A_{343nm} absorbance, before and after reaction was recorded to quantify labeling ratio. High salt concentration buffer was used to get rid of extra DNA with Amicon 50kD. A_{260} and A_{280} were recorded to quantify enzyme-DNA complex concentration and labeling ratio.

Enzyme DNA Origami assembly and purification: DNA Origami structures were designed with caDNAno, and oligonucleotides were ordered from IDT. M13 was mixed with helpers with 1:10 ratio in 1×TAE-Mg buffer (16mM $MgCl_2$), annealed from 80°C to 4°C over the time course of 37h. 100kD Amicon was applied to get rid of free helpers, and purified DNA origami was mixed with enzyme-DNA complex with 1:15 ratio, annealed from 37°C to 4°C over the time course of 2h in 1×TAE-Mg buffer (12.5mM $Mg(OAc)_2$). Agarose gel electrophoresis (2%, 1×TAE-Mg) was used to get rid of extra enzymes with 70V, 2h. DNA origami concentration was quantified with A_{260} absorbance, and calculated with Ext. Co=0.109.

TEM imaging: EM grid was negatively charged with Machine. Samples were deposited onto grid for 1min, and stained with 1% uranyl formate for 15sec, and imaged with CM12.

Enzyme assay: 96-well-plate was used to monitor enzyme activity through absorbance change. Final DNA structure and free enzyme concentration used in assay was 0.5nM. GOx and HRP enzyme assay were monitored at 410nm, and G6pD, LDH, MDH enzyme assay were monitored at 340nm.

6.5. Conclusions

In conclusion, we have designed DNA Origami cage to encapsulate enzymes. With the internalization of cascade enzymes, 10 folds of activity enhancement was observed, which demonstrated the improvement of intermediate flux; five enzyme Kcat value increased 5-10 folds after internalized inside DNA cage structure, which proved DNA cage environment could boost enzyme catalytic turnover numbers, which made DNA cage as ideal material to mimic in vivo environment to study biomolecular

behavior; DNA cage could also protect inside enzymes against many factors, which can be used in future in vivo experiment, such as drug delivery.

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Chapter 7

Summary and Outlook

DNA nanotechnology field has been developed over three decades, and many different DNA structure have been created, including DNA tiles and DNA Origami, 2D and 3D structure, curvature structure, which provide enough candidates for application. With excellent spatial addressability, DNA structure is an ideal template to organize nanoscale subjects for different purposes. Previously, many works have been done on developing method to assemble different nanomaterials on DNA structure, including metal or semiconducting nanoparticles, nanowires and biomolecules. With proper control of spatial distance and orientation, different properties of the assembled functional nanomaterials can be studied, including photonics, electronics and molecular biophysics. There are several interesting directions that is interested in future, as listed belo

7.1 DNA Cage system

Previous result proved that DNA cage can serve as an ideal compartment to study internalized biomolecular behavior, because of the high density of phosphate and negative charge.

7.1.1 Construction of integrated ‘catalytic DNA’

DNAzyme has been developed to mimic enzyme, however unlike enzyme, DNAzyme do not have protection shell. Here we can use DNA cage as shell for inside core, DNAzyme, to construct integrated ‘catalytic DNA’. DNA cage can protect inside DNAzyme from degradation, such as digestion enzyme. In addition, previous research demonstrated that DNA cage can enhance inside enzyme activity with high concentration of surrounding phosphate and negative charge. Phosphate is an ideal kosmotropic anion,

which could accumulate high density water for protein. With the same principle, phosphate backbone will have the same effect on stabilizing inside DNAzyme. The construction of integrated 'catalytic DNA' will open one door to understand life evolution.

7.1.2 DNA cage as drug delivery carrier

From previous study, DNA cage can not only enhance inside enzyme activity, but also protect inside target from degradation, including protease and BSA binding. With great spatial addressability, DNA cage can be applied to encapsulate target molecules, including enzyme, regulation hormones or drug, with specific ligands for targeted delivery. In addition, with proper design, controllable switch to open and close cage for releasing of target molecules can be accomplished.

7.2 Apply DNA scaffold to study surface protein, ligands interaction

Cell membrane protein ligands interaction is essential in biology, which induce signals between cell's internal and external environment and intercellular communication. Interaction between membrane protein and ligands is affected with many factors, including distance between ligands and numbers of ligands. DNA structure is an ideal template with excellent spatial addressability and with proper control of ligands density and distance on DNA scaffold, cell membrane protein and ligands interaction can be studied.

Construction of artificial metabolism pathway in vivo

With the great spatial addressability of DNA structures, integrated metabolism pathway can be constructed based on DNA structures. Firstly, DNA cage can be constructed to mimic compartment environment; secondly, DNA scaffold can be used to

direct the assembly of metabolism enzymes with controlled ratio, order and distance; thirdly, substrate, intermediate or cofactors can be linked on DNA scaffold in between metabolism enzymes, serving as swing arm to improve flux. Overall, DNA structure can construct artificial metabolism pathway with integrated function.

7.3 DNA structure based mask or template

DNA structure approach can be bridged with top-down method. DNA structure provided great controllability in nanometer scale, which is in demand in many top-down methods, such as Electron Beam Lithography (EBL) or Atomic Layer Deposition (ALD). However,these methods usually need template have high stability over high temperature or high energy electron density. To improve the stability of DNA structure, polymer, such as polyaniline, can be utilized. Aniline monomer can attach onto DNA structure through electrostatic interaction, and after reduction by HRP, aniline monomer on DNA structure surface can be linked together to form polyaniline, with excellent conductivity and high stability. The resulted polymer-DNA complex can be used as mask for electron beam lithography or template for atomic layer deposition.

7.4 Conformational switchable DNA origami

DNA origami has been developed for several years, expanded from 2D to 3D, with curvature. However, compared with paper origami, whose conformation can be changed, DNA origami morphology is identical after annealing. Here we want to develop conformational switchable DNA origami. With strand displacement method or riboswitch method, DNA origami shape can be altered. Previously we have demonstrated that with fuel strand, 2D DNA origami can be rolled into tube shape as initial demonstration. With proper design, different origami conformation can be changed.

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APPENDIX A
SUPPLEMENTAL INFORMATION FOR CHAPTER 2

Supplemental Information

A Route to Scale Up DNA Origami Using DNA Tiles as

Folding Staples

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Experimental Materials and Methods

Materials: All strands including 8HX strands and helper strands were purchased from Integrated Technologies, Inc. (www.IDTDNA.com). 8HX strands were purified by 10% denaturing polyacrylamide gel electrophoresis (PAGE), and the concentration of each strand was estimated by measuring OD260. All helper strands were in the format of 96-well plates normalized to 100uM×60uL, and were used without further purification. M13 viral DNA was purchased from New England Biolabs, Inc. (NEB, Catalog number: #N4040S).

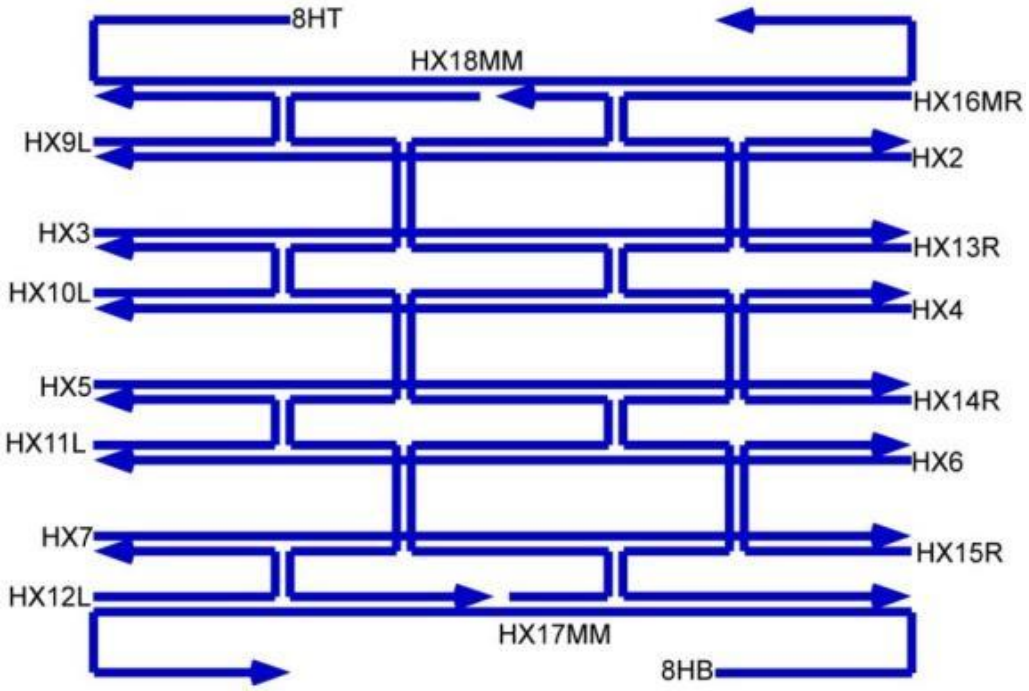
Folding: Assembly of 8HX was accomplished in a one-step annealing reaction. Each individual tile was assembled by mixing a stoichiometric quantity of the strands involved in the tile in 1×TAE-Mg^{2+} buffer (20mM Tris, pH 7.6, 2mM EDTA, 12.5 mM $MgCl_2$). The final concentration was 2.0 uM for each strand, and the final volume was 30 uL. The oligo mixtures were subjected to a thermal-annealing ramp that cooled from 90 to 70 over the couse of 90 min and then cooled from 70 to 25 over 620 min. The 8HX Origami structure was annealed in a two-steps annealing reaction by mixing 10 nM scaffold strands with 100 nM of helper strands in 1.5×TAE-Mg^{2+}, cooling from 90 to 70 over the couse of 90 min and then cooled from 70 to 25 over 620 min first, then added 20

nM 8HX tiles, cooling from 45 to 40 over the course of 500 min and then cooled from 40 to 20 over 60h.

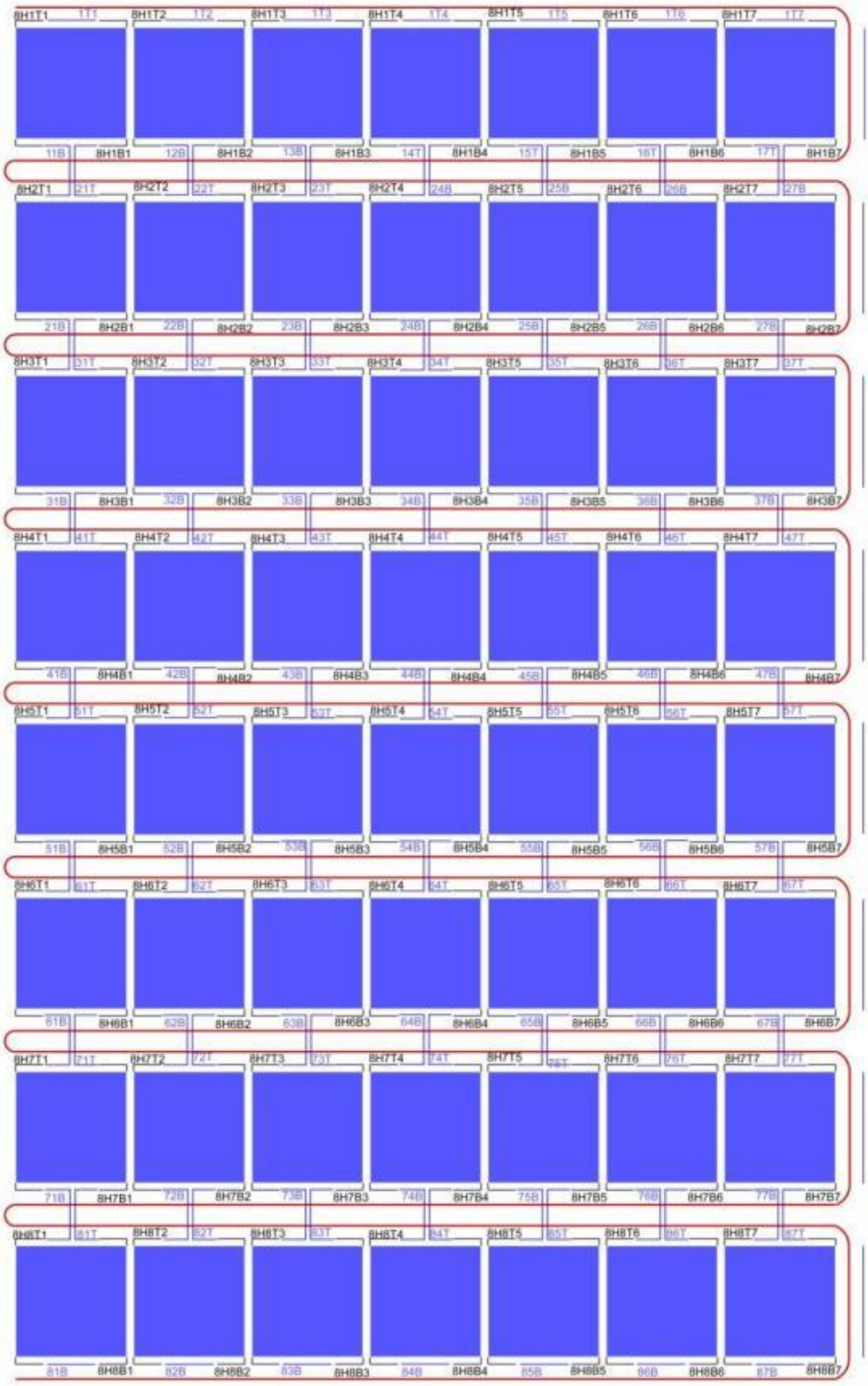
Gel purification: Folding products were electrophoresed on 0.3% or 0.7% agarose gel containing 1×TAE-Mg^{2+}, 0.5 ug/mL ethidium bromide at 80V for one hour in a gel box. Monomer bands were excised and DNA recovered by pestlecrushing excised bands followed by centrifugation for 4 min at 3000 rpg using Freeze 'N Squeeze DNA Gel Extraction spin columns (Bio-Rad). Recovered material in the flow-through was stored at 4 degree Centigrade for further use.

AFM imaging: The sample (2uL) was deposited onto a freshly cleaved mica (Ted Pella, Inc.) and left to absorb for 3 min. Buffer (1×TAE-Mg^{2+}, 400uL) was added to the liquid cell and the sample was scanned in a tapping mode on a Pico-Plus AFM (Molecular Imaging, Agilent Technologies) with NP-S tips (Veeco, Inc.).

DNA sequences:


8HT
HX18MM
HX16MR
HX9L
HX2
HX3
HX13R
HX10L
HX4
HX5
HX14R
HX11L
HX6
HX7
HX15R
HX12L
HX17MM
8HB


8H1T1
1T1
8H1T2
1T2
8H1T3
1T3
8H1T4
1T4
8H1T5
1T5
1
11L
8H1B1
12L
8H1B2
13L
8H1B3
14L
8H1B4
15L
8H1B5
8H2T1
11R
8H2T2
12R
8H2T3
13R
8H2T4
14R
8H2T5
15R
2
21L
8H2B1
22L
8H2B2
23L
8H2B3
24L
8H2B4
25L
8H2B5
8H3T1
21R
8H3T2
22R
8H3T3
23R
8H3T4
24R
8H3T5
25R
3
31L
8H3B1
32L
8H3B2
33L
8H3B3
34L
8H3B4
35L
8H3B5
8H4T1
31R
8H4T2
32R
8H4T3
33R
8H4T4
34R
8H4T5
35R
4
41L
8H4B1
42L
8H4B2
43L
8H4B3
44L
8H4B4
45L
8H4B5
8H5T1
41R
8H5T2
42R
8H5T3
43R
8H5T4
44R
8H5T5
45R
5
5B1
8H5B1
5B2
8H5B2
5B3
8H5B3
5B4
8H5B4
5B5
8H5B5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8H2T1 21T 8H2T2 22T 8H2T3 23T 8H2T4 24B 8H2T5 25B 8H2T6 26B 8H2T7 27B
21B 8H2B1 22B 8H2B2 23B 8H2B3 24B 8H2B4 25B 8H2B5 26B 8H2B6 27B 8H2B7
8H3T1 31T 8H3T2 32T 8H3T3 33T 8H3T4 34T 8H3T5 35T 8H3T6 36T 8H3T7 37T
31B 8H3B1 32B 8H3B2 33B 8H3B3 34B 8H3B4 35B 8H3B5 36B 8H3B6 37B 8H3B7
8H4T1 41T 8H4T2 42T 8H4T3 43T 8H4T4 44T 8H4T5 45T 8H4T6 46T 8H4T7 47T
41B 8H4B1 42B 8H4B2 43B 8H4B3 44B 8H4B4 45B 8H4B5 46B 8H4B6 47B 8H4B7
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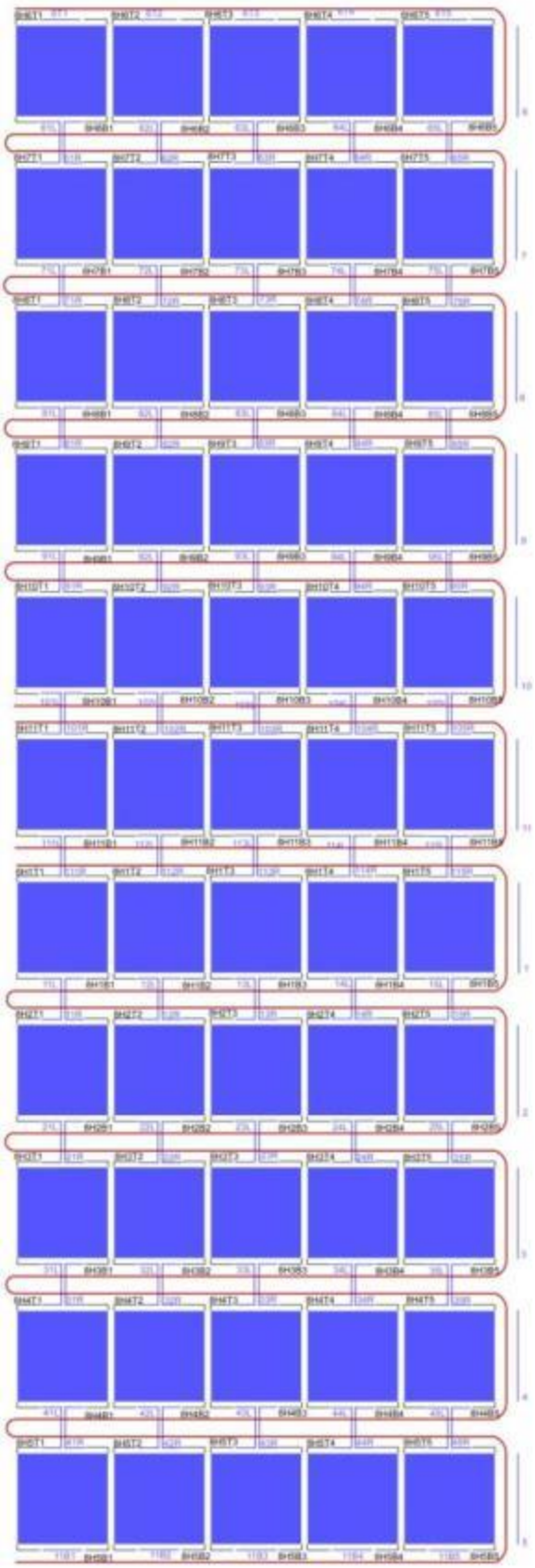

Table S1. 8HX strands other strands except top and bottom strands

HX2;AACAGAGTTCCCTGTCTCCTGTATTCGAGATCCTGGTTCCTGGCTCCTTC
TG

HX3;TACTGGGCTAGGACATGGGACAACACGGTGCGGACGCTGGACAGACCA
AGCT

HX4;AGTAGGGCGGCCTGATACCTGAGTCCAAGGTCCTGCAACCTGGGGCCCT
CTT

HX5;GATGAGGAACGGACTATGGACGCTCCGAGTAGGACAAGGGACGACTCG
TTTC

HX6;GCTTCGATGCCCTGCTGCCTGGCTCCGGTCCCCTGACTCCTGAGTCCCTT
TC

HX7;GGTTAGGTAAGGACCGAGGACTATCCGATTCGGACTAAGGACGGCTCAC
TAC

HX9L;TTCAGAAGGAGCCACCGCCTCCAGCC

HX10L;TTAAGAGGGCCCCACCTAGCCCAGTATT

HX11L;TTGAAAGGGACTCACCGTTCCTCATCTT

HX12L;GGCGCGACTTCACCTTACCTAACCTT

HX13R;TTAGCTTGGTCTGTGGGAACTCTGTTTT

HX14R;TTGAAACGAGTCGTGGCCGCCCTACTTT

HX15R;TTGTAGTGAGCCGTGGGCATCGAAGCTT

HX16MR;AGCAAGGAAGAGGAAACGTGGAGACACCAGCGTGGTATCACCCTT
GTGGCAGCACCTTAGTGGGCTTCCATTCTTATCGC

HX17MM;CGACCCACCGAATCGGATAGTGGGGACCGGAGCCACCTACTCGGA

GCGTGGACCTTGGACTCACCGCACC

HX18MM;GTGTTGTGGATCTCGAATACACCCGCCAAACCGACGGAATGTGGA

ACCACCCATGTGGTTGCACCATAGTGGAGTCACCTCGGTGGAATCCTACGGA

A

Table S2. 8HX strands top and bottom strands for 5×5 structure

8H1T1;TATTTCGGAACCTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGAGTAACAGTGCC

8H1T2;GGGTCAGTGCCTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTTTGATGATACAG

8H1T3;GTCATACATGGCTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTATGGAAAGCGCAG

8H1T4;CATTAAAGCCAGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCAGACGATTGGCC

8H1T5;GGTTGAGGCAGGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCCAGAACCACCAC

8H1B1;TTAGAGCCAGCAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGGTGAATTATCAC

8H1B2;CGTCACCAATGAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAATCACCAGTAGC

8H1B3;AAGTTTGCCTTTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCACCATCGATAGCA

8H1B4;ATAGCCCCCTTATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCGCGTCAGACTGTA

8H1B5;CAGAGCCACCACCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTAGCGTTTGCCAT

8H2T1;ATTATTCATTAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTTCAACCGATTGA

8H2T2;CAAAAGGGCGACAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATCAATAGAAAA

8H2T3;TTTATTTTGTCACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGCAACATATAAAA

8H2T4;ATACATAAAGGTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCTCCTTATTACGC

8H2T5;GGCATGATTAAGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCCGAGGAAACGCA

8H2B1;TTATCCCAATCCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAGCCTAATTTGCC

8H2B2;TAGCAGCCTTTACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAATAAGAAACGAT

8H2B3;GAGAATTAACTGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAGAGAGAATAACA

8H2B4;TCAGAGAGATAACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCACACCCTGAACAA

8H2B5;ACAATGAAATAGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCCACAAGAATTGA

8H3T1;AGCGTCTTTCCAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCCAGCTACAATTT

8H3T2;TGCTATTTTGCACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGACTTGCGGGAGG

8H3T3;TAGCGAACCTCCCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTTAGAAGGCTTATC

8H3T4;AGCAAATCAGATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTTTATTTTCATCGT

8H3T5;AAGCAAGCCGTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAGAACGGGTATTA

8H3B1;ATAAAGCCAACGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCTGTTTAGTATCA

8H3B2;ACGCCAACATGTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTCAACAGTAGGGC

8H3B3;ATAAAGTACCGACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATTTAGGCAGAGG

8H3B4;AACATGTTCAGCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAAAAGGTAAAGTA

8H3B5;TGAACAAGAAAAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAATGCAGAACGCG

8H4T1;TACTAGAAAAAGCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATAAGGCGTTAA

8H4T2;CGACCGTGTGATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATTTCATCTTCT

8H4T3;ATATATTTTAGTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTCCAATCGCAAGA

8H4T4;ATGCTGATGCAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTTAACCTCCGGCTT

8H4T5;GAGACTACCTTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGAAGAGTCAATAG

8H4B1;CGGGAGAAACAATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTAACGTCAGATGA

8H4B2;ATCGCGCAGAGGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAACGGATTCGCCT

8H4B3;GAAACAAACATCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGAATTATTCATTT

8H4B4;TTACCTTTTTTAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAGAAAACAAAATT

8H4B5;CTTGCTTCTGTAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTGGAAACAGTACA

8H5T1;AGATTTTCAGGTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTAAATTATTTGCAC

8H5T2;ACCTACCATATCAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTATTGTTTGGATTA

8H5T3;CAATATAATCCTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTATCATCATATTC

8H5T4;GAAGGAGCGGAATGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTTGAGTAACATTAT
8H5T5;AATTTTAAAAGTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTTTCGACAACTCGT
8H5B1;ACCGAACGAACCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCTGCGCGAACTGAT
8H5B2;ACACCGCCTGCAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCCCAGCAGAAGATA
8H5B3;AAGCATCACCTTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCCAGTGCCACGCTG
8H5B4;AGTTGGCAAATCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCCTGAACCTCAAAT
8H5B5;TTAGGAGCACTAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCACAGTTGAAAGGA

Table S3. 8HX strands top and bottom strands for 7×8 structure

8H1T1;CCTGTTTGATGGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTGCAAGCGGTCCAC
8H1T2;TGAGAGAGTTGCAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTGAGACGGGCAACA
8H1T3;TCTTTTCACCAGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTGGGAGAGGCGGTT
8H1T4;CGGCCAACGCGCGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCCAGTCGGGAAAC

8H1T5;CACTGCCCGCTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCCTAATGAGTGAG

8H1T6;AAAGCCTGGGGTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACAATTCCACACA

8H1T7;TTGTTATCCGCTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGAATTCGTAATCA

8H1B1;TCGGATTCTCCGTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAGCTTTCATCAAC

8H1B2;GTTGGTGTAGATGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGGGAACAAACGGC

8H1B3;ACGACAGTATCGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGGCGCATCGTAAC

8H1B4;CTTCTGGTGCCGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCCCTCAGGAAGATC

8H1B5;CTGTTGGGAAGGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAAACCAGGCAAAG

8H1B6;AAAGGGGGATGTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCGATCGGTGCGGG

8H1B7;AGTCACGACGTTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCTGCAAGGCGATT

8H2T1;CCTTCCTGTAGCCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTAACCAATAGGAA

8H2T2;TCAGCTCATTTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTTAATATTTTGTT

8H2T3;TAAATTGTAAACGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAAAGCCCCAAAA

8H2T4;GGTTGATAATCAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCGGTAATCGTAAA

8H2T5;GAGAATCGATGAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAGGCTATCAGGTC

8H2T6;GAGAGATCTACAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCTAGCTGATAAAT

8H2T7;ATATTCAACCGTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGTGAGAAAGGCCG

8H2B1;AAAGTACGGTGTCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATATAATGCTGTA

8H2B2;GCGAACGAGTAGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTGGAAGTTTCATT

8H2B3;AACCTGTTTAGCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTTTAGTTTGACCA

8H2B4;ATTCTACTAATAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCATATTTTCATTTG

8H2B5;AAGAATTAGCAAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

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8H2B7;TCAACGCAAGGATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTTATGACCCTGTA

8H3T1;GCTTAATTGCTGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCTCCTTTTGATAA

8H3T2;GTACCTTTAATTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCCAGACCGGAAGC

8H3T3;GCTTCAAAGCGAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGGAAGCCCGAAAG

8H3T4;AAAAAGATTAAGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACCCTGACTATTA

8H3T5;AAATCAGGTCTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCTTTAAACAGTTC

8H3T6;TCCCCCTCAAATGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGCGTCCAATACTG

8H3T7;TTTAGACTGGATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTGCAAAAGAAGTT

8H3B1;GACAAGAACCGGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAGGCGCATAGGCT

8H3B2;AGTGAATAAGGCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTATTCATTACCCA

8H3B3;CTTGAGATGGTTTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTGCCCTGACGAGA

8H3B4;TTAAGAACTGGCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAATTTCAACTTTA

8H3B5;TAATAAAACGAACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCATTATACCAGTC

8H3B6;TTGAGATTTAGGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTAACGGAACAACA

8H3B7;GAATTACGAGGCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATACCACATTCAA

8H4T1;CGGTGTACAGACCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGGGAACCGAACTG

8H4T2;CGGTCAATCATAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCGACCTGCTCCAT

8H4T3;GTGTCGAAATCCGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCAAAGTACAACGG

8H4T4;ACCAAGCGCGAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATACACTAAAAC

8H4T5;AAAGAGGCAAAAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAATACGTAATGC

8H4T6;CATTAAACGGGTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAGGCTTTGAGGAC

8H4T7;GCAACGGCTACAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTTCACCCTCAGCAG

8H4B1;ACCAGTACAAACTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCCCAATAGGAACC

8H4B2;GCGTAACGATCTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCACAACGCCTGTAG

8H4B3;CTGTATGGGATTTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAAGTTTTGTCGTC

8H4B4;GAAAGGAACAACTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTGCTAAACAACTT

8H4B5;TCCAAAAAAAAAGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAAAGGAATTGCGA

8H4B6;GCTTTCGAGGTGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCTCCAAAAGGAGC

8H4B7;TGACAACAACCATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATTTCTTAAACAG

8H5T1;CAGGGATAGCAAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCCTCAGAACCGCC

8H5T2;TCAGAACCGCCACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGGTGTATCACCGT

8H5T3;ATAGCCCGGAATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACCAGGCGGATAA

8H5T4;GGTTTTGCTCAGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGAGGCTGAGACTC

8H5T5;ATGAAAGTATTAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATGCCCCCTGCC

8H5T6;CGTATAAACAGTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTATAAGTTTTAACG
8H5T7;GAGTGTACTGGTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTCGTTCCAGTAAGC
8H5B1;ACCATTACCATTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG
ATTCCTGAAGTCGCGCCAGCCATTTGGGAA
8H5B2;GCACCGTAATCAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCGCAAGGCCGGAAA
8H5B3;GCGCGTTTTCATCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG
ATTCCTGAAGTCGCGCCTAGCGACAGAATC
8H5B4;CTTTTCATAATCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG
ATTCCTGAAGTCGCGCCGGCATTTTCGGTC
8H5B5;TCAGAGCCGCCACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCAAATCACCGGAAC
8H5B6;CGCCACCAGAACCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCCCTCAGAACCGCC
8H5B7;CAGGTCAGACGATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCACCACCAGAGCCG
8H6T1;CGTCACCGACTTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTAATATTGACGGAA
8H6T2;GGGAGGGAAGGTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTCCAGCGCCAAAGA
8H6T3;TTCATATGGTTTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTACCACGGAATAAG

8H6T4;GAAACGCAAAGACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACGTAGAAAATAC

8H6T5;AGTATGTTAGCAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACCCAAAAGAACT

8H6T6;ATAATAACGGAATGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

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8H6T7;AAAGTAAGCAGATGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

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8H6B1;CGGTATTCTAAGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

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8H6B2;TTTTGAAGCCTTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

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8H6B3;TATCCTGAATCTTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAATCAAGATTAGT

8H6B4;AGTTACAAAATAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCACCAACGCTAACG

8H6B5;TTTTTGTTTAACGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

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8H6B7;AGTCAGAGGGTAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGCGCATTAGACGG

8H7T1;AGGAATCATTACCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACTCATCGAGAAC

8H7T2;AACCAAGTACCGCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTATCGGCTGTCTTT

8H7T3;AAACCAATCAATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAGAAAAATAATA

8H7T4;ATAAGTCCTGAACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGTTCAGCTAATGC

8H7T5;CAATAAACAACATGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGTACCGACAAAAG

8H7T6;AAGAGAATATAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAACATGTAATTTA

8H7T7;ATTTAACAACGCCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGCCAACGCTCAAC

8H7B1;TGAATAACCTTGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTTTTTTAATGGAA

8H7B2;TCCTTGAAAACATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTTCTGTAAATCGT

8H7B3;TGAATTTATCAAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAGCGATAGCTTAG

8H7B4;AGGTTGGGTTATAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATCATAGGTCTGA

8H7B5;CAAAGAACGCGAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTAACTATATGTAA

8H7B6;GACCTAAATTTAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAAAACTTTTTCAA

8H7B7;ATAAGAATAAACAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTGGTTTGAAATAC

8H8T1;CATTTGAATTACCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTAAACATCAAGAAA

8H8T2;AAGATGATGAAACGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGCAGAGGCGAATT

8H8T3;GTTACAAAATCGCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGAAACAATAACGG

8H8T4;TTTTACATCGGGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTTCAGGTTTAACG

8H8T5;AATTGCGTAGATTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCCATATCAAAATT

8H8T6;GGGTTAGAACCTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTTAATCCTGATTGT

8H8T7;CAATTCATCAATAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTAGCGGAATTATCA

8H8B1;TTAAAAATACCGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGTCTTTAATGCGC

8H8B2;CAGTATTAACACCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCACGAACCACCAGC

8H8B3;AAAATCTAAAGCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCGCCTGCAACAGTG
8H8B4;ATCTGGTCAGTTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG
ATTCCTGAAGTCGCGCCTCACCTTGCTGAA
8H8B5;AAATATCTTTAGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCGCAAATCAACAGT
8H8B6;TACATTTGAGGATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCAGCACTAACAACT
8H8B7;ATTAAATCCTTTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG
ATTCCTGAAGTCGCGCCTTAGAAGTATTAG

Table S4. 8HX strands top and bottom strands for 5×11 structure (the top 5 layer is the same with 5*5, so the sequence is the same, I just list the bottom 6 layer 8HX top and bottom strands)

8H6T1;GGACTCCAACGTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTTGTTCCAGTTTGG
8H6T2;TAGGGTTGAGTGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC
GTTTCCTCTTCCTTGCTTCGGCAAAATCCC
8H6T3;GGTGGTTCCGAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTCACGCTGGTTTGC
8H6T4;GCAGCAAGCGGTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTACAGCTGATTGCC
8H6T5;AGTGAGACGGGCAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGTTTGCGTATTGG

8H6B1;TTGTAAAACGACGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATTAAGTTGGGTA

8H6B2;GGATCCCCGGGTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGCCAGTGCCAAGC

8H6B3;GTGTGAAATTGTTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCCCGAGCTCGAATT

8H6B4;TAAAGTGTAAAGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATCCGCTCACAAT

8H6B5;GTTGCGCTCACTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCCTGGGGTGCCTAA

8H7T1;GTGCTGCAAGGCGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGGGCCTCTTCGCT

8H7T2;GGGCGATCGGTGCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAGCGCCATTCGC

8H7T3;CGGAAACCAGGCAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTATCGCACTCCAGC

8H7T4;CGGCCTCAGGAAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAACCGTGCATCTG

8H7T5;ATGGGCGCATCGTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGGCGGATTGACCG

8H7B1;GCAAACAAGAGAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATCTACAAAGGCT

8H7B2;TGTACCCCGGTTGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTCGATGAACGGTA

8H7B3;CAAATATTTAAATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATAATCAGAAAAG

8H7B4;TTGTTAAATCAGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTGTAAACGTTAAT

8H7B5;GCGTCTGGCCTTCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCTCATTTTTTAACC

8H8T1;CTATTTTTGAGAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTCAACCGTTCTAGC

8H8T2;TCAATATGATATTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTTCAAAAGGGTGAG

8H8T3;TGTAGGTAAAGATGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAGAACCCTCATAT

8H8T4;GATAAAAATTTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGTAATACTTTTGC

8H8T5;ACATTATGACCCTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTAAAGCCTCAGAGC

8H8B1;GGCTTAGAGCTTAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCTTTAATTGCTCCT

8H8B2;ATGCAACTAAAGTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATTGCTGAATATA

8H8B3;CCAATTCTGCGAAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCACGGTGTCTGGAA

8H8B4;TGGTCAATAACCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCGAGTAGATTTAG

8H8B5;TGGCATCAATTCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCGTTTAGCTATATT

8H9T1;ATTAGAGAGTACCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAAGCGAACCAGA

8H9T2;TAATTCGAGCTTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTGATTAAGAGGAAG

8H9T3;ATTGCATCAAAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAGGTCTTTACCCT

8H9T4;TAAATCAAAAATCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCTCAAATGCTTTA

8H9T5;TCATTGAATCCCCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGAC

GTTTCCTCTTCCTTGCTACTGGATAGCGTC

8H9B1;ATGCGATTTTAAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGATGGTTTAATTT

8H9B2;ATCTACGTTAATAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAACTGGCTCATTA

8H9B3;TTCATCAGTTGAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGG

ATTCCTGAAGTCGCGCCAAACGAACTAACG

8H9B4;GCCAAAAGGAATTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCATTTAGGAATACC

8H9B5;TACCAGACGACGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCACGAGGCATAGTA
8H10T1;AAATTGGGCTTGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTATAAGGCTTGCCC
8H10T2;GCTCATTCAGTGAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTGAACCGGATATTC
8H10T3;GTAATCTTGACAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA
CGTTTCCTCTTCCTTGCTTACAGACCAGGCG
8H10T4;CAGATGAACGGTGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGG
ACGTTTCCTCTTCCTTGCTAATCATAAGGGAA
8H10T5;GGCGCAGACGGTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGG
ACGTTTCCTCTTCCTTGCTGAAATCCGCGACC
8H10B1;GAGGCTTGCAGGGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA
GGATTCCTGAAGTCGCGCCACAACCATCGCCC
8H10B2;CGAAAGACAGCATGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA
GGATTCCTGAAGTCGCGCCAGTTAAAGGCCGC
8H10B3;TAAAGACTTTTTCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG
GATTCCTGAAGTCGCGCCCGGAACGAGGGTA
8H10B4;CACTACGAAGGCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA
GGATTCCTGAAGTCGCGCCATGAGGAAGTTTC
8H-
10B5;ACTCATCTTTGACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAGGA
TTCCTGAAGTCGCGCCCCAACCTAAAACG

8H11T1;GCCGACAATGACAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGG

ACGTTTCCTCTTCCTTGCTCGAGGTGAATTTC

8H11T2;ATCAGCTTGCTTTGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAAAAAAGGCTCCA

8H11T3;TGAAAATCTCCAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGAACAACTAAAGG

8H11T4;TGAGAATAGAAAGGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGG

ACGTTTCCTCTTCCTTGCTTGGGATTTTGCTA

8H11T5;TGAATTTTCTGTAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTACGATCTAAAGTT

8H11B1;CTCAAGAGAAGGAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCATTATTCTGAAAC

8H11B2;GTGCCGTCGAGAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCTTAGGATTAGCGG

8H11B3;ACTCAGGAGGTTTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCGGTTGATATAAGT

8H11B4;ACCCTCAGAGCCAGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCAGTACCGCCACCC

8H11B5;CATGTACCGTAACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCCCACCCTCATTTT

8H12T1;TATTAGTCTTTAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGCGTAAGAATACG

8H12T2;TTCTGACCTGAAAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGTAATAAAAGGGA

8H12T3;AGTCACACGACCAGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTAATCGTCTGAAAT

8H12T4;CATTTTGACGCTCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTCAGCCATTGCAAC

8H12T5;ACAATATTACCGCGGCTGGAGGCGGACATTCCGTCGGTTTGGCGGGA

CGTTTCCTCTTCCTTGCTGAAGAACTCAAAC

8H12B1;TAGCGGTCACGCTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTAG

GATTCCTGAAGTCGCGCCAGAAAGCGAAAGG

8H12B2;ACAGGGCGCGTACGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCGCGCGTAACCACC

8H12B3;GTTAGAATCAGAGGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCTATGGTTGCTTTG

8H12B4;AGGAACGGTACGCGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCCGGGAGCTAAACA

8H12B5;CGAGTAAAAGAGTGCGATAAGAATGGAAGCCCTGGGTCGTTCCGTA

GGATTCCTGAAGTCGCGCCCAGAATCCTGAGA

Table S5. Bridge strands for 5×5

1T1;CGTATAAACAGTTAATGCCCCCTGCC

1T2;GAGTGTACTGGTAATAAGTTTTAACG

1T3;TCTCTGAATTTACCGTTCCAGTAAGC

1T4;TTGATATTCACAAACAAATAAATCCT

1T5;CAGAGCCGCCGCCAGCATTGACAGGA

1;CCCTCAGAGCCGCCACCCTCAGAACCGCCACCCTCAGAGCCACCACCCTC

11L;CGTCACCGACTTGAATATTGACGGAA

11R;GGGAGGGAAGGTAAGCCATTTGGGAA

12L;ACCATTACCATTACCAGCGCCAAAGA

12R;TTCATATGGTTTAGCAAGGCCGGAAA

13L;GCACCGTAATCAGACCACGGAATAAG

13R;GAAACGCAAAGACTAGCGACAGAATC

14L;GCGCGTTTTCATCACGTAGAAAATAC

14R;AGTATGTTAGCAAGGCATTTTCGGTC

15L;CTTTTCATAATCAACCCAAAAGAACT

15R;ATAATAACGGAATAAATCACCGGAAC

2;TTACCGAAGCCCTTTTTAAGAAAAGTAAGCAGATAGCCGAACAAAGTTAC

21L;AGTTACAAAATAAACCAACGCTAACG

21R;TATCCTGAATCTTACAGCCATATTAT

22L;TTTTTGTTTAACGAATCAAGATTAGT

22R;TTTTGAAGCCTTATCAAAAATGAAAA

23L;TAAAAACAGGGAAACGCGAGGCGTTT

23R;CGGTATTCTAAGAGCGCATTAGACGG

24L;AGTCAGAGGGTAAGCGCCCAATAGCA

24R;AGGAATCATTACCTTGAGCGCTAATA

25L;GTTAAGCCCAATAACTCATCGAGAAC

25R;AACCAAGTACCGCATAAGAGCAAGAA

3;TCCTAATTTACGAGCATGTAGAAACCAATCAATAATCGGCTGTCTTTCCT

31L;TATGCGTTATACACCGGAATCATAAT

31R;ATAAGAATAAACAAATTCTTACCAGT

32L;TTAATTGAGAATCTGGTTTGAAATAC

32R;GACCTAAATTTAAGCCATATTTAACA

33L;CATTTTCGAGCCAAAAACTTTTTCAA

33R;CAAAGAACGCGAGGTAATAAGAGAAT

34L;ATTCTGTCCAGACTAACTATATGTAA

34R;AGGTTGGGTTATAGACGACAATAAAC

35L;CCTGTTTATCAACATCATAGGTCTGA

35R;TGAATTTATCAAAAATAGATAAGTCC

4;TTAATTAATTTTCCCTTAGAATCCTTGAAAACATAGCGATAGCTTAGATT

41L;ATATACAGTAACAAAAGAAATTGCGT

41R;GTAAAACAGAAATGTACCTTTTACAT

42L;GATTGCTTTGAATTGGAAGGGTTAGA

42R;TACTTCTGAATAAACCAAGTTACAAA

43L;CAATTACCTGAGCGATGGCAATTCAT

43R;CTGATTATCAGATAAAAGAAGATGAT

44L;AATTACATTTAACAAAGAAACCACCA

44R;CATTTTGCGGAACAATTTCATTTGAA

45L;TAAATCAATATATCCCGAACGTTATT

45R;ATTAAATCCTTTGGTGAGTGAATAAC

5;ATTAGAGCCGTCAATAGATAATACATTTGAGGATTTAGAAGTATTAGACT

5B1;AGCCCTAAAACATCGCCATTAAAAAT

5B2;AAACAGAGGTGAGGCGGTCAGTATTA

5B3;AGAGCCAGCAGCAAATGAAAAATCTA

5B4;ATCAAACCCTCAATCAATATCTGGTC

5B5;ATTGAGGAAGGTTATCTAAAATATCT

Table S6. Bridge strands for 7×8 strcuture

1T1;GCTGGTTTGCCCCAGCAGGCGAAAAT

1T2;GCTGATTGCCCTTCACCGCCTGGCCC

1T3;TGCGTATTGGGCGCCAGGGTGGTTTT

1T4;CTGTCGTGCCAGCTGCATTAATGAAT

1T5;CTAACTCACATTAATTGCGTTGCGCT

1T6;ACATACGAGCCGGAAGCATAAAGTGT

1T7;TGGTCATAGCTGTTTCCTGTGTGAAA

2T1L;ATTAAATGTGAGCAATTCGCGTCTGG

2T1R;CGCCATCAAAAATGAGTAACAACCCG

2T2L;GGATTGACCGTAAAATTTTTGTTAAA

2T2R;AAAATTCGCATTATGGGATAGGTCAC

2T3L;CGTGCATCTGCCAATAAGCAAATATT

2T3R;ACAGGAAGATTGTGTTTGAGGGGACG

2T4L;GCACTCCAGCCAGTCATATGTACCCC

2T4R;ACTAGCATGTCAACTTTCCGGCACCG

2T5L;CGCCATTCGCCATCTGGAGCAAACAA

2T5R;ATTGCCTGAGAGTTCAGGCTGCGCAA

2T6L;CCTCTTCGCTATTGGTAGCTATTTTT

2T6R;TAATGCCGGAGAGACGCCAGCTGGCG

2T7L;AAGTTGGGTAACGCACCATCAATATG

2T7R;GAGACAGTCAAATCCAGGGTTTTCCC

3T1L;GCTCAACATGTTTCGGATGGCTTAGA

3T1R;GAGGTCATTTTTGTAAATATGCAACT

3T2L;CCATATAACAGTTTCAGGATTAGAGA

3T2R;AAACTCCAACAGGGATTCCCAATTCT

3T3L;TTAGATACATTTCCGTTTTAATTCGA

3T3R;ACTTCAAATATCGGCAAATGGTCAAT

3T4L;GGGCGCGAGCTGAAGCGGATTGCATC

3T4R;TAGTCAGAAGCAAAAAGGTGGCATCA

3T5L;ATCCAATAAATCAGACCATAAATCAA

3T5R;AGAAAACGAGAATTACAGGCAAGGCA

3T6L;GCCTCAGAGCATAAATATTCATTGAA

3T6R;CGGAATCGTCATAAAGCTAAATCGGT

3T7L;ATACTTTTGCGGGTAATAGTAAAATG

3T7R;TTGCCAGAGGGGGAGAAGCCTTTATT

4T1L;GGCTGACCTTCATGAGGACAGATGAA

4T1R;ACCAACTTTGAAACAAGAGTAATCTT

4T2L;AATCAACGTAACAAACGAGGCGCAGA

4T2R;GTTACTTAGCCGGAAGCTGCTCATTC

4T3L;AACACCAGAACGACGCCTGATAAATT

4T3R;AGATTTGTATCATGTAGTAAATTGGG

4T4L;ATCATTGTGAATTCCCCAGCGATTAT

4T4R;ACTCATCTTTGACACCTTATGCGATT

4T5L;AGGACGTTGGGAACCAACCTAAAACG

4T5R;CACTACGAAGGCAGAAAAATCTACGT

4T6L;TTATTACAGGTAGATGAGGAAGTTTC

4T6R;TAAAGACTTTTTCAAAGATTCATCAG

4T7L;CTAATGCAGATACCGGAACGAGGGTA

4T7R;CGAAAGACAGCATATAACGCCAAAAG

5T1L;CATGTACCGTAACCCACCCTCATTTT

5T1R;ACCCTCAGAGCCAACTGAGTTTCGTC

5T2L;CATTCCACAGACAAGTACCGCCACCC

5T2R;ACTCAGGAGGTTTGCCCTCATAGTTA

5T3L;TTTCCAGACGTTAGGTTGATATAAGT

5T3R;GTGCCGTCGAGAGGTAAATGAATTTT

5T4L;TCAACAGTTTCAGTTAGGATTAGCGG

5T4R;CTCAAGAGAAGGACGGAGTGAGAATA

5T5L;ATAATAATTTTTTATTATTCTGAAAC

5T5R;TATTTCGGAACCTCACGTTGAAAATC

5T6L;CTTTAATTGTATCGAGTAACAGTGCC

5T6R;GGGTCAGTGCCTTGGTTTATCAGCTT

5T7L;CTTGATACCGATATTTGATGATACAG

5T7R;GTCATACATGGCTGTTGCGCCGACAA

6T1L;TTAGAGCCAGCAAGGTGAATTATCAC

6T1R;ATTATTCATTAAAAATCACCAGTAGC

6T2L;CGTCACCAATGAATTCAACCGATTGA

6T2R;CAAAAGGGCGACAACCATCGATAGCA

6T3L;AAGTTTGCCTTTAAATCAATAGAAAA

6T3R;TTTATTTTGTCACGCGTCAGACTGTA

6T4L;ATAGCCCCCTTATGCAACATATAAAA

6T4R;ATACATAAAGGTGTAGCGTTTGCCAT

6T5L;CAGAGCCACCACCCTCCTTATTACGC

6T5R;GGCATGATTAAGAGGAACCGCCTCCC

6T6L;ACCCTCAGAGCCACCGAGGAAACGCA

6T6R;TACCAGAAGGAAACCACCCTCAGAGC

6T7L;CCGCCAGCATTGAGCCCTTTTTAAGA

6T7R;CTATCTTACCGAACAGGAGGTTGAGG

7T1L;AGCAAATCAGATATTATTTTCATCGT

7T1R;AAGCAAGCCGTTTTAGAAGGCTTATC

7T2L;TAGCGAACCTCCCAGAACGGGTATTA

7T2R;CCTTATCATTCCAGACTTGCGGGAGG

7T3L;TGCTATTTTGCACTACGAGCATGTAG

7T3R;TCCCATCCTAATTCCAGCTACAATTT

7T4L;AGCGTCTTTCCAGTTATCAACAATAG

7T4R;AGAACGCGCCTGTAGCCTAATTTGCC

7T5L;TTATCCCAATCCAGTCCAGACGACGA

7T5R;GTAAAGTAATTCTAATAAGAAACGAT

7T6L;TAGCAGCCTTTACTCGAGCCAGTAAT

7T6R;GGCAGAGGCATTTAGAGAGAATAACA

7T7L;GAGAATTAACTGATGAGAATCGCCAT

7T7R;AGTAGGGCTTAATACACCCTGAACAA

8T1L;ACAGTACATAAATCATTTAACAATTT

8T1R;ACAAAATTAATTACAATATATGTGAG

8T2L;CGCTATTAATTAAACCTGAGCAAAAG

8T2R;ATTCATTTCAATTTTTTCCCTTAGAA

8T3L;ATTAAGACGCTGACTTTGAATACCAA

8T3R;ATTCGCCTGATTGGAAGAGTCAATAG

8T4L;GAGACTACCTTTTCAGTAACAGTACC

8T4R;TCAGATGAATATATAACCTCCGGCTT

8T5L;ATGCTGATGCAAAACAGAAATAAAGA

8T5R;ATTTGCACGTAAATCCAATCGCAAGA

8T6L;ATATATTTTAGTTCTGAATAATGGAA

8T6R;TTGGATTATACTTAATTTCATCTTCT

8T7L;CGACCGTGTGATATATCAGATGATGG

8T7R;TCATATTCCTGATAATAAGGCGTTAA

8B1;GAACTGATAGCCCTAAAACATCGCCA

8B2;AGAAGATAAAACAGAGGTGAGGCGGT

8B3;CCACGCTGAGAGCCAGCAGCAAATGA

8B4;CCTCAAATATCAAACCCTCAATCAAT

8B5;TGAAAGGAATTGAGGAAGGTTATCTA

8B6;AATAGATTAGAGCCGTCAATAGATAA

8B7;ACTTTACAAACAATTCGACAACTCGT

Hel1;GCCAGTGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGG
G

Hel2;AGAACCCTCATATATTTTAAATGCAATGCCTGAGTAATGTGTAGGTAAA
G

Hel3;AACACTATCATAACCCTCGTTTACCAGACGACGATAAAAACCAAAATAG
C

Hel4;TAACCGATATATTCGGTCGCTGAGGCTTGCAGGGAGTTAAAGGCCGCTT
T

Hel5;ATTCACAAACAAATAAATCCTCATTAAAGCCAGAATGGAAAGCGCAGTC
T

Hel6;ATATCAGAGAGATAACCCACAAGAATTGAGTTAAGCCCAATAATAAGA
GC

Hel7;AATTACTAGAAAAAGCCTGTTTAGTATCATATGCGTTATACAAATTCTTA

Hel8:ATTAATTTTAAAAGTTTGAGTAACATTATCATTTTGCGGAACAAAGAAA
C

Table S7. Bridge strands for 5×11 structure

6T1;AACAAGAGTCCACTATTAAAGAACGT

6T2;TTATAAATCAAAAGAATAGCCCGAGA

6T3;CCCAGCAGGCGAAAATCCTGTTTGAT

6T4;CTTCACCGCCTGGCCCTGAGAGAGTT

6T5;GCGCCAGGGTGGTTTTTCTTTTCACC

61L;ACGCCAGGGTTTTGCGAAAGGGGGAT

61R;ATTACGCCAGCTGCCCAGTCACGACG

62L;TTGCATGCCTGCACAACTGTTGGGAA

62R;CATTCAGGCTGCGGGTCGACTCTAGA

63L;CGTAATCATGGTCCCGCTTCTGGTGC

63R;CAGCTTTCCGGCAATAGCTGTTTCCT

64L;TCCACACAACATAACGACGACAGTAT

64R;CCAGTTTGAGGGGCGAGCCGGAAGCA

65L;TGAGTGAGCTAACCACGTTGGTGTAG

65R;TAATGGGATAGGTTCACATTAATTGC

71L;ATCAGGTCATTGCCCGGAGAGGGTAG

71R;TGATAAATTAATGCTGAGAGTCTGGA

72L;ATCGTAAAACTAGAGTCAAATCACCA

72R;AAAGGCCGGAGACCATGTCAATCATA

73L;CCCCAAAAACAGGTGCCTGAGTAATG

73R;ATTTTAAATGCAAAAGATTGTATAAG

74L;ATTTTGTTAAAATATTTCAACGCAAG

74R;GGGAGAAGCCTTTTCGCATTAAATTT

75L;AATAGGAACGCCAGGTTGTACCAAAA

75R;ATAAAGCTAAATCTCAAAAATAATTC

81L;TTTGATAAGAGGTCCAACAGGTCAGG

81R;CCGGAAGCAAACTCATTTTTGCGGAT

82L;ATGCTGTAGCTCAAAATATCGCGTTT

82R;CCCGAAAGACTTCACATGTTTTAAAT

83L;GTTTCATTCCATAAGAAGCAAAGCGG

83R;GACTATTATAGTCTAACAGTTGATTC

84L;TTTGACCATTAGAACGAGAATGACCA

84R;AACAGTTCAGAAATACATTTCGCAAA

85L;TTCATTTGGGGCGTCGTCATAAATAT

85R;CAATACTGCGGAACGAGCTGAAAAGG

91L;CAACTTTAATCATCAGAACGAGTAGT

91R;TGACGAGAAACACTGTGAATTACCTT

92L;TACCAGTCAGGACACGTAACAAAGCT

92R;ATTACCCAAATCAGTTGGGAAGAAAA

93L;GAACAACATTATTACCTTCATCAAGA

93R;CATAGGCTGGCTGACAGGTAGAAAGA

94L;ACATTCAACTAATCTTTGAAAGAGGA

94R;CCGAACTGACCAAGCAGATACATAAC

95L;AGAGCAACACTATTTAGCCGGAACGA

95R;TGCTCCATGTTACCATAACCCTCGTT

101L;ACGCATAACCGATTACCGATAGTTGC

101R;TTAAACAGCTTGAATATTCGGTCGCT

102L;TTTTGCGGGATCGATTGTATCGGTTT

102R;AAAGGAGCCTTTATCACCCTCAGCAG

103L;GCAACGGCTACAGAATTTTTTCACGT

103R;AATTGCGAATAATAGGCTTTGAGGAC

104L;CATTAAACGGGTAAGTTTCAGCGGAG

104R;AACAACTTTCAACAAATACGTAATGC

105L;AAAGAGGCAAAAGAGACGTTAGTAAA

105R;TTGTCGTCTTTCCAATACACTAAAAC

111L;ATGAAAGTATTAAAATGCCCCCTGCC

111R;CGTATAAACAGTTGAGGCTGAGACTC

112L;GGTTTTGCTCAGTATAAGTTTTAACG

112R;GAGTGTACTGGTAACCAGGCGGATAA

113L;ATAGCCCGGAATACGTTCCAGTAAGC

113R;TCTCTGAATTTACGGTGTATCACCGT

114L;TCAGAACCGCCACACAAATAAATCCT

114R;TTGATATTCACAACCTCAGAACCGCC

115L;CAGGGATAGCAAGAGCATTGACAGGA

115R;CAGAGCCGCCGCCCCCAATAGGAACC

Hel6;AGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC
G

Hel7;CTTTCATCAACATTAAATGTGAGCGAGTAACAACCCGTCGGATTCTCCG
T

Hel8;GTAGCATTAACATCCAATAAATCATACAGGCAAGGCAAAGAATTAGCA
AA

Hel9;AATAGCGAGAGGCTTTTGCAAAAGAAGTTTTGCCAGAGGGGGTAATAGT

A

Hel10;TATACCAAGCGCGAAACAAAGTACAACGGAGATTTGTATCATCGCCTG

AT

Hel11;GTCACCAGTACAAACTACAACGCCTGTAGCATTCCACAGACAGCCCTC

AT

AFM images

Figure S1.1 5×5 structure up band (AGE) AFM images

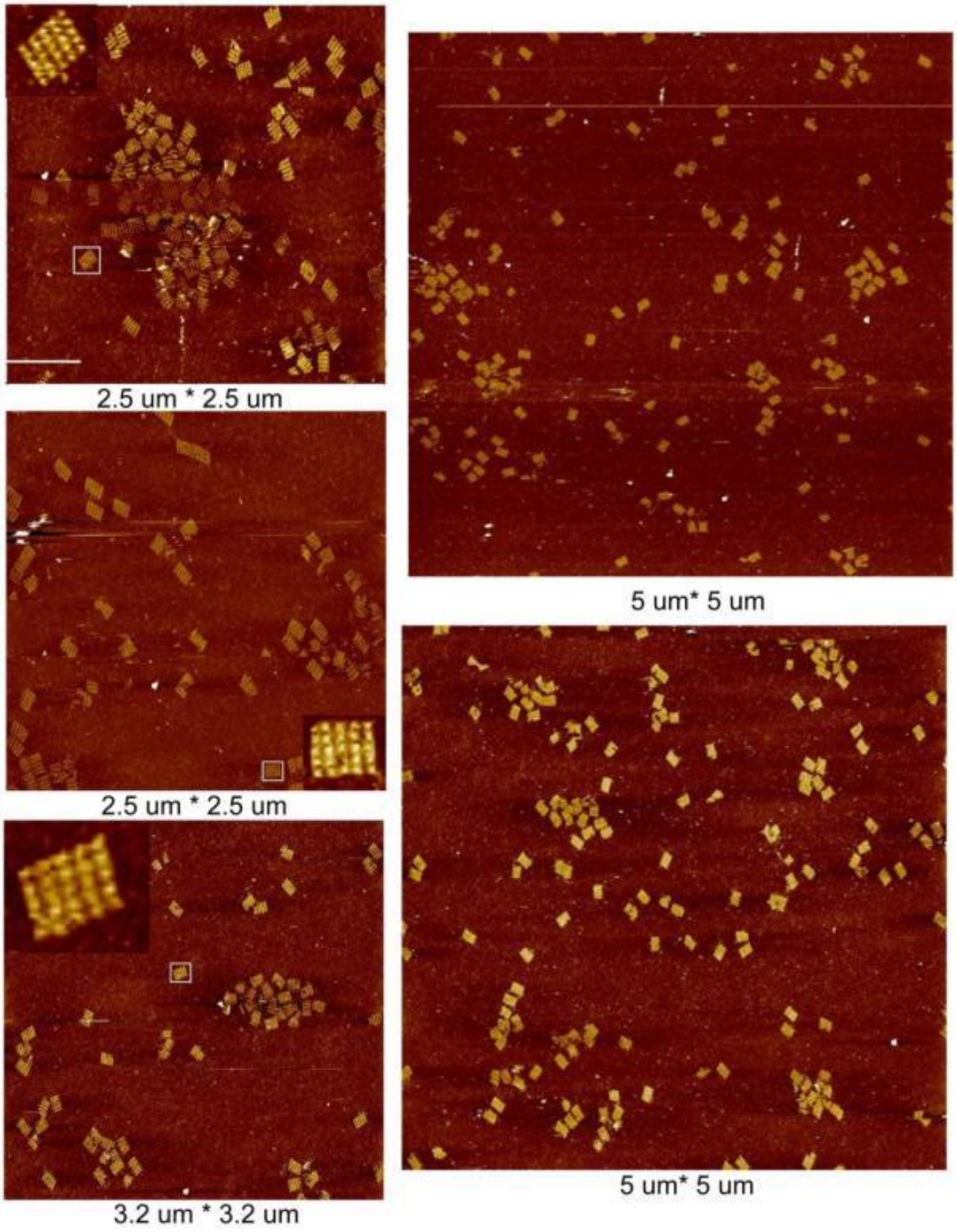
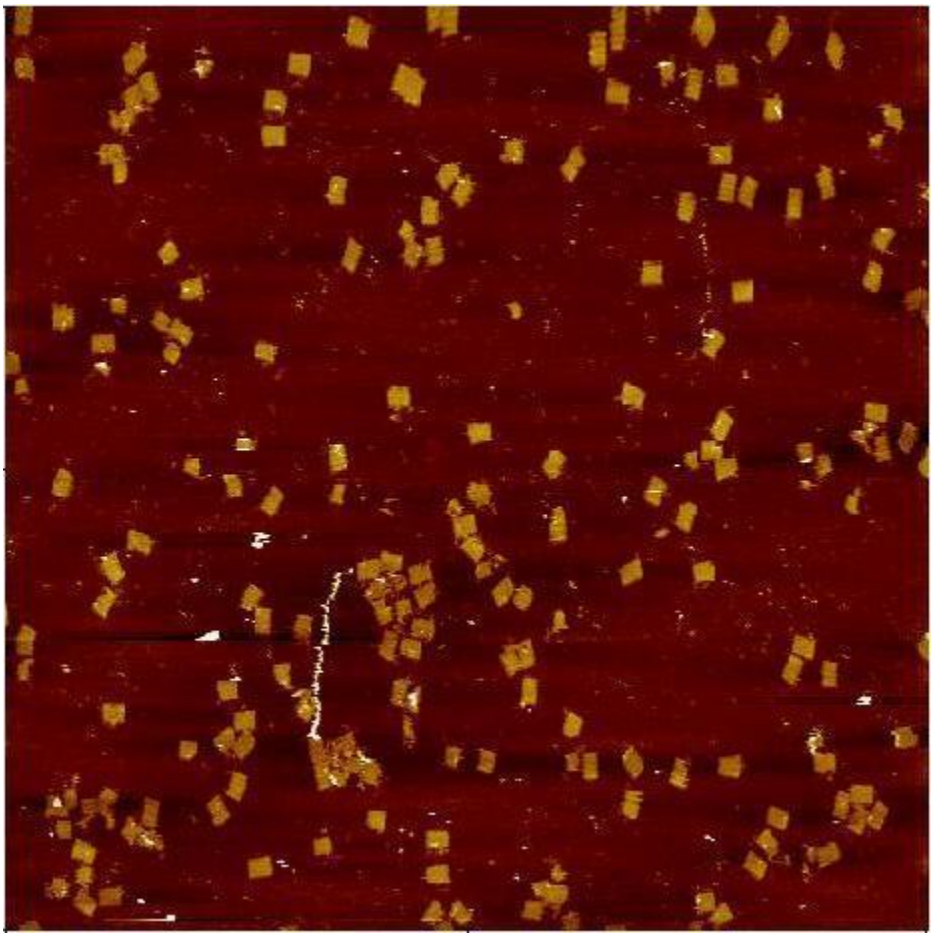
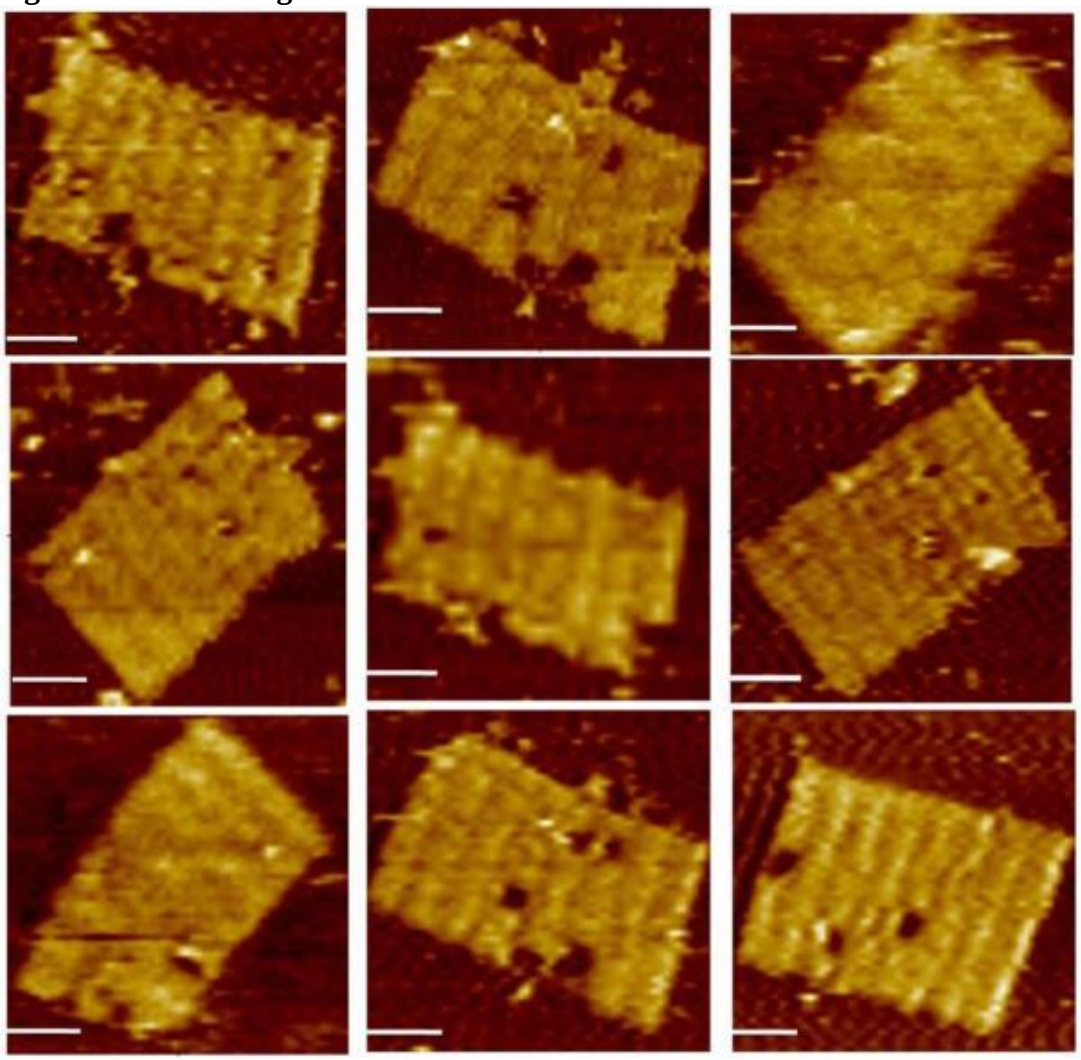


Figure S1.2 AFM images for 5×5 structure down band (AGE) AFM images



5um*5um

Figure S2. AFM images for 7×8 structure.



40nm scale bar

Figure S3. Design of 5×11 structure

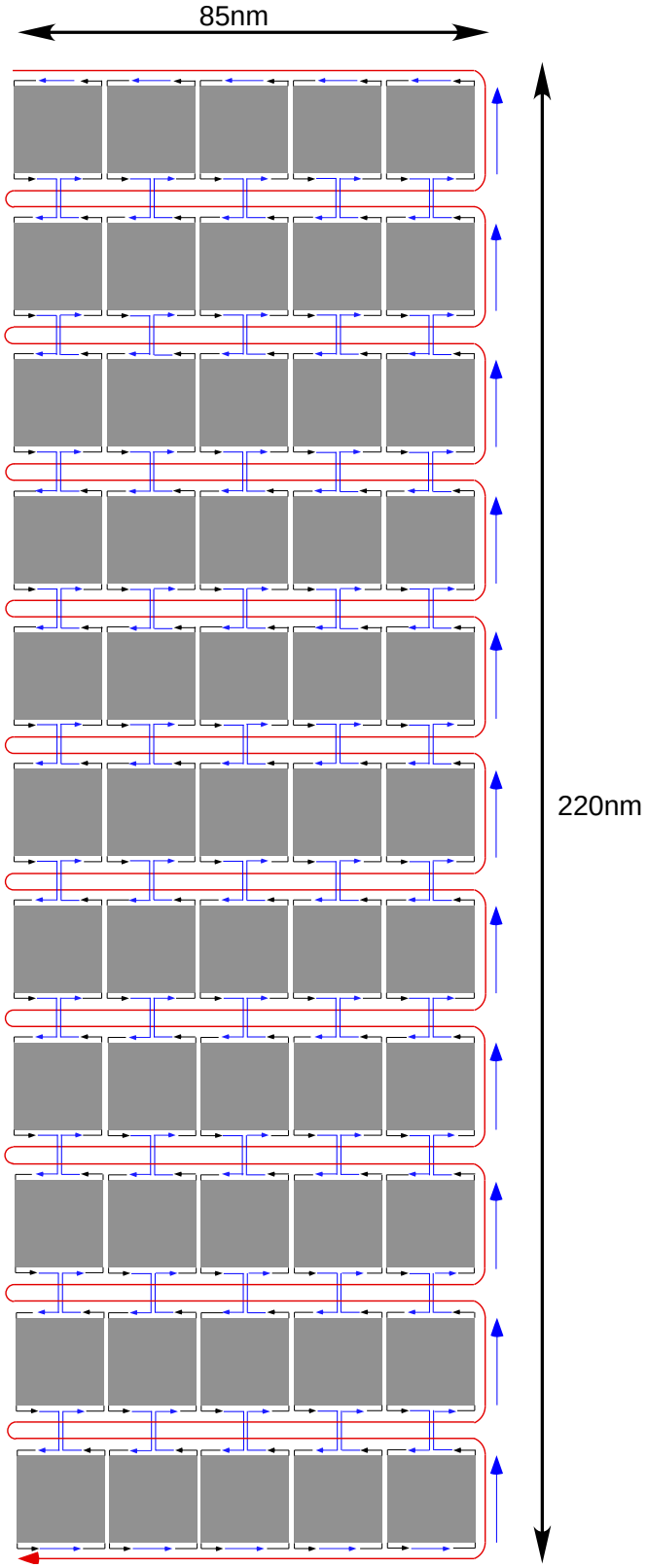


Figure S4. Gel images for 5×11 structure

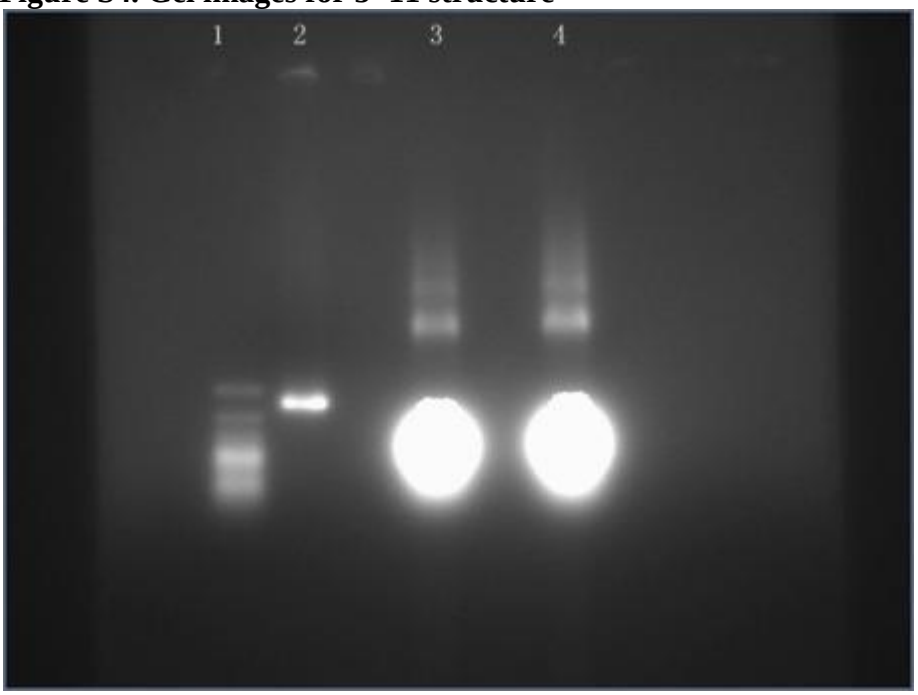
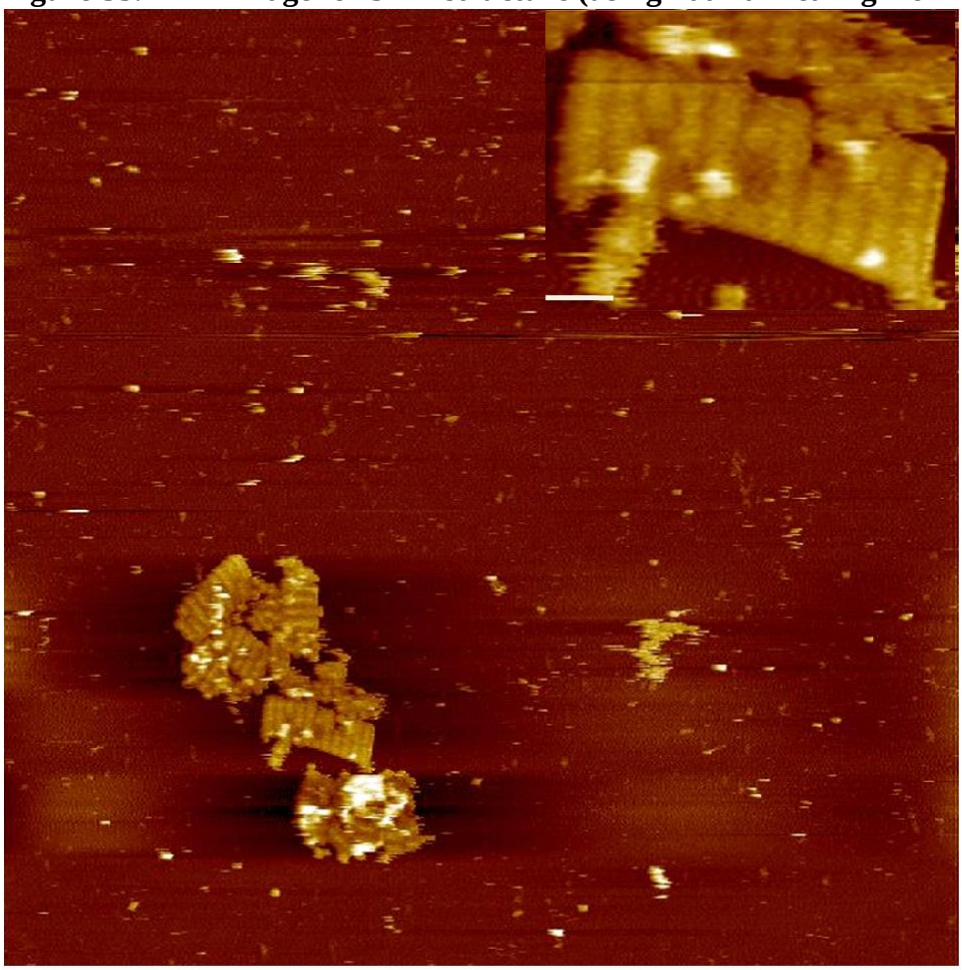
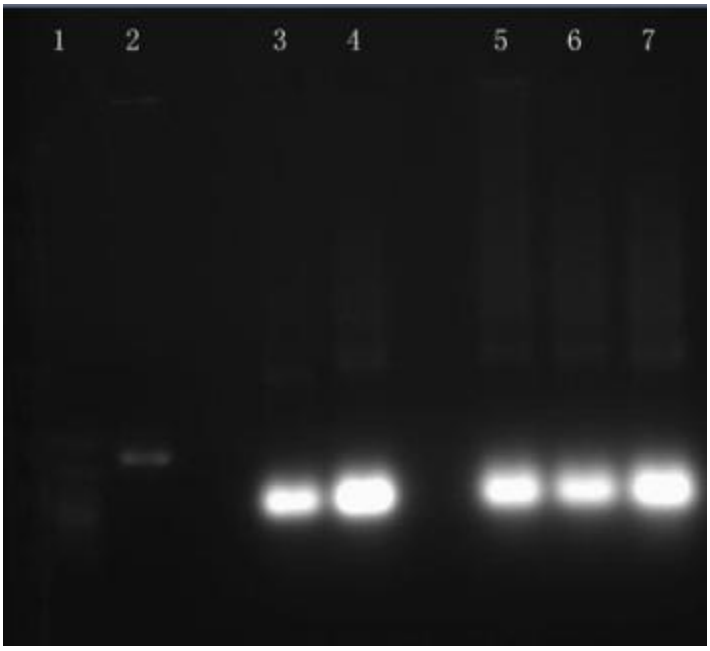


Figure S5. AFM image for 5×11 structure (using 100h annealing from 45C to 4C)



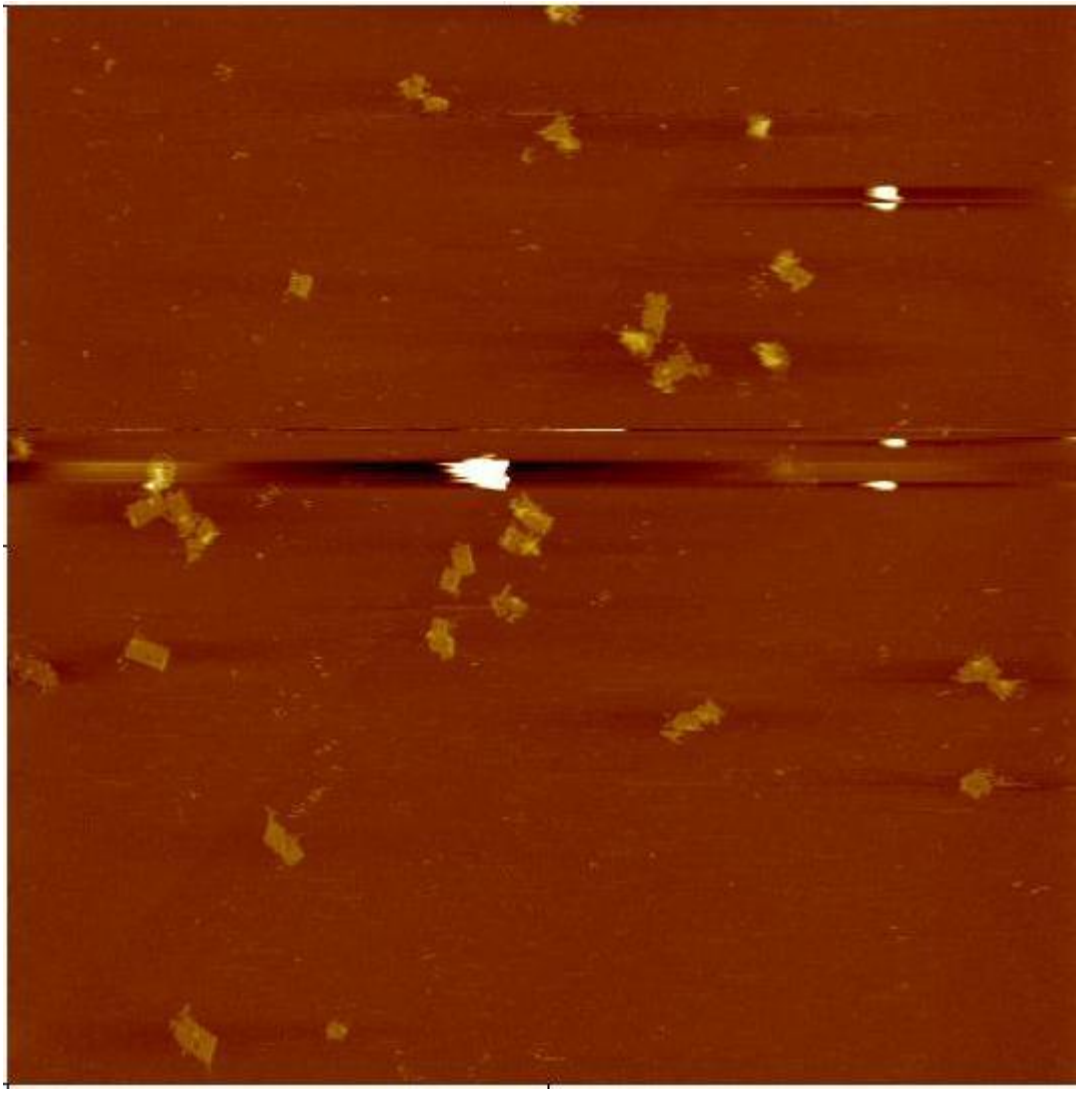
2.35 um*2.35um

Figure S6 . AGE picture for 5*n layer structure (n=) using 30h annealing



1, 100bp marker; 2, M13; 3, 8 layer structure(1.2*Mg); 4, 10 layer structure (1.2*Mg); 5, 6, 7, 11 layer structure at different Mg conditions, 1.5, 1.2. 1.0

Figure S7. AFM images for 8 layer structure



5um*5um

Figure S8. AFM for 10 layer structure

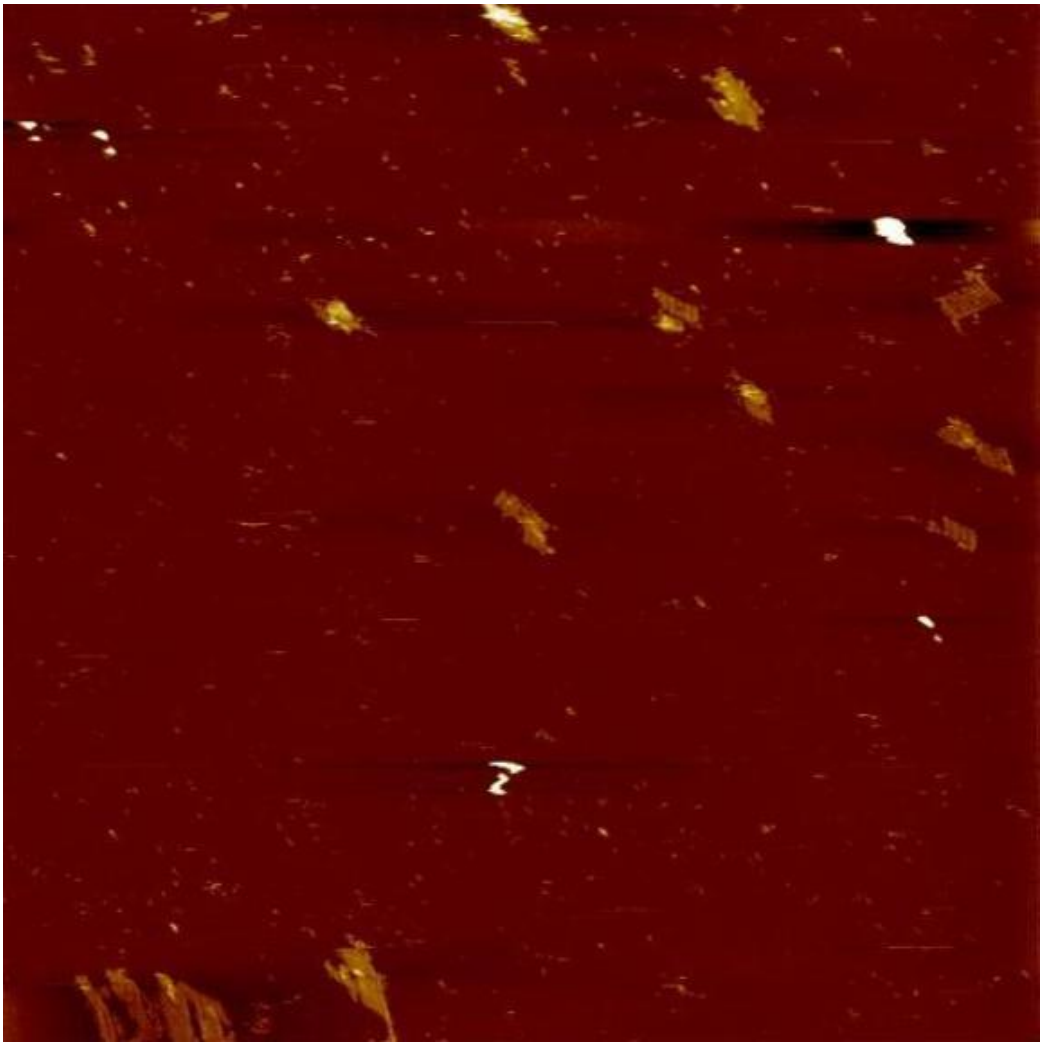
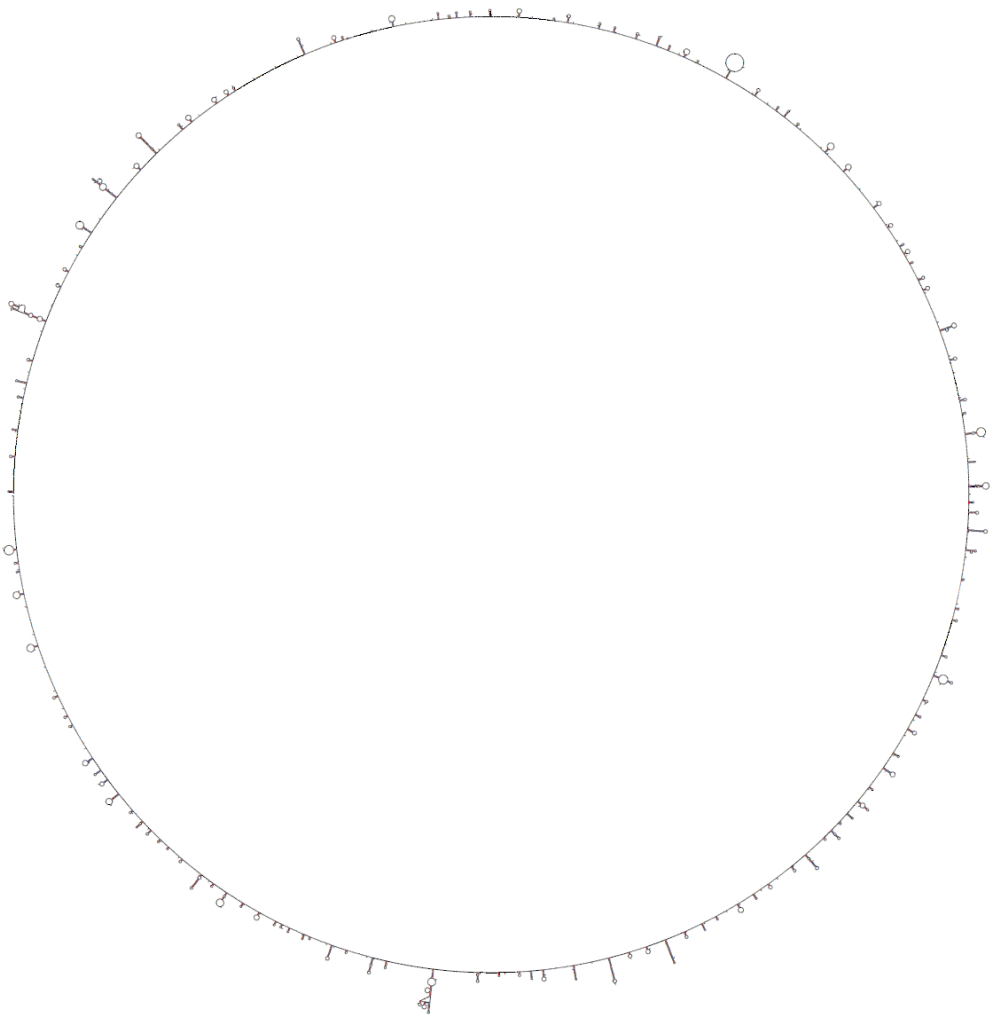


Figure S9. Secondary structure of M13 strand at 45 °C with 10 mM NaCl and 15 mM Mg2+ using Mfold (http://mfold.bioinfo.rpi.edu/cgi-bin/dna-form1.cgi). The secondary structure contains one 20 bp hairpin, one 13 bp hairpin and the rest are all equal or less than < 10 bp. Since the number of base-pairing between the staple tiles and the M13, and between the bridge strands and the M13 are all 13 bp, the only hairpin remains a concern is the one with 20bp. In our design the 20 bp hairpin is located in the unused loop in the 5x5 structure, but used in the 7x8 and 5x11 structures. This may partially explain the reduced yield for the larger structures.



APPENDIX B

SUPPLEMENTAL INFORMATION FOR CHAPTER 3

Supplemental Information

Organizing DNA Origami Tiles Into Larger Structures Using Pre-formed Scaffold Frames

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Arizona State University, Tempe, AZ 85287

Experimental Materials and Methods

Materials: All DNA staple strands were purchased from Integrated Technologies, Inc. (www.IDTDNA.com) in the format of 96-well plates and desalted with concentrations normalized to 100 μM. Single stranded M13mp18 viral DNA and ΦX 174 DNA were purchased from New England Biolabs, Inc. (NEB, Catalog number: N4040S and N3023S). All DNA strands were used without further purification.

Assembly Procedure: 1) Each individual DNA origami staple tile was assembled by mixing M13mp18 DNA (10 nM) with the corresponding staple strands with a 1:5 molar ratio in 1 $\times$TAE-Mg^{2+} buffer (pH 8.0, 20mM Tris, 2 mM EDTA, 12.5 mM $Mg(OAc)_2$). The final volume of each reaction was 100 uL. The oligo mixtures were annealed in a PCR thermocycler, cooled from 90°C to 70°C at a rate of -0.5°C/min and subsequently cooled from 70°C to 4°C at a rate of -0.1°C/min. Following the anneal, the structures were purified with 100 kD MWCO Microcon centrifugal filter devices (Amicon, Catalog number: UFC510096).

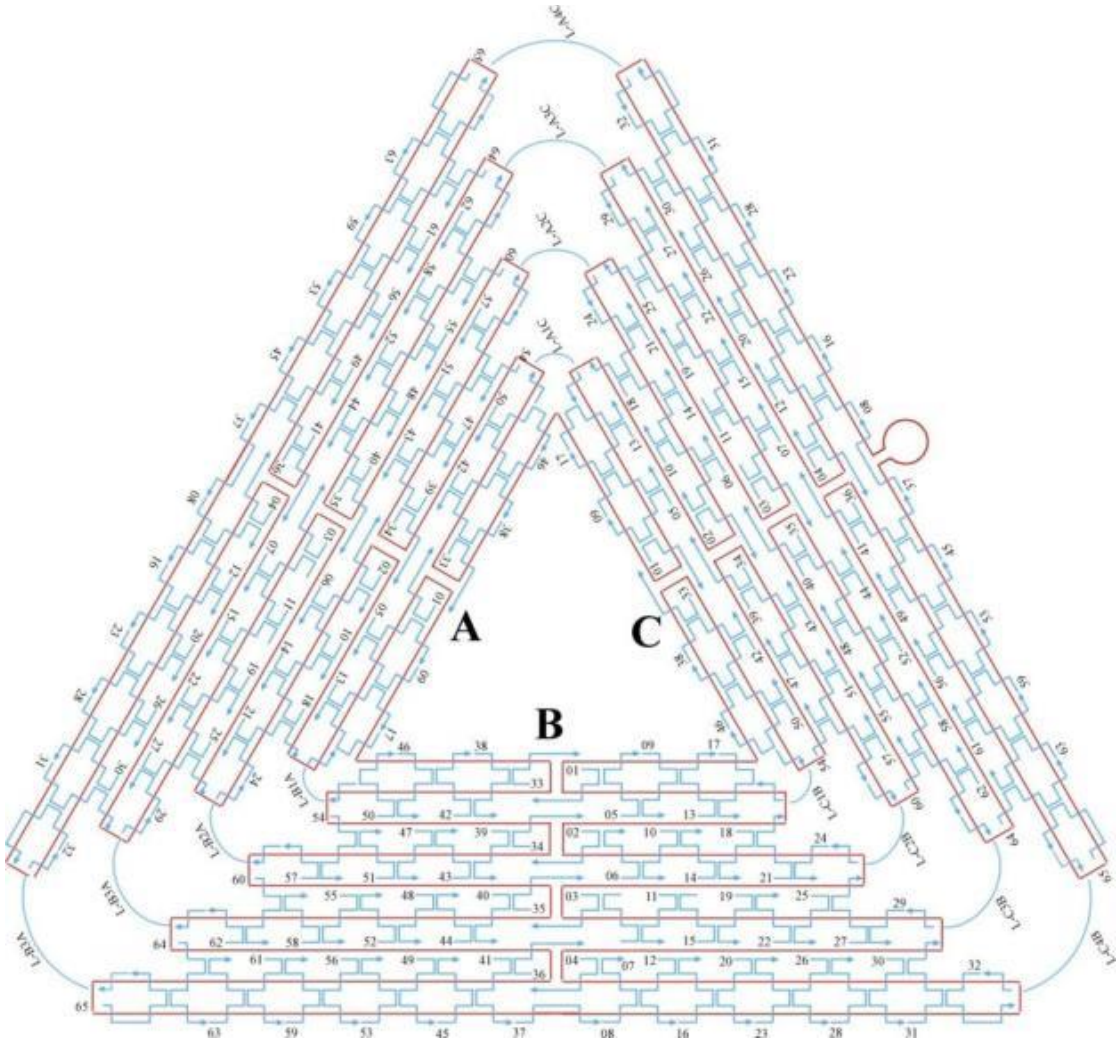
2) Origami super-structures were assembled in a two-step annealing process. Individual origami staple tiles bearing unique single stranded probes along two edges at designed positions were annealed in separate tubes as described above and subsequently purified

with 100 KD MWCO Microcon centrifugal filters to remove any excess staple strands. At the same PhiX174 scaffold strand (10 nM) and a complete set of bridges strands were mixed in a separate tube (molar ratio 1:10) and annealed from 90 °C to 4 °C over 10 h in 1×TAE-Mg^{2+} buffer. The two solutions were mixed together (molar ratio 1.5:1 or 2:1) and annealed from 45 °C to 4 °C at a rate of -2°C/h. The annealing cycle was repeated 10 times, and in each consecutive cycle the starting temperature was decreased by 0.5 °C from the prior cycle. The entire annealing program took approximately 100 hrs.

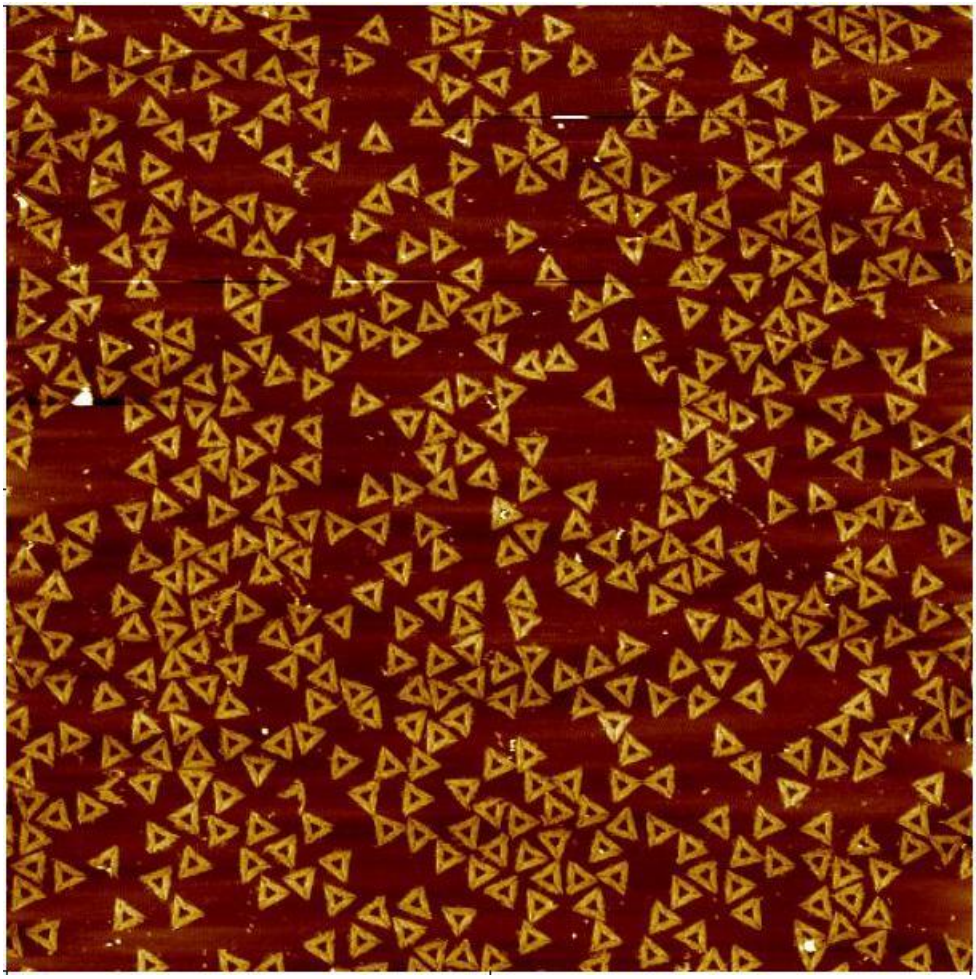
Agarose gel electrophoresis: The assembled products were loaded into agarose gels (0.3% agarose in 1×TAE-Mg^{2+} aqueous buffer, containing 0.5 µg/mL ethidium bromide) and subject to gel electrophoresis at 80V for one hour.

AFM imaging: The samples (2 µL) were deposited onto freshly cleaved mica (Ted Pella, Inc.) and left to adsorb for 3 min. Buffer (1×TAE-Mg^{2+}, 400 µL) was added on top of the sample and the sample was imaged in fluid tapping mode on a Pico-Plus AFM (Molecular Imaging, now Agilent Technologies) with SNL tips (Veeco Probes, Inc.).

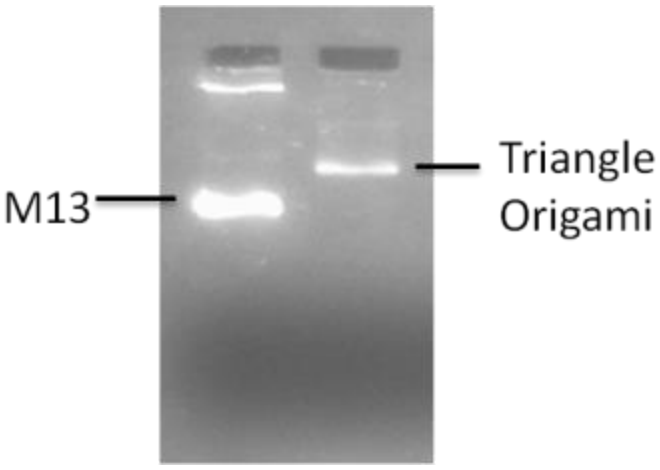
S1. Design of the triangular DNA origami staple tile. The red strand represents the M13 scaffold. The blue strands are the staple strands with arrows pointing to the 3' ends. The spacing between consecutive staple crossovers connecting neighboring parallel helices is 32 bps. The outermost helices are 384 bps or approximately 125 nm.



S2. AFM image of the individual triangular shaped DNA Origami (the size of the image is 3.5 um × 3.5 um)

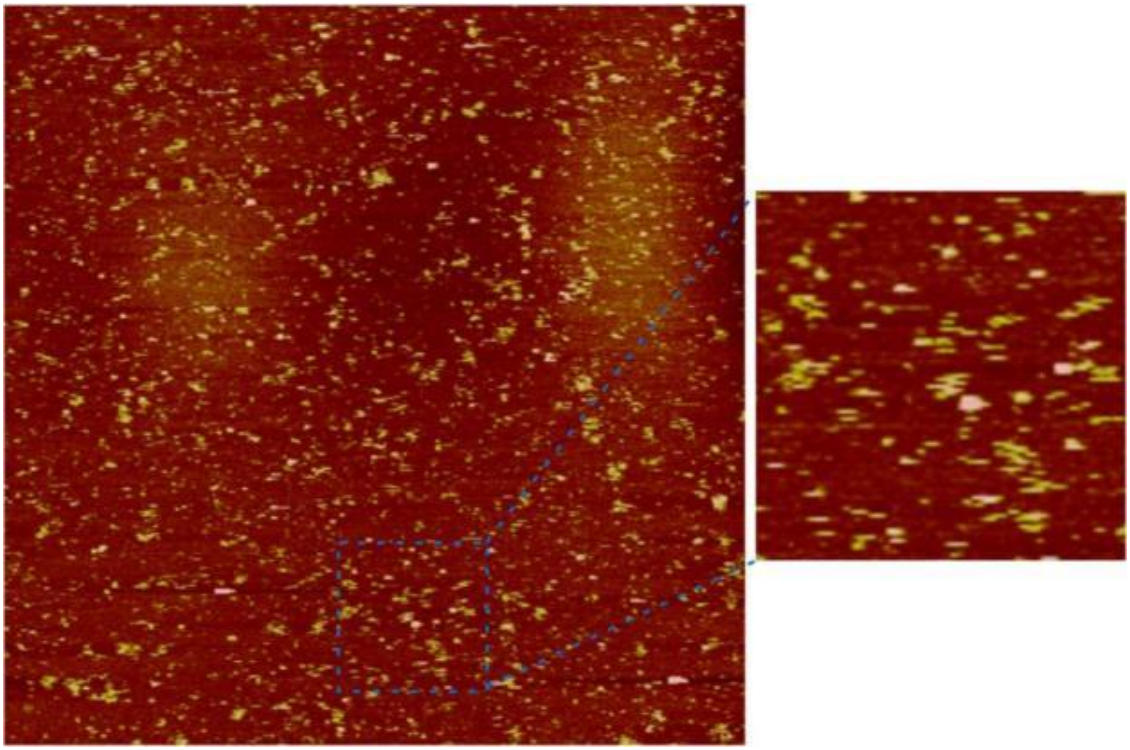


S3. Agarose gel electrophoresis result for the triangular DNA Origami. (1.5% agarose gel)

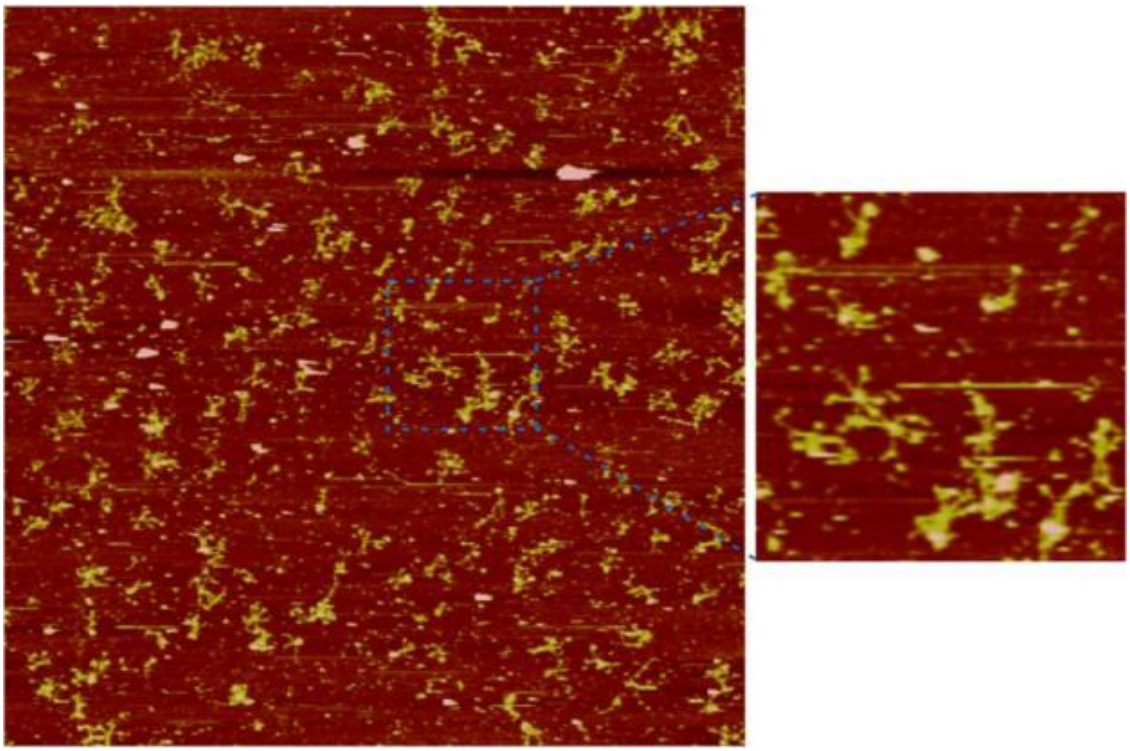

M13
Triangle
Origami

S4. AFM images of the pre-formed scaffold frames of triangle Origami based super Origami with three different designs. (the size of the AFM images are 5 um × 5 um)

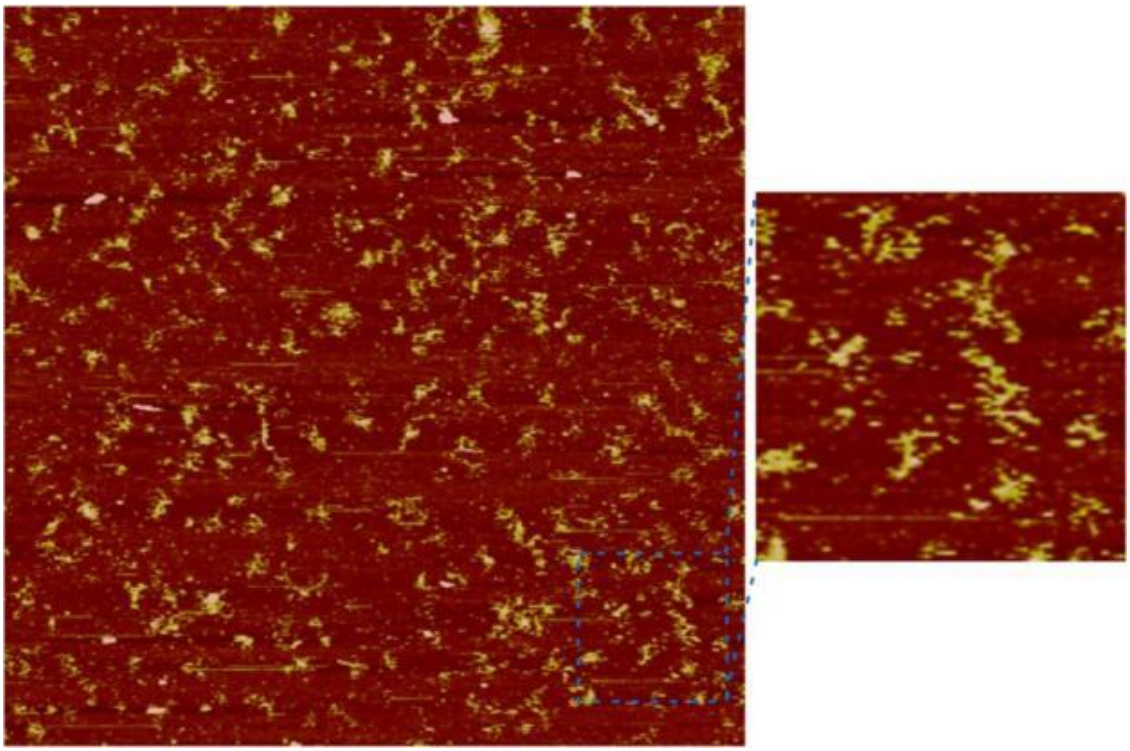
Design 1



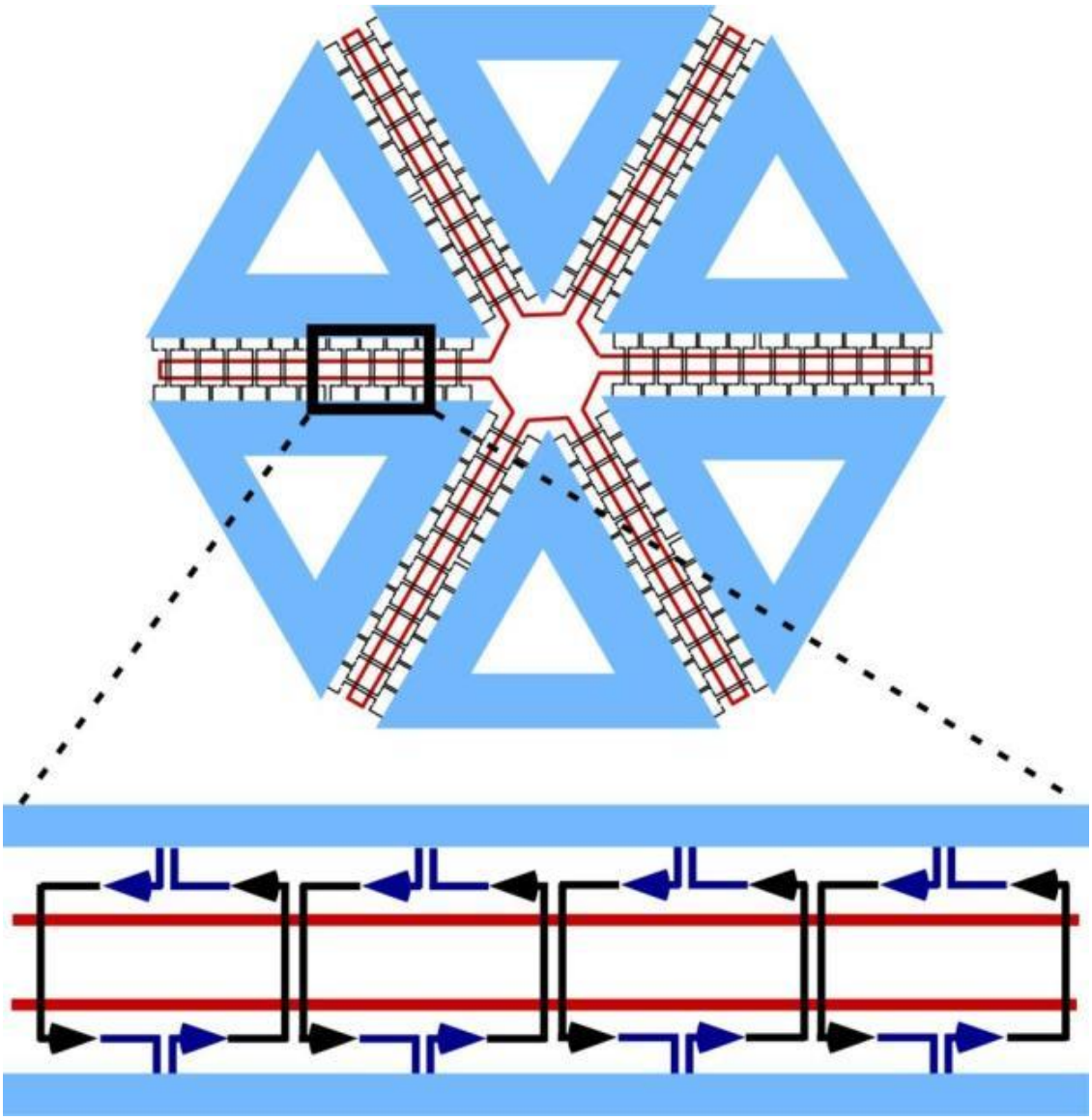
Design 2

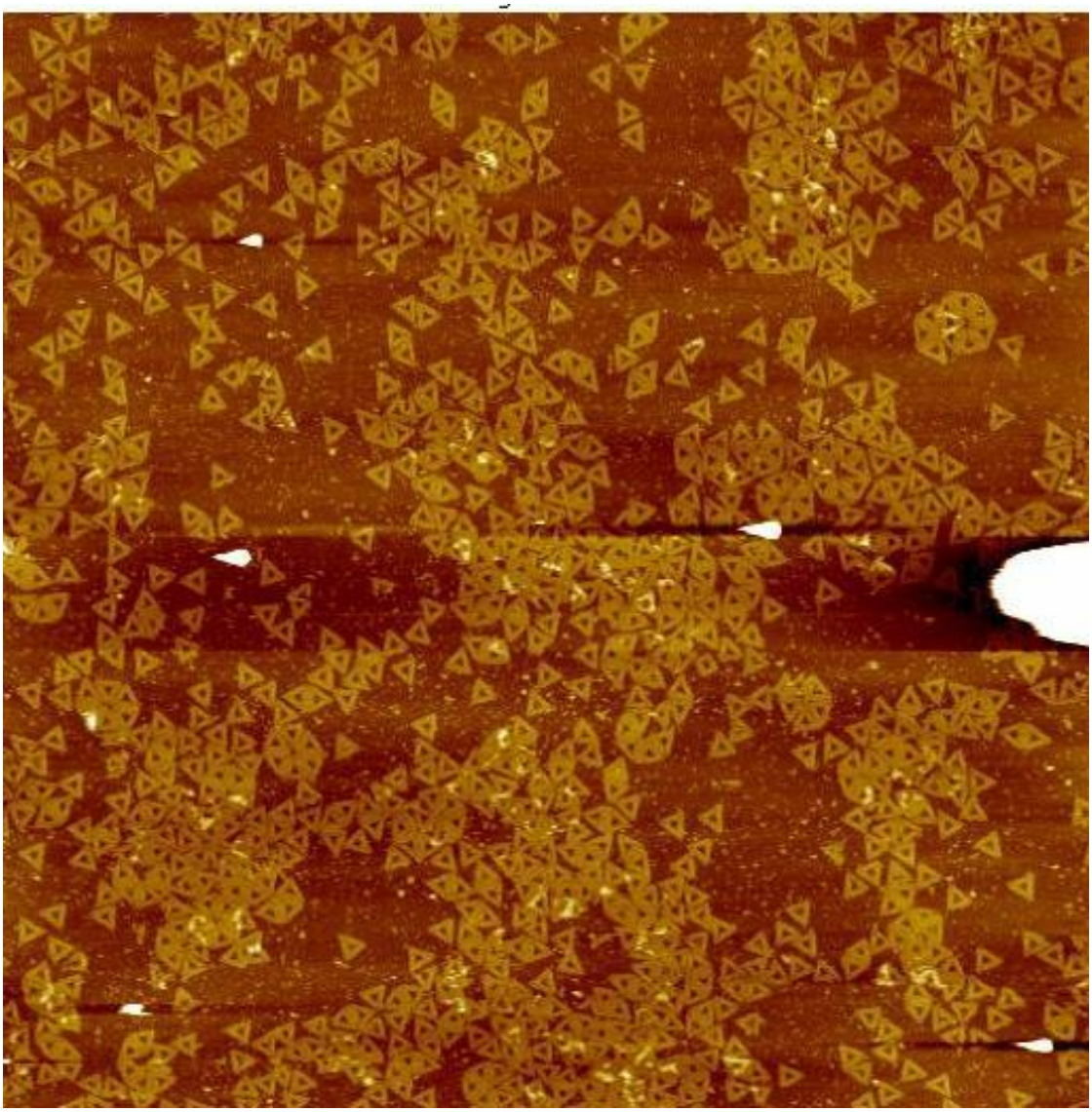


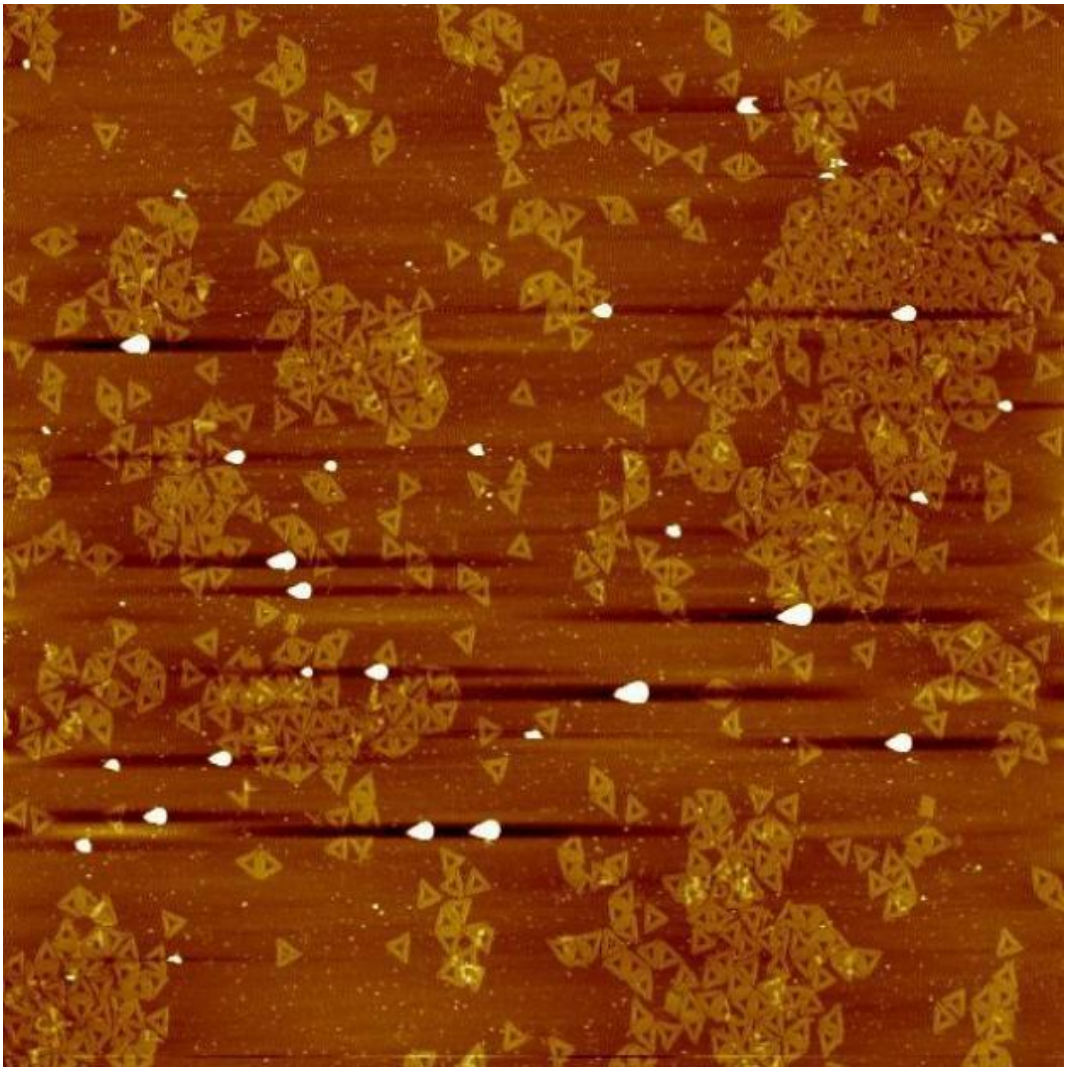
Design 3

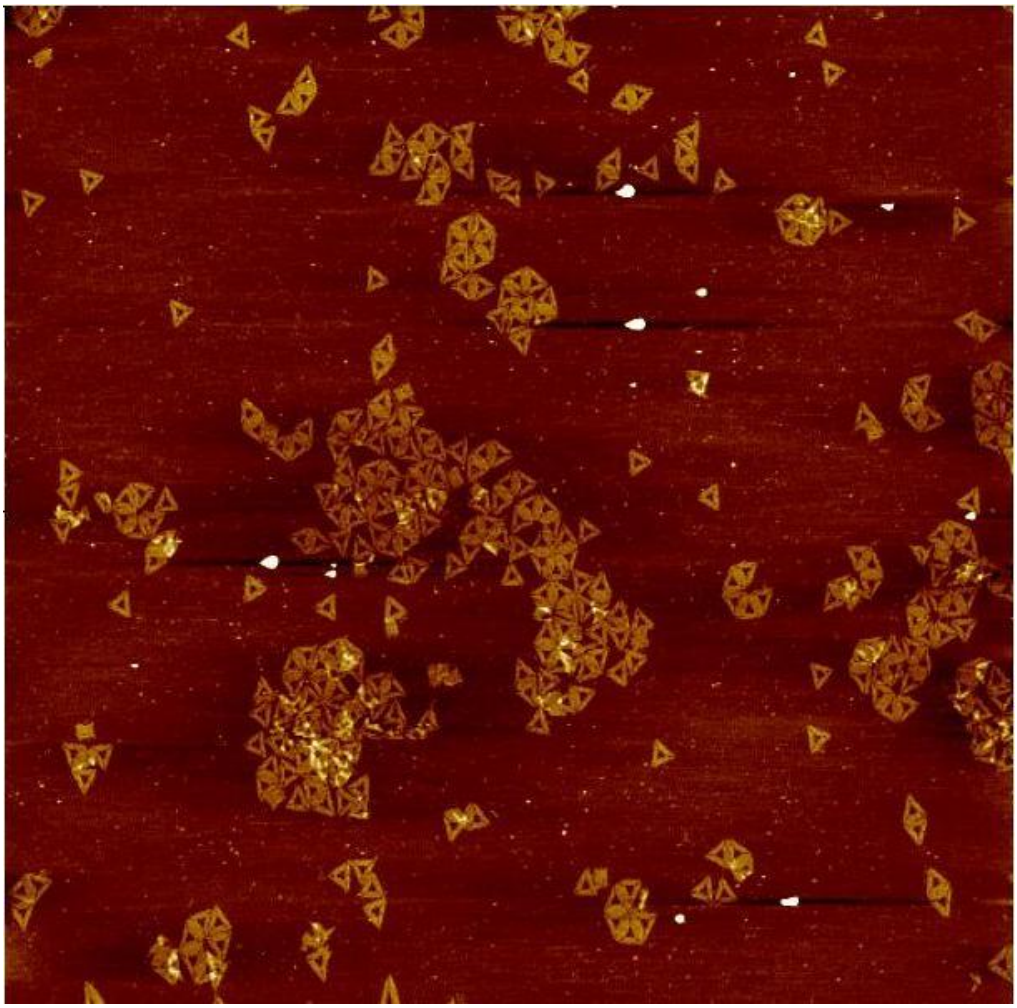


S5. Design and AFM images of the triangular origami staple tile based super-structure using design 1 (the size of the AFM images are 5 um × 5 um)

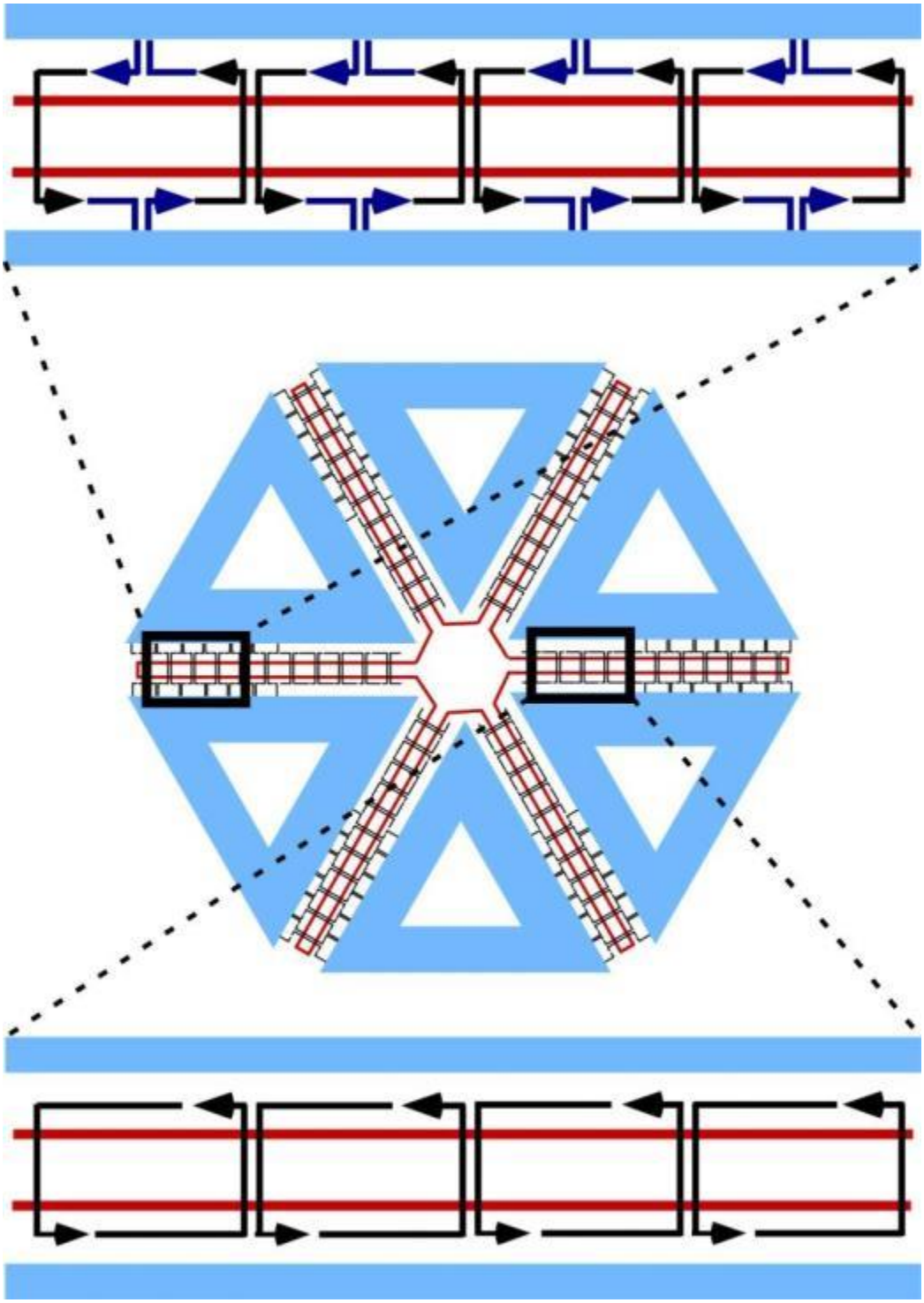


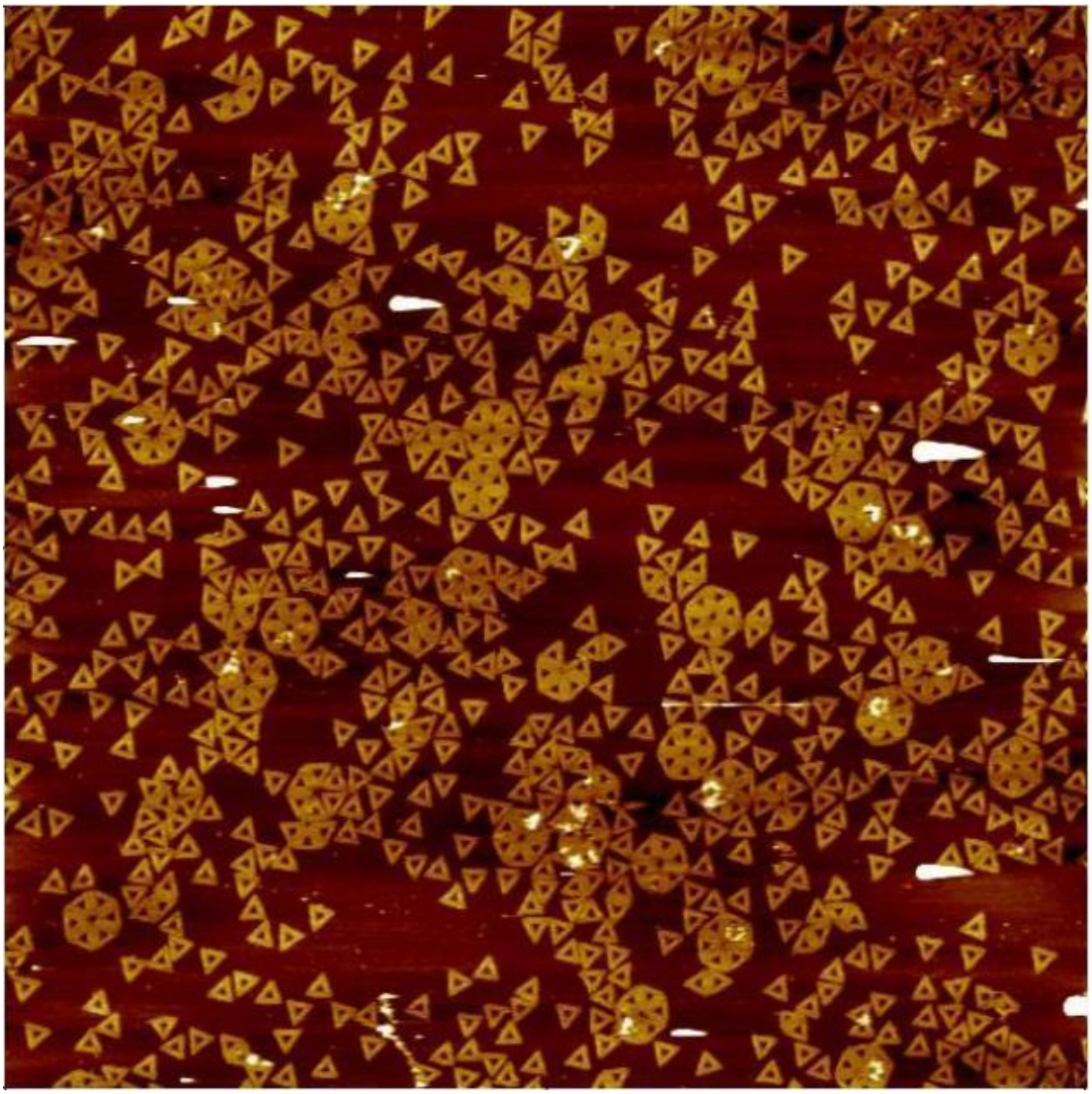


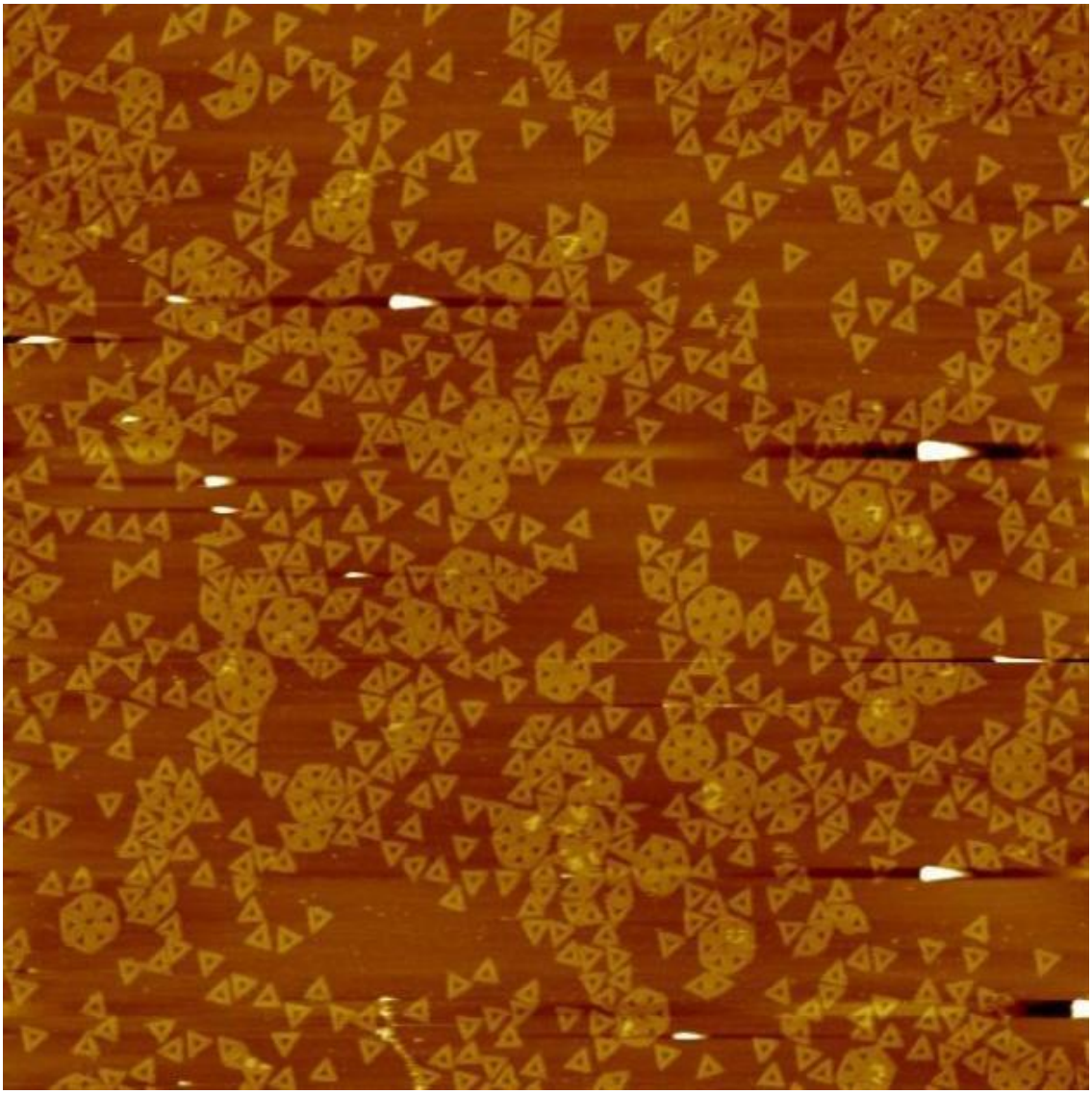


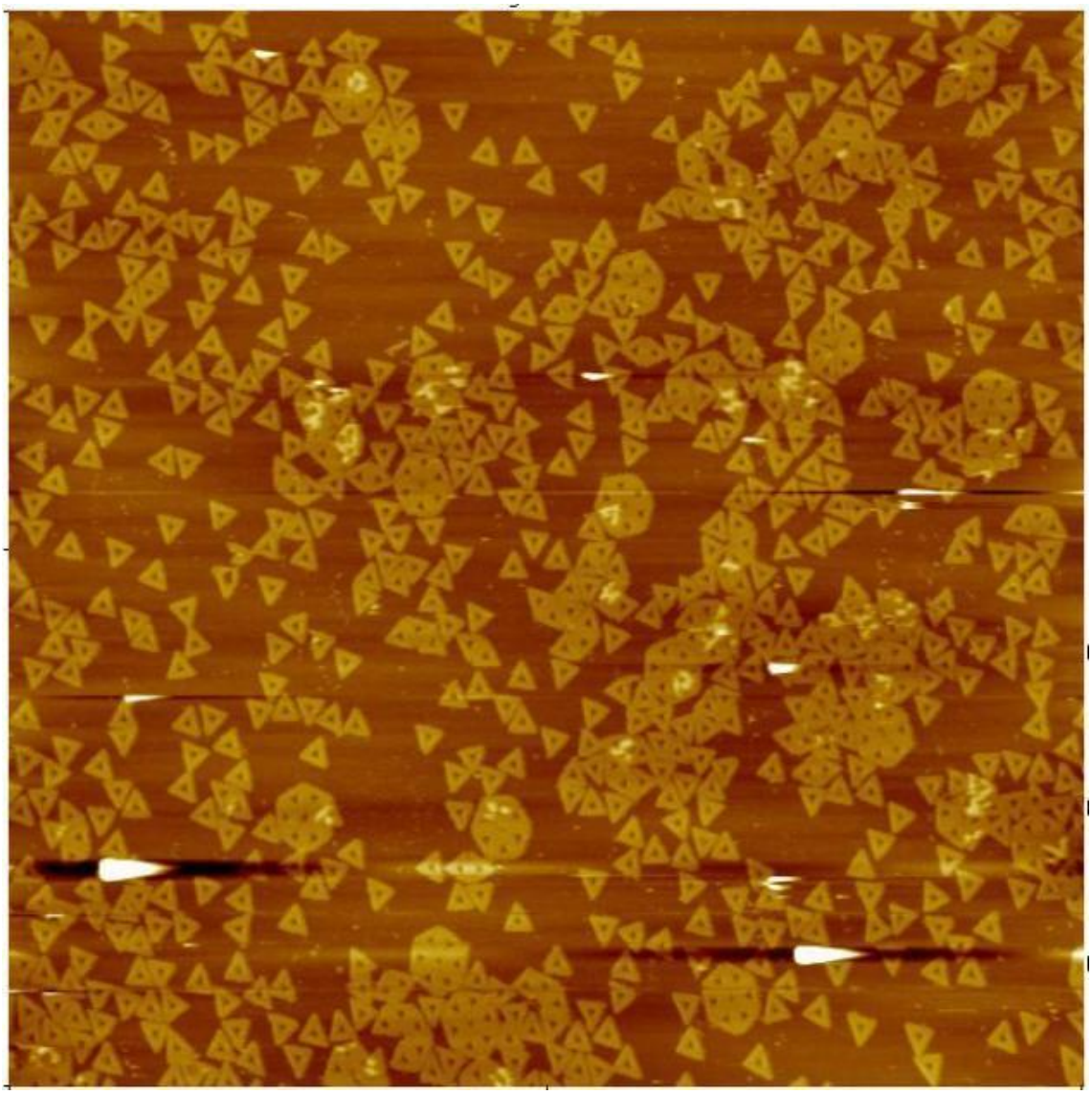


S6. Design and AFM images of the triangular origami staple tile based super-structure using design 2 (the size of the AFM images are 5 um × 5 um)



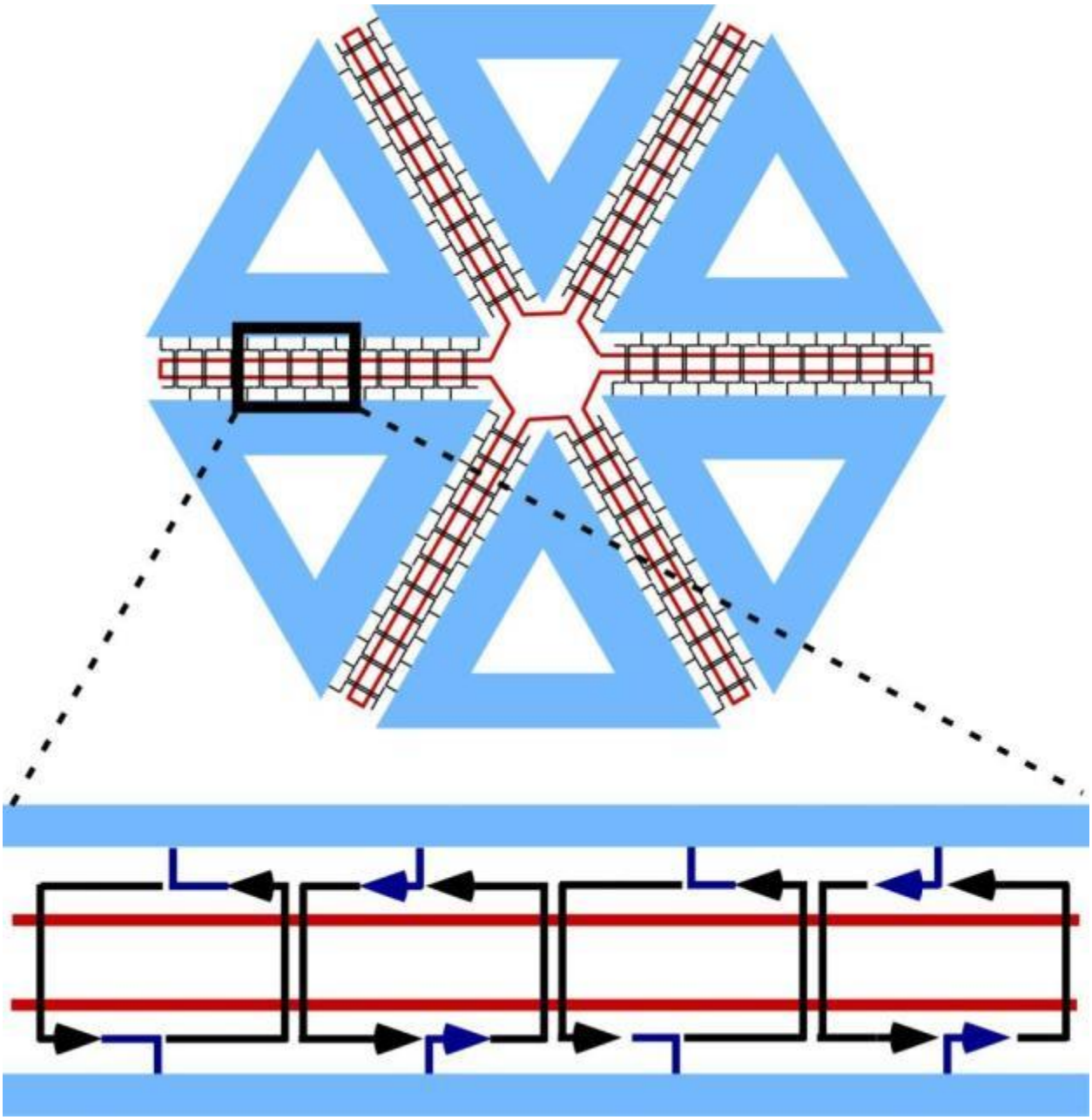


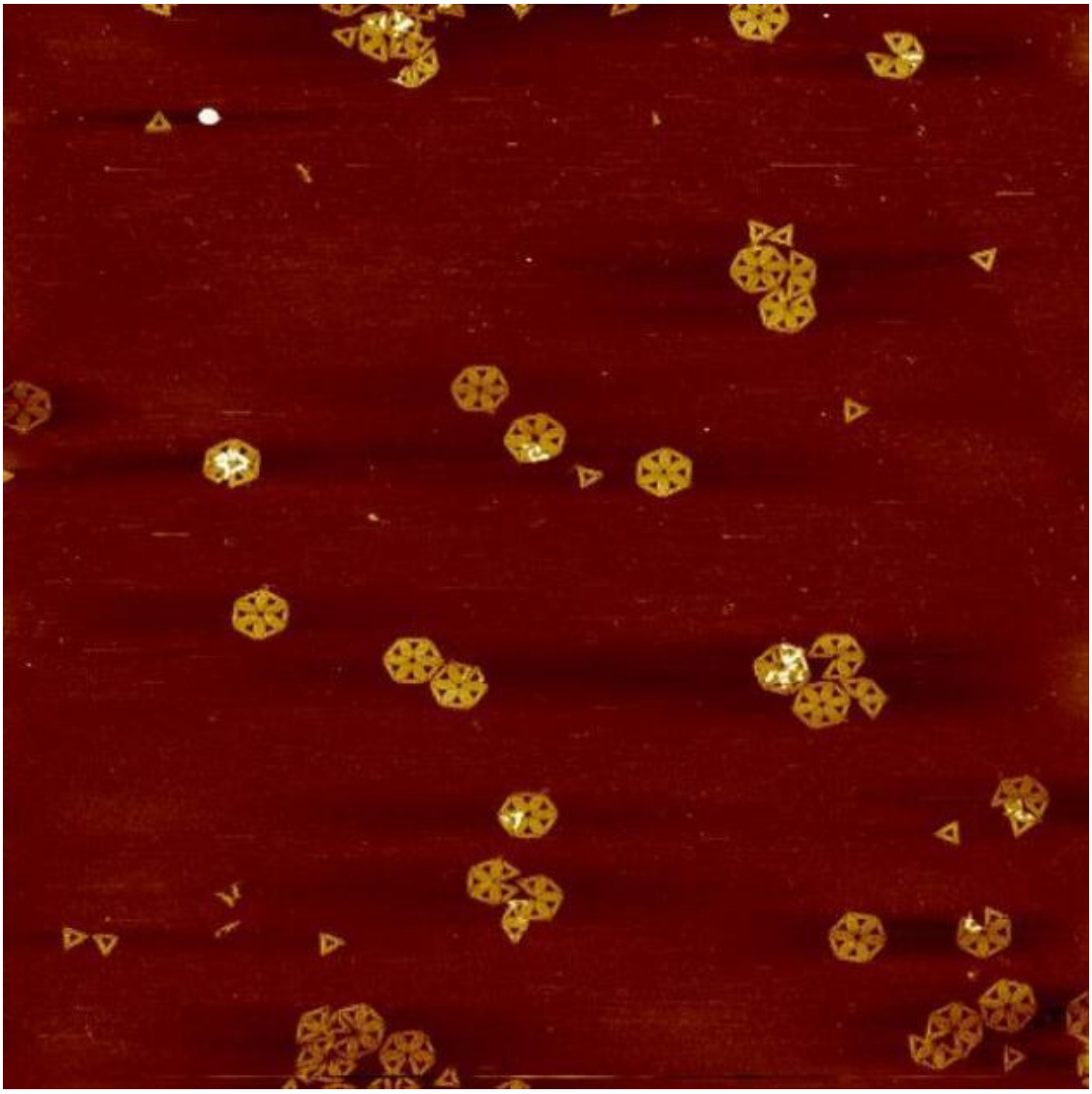


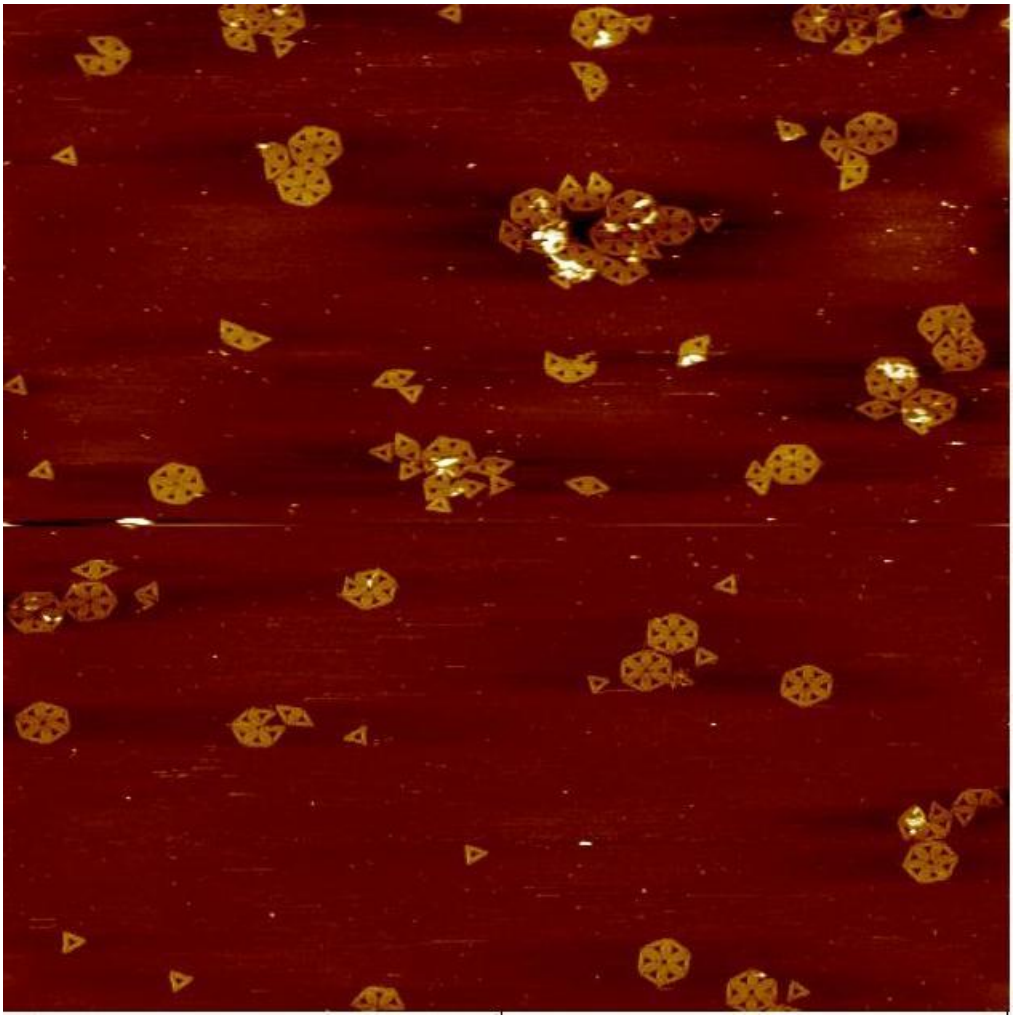


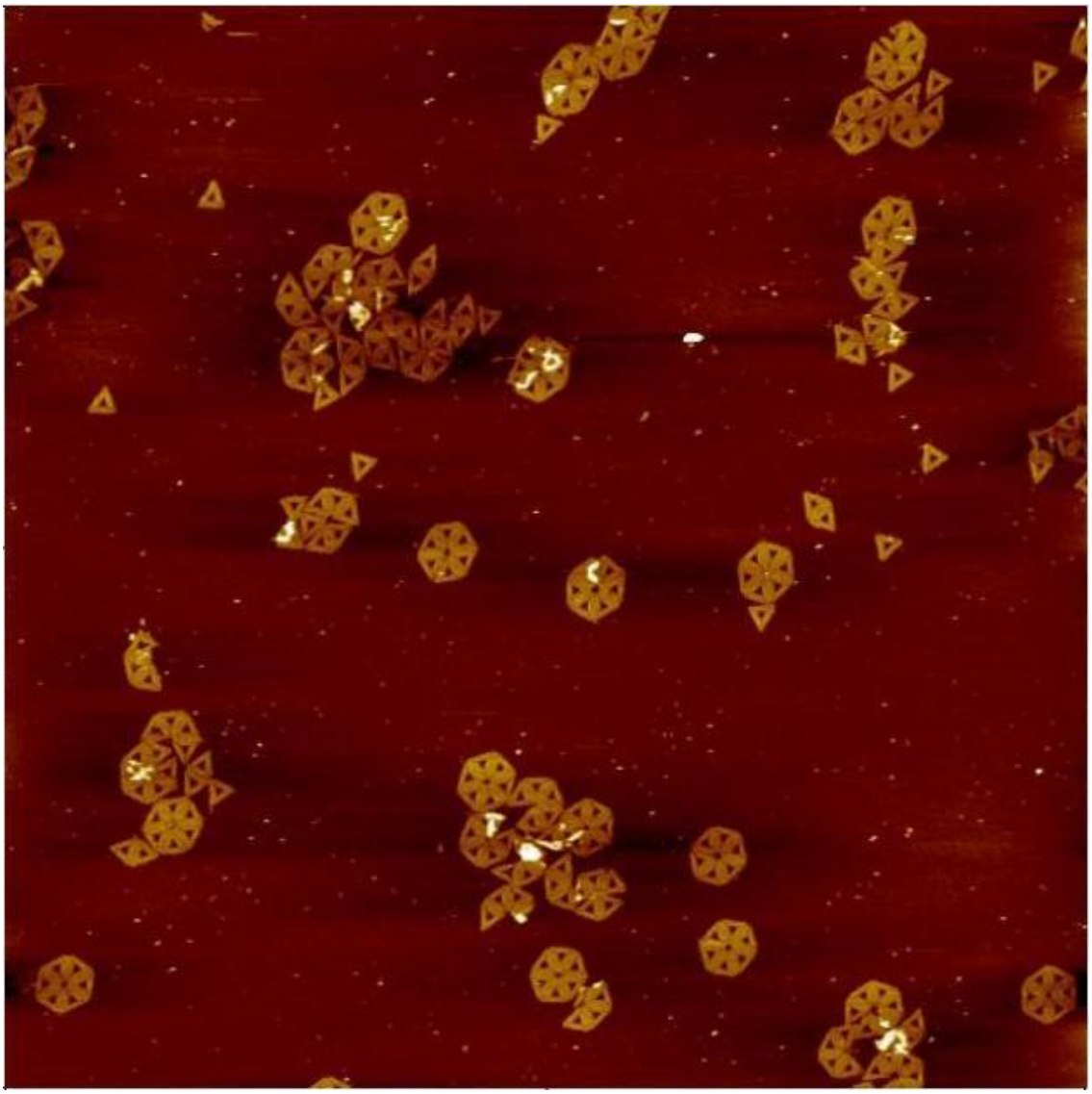
S7. Design and AFM images (zoom out and zoom in) of the triangular origami staple tile based super-structure using design 3 (the size of the AFM images are 5 um × 5 um)

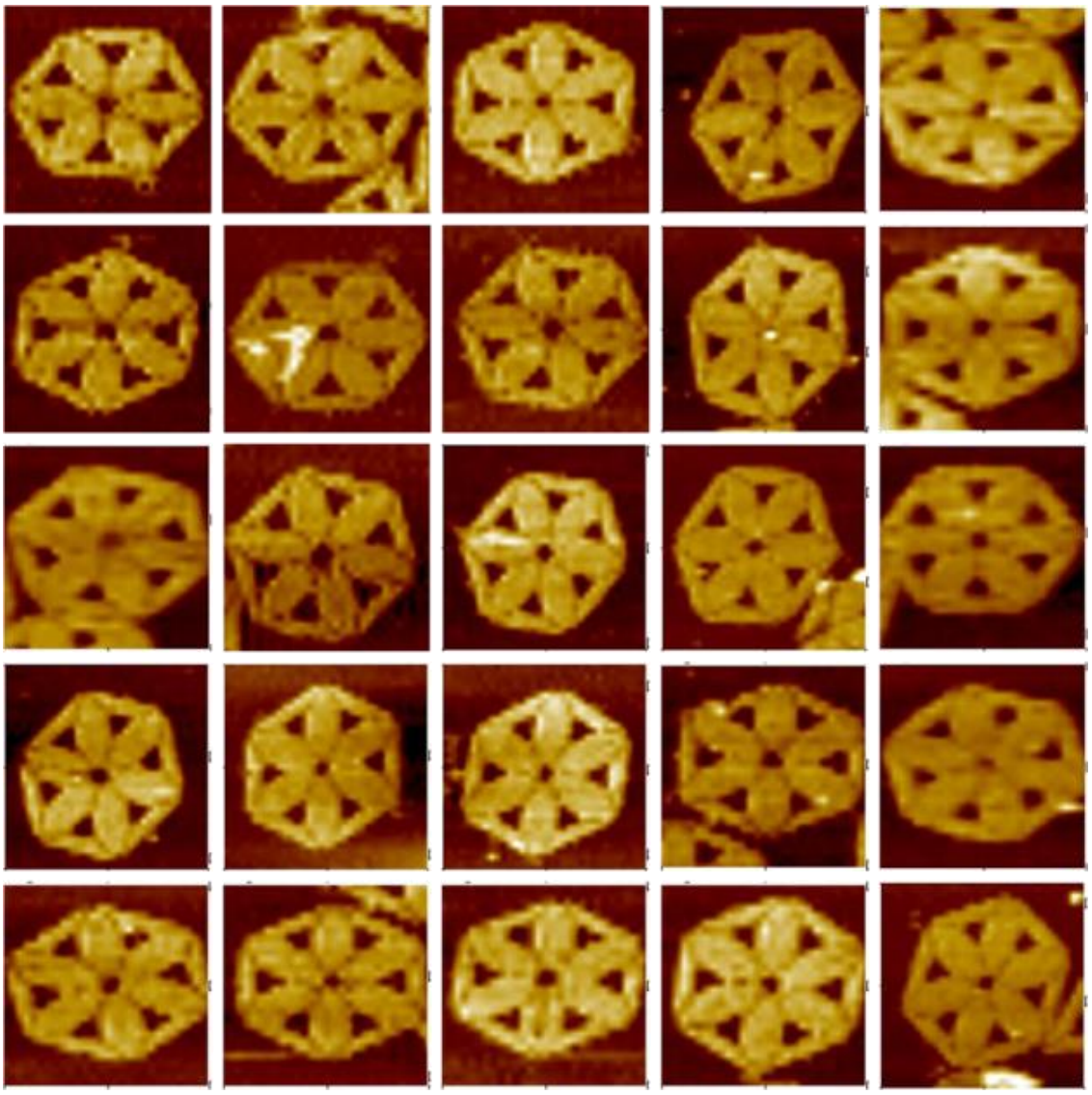
(the size of the zoom out AFM images are 5 um × 5 um and the size of the zoom in images are 270 nm x 270 nm)



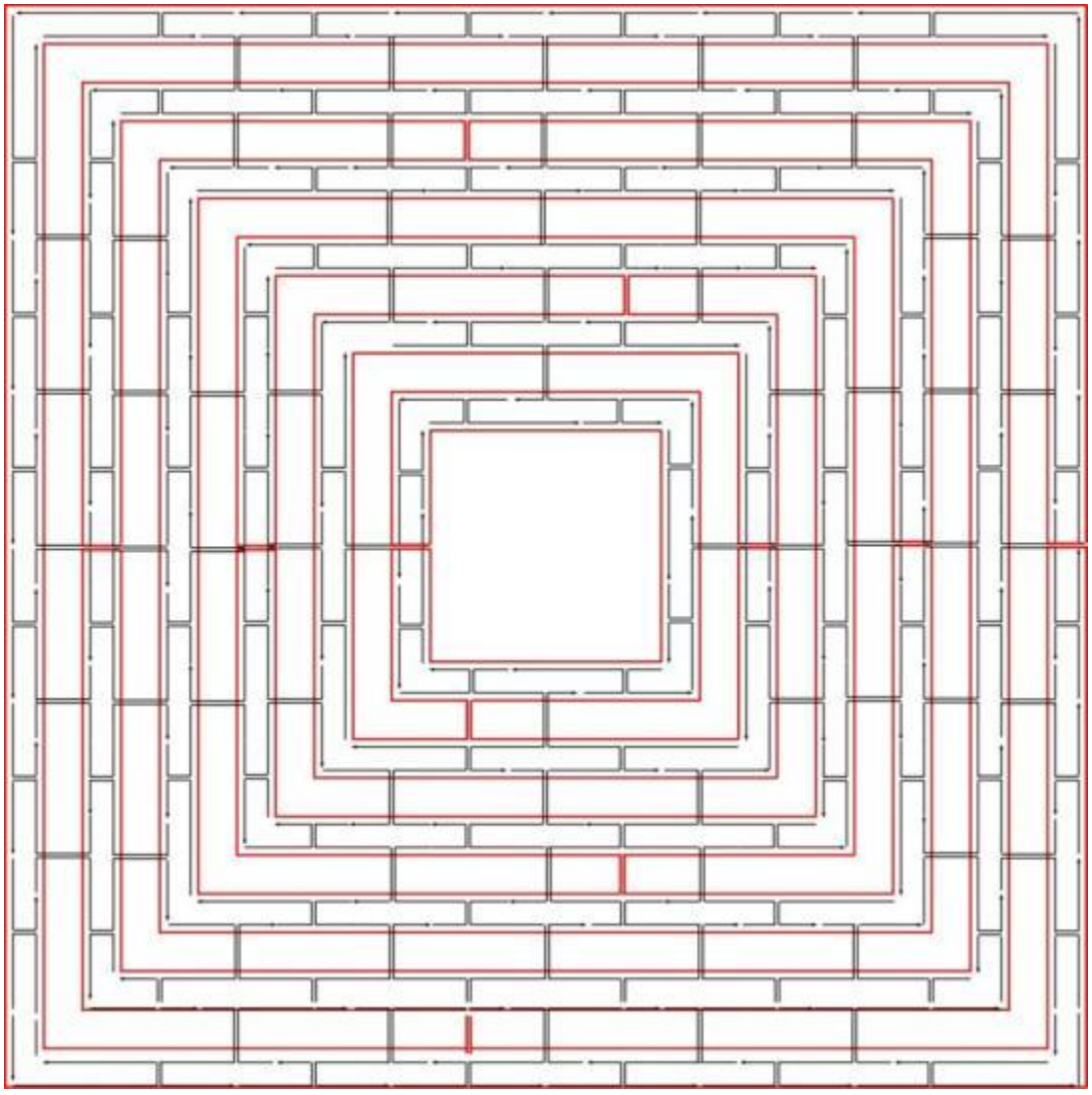




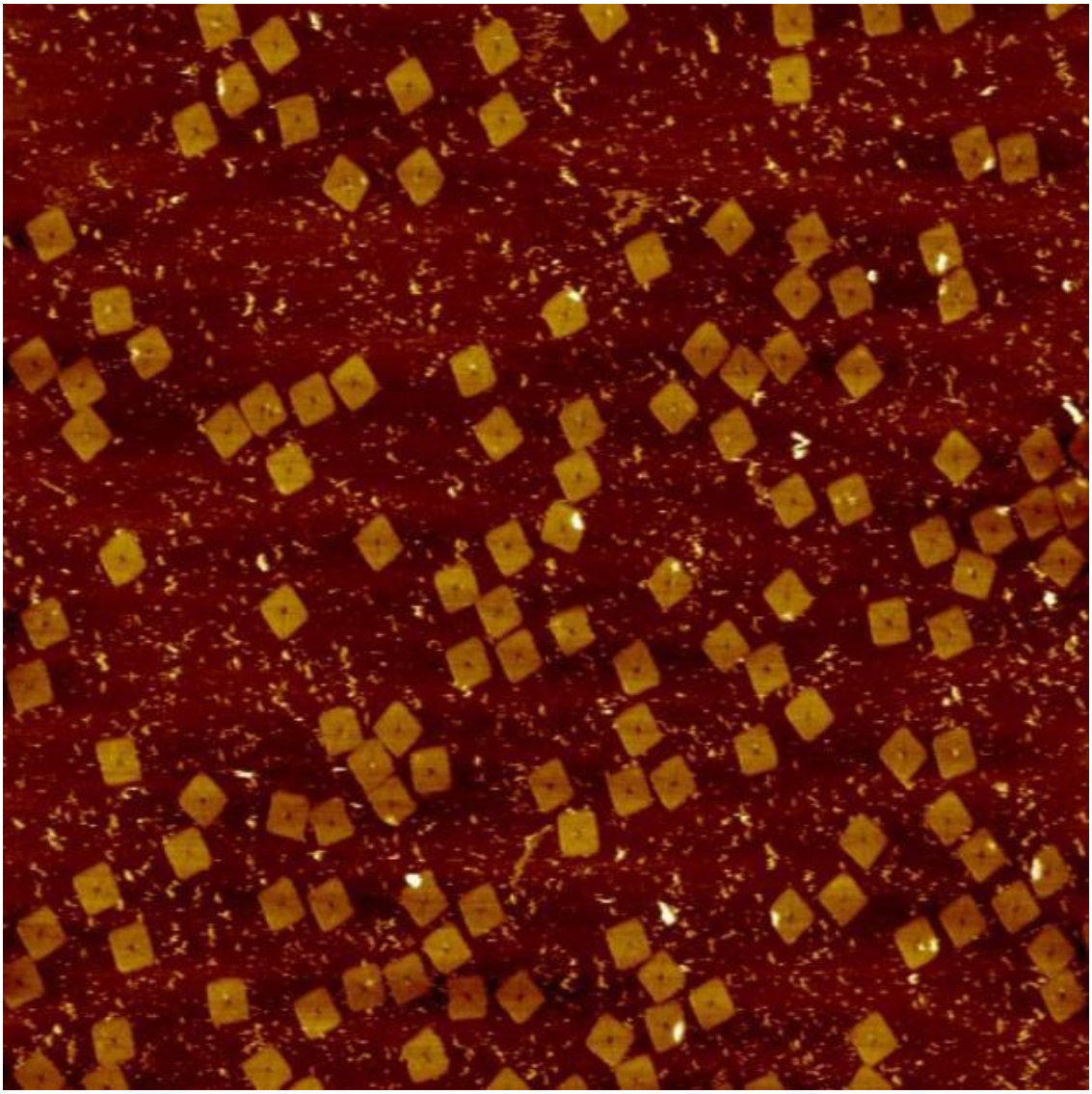




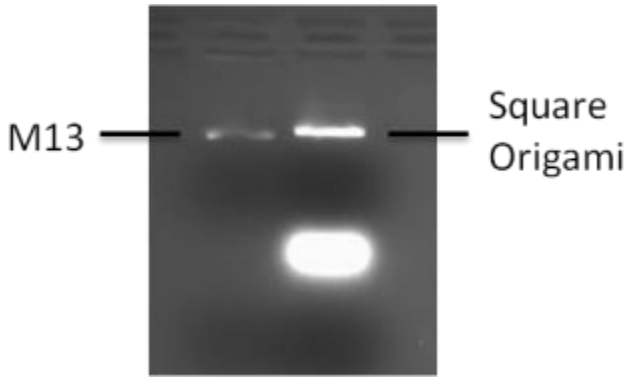
S8. Design of the square DNA origami staple tile. The red strand represents the M13 scaffold. The black strands are the staple strands with arrows pointing to the 3' ends. The spacing between consecutive crossovers connecting neighboring parallel helices is 32 base-pairs. The outermost helices are 224 bps or approximately 21 full turns. To make 90 degree angles at each corner, each consecutive helix is 8 bps shorter (on both ends) than the outer, adjacent helix.



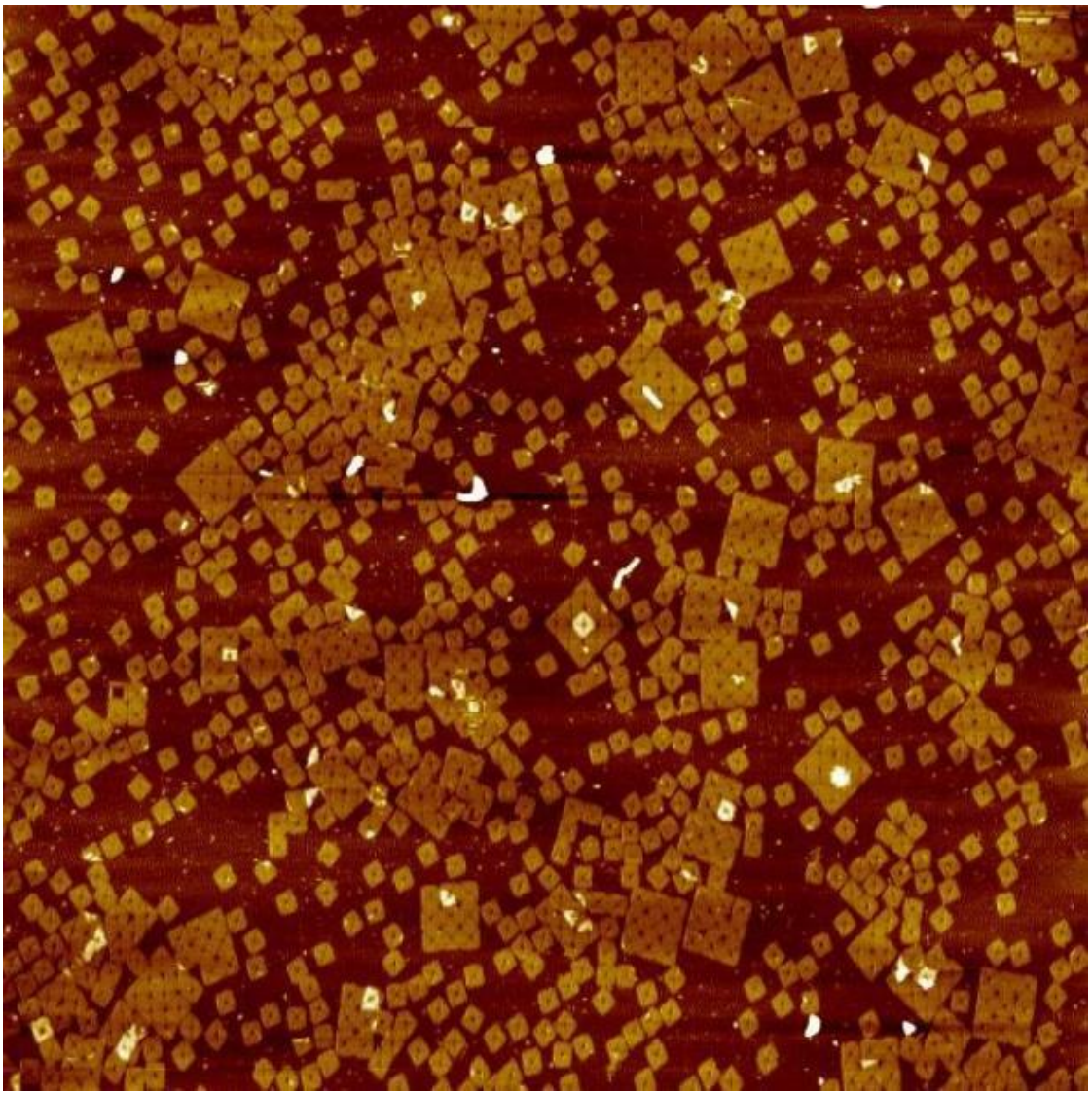
S9. AFM image of the individual square shaped DNA origami staple tile (the size of the image is 2.5 um × 2.5 um)

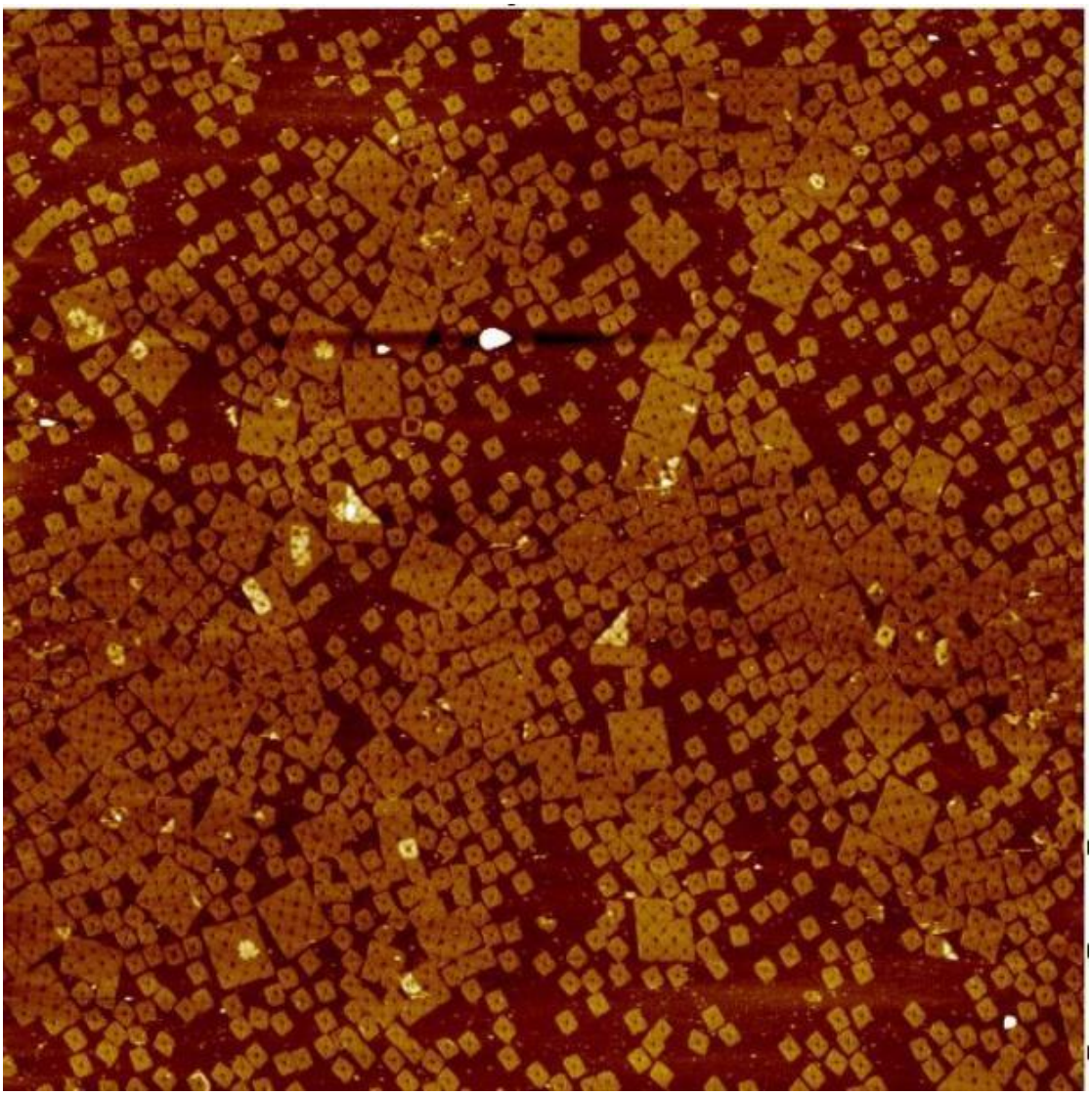


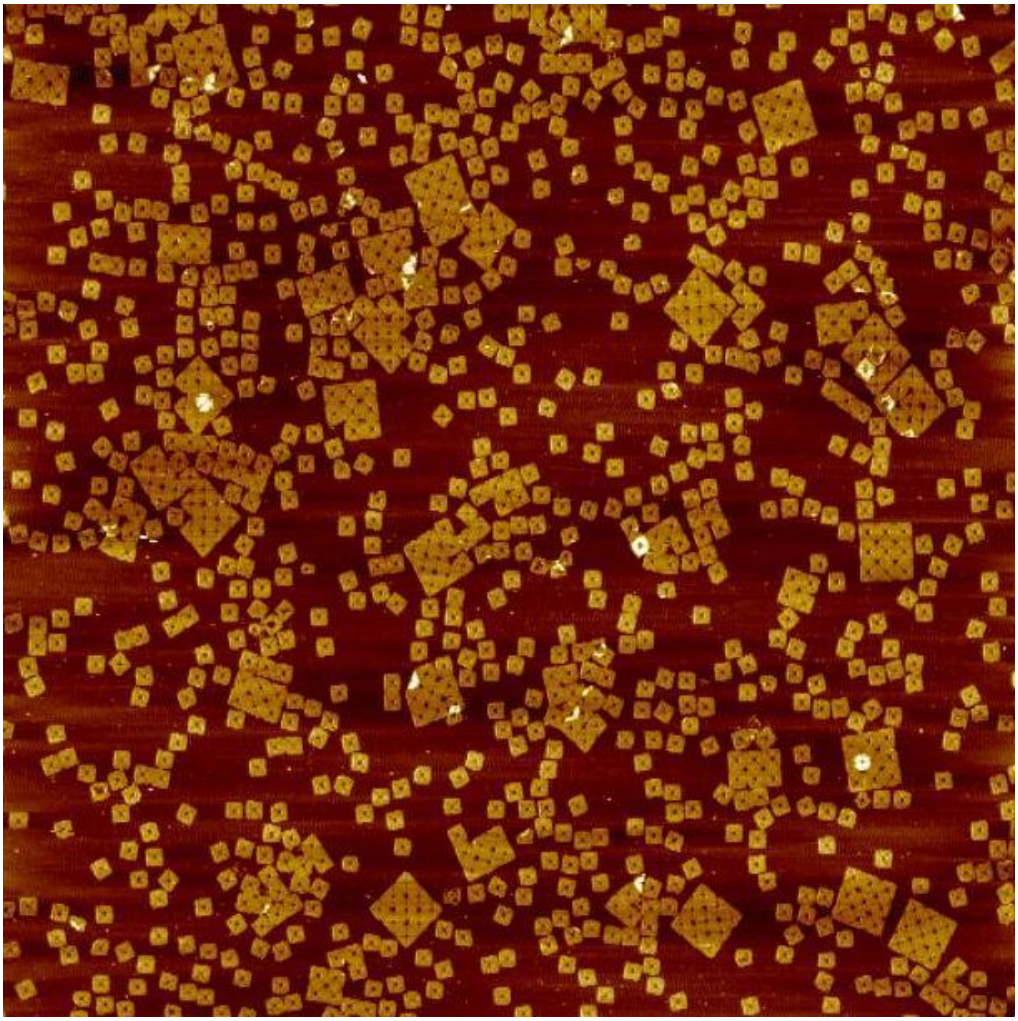
S10. Agarose gel electrophoresis result for the square DNA origami. (1.5% agarose gel)

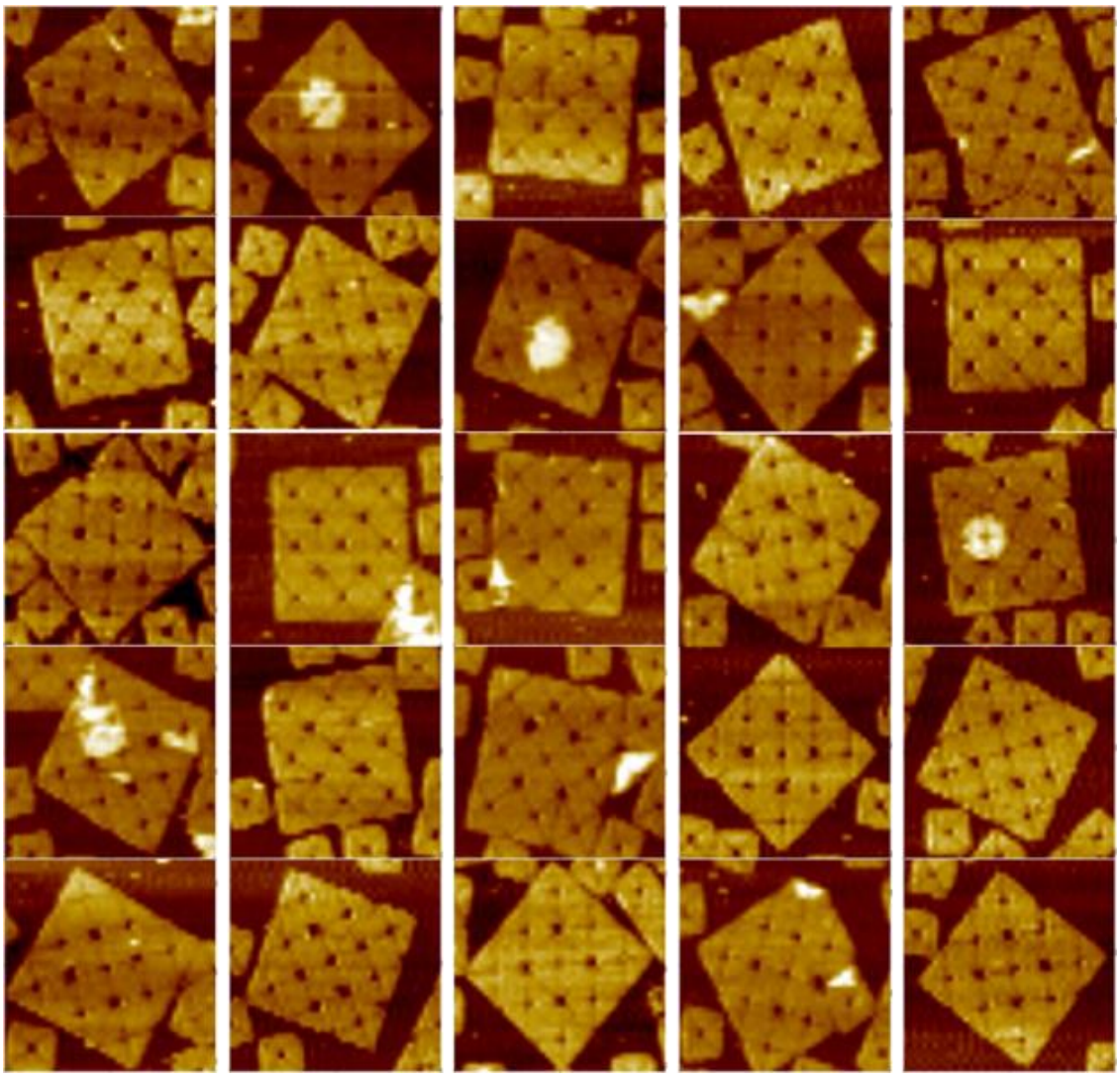


S11. Zoom out and zoom in AFM images for 3 x 3 square staple tile based super-structures. (The size of the zoom out images are 5 um × 5 um, and the size of the zoom in images are 340 nm x 340 nm).

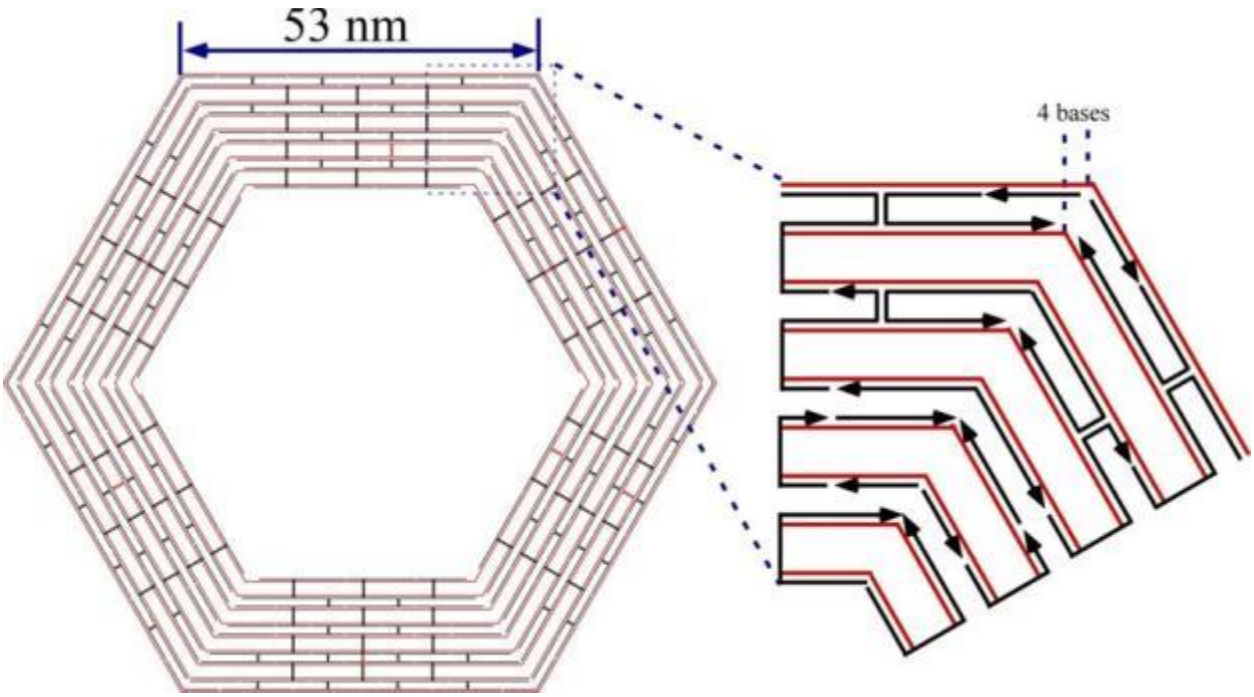




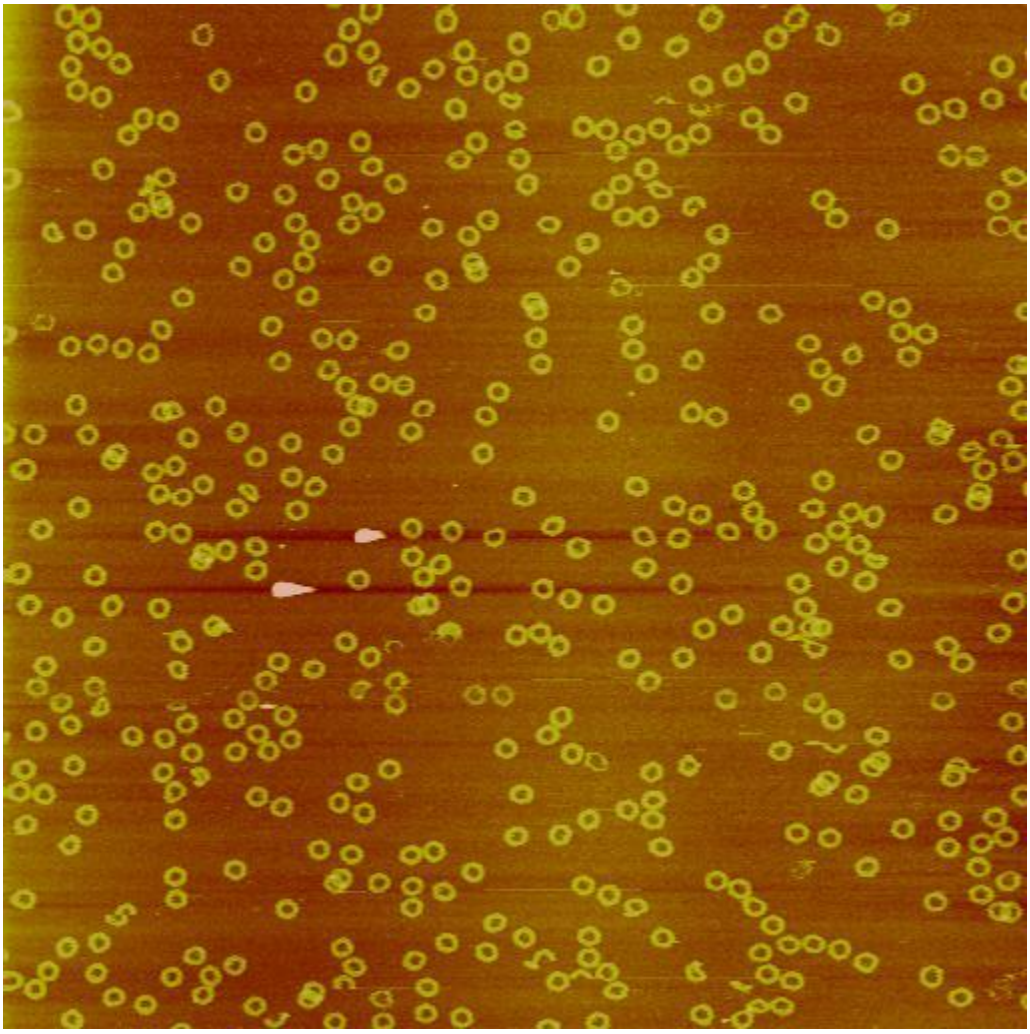




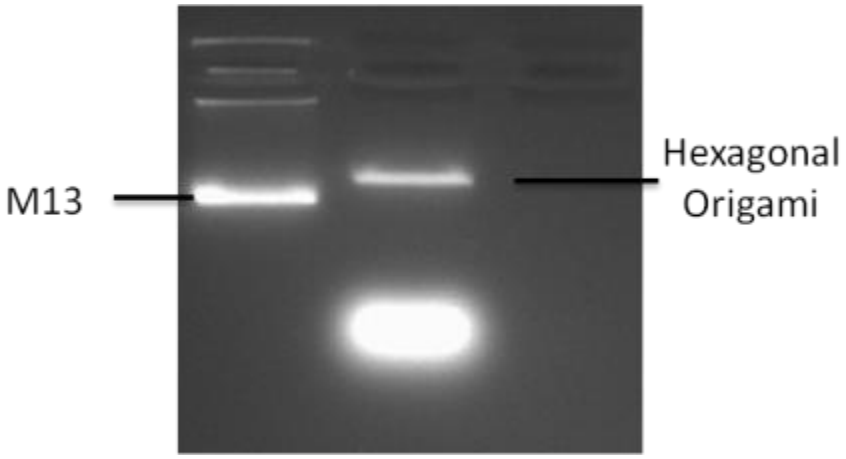
S12. Design of the hexagonal DNA origami staple tile. The red strand represents the M13 scaffold. The black strands are the staple strands with arrows pointing to the 3' ends. The design principle is the same as for the square origami. 9 parallel helices are arranged in a plane forming each side. The spacing between consecutive crossovers connecting neighboring parallel helixes is 32 bps. The outermost helices are 160 bps or approximately 15 full turns. To make 120 degree turns at each corner, each consecutive helix is 4 bps shorter (on both ends) than the outer, adjacent helix.



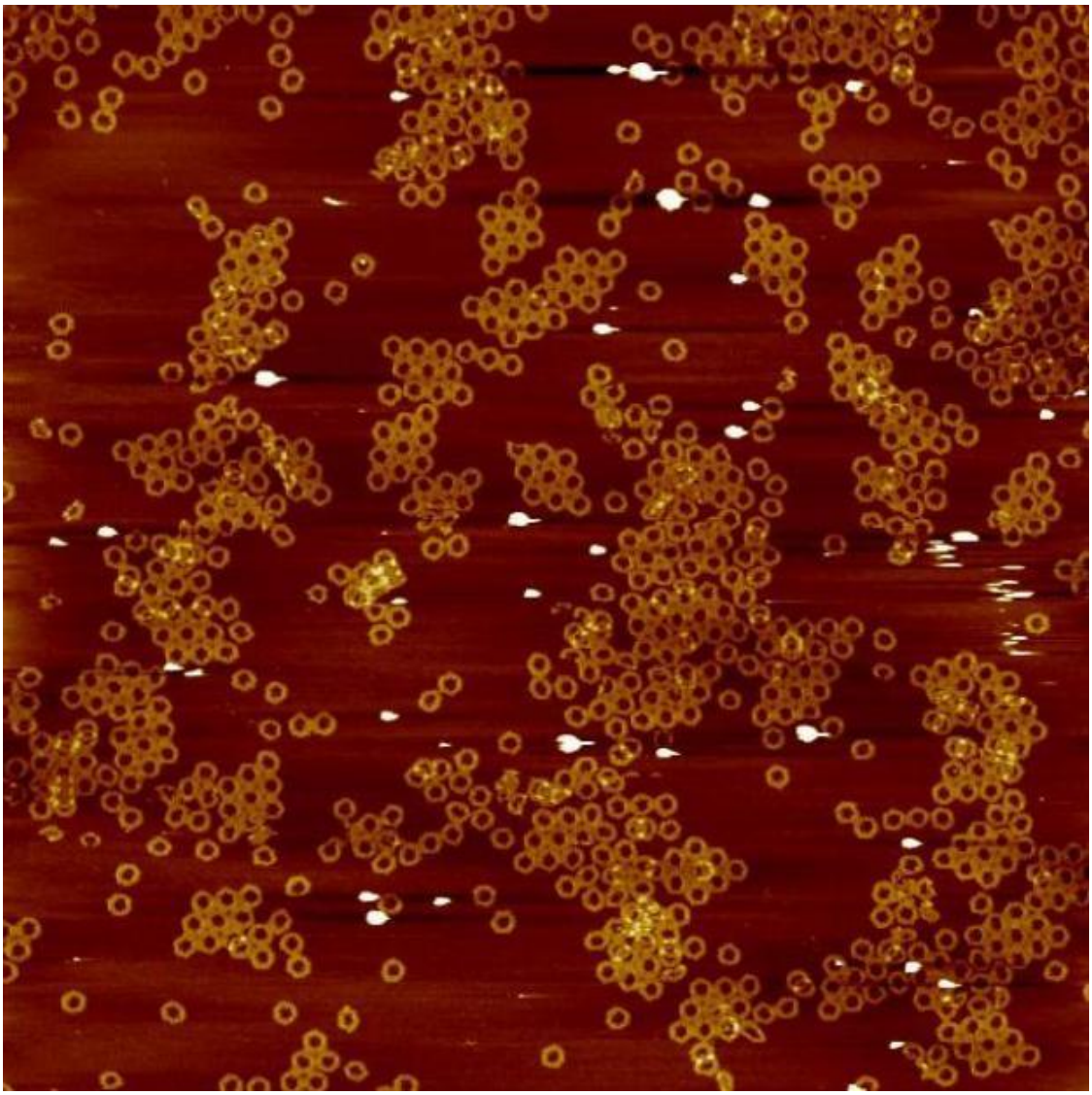
S13. AFM image of individual hexagonal DNA origami staple tiles. (The size of image is 5 um × 5 um)

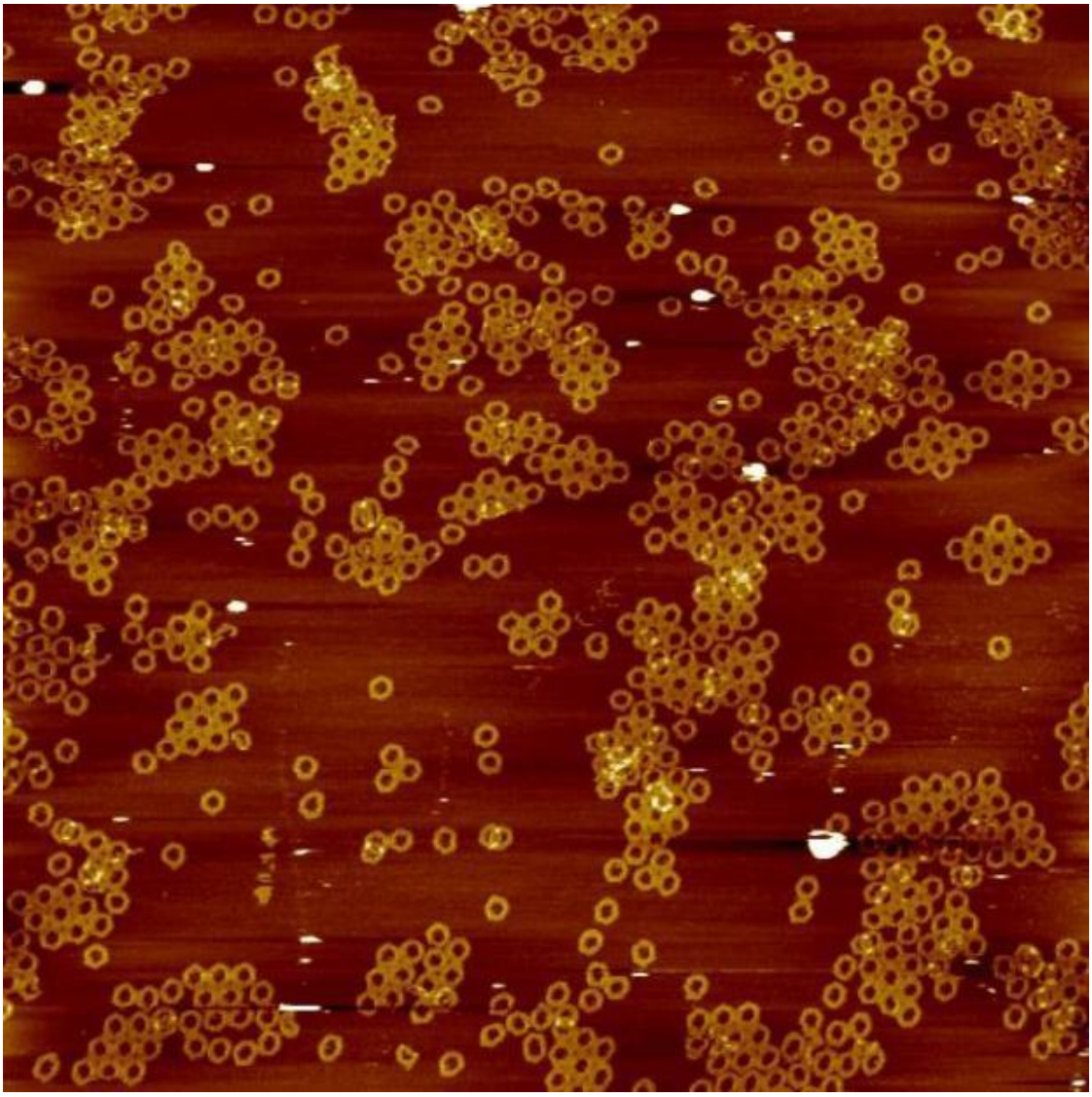


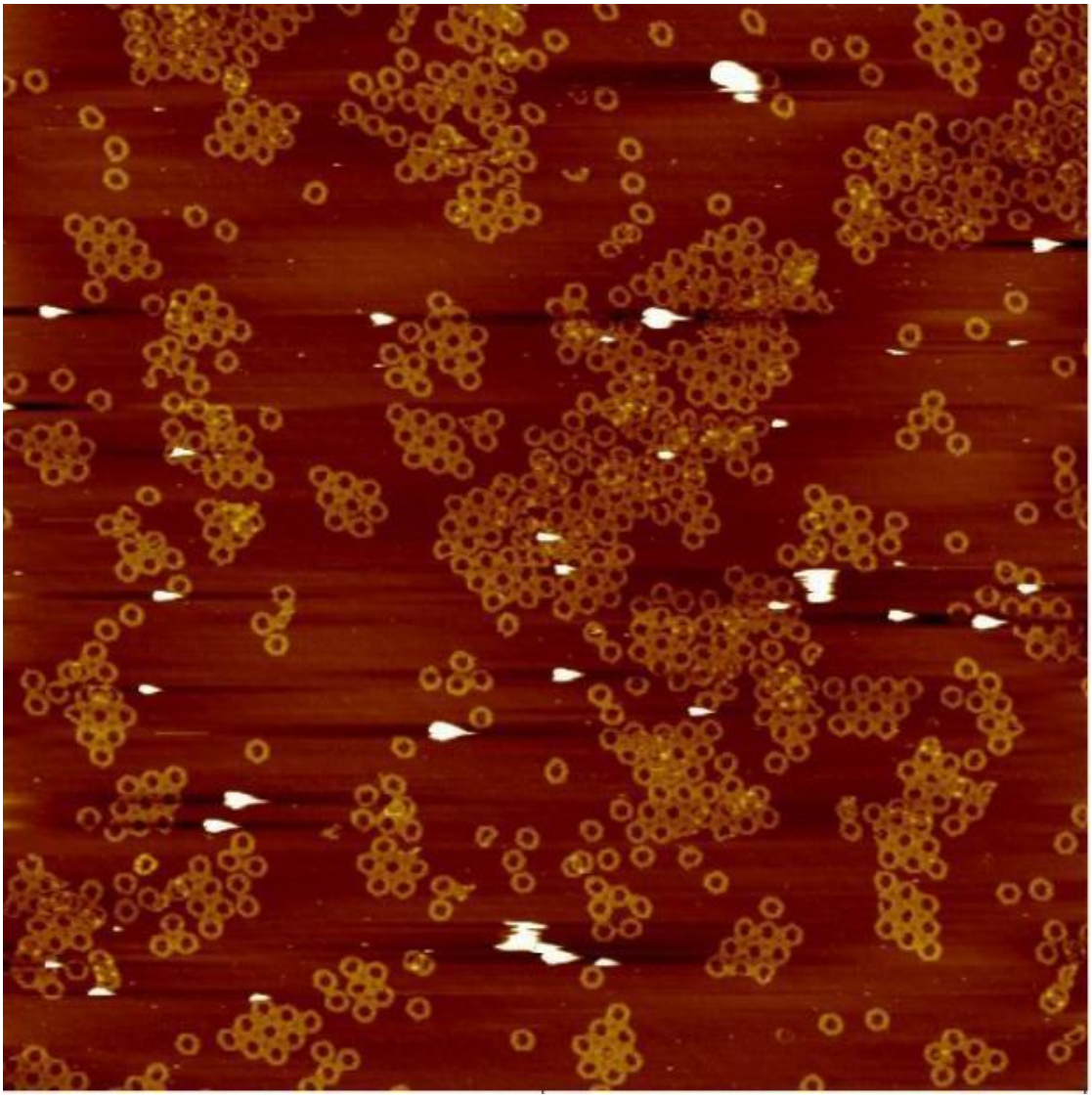
S14. Agarose gel electrophoresis result for hexagonal shaped DNA Origami.

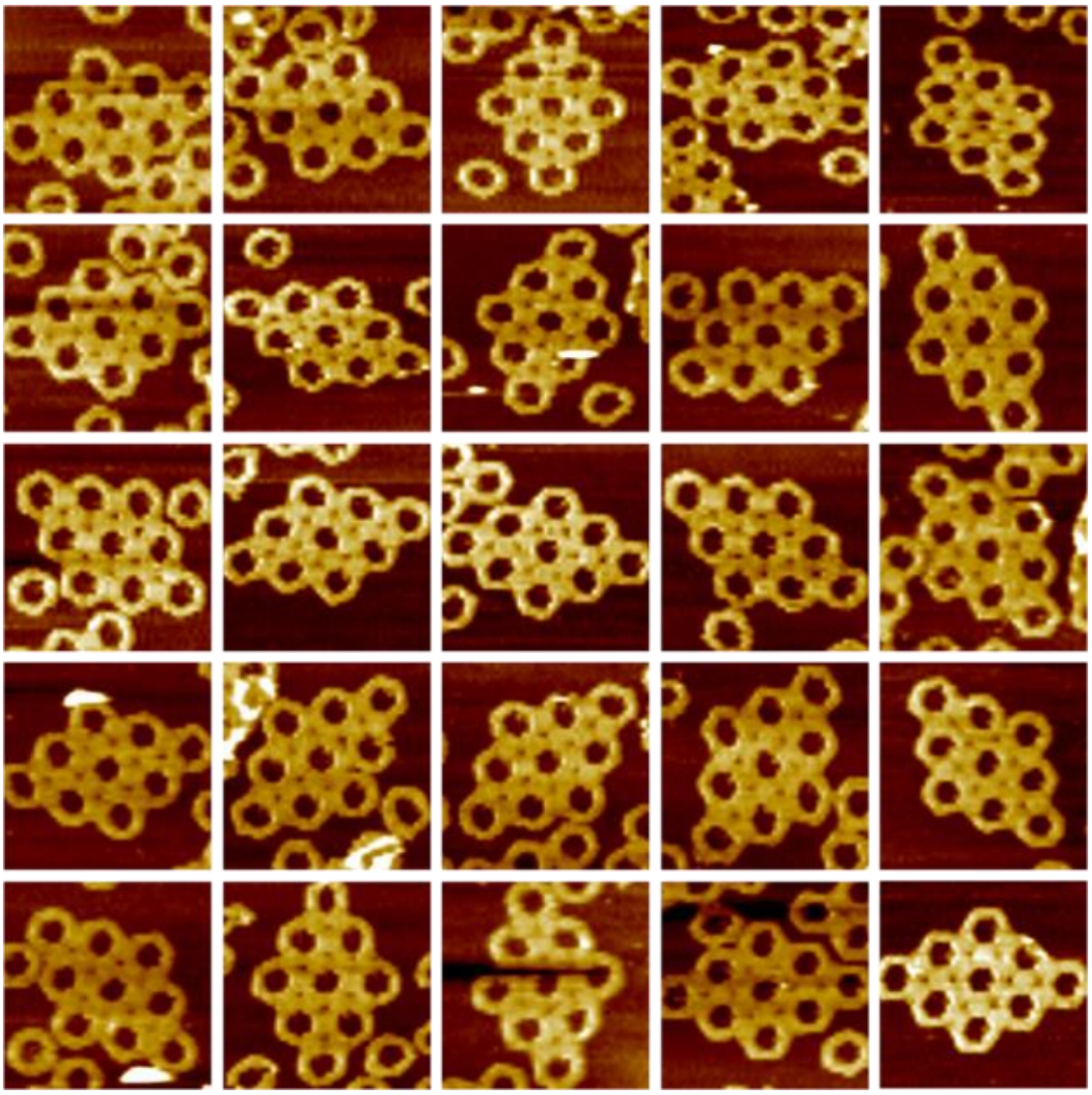


S15. Zoom out and zoom in AFM images of 3 x 3 hexagonal staple tile based origami super-structures. (The size of the zoom out images are 5 um × 5 um, and the size of the zoom in images are 470 nm x 470 nm)

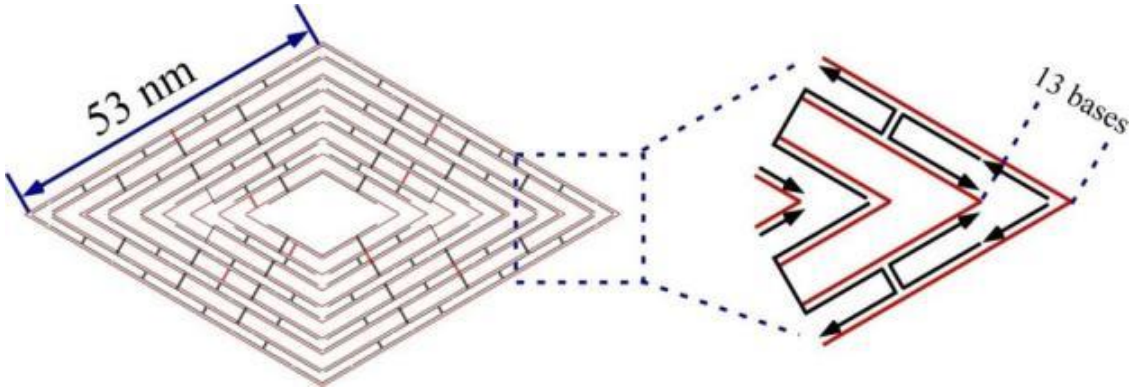




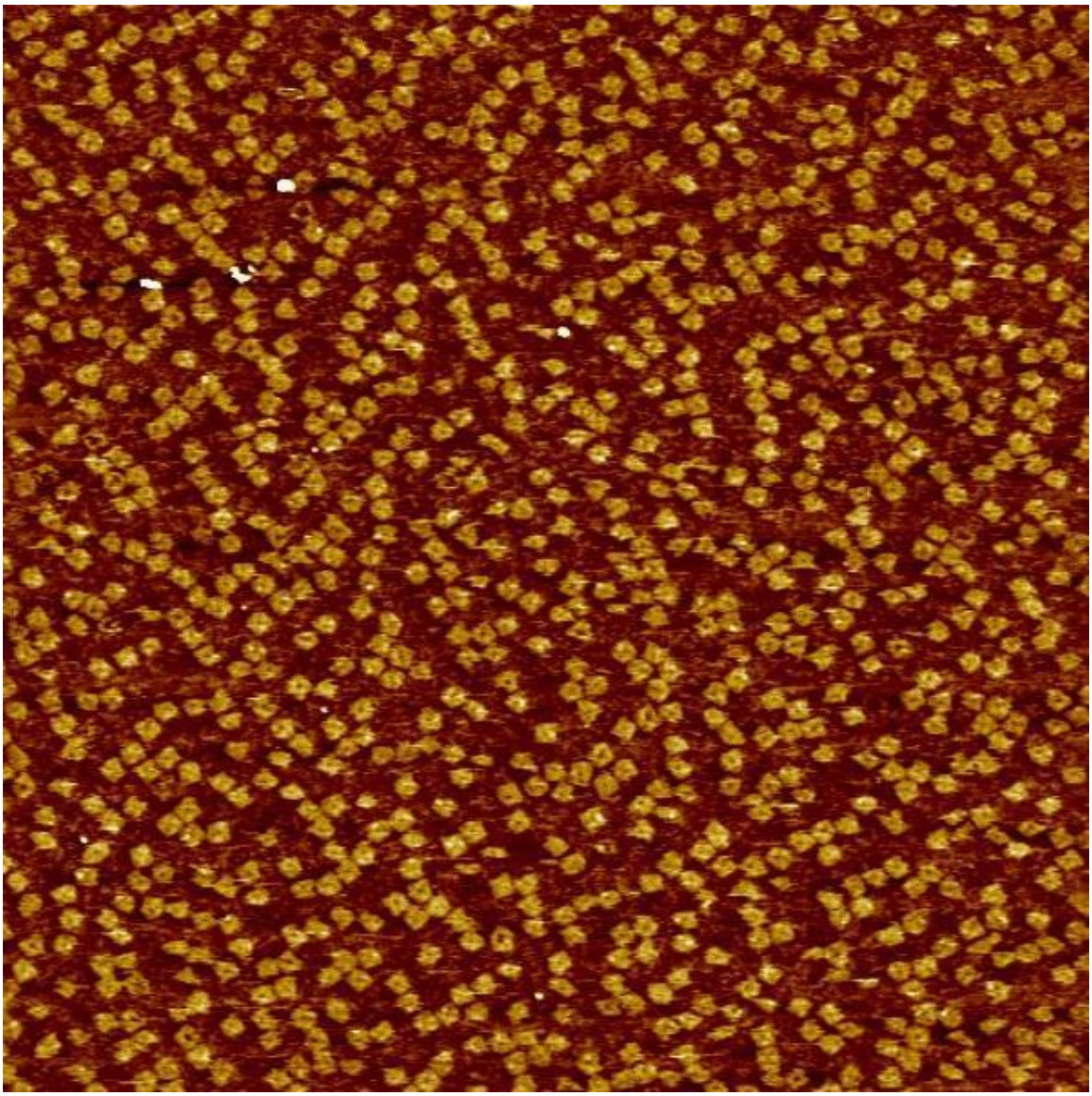




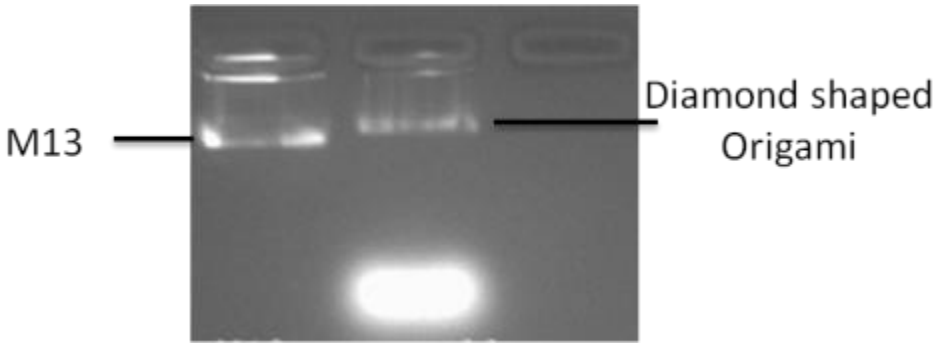
S16. Design for the diamond shaped DNA origami staple tiles.



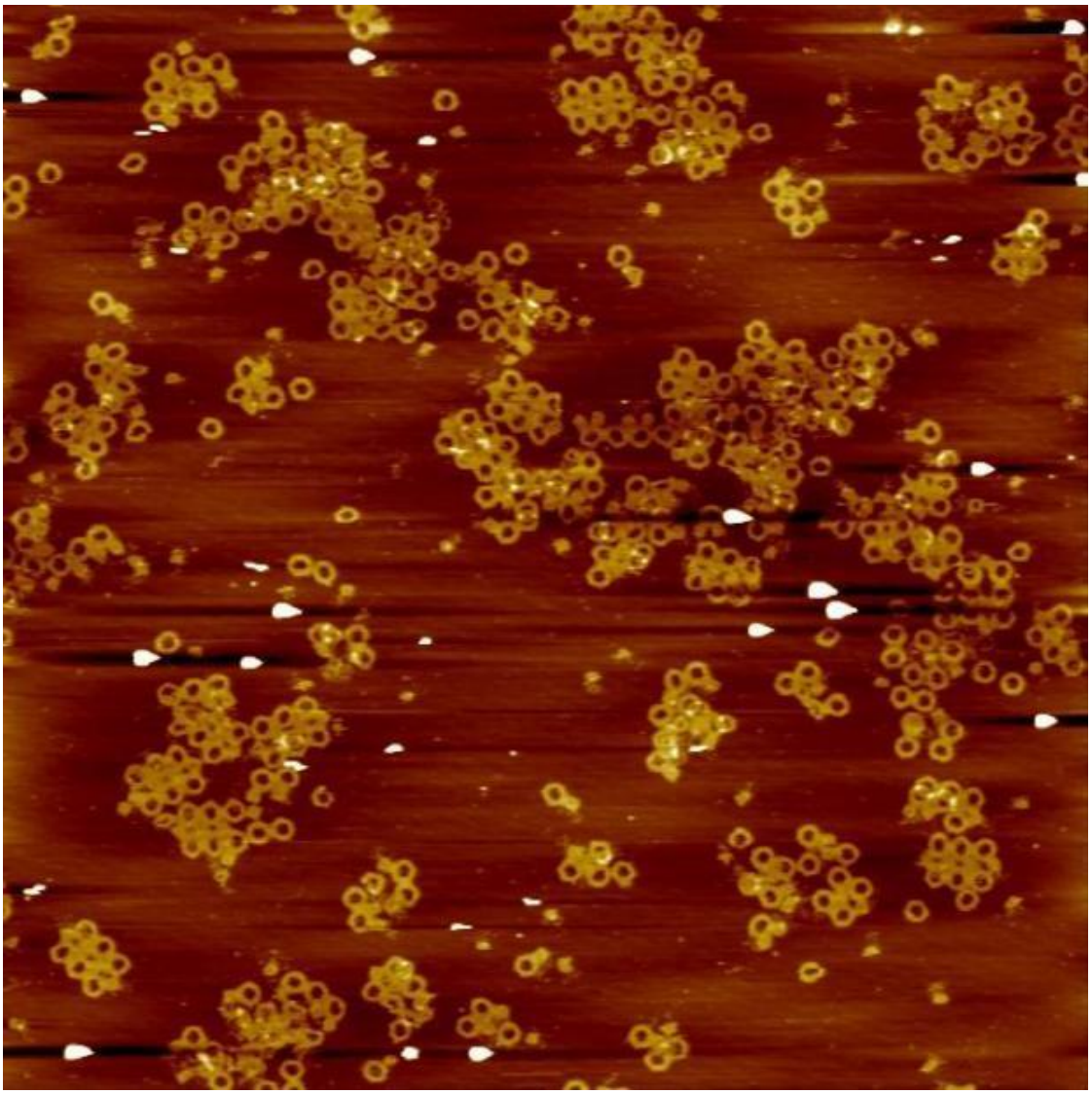
S17. AFM image of the individual diamond shaped DNA origami staple tiles. (The size of the image is 3 um × 3 um)

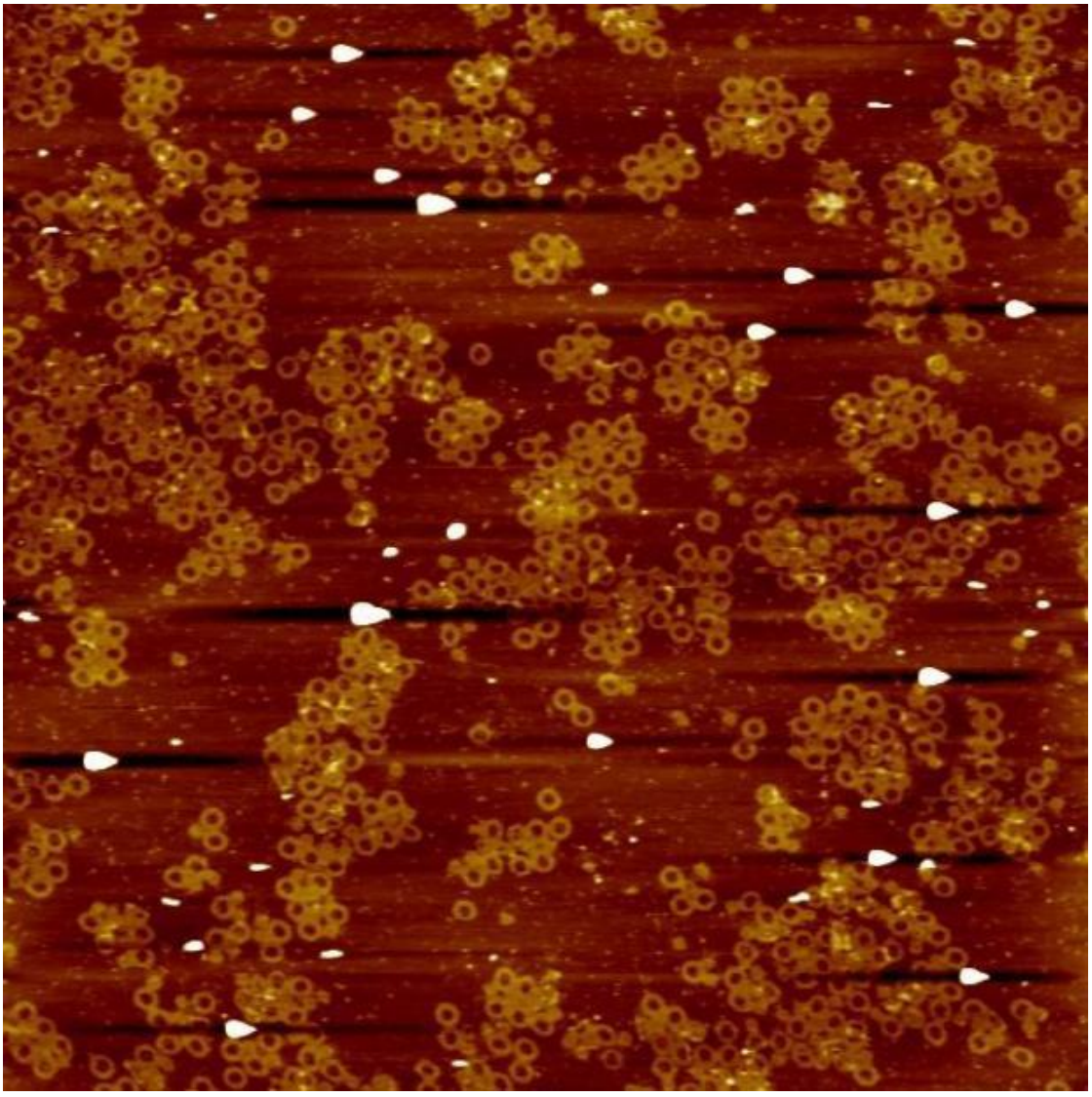


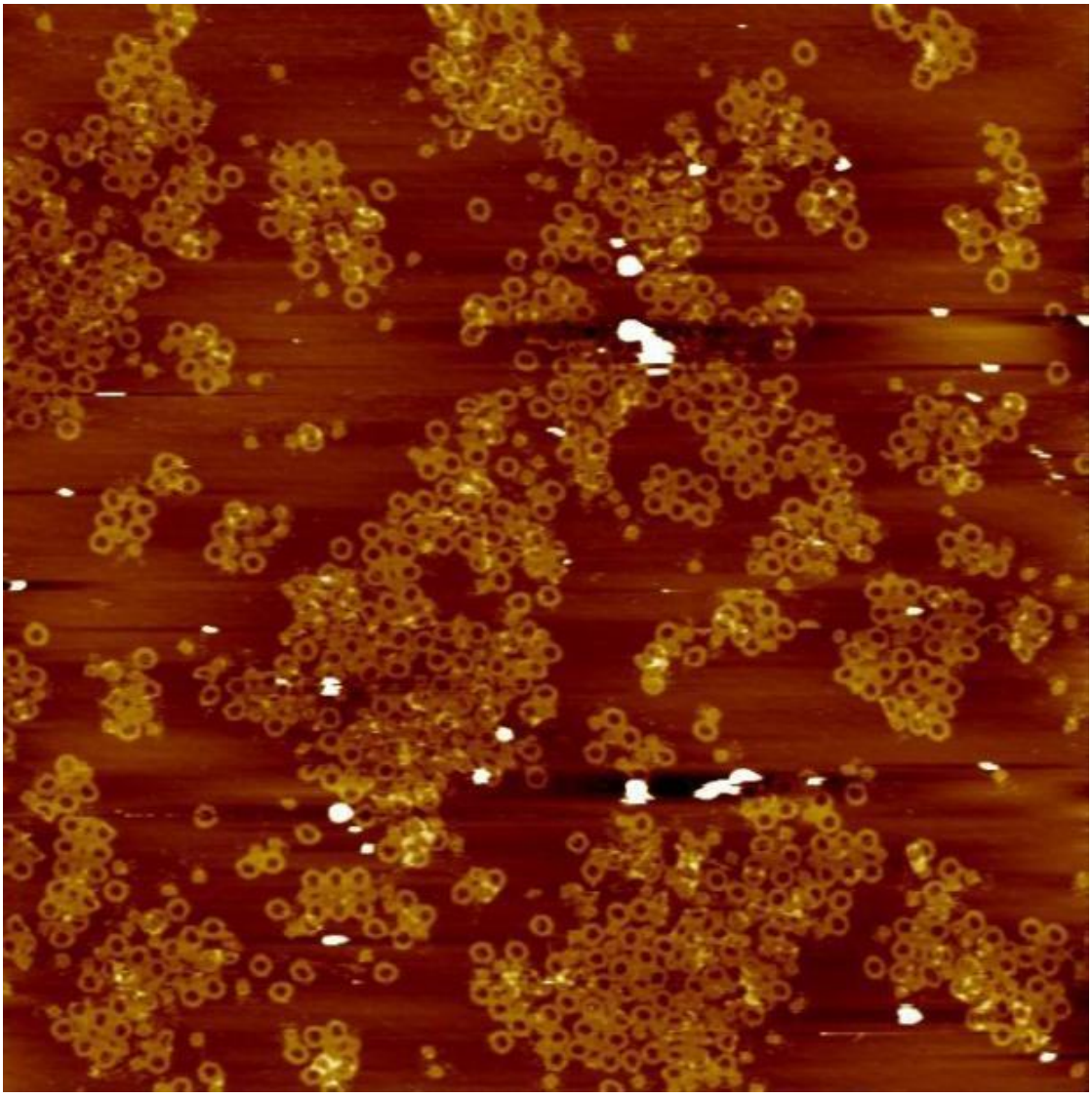
S18. Agarose gel electrophoresis result for the diamond shaped DNA Origami.

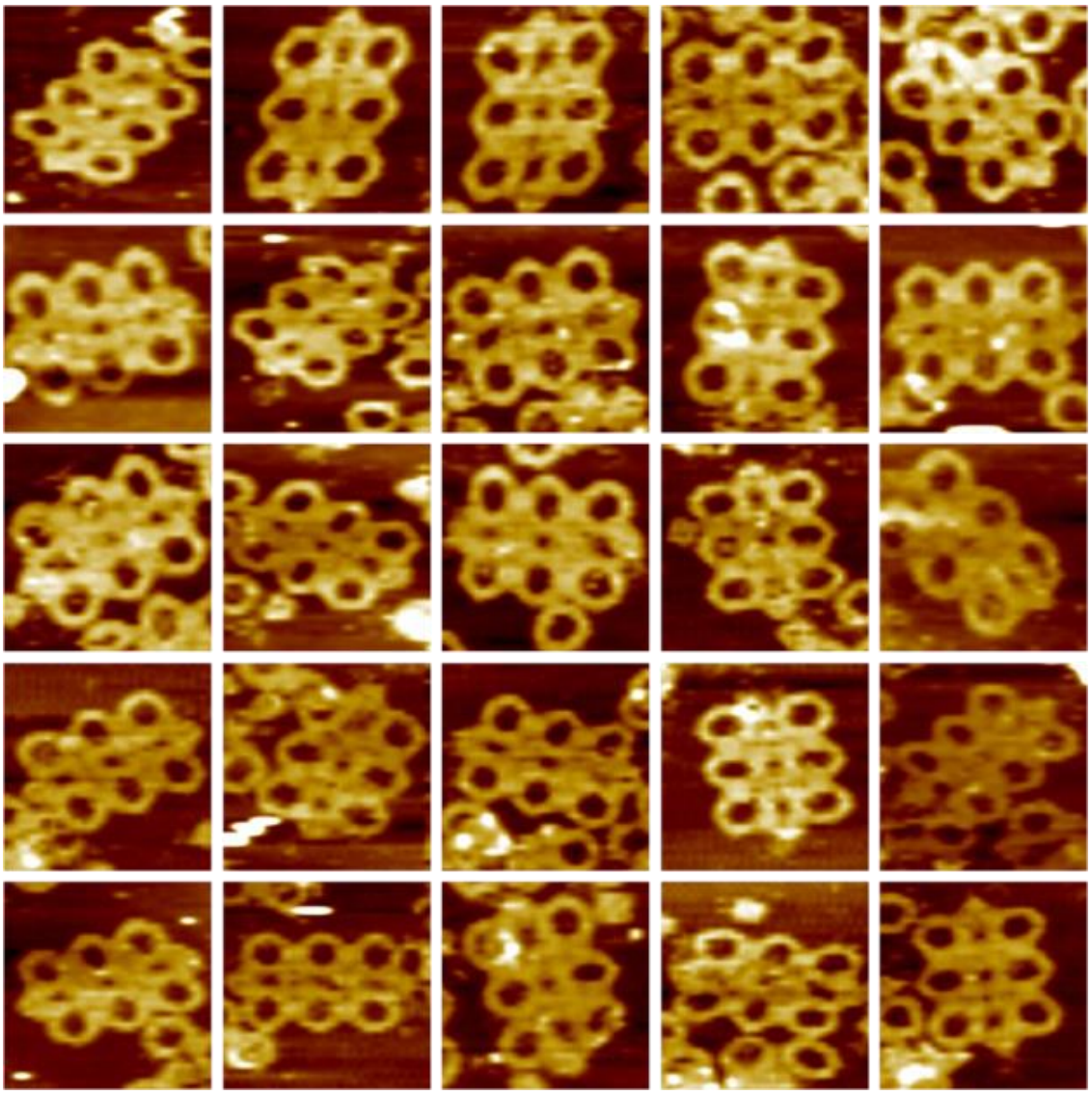


S19. Zoom out and zoom in AFM images of the origami super-structures assembled from a mixture of hexagonal and diamond shaped origami into a 3 row closely packed pattern. (The size of the zoom out images are 5 um × 5 um and the size of the zoom in images are 400 nm x 400 nm)









DNA sequences:

Table S1. Unmodified triangle origami staples

A01, CGGGGTTTCCTCAAGAGAAGGATTTTGAATTA,

A02, AGCGTCATGTCTCTGAATTTACCGACTACCTT,

A03, TTCATAATCCCCTTATTAGCGTTTTTCTTACC,

A04, ATGGTTTATGTCACAATCAATAGATATTAAAC,

A05, TTTGATGATTAAGAGGCTGAGACTTGCTCAGTACCAGGCG,

A06, CCGGAACCCAGAATGGAAAGCGCAACATGGCT,

A07, AAAGACAACATTTTCGGTCATAGCCAAAATCA,

A08, GACGGGAGAATTAACTCGGAATAAGTTTATTTCCAGCGCC,

A09, GATAAGTGCCGTCGAGCTGAAACATGAAAGTATACAGGAG,

A10, TGTACTGGAAATCCTCATTAAAGCAGAGCCAC,

A11, CACCGGAAAGCGCGTTTTCATCGGAAGGGCGA,

A12, CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAA,

A13, TTTAACGGTTCGGAACCTATTATTAGGGTTGATATAAGTA,

A14, CTCAGAGCATATTCACAAACAAATTAATAAGT,

A15, GGAGGGAATTTAGCGTCAGACTGTCCGCCTCC,

A16, GTCAGAGGGTAATTGATGGCAACATATAAAAGCGATTGAG,

A17, TAGCCCGGAATAGGTGAATGCCCCCTGCCTATGGTCAGTG,

A18, CCTTGAGTCAGACGATTGGCCTTGCGCCACCC,

A19, TCAGAACCCAGAATCAAGTTTGCCGGTAAATA,

A20, TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGA,

A21, CAGAGCCAGGAGGTTGAGGCAGGTAACAGTGCCCG,

A22, ATTAAAGGCCGTAATCAGTAGCGAGCCACCCT,

A23, GATAACCCACAAGAATGTTAGCAAACGTAGAAAATTATTC,

A24, GCCGCCAGCATTGACACCACCCTC,

A25, AGAGCCGCACCATCGATAGCAGCATGAATTAT,

A26, CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATA,

A27, AGCCATTTAAACGTCACCAATGAACACCAGAACCA,

A28, ATAAGAGCAAGAAACATGGCATGATTAAGACTCCGACTTG,

A29, CCATTAGCAAGGCCGGGGGAATTA,

A30, GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGC,

A31, TATCTTACCGAAGCCCAAACGCAATAATAACGAAAATCACCAG,

A32, CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGCAGATAGCCG,

A33, CCTTTTTTCATTTAACAATTTCATAGGATTAG,

A34, TTTAACCTATCATAGGTCTGAGAGTTCCAGTA,

A35, AGTATAAAATATGCGTTATACAAAGCCATCTT,

A36, CAAGTACCTCATTCCAAGAACGGGAAATTCAT,

A37, AGAGAATAACATAAAAACAGGGAAGCGCATTA,

A38, AAAACAAAATTAATTAAATGGAAACAGTACATTAGTGAAT,

A39, TTATCAAACCGGCTTAGGTTGGGTAAGCCTGT,

A40, TTAGTATCGCCAACGCTCAACAGTCGGCTGTC,

A41, TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAG,

A42, AGAGTCAAAAATCAATATATGTGATGAAACAAACATCAAG,

A43, ACTAGAAATATATAACTATATGTACGCTGAGA,

A44, TCAATAATAGGGCTTAATTGAGAATCATAATT,

A45, AACGTCAAAAATGAAAAGCAAGCCGTTTTTATGAAACCAA,

A46, GAGCAAAAGAAGATGAGTGAATAACCTTGCTTATAGCTTA,

A47, GATTAAGAAATGCTGATGCAAATCAGAATAAA,

A48, CACCGGAATCGCCATATTTAACAAAATTTACG,

A49, AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTT,

A50, ACATAGCGCTGTAAATCGTCGCTATTCATTTCAATTACCT,

A51, GTTAAATACAATCGCAAGACAAAGCCTTGAAA,

A52, CCCATCCTCGCCAACATGTAATTTAATAAGGC,

A53, TCCCAATCCAAATAAGATTACCGCGCCCAATAAATAATAT,

A54, TCCCTTAGAATAACGCGAGAAAACTTTTACCGACC,

A55, GTGTGATAAGGCAGAGGCATTTTCAGTCCTGA,

A56, ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTA,

A57, GTTTGAAATTCAAATATATTTTAG,

A58, AATAGATAGAGCCAGTAATAAGAGATTTAATG,

A59, GCCAGTTACAAAATAATAGAAGGCTTATCCGGTTATCAAC,

A60, TTCTGACCTAAAATATAAAGTACCGACTGCAGAAC,

A61, GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTT,

A62, TCAGCTAAAAAAGGTAAAGTAATT,

A63, ACGCTAACGAGCGTCTGGCGTTTTAGCGAACCCAACATGT,

A64, ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCA,

A65, TGCTATTTTGCACCCAGCTACAATTTTGTTTTGAAGCCTTAAA,

B01, TCATATGTGTAATCGTAAAACTAGTCATTTTC,

B02, GTGAGAAAATGTGTAGGTAAAGATACAACTTT,

B03, GGCATCAAATTTGGGGCGCGAGCTAGTTAAAG,

B04, TTCGAGCTAAGACTTCAAATATCGGGAACGAG,

B05, ACAGTCAAAGAGAATCGATGAACGACCCCGGTTGATAATC,

B06, ATAGTAGTATGCAATGCCTGAGTAGGCCGGAG,

B07, AACCAGACGTTTAGCTATATTTTCTTCTACTA,

B08, GAATACCACATTCAACTTAAGAGGAAGCCCGATCAAAGCG,

B09, AGAAAAGCCCCAAAAAGAGTCTGGAGCAAACAATCACCAT,

B10, CAATATGACCCTCATATATTTTAAAGCATTAA,

B11, CATCCAATAAATGGTCAATAACCTCGGAAGCA,

B12, AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAA,

B13, CGTTCTAGTCAGGTCATTGCCTGACAGGAAGATTGTATAA,

B14, CAGGCAAGATAAAAATTTTTAGAATATTCAAC,

B15, GATTAGAGATTAGATACATTTCGCAAATCATA,

B16, CGCCAAAAGGAATTACAGTCAGAAGCAAAGCGCAGGTCAG,

B17, GCAAATATTTAAATTGAGATCTACAAAGGCTACTGATAAA,

B18, TTAATGCCTTATTTCAACGCAAGGGCAAAGAA,

B19, TTAGCAAATAGATTTAGTTTGACCAGTACCTT,

B20, TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGC,

B21, ATAAAGCCTTTGCGGGAGAAGCCTGGAGAGGGTAG,

B22, TAAGAGGTCAATTCTGCGAACGAGATTAAGCA,

B23, AACACTATCATAACCCATCAAAAATCAGGTCTCCTTTTGA,

B24, ATGACCCTGTAATACTTCAGAGCA,

B25, TAAAGCTATATAACAGTTGATTCCCATTTTTG,

B26, CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGAC,

B27, TAATTGCTTGGAAGTTTCATTCCAAATCGGTTGTA,

B28, GATAAAAACCAAAATATTAAACAGTTCAGAAATTAGAGCT,

B29, ACTAAAGTACGGTGTCGAATATAA,

B30, TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCA,

B31, AAAGAAGTTTTGCCAGCATAAATATTCATTGACTCAACATGTT,

B32, AATACTGCGGAATCGTAGGGGGTAATAGTAAAATGTTTAGACT,

B33, AGGGATAGCTCAGAGCCACCACCCCATGTCAA,

B34, CAACAGTTTATGGGATTTTGCTAATCAAAAGG,

B35, GCCGCTTTGCTGAGGCTTGCAGGGGAAAAGGT,

B36, GCGCAGACTCCATGTTACTTAGCCCGTTTTAA,

B37, ACAGGTAGAAAGATTCATCAGTTGAGATTTAG,

B38, CCTCAGAACCGCCACCCAAGCCCAATAGGAACGTAAATGA,

B39, ATTTTCTGTCAGCGGAGTGAGAATACCGATAT,

B40, ATTCGGTCTGCGGGATCGTCACCCGAAATCCG,

B41, CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATT,

B42, AGACGTTACCATGTACCGTAACACCCCTCAGAACCGCCAC,

B43, CACGCATAAGAAAGGAACAACTAAGTCTTTCC,

B44, ATTGTGTCTCAGCAGCGAAAGACACCATCGCC,

B45, TTAATAAAACGAACTAACCGAACTGACCAACTCCTGATAA,

B46, AGGTTTAGTACCGCCATGAGTTTCGTCACCAGGATCTAAA,

B47, GTTTTGTCAGGAATTGCGAATAATCCGACAAT,

B48, GACAACAAGCATCGGAACGAGGGTGAGATTTG,

B49, TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACG,

B50, AGCGTAACTACAAACTACAACGCCTATCACCGTACTCAGG,

B51, TAGTTGCGAATTTTTTCACGTTGATCATAGTT,

B52, GTACAACGAGCAACGGCTACAGAGGATACCGA,

B53, ACCAGTCAGGACGTTGGAACGGTGTACAGACCGAAACAAA,

B54, ACAGACAGCCCAAATCTCCAAAAAAAAATTTCTTA,

B55, AACAGCTTGCTTTGAGGACTAAAGCGATTATA,

B56, CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTAT,

B57, CGAGGTGAGGCTCCAAAAGGAGCC,

B58, ACCCCCAGACTTTTTCATGAGGAACTTGCTTT,

B59, ACCTTATGCGATTTTATGACCTTCATCAAGAGCATCTTTG,

B60, CGGTTTATCAGGTTTCCATTAAACGGGAATACACT,

B61, AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATT,

B62, GGCAAAAGTAAAATACGTAATGCC,

B63, TGGTTTAATTTCAACTCGGATATTCATTACCCACGAAAGA,

B64, ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGA,

B65, CCTGACGAGAAACACCAGAACGAGTAGGCTGCTCATTCAGTGA,

Link-A1C, TTAATTAATTTTTTACCATATCAAA,

Link-A2C, TTAATTTCATCTTAGACTTTACAA,

Link-A3C, CTGTCCAGACGTATACCGAACGA,

Link-A4C, TCAAGATTAGTGTAGCAATACT,

Link-B1A, TGTAGCATTCCTTTTATAAACAGTT,

Link-B2A, TTTAATTGTATTTCCACCAGAGCC,

Link-B3A, ACTACGAAGGCTTAGCACCATTA,

Link-B4A, ATAAGGCTTGCAACAAAGTTAC,

Link-C1B, GTGGGAACAAATTTCTATTTTTGAG,

Link-C2B, CGGTGCGGGCCTTCCAAAAACATT,

Link-C3B, ATGAGTGAGCTTTTAAATATGCA,

Link-C4B, ACTATTAAAGAGGATAGCGTCC,

Loop, GCGCTTAATGCGCCGCTACAGGGC,

C01, TCGGGAGATATACAGTAACAGTACAAATAATT,

C02, CCTGATTAAAGGAGCGGAATTATCTCGGCCTC,

C03, GCAAATCACCTCAATCAATATCTGCAGGTCGA,

C04, CGACCAGTACATTGGCAGATTCACCTGATTGC,

C05, TGGCAATTTTTAACGTCAGATGAAAACAATAACGGATTCG,

C06, AAGGAATTACAAAGAAACCACCAGTCAGATGA,

C07, GGACATTCACCTCAAATATCAAACACAGTTGA,

C08, TTGACGAGCACGTATACTGAAATGGATTATTTAATAAAAG,

C09, CCTGATTGCTTTGAATTGCGTAGATTTTCAGGCATCAATA,

C10, TAATCCTGATTATCATTTTGCGGAGAGGAAGG,

C11, TTATCTAAAGCATCACCTTGCTGATGGCCAAC,

C12, AGAGATAGTTTGACGCTCAATCGTACGTGCTTTCCTCGTT,

C13, GATTATACACAGAAATAAAGAAATACCAAGTTACAAAATC,

C14, TAGGAGCATAAAAGTTTGAGTAACATTGTTTG,

C15, TGACCTGACAAATGAAAAATCTAAAATATCTT,

C16, AGAATCAGAGCGGGAGATGGAAATACCTACATAACCCTTC,

C17, GCGCAGAGGCGAATTAATTATTTGCACGTAAATTCTGAAT,

C18, AATGGAAGCGAACGTTATTAATTTCTAACAAC,

C19, TAATAGATCGCTGAGAGCCAGCAGAAGCGTAA,

C20, GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGA,

C21, TCAATAGATATTAAATCCTTTGCCGGTTAGAACCT,

C22, CAATATTTGCCTGCAACAGTGCCATAGAGCCG,

C23, TTAAAGGGATTTTAGATACCGCCAGCCATTGCGGCACAGA,

C24, ACAATTCGACAACTCGTAATACAT,

C25, TTGAGGATGGTCAGTATTAACACCTTGAATGG,

C26, CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCA,

C27, CGCGAACTAAAACAGAGGTGAGGCTTAGAAGTATT,

C28, GAATCCTGAGAAGTGTATCGGCCTTGCTGGTACTTTAATG,

C29, ACCACCAGCAGAAGATGATAGCCC,

C30, TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAG,

C31, GCCACCGAGTAAAAGAACATCACTTGCCTGAGCGCCATTAAAA,

C32, TCTTTGATTAGTAATAGTCTGTCCATCACGCAAATTAACCGTT,

C33, CGCGTCTGATAGGAACGCCATCAACTTTTACA,

C34, AGGAAGATGGGGACGACGACAGTAATCATATT,

C35, CTCTAGAGCAAGCTTGCATGCCTGGTCAGTTG,

C36, CCTTCACCGTGAGACGGGCAACAGCAGTCACA,

C37, CGAGAAAGGAAGGGAAGCGTACTATGGTTGCT,

C38, GCTCATTTTTTAACCAGCCTTCCTGTAGCCAGGCATCTGC,

C39, CAGTTTGACGCACTCCAGCCAGCTAAACGACG,

C40, GCCAGTGCGATCCCCGGGTACCGAGTTTTTCT,

C41, TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGG,

C42, GTAACCGTCTTTCATCAACATTAAAATTTTTGTTAAATCA,

C43, ACGTTGTATTCCGGCACCGCTTCTGGCGCATC,

C44, CCAGGGTGGCTCGAATTCGTAATCCAGTCACG,

C45, TAGAGCTTGACGGGGAGTTGCAGCAAGCGGTCATTGGGCG,

C46, GTTAAAATTCGCATTAATGTGAGCGAGTAACACACGTTGG,

C47, TGTAGATGGGTGCCGGAAACCAGGAACGCCAG,

C48, GGTTTTCCATGGTCATAGCTGTTTGAGAGGCG,

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C50, GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTT,

C51, AGTTGGGTCAAAGCGCCATTCGCCCCGTAATG,

C52, CGCGCGGGCCTGTGTGAAATTGTTGGCGATTA,

C53, CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAA,

C54, CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATG,

C55, TGCTGCAAATCCGCTCACAATTCCCAGCTGCA,

C56, TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCA,

C57, TGGCGAAATGTTGGGAAGGGCGAT,

C58, TGTCGTGCACACAACATACGAGCCACGCCAGC,

C59, CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACC,

C60, TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCT,

C61, TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAAT,

C62, GCGCTCACAAGCCTGGGGTGCCTA,

C63, CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTT,

C64, AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGG,

C65, ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCC,

S2. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 1

Modified helpers for each triangle origami

6B Part

6B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACATGGTCA

6B31-1;TAACAGTCAAAGAAGTTTTGCCAGCATAAATA

6B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAGGGAGAGG

6B28-1;TCCTTCATGATAAAAACCAAAATATTAAACAG

6B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACGAACTTAA

6B23-1;AACGTGACAACACTATCATAACCCATCAAAAA

6B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCGATGAGGG

6B16-1;TGTCTACACGCCAAAAGGAATTACAGTCAGAA

6B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAAGTAGAGTC

6B08-1;CGCAATGGGAATACCACATTCAACTTAAGAGG

6B37;GTCCATCTACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGAAAGAC

6B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTCGAAGGAG

6B45-1;GAGTAGTTTTAATAAAACGAACTAACCGAACT

6B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGGAAATGGT

6B53-1;TGACCAGCACCAGTCAGGACGTTGGAACGGTG

6B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATAAGGAAGC

6B59-1;ATGCGGCAACCTTATGCGATTTTATGACCTTC

6B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTACGCTCG

6B63-1;TAGACATATGGTTTAATTTCAACTCGGATATT

6B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAATTTA

TCC

6B65;AGCCCCTGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

6A Part

6A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAACCACCTA

6A31-1;GCCTTTACTATCTTACCGAAGCCCAAACGCAA

6A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCGCTTGCCT

6A28-1;GCTGCGGAATAAGAGCAAGAAACATGGCATGA

6A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACGACCAGG

6A23-1;TTTTTACCGATAACCCACAAGAATGTTAGCAA

6A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGATTTAGACA

6A16-1;GCACGTAAGTCAGAGGGTAATTGATGGCAACA

6A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAATTTTTGAC

6A08-1;GTCAGTAAGACGGGAGAATTAACTCGGAATAA

6A37;CACGCAAGAGAGAATAACATAAAAACAGGGAAGCGCATTAGAACGTC

A

6A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGGTAAACGC

6A45-1;TTAACCGGAACGTCAAAAATGAAAAGCAAGCC

6A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTACGCTCGA

6A53-1;TTCCGTAATCCCAATCCAAATAAGATTACCGC

6A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAATTCAGCG

6A59-1;AGGCCGTTGCCAGTTACAAAATAATAGAAGGC

6A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTGAATGTT

6A63-1;TAAGCAATACGCTAACGAGCGTCTGGCGTTTT

6A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAGACGG

CAG

6A65;AGCAGGAAACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

5B Part

5B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAAGCGAGGG

5B31-1;GCGTACCAAAAGAAGTTTTGCCAGCATAAATA

5B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCATAAACGCA

5B28-1;CGAGCACGGATAAAAACCAAAATATTAAACAG

5B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACAGAGCGGT

5B23-1;TTTGTTACAACACTATCATAACCCATCAAAAA

5B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTCGTCAGA

5B16-1;CGGTTAAACGCCAAAAGGAATTACAGTCAGAA

5B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCCAAAAC

5B08-1;AGCTTAATGAATACCACATTCAACTTAAGAGG

5B37;TACGGATTACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGAGGCCA

5B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTGTTCAGTA

5B45-1;CTTACCTATTAATAAAACGAACTAACCGAACT

5B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGTTAGTGGT

5B53-1;CAGATAGTACCAGTCAGGACGTTGGAACGGTG

5B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATAATCCACG

5B59-1;ACAAGAGAACCTTATGCGATTTTATGACCTTC

5B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTATCTCTAC

5B63-1;CTCATATCTGGTTTAATTTCAACTCGGATATT

5B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGATAAAC

CAG

5B65;CAAGCATAACACCAGAACGAGTAGGCTGCTCATTCAGTGA

5A Part

5A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAATCATCCAA

5A31-1;AGAATCGTTATCTTACCGAAGCCCAAACGCAA

5A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTAGTTGAT

5A28-1;GTAAGAGCATAAGAGCAAGAAACATGGCATGA

5A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATTCTCGAG

5A23-1;CGAATTTTGATAACCCACAAGAATGTTAGCAA

5A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGACTCATTTT

5A16-1;TCGATTTAGTCAGAGGGTAATTGATGGCAACA

5A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAATTCGTAA

5A08-1;CCTGCTTTGACGGGAGAATTAACTCGGAATAA

5A37;AGAAATATAGAGAATAACATAAAAACAGGGAAGCGCATTAATCAAGAT

5A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGCCGAAAGT

5A45-1;TGGAAGCGAACGTCAAAAATGAAAAGCAAGCC

5A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTATAAAACT

5A53-1;CCAATCATTCCCAATCCAAATAAGATTACCGC

5A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTATTTTATCG

5A59-1;GAGCAGATGCCAGTTACAAAATAATAGAAGGC

5A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTTGTCGTC

5A63-1;AAACGTCGACGCTAACGAGCGTCTGGCGTTTT

5A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAGCTAC

AGT

5A65;AATCTCATACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

4B Part

4B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACTCTCTTT

4B31-1;TATCTGGTAAAGAAGTTTTGCCAGCATAAATA

4B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCATGAACGGC

4B28-1;GCTTGGTAGATAAAAACCAAAATATTAAACAG

4B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACAGTTGGAT

4B23-1;AGATTTGTAACACTATCATAACCCATCAAAAA

4B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCCATTGTGA

4B16-1;GTTGCGGCCGCCAAAAGGAATTACAGTCAGAA

4B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCATTCTG

4B08-1;TGGGAAGTGAATACCACATTCAACTTAAGAGG

4B37;TTGTTCCAACAGGTAGAAAGATTCATCAGTTGAGATTTAGAGCGACAG

4B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTTTCTTTAG

4B45-1;AGCAAGGTTTAATAAAACGAACTAACCGAACT

4B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGCCATATCT

4B53-1;ATTTAGCCACCAGTCAGGACGTTGGAACGGTG

4B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATACATAGAA

4B59-1;CTGGTAGCACCTTATGCGATTTTATGACCTTC

4B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTTTAAGCG

4B63-1;AACAGGCCTGGTTTAATTTCAACTCGGATATT

4B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAACAAC

CAA

4B65;CGTCCTGCACACCAGAACGAGTAGGCTGCTCATTCAGTGA

4A Part

4A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAATGGGCAT

4A31-1;CACGTATTTATCTTACCGAAGCCCAAACGCAA

4A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTTGCAAGC

4A28-1;ATTGCGTAATAAGAGCAAGAAACATGGCATGA

4A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACCCGACGA

4A23-1;CGCTACCTGATAACCCACAAGAATGTTAGCAA

4A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAGTAGGAAG

4A16-1;ACCGCATGGTCAGAGGGTAATTGATGGCAACA

4A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGAAATGA

A

4A08-1;ACCATACTGACGGGAGAATTAACTCGGAATAA

4A37;AGTCGGCGAGAGAATAACATAAAAACAGGGAAGCGCATTACAGGCAC

A

4A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGTGTGAATC

4A45-1;TCGGCAGCAACGTCAAAAATGAAAAGCAAGCC

4A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTAAGAACCA

4A53-1;AAAATAGTTCCCAATCCAAATAAGATTACCGC

4A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTACACGCAAA

4A59-1;AAAACGCCGCCAGTTACAAAATAATAGAAGGC

4A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTCTAATCG

4A63-1;AGAGTGTCACGCTAACGAGCGTCTGGCGTTTT

4A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAAAAAA

CGA

4A65;ATGAGCCTACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

3B Part

3B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAGTCGCATT

3B31-1;GAATAGCAAAAGAAGTTTTGCCAGCATAAATA

3B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAAAGCCTCT

3B28-1;GAGGCCTCGATAAAAACCAAAATATTAAACAG

3B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACCAGCAATC

3B23-1;AATACCTTAACACTATCATAACCCATCAAAAA

3B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTCTTTTTG

3B16-1;CGCGAATACGCCAAAAGGAATTACAGTCAGAA

3B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATCCTTAAG

3B08-1;AGCTTGCGGAATACCACATTCAACTTAAGAGG

3B37;GTTCTCTAACAGGTAGAAAGATTCATCAGTTGAGATTTAGGCAAAACT

3B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTAAAACCAT

3B45-1;GGCGGTGGTTAATAAAACGAACTAACCGAACT

3B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGTCTATAGT

3B53-1;TGGGGGAGACCAGTCAGGACGTTGGAACGGTG

3B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATCACATTGT

3B59-1;ATCCATTAACCTTATGCGATTTTATGACCTTC

3B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTACTTCTCA

3B63-1;CATCACGATGGTTTAATTTCAACTCGGATATT

3B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAACGTC

AGA

3B65;TCAACATAACACCAGAACGAGTAGGCTGCTCATTCAGTGA

3A Part

3A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGAACTCAA

3A31-1;AGACAGAATATCTTACCGAAGCCCAAACGCAA

3A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTCTCTTCC

3A28-1;TATCCATCATAAGAGCAAGAAACATGGCATGA

3A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATGCTTATG

3A23-1;GATTGAGAGATAACCCACAAGAATGTTAGCAA

3A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAAAGAGTAG

3A16-1;AATAGCAGGTCAGAGGGTAATTGATGGCAACA

3A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGTTTAAGA

3A08-1;AGTCAAAAGACGGGAGAATTAACTCGGAATAA

3A37;TAATAAGAAGAGAATAACATAAAAACAGGGAAGCGCATTATAATCAGC

3A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGACGAACCA

3A45-1;ATTTGGAGAACGTCAAAAATGAAAAGCAAGCC

3A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTGCATGAAA

3A53-1;GTGTCAATTCCCAATCCAAATAAGATTACCGC

3A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTACCTGACGG

3A59-1;TTAGAGCCGCCAGTTACAAAATAATAGAAGGC

3A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTAATACCAT

3A63-1;CCAGAAATACGCTAACGAGCGTCTGGCGTTTT

3A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCATGTTCC

AA

3A65;TATCAATAACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

2B Part

2B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAACCATGAAA

2B31-1;GAAGCAGCAAAGAAGTTTTGCCAGCATAAATA

2B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCAATCAGTGA

2B28-1;CTTTGCAGGATAAAAACCAAAATATTAAACAG

2B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACTAGCGCCA

2B23-1;ACCGCTGAAACACTATCATAACCCATCAAAAA

2B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTTCTGCGT

2B16-1;TCAACCTCCGCCAAAAGGAATTACAGTCAGAA

2B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAAAGCACTAA

2B08-1;TTTGATTTGAATACCACATTCAACTTAAGAGG

2B37;CCGTTTGAACAGGTAGAAAGATTCATCAGTTGAGATTTAGGGTCATTG

2B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTGCTTGAGT

2B45-1;ATCTCGGATTAATAAAACGAACTAACCGAACT

2B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGAACCTGCT

2B53-1;GGTGTTTTACCAGTCAGGACGTTGGAACGGTG

2B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATCCATAATA

2B59-1;TAGACTCCACCTTATGCGATTTTATGACCTTC

2B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTTCTGTTG

2B63-1;TTTTGTGCTGGTTTAATTTCAACTCGGATATT

2B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAATATA

CCT

2B65;GCGTGAAGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

2A Part

2A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAACAGCAATC

2A31-1;TTTGCATCTATCTTACCGAAGCCCAAACGCAA

2A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTCGGCAAT

2A28-1;AGTTGCATATAAGAGCAAGAAACATGGCATGA

2A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATTTAGTAA

2A23-1;AAATCCGGGATAACCCACAAGAATGTTAGCAA

2A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGACGTCAACC

2A16-1;CATCAGCAGTCAGAGGGTAATTGATGGCAACA

2A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAACCAGCACG

2A08-1;TCAGGAAAGACGGGAGAATTAACTCGGAATAA

2A37;ATCCTTTCAGAGAATAACATAAAAACAGGGAAGCGCATTATGCAGCAG

2A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGCTTTATCA

2A45-1;CAAGTCCAAACGTCAAAAATGAAAAGCAAGCC

2A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTACCAAATC

2A53-1;ACGGCAGATCCCAATCCAAATAAGATTACCGC

2A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAAGTGCCAG

2A59-1;AAGAAGTCGCCAGTTACAAAATAATAGAAGGC

2A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTCTTTACCA

2A63-1;CAGAAACAACGCTAACGAGCGTCTGGCGTTTT

2A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCAAAACT

AGG

2A65;TTAGGAACACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

1B Part

1B32;AATACTGCGGAATCGTAGGGGGTAATAGTAAAATTAGAGC

1B31-1;AATACCAGAAAGAAGTTTTGCCAGCATAAATA

1B30;TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCACATCACCC

1B28-1;TATCGGTAGATAAAAACCAAAATATTAAACAG

1B26;CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACGCAAGCAC

1B23-1;CCGGAGGCAACACTATCATAACCCATCAAAAA

1B20;TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCGGCTTTTT

1B16-1;TTTAGACACGCCAAAAGGAATTACAGTCAGAA

1B12;AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATGGCGCCA

1B08-1;CAATACCGGAATACCACATTCAACTTAAGAGG

1B37;CACCTCACACAGGTAGAAAGATTCATCAGTTGAGATTTAGCCAGCAAT

1B41;CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTTTAAGTGG

1B45-1;TCTTTAATTTAATAAAACGAACTAACCGAACT

1B49;TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGAACCTGAT

1B53-1;GCGGCATTACCAGTCAGGACGTTGGAACGGTG

1B56;CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATTAGTAGCG

1B59-1;CCATGAAAACCTTATGCGATTTTATGACCTTC

1B61;AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTCCAACATA

1B63-1;GTACGGGGTGGTTTAATTTCAACTCGGATATT

1B64;ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGAAAGGA
CGT

1B65;CTTGACGGACACCAGAACGAGTAGGCTGCTCATTCAGTGA

1A Part

1A32;CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAACATGGCGA

1A31-1;CATCATAGTATCTTACCGAAGCCCAAACGCAA

1A30;GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCGCAGTCG
G

1A28-1;GAAGAAGAATAAGAGCAAGAAACATGGCATGA

1A26;CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATACTCAAAGC

1A23-1;AAATTTAGGATAACCCACAAGAATGTTAGCAA

1A20;TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGAGGTCGGCA

1A16-1;CACCAACAGTCAGAGGGTAATTGATGGCAACA

1A12;CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAAGAAACAA
C

1A08-1;ACAGATGTGACGGGAGAATTAACTCGGAATAA

1A37;ACCACCATAGAGAATAACATAAAAACAGGGAAGCGCATTAATCCATCT

1A41;TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGTACCAGCA

1A45-1;CAAAATATAACGTCAAAAATGAAAAGCAAGCC

1A49;AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTAACGTTGA

1A53-1;GTCTGTAATCCCAATCCAAATAAGATTACCGC

1A56;ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTAAACAGGTG

1A59-1;AACAGAAGGCCAGTTACAAAATAATAGAAGGC

1A61;GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTGAGAACC

1A63-1;AGTTTGAAACGCTAACGAGCGTCTGGCGTTTT

1A64;ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCATTATGG

CG

1A65;AACATGATACCCAGCTACAATTTTGTTTTGAAGCCTTAAA

Bridges

611;ATATAACCAAGTCTGA

612;AGAAATAAAGTAGTGT

621;AGTGGCATAGAAAAAA

622;AGCTTATCTAACACCA

631;TCCACTGTGCTGGAGT

632;CCGAAGAATCACCATA

641;ACATAAAACTTTAGGT

642;CGATGTAGAGTAAAAA

651;AATAGCAACAAACTAT

652;TTAACCGTGGCCACGA

661;GGAGAGCGTGAAGAAA

662;GAATGCAACCAACGGC

671;TCGCCAGCCGGCGTTG

672;CTGATTAGGATAACCG

681;AATAAGACAATATCAG

682;TCAAAAGCGACCAATC

691;CAAGATGGCAGGCAAA

692;GAACCAAAGAAAGGTC

6101;GCGCCAGTTCGGAACC

6102;GAGGGTAGTTGAATAT

6111;TCAAGTAAAGGATAAA

6112;CCATTCAAGGGGCCGA

5 Triangle Origami(65)

511;CATACCAAGAACGTGC

512;TCCTTGACAGACGAGC

521;TTAGTACCAAATGTGA

522;CATGAACATCGCAACG

531;GCGAGCGCAAATGTCA

532;CTCTTTTACAGAACGT

541;TTACATCAATCGGACT

542;TGAACAGCCTCCTTCC

551;GCACGTTTCATGATTT

552;ACTTGACTTCTTCTGC

561;GTGTTTCCTGGAAACG

562;AAGCGGTCTGCGCGTA

571;GAACAATTCCTGAATG

572;GGCAGAAGCAGCGGCT

581;CGCCATTAATCATCTT

582;AAATCGAAATAATGTT

591;CCTTCCATATCCAAAC

592;CAGTAGCAGATGAGAC

5101;GACGGGATCGCAGCGA

5102;AGCCTCAAGAACATAA

5111;CAATAAACAAAGTCCA

5112;TATCCCACTCAACAGG

4 Triangle Origami(54)

411;CGCGTCAGTGAAAAAG

412;CCAGAACGTTTTTGAC

421;GGCGAAAGTTAGCATC

422;GCTCACCTGTCGCAAA

431;CTGCGCAACCATATAA

432;ACCAACAGGGATAGGT

441;CCGCCAGCGTTAACGT

442;GACTTTTTAGTCCACT

451;ACAAGCAGCCTTTAGC

452;CTCCTAGATAGTAATT

461;AATTTTTCTTAGTGAG

462;CTTGGTTTGACTCATC

471;GTTAACTTCAGCTTCT

472;ATTCTGAACTGCGTCA

481;CTGCAGGTATCCCGAA

482;GCATTTTCTGGATACG

491;AAGCGCGCCCGTGGAC

492;TAAGCACTATAAATTT

4101;ACAGGTTGGTAACCCA

4102;GTCGCGTCCGCCGCCA

4111;AACTTTTCTGCTTCAA

4112;TTGCGTTCCCAGCCTC

3 Triangle Origami(43)

311;ACTGTAACTATGGCCG

312;AGCAGCCTCATAAGGC

321;TATTTAACTACAAACT

322;GTAACAGATGGCGGCG

331;CCAAAATTGCCAATTC

332;AGCATTGTAGGGTCAA

341;TGTCCGCATATCAAGT

342;GTTATTAATAAAGTGC

351;GACGGCCACCCTTCGG

352;TTTTCGTCTTAGCTGT

361;CAAAAATAGTCTTCTC

362;GCGTAACCCTGATAGC

371;ATTAGCCTCAGCAGCC

372;AGGGCGTTTGCGACCC

381;TACGACCAATACTCAT

382;GGGTAATTATATCACG

391;GCATTGGGTCATCCTT

392;TTGAACACATTATCAT

3101;GTCGTCAGTCATAGTG

3102;ACGCGATTCCAACGTG

3111;TAAACCAACAAACGCT

3112;GCATTCATCCATCAGC

2 Triangle Oriami(32)

211;CGCCCTGCGTATTCTG

212;GGTCTTTCATACGAAA

221;AAGAGCTTGCATCTCA

222;ATAAGCAAGATGCGGT

231;GAAGCCAAGCGAGCAG

232;GACGCAACGCATTGGG

241;AAATGCCAGAAAGATT

242;GTTGCTTGCAAGCCTC

251;GCCTCGATGGCGCATA

252;AAGCATTTACGCTCAA

261;GTGACATTCTGACCAG

262;GTAAAATACAGAAGGG

271;TAAAAAAGGTCATTTC

272;CCTTGCGACCTCCAAG

281;ACATACAAGAACTAAG

282;TTGCTGATTTGGGAGG

291;TTATTTCCAGAGCCAT

292;ATATGAGATAGACAAA

2101;CAGCTTTAGAAATATC

2102;CGACATTACCGTCTTT

2111;GTATCGGCCCACACCA

2112;AATATCAAAACAGCTT

1 Triangle Origami(21)

111;TCTTTTTGACACAGTC

112;CAATAGTCAGTCTCAT

121;CTCTTTCTTGCCCGGC

122;AACGTTATGATTGTCC

131;GCTCTTTTAGACCAAA

132;GTAAAGTTTGATTCTC

141;ATACCAGCACCAATCC

142;TCAGCGAAAGAGGAAG

151;CTCCCAAGAAATAATC

152;CTGGAGACCATTAAGC

161;CAAGATAAACATAAAT

162;AGCACCAATCACGAGT

171;GCGGCAGAAGCAGAAG

172;CCAGCAAGCTTGCCAC

181;AAGCAACTCCAAACAA

182;GACCGCCTTATCAGAA

191;CCTGCAACGAATGCCA

192;ATCACCTTGTACCTTC

1101;GCTTTAGCAGTATTGT

1102;ATGCCTACCATAGCAC

1111;GGCGGCCTGCAGATTT

1112;CTTGAATGCATCAGGG

S3. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 2

Modified helpers for each triangle origami

6I1;CGAAGGAGTCGCCAGCCGGCGTTGACAGATGT

6I21;CACCAACAGAAACAACCTGATTAGGATAACCG

6T22;GAGTAGTTGAAATGGTAATAAGACAATATCAG

6I31;AAATTTAGGGTCGGCATCAAAAGCGACCAATC

6I32;TGACCAGCAAGGAAGCCAAGATGGCAGGCAAA

6I41;GAAGAAGACTCAAAGCGAACCAAAGAAAGGTC

6I42;ATGCGGCATACGCTCGGCGCCAGTTCGGAACC

6I51;CATCATAGGCAGTCGGGAGGGTAGTTGAATAT

6I52;TAGACATAATTTATCCTCAAGTAAAGGATAAA

6I6;CATGGCGACCATTCAAGGGGCCGAAGCCCCTG

5I1;GTTCAGTAACTTGACTTCTTCTGCGTCAGTAA

5I21;GCACGTAATTTTTGACGCACGTTTCATGATTT

5T22;CTTACCTATTAGTGGTTGAACAGCCTCCTTCC

5I31;TTTTTACCTTTAGACATTACATCAATCGGACT

5I32;CAGATAGTAATCCACGCTCTTTTACAGAACGT

5I41;GCTGCGGACGACCAGGGCGAGCGCAAATGTCA

5I42;ACAAGAGAATCTCTACCATGAACATCGCAACG

5I51;GCCTTTACGCTTGCCTTTAGTACCAAATGTGA

5I52;CTCATATCTAAACCAGTCCTTGACAGACGAGC

5I6;ACCACCTACATACCAAGAACGTGCCAAGCATA

4I1;TTCTTTAGCTCCTAGATAGTAATTCCTGCTTT

4I21;TCGATTTAATTCGTAAACAAGCAGCCTTTAGC

4T22;AGCAAGGTCCATATCTGACTTTTTAGTCCACT

4I31;CGAATTTTCTCATTTTCCGCCAGCGTTAACGT

4I32;ATTTAGCCACATAGAAACCAACAGGGATAGGT

4I41;GTAAGAGCTTCTCGAGCTGCGCAACCATATAA

4I42;CTGGTAGCTTTAAGCGGCTCACCTGTCGCAAA

4I51;AGAATCGTTAGTTGATGGCGAAAGTTAGCATC

4I52;AACAGGCCACAACCAACCAGAACGTTTTTGAC

4I6;TCATCCAACGCGTCAGTGAAAAAGCGTCCTGC

3I1;AAAACCATTTTTCGTCTTAGCTGTACCATACT

3I21;GGCGGTGGTCTATAGTGTTATTAATAAAGTGC

3I22;ACCGCATGGAAATGAAGACGGCCACCCTTCGG

3I31;TGGGGGAGCACATTGTAGCATTGTAGGGTCAA

3I32;CGCTACCTGTAGGAAGTGTCCGCATATCAAGT

3I41;ATCCATTAACTTCTCAGTAACAGATGGCGGCG

3I42;ATTGCGTACCCGACGACCAAAATTGCCAATTC

3I51;CATCACGAACGTCAGAAGCAGCCTCATAAGGC

3T52;CACGTATTTTGCAAGCTATTTAACTACAAACT

3I6;ATGGGCATACTGTAACTATGGCCGTCAACATA

2I1;GCTTGAGTAAGCATTTACGCTCAAAGTCAAAA

2I21;AATAGCAGGTTTAAGAGCCTCGATGGCGCATA

2T22;ATCTCGGAAACCTGCTGTTGCTTGCAAGCCTC

2I31;GATTGAGAAAGAGTAGAAATGCCAGAAAGATT

2I32;GGTGTTTTCCATAATAGACGCAACGCATTGGG

2I41;TATCCATCTGCTTATGGAAGCCAAGCGAGCAG

2I42;TAGACTCCTTCTGTTGATAAGCAAGATGCGGT

2I51;AGACAGAATCTCTTCCAAGAGCTTGCATCTCA

2I52;TTTTGTGCATATACCTGGTCTTTCATACGAAA

2I6;GAACTCAACGCCCTGCGTATTCTGGCGTGAAG

1I1;TTAAGTGGCTGGAGACCATTAAGCTCAGGAAA

1I21;CATCAGCACCAGCACGCTCCCAAGAAATAATC

1T22;TCTTTAATAACCTGATTCAGCGAAAGAGGAAG

1I31;AAATCCGGCGTCAACCATACCAGCACCAATCC

1I32;GCGGCATTTAGTAGCGGTAAAGTTTGATTCTC

1I41;AGTTGCATTTTAGTAAGCTCTTTTAGACCAAA

1I42;CCATGAAACCAACATAAACGTTATGATTGTCC

1I51;TTTGCATCTCGGCAATCTCTTTCTTGCCCGGC

1I52;GTACGGGGAAGGACGTCAATAGTCAGTCTCAT

1I6;CAGCAATCTCTTTTTGACACAGTCCTTGACGG

S4. Triangle origami modified staples and bridges that hybridize with ΦX 174 scaffolds for design 3

Modified helpers for each triangle origami

111;CATGGTCAATATAACCAAGTCTGA

112;AGAAATAAAGTAGTGTTAACAGTC

121;AGTGGCATAGAAAAAAAGTTTGAA

122;TGAGAACCAGCTTATCTAACACCA

131;GAACTTAATCCACTGTGCTGGAGT

132;CCGAAGAATCACCATAAACGTGAC

141;ACATAAAACTTTAGGTGTCTGTAA

142;AACGTTGACGATGTAGAGTAAAAA

151;GTAGAGTCAATAGCAACAAACTAT

152;TTAACCGTGGCCACGACGCAATGG

161;GGAGAGCGTGAAGAAAACCACCAT

162;ATCCATCTGAATGCAACCAACGGC

171;CGAAGGAGTCGCCAGCCGGCGTTG

172;CTGATTAGGATAACCGGAGTAGTT

181;AATAAGACAATATCAGCACCAACA

182;GGTCGGCATCAAAAGCGACCAATC

191;AAGGAAGCCAAGATGGCAGGCAAA

192;GAACCAAAGAAAGGTCATGCGGCA

1101;GCGCCAGTTCGGAACCGAAGAAGA

1102;GCAGTCGGGAGGGTAGTTGAATAT

1111;ATTTATCCTCAAGTAAAGGATAAA

1112;CCATTCAAGGGGCCGAAGCCCCTG

211;AGCGAGGGTATCCCACTCAACAGG

212;CAATAAACAAAGTCCAGCGTACCA

221;AGCCTCAAGAACATAATAAGCAAT

222;TGAATGTTGACGGGATCGCAGCGA

231;AGAGCGGTCAGTAGCAGATGAGAC

232;CCTTCCATATCCAAACTTTGTTAC

241;AAATCGAAATAATGTTTTCCGTAA

242;ACGCTCGACGCCATTAATCATCTT

251;TCCAAAACGGCAGAAGCAGCGGCT

252;GAACAATTCCTGAATGAGCTTAAT

261;AAGCGGTCTGCGCGTACACGCAAG

262;GAACGTCAGTGTTTCCTGGAAACG

271;GTTCAGTAACTTGACTTCTTCTGC

272;GCACGTTTCATGATTTCTTACCTA

281;TGAACAGCCTCCTTCCGCACGTAA

282;TTTAGACATTACATCAATCGGACT

291;AATCCACGCTCTTTTACAGAACGT

292;GCGAGCGCAAATGTCAACAAGAGA

2101;CATGAACATCGCAACGGCTGCGGA

2102;GCTTGCCTTTAGTACCAAATGTGA

2111;TAAACCAGTCCTTGACAGACGAGC

2112;CATACCAAGAACGTGCCAAGCATA

311;CTCTCTTTTTGCGTTCCCAGCCTC

312;AACTTTTCTGCTTCAATATCTGGT

321;GTCGCGTCCGCCGCCAAAACGTCG

322;TTGTCGTCACAGGTTGGTAACCCA

331;AGTTGGATTAAGCACTATAAATTT

332;AAGCGCGCCCGTGGACAGATTTGT

341;GCATTTTCTGGATACGCCAATCAT

342;ATAAAACTCTGCAGGTATCCCGAA

351;TCATTCTGATTCTGAACTGCGTCA

352;GTTAACTTCAGCTTCTTGGGAAGT

361;CTTGGTTTGACTCATCAGAAATAT

362;ATCAAGATAATTTTTCTTAGTGAG

371;TTCTTTAGCTCCTAGATAGTAATT

372;ACAAGCAGCCTTTAGCAGCAAGGT

381;GACTTTTTAGTCCACTTCGATTTA

382;CTCATTTTCCGCCAGCGTTAACGT

391;ACATAGAAACCAACAGGGATAGGT

392;CTGCGCAACCATATAACTGGTAGC

3101;GCTCACCTGTCGCAAAGTAAGAGC

3102;TAGTTGATGGCGAAAGTTAGCATC

3111;ACAACCAACCAGAACGTTTTTGAC

3112;CGCGTCAGTGAAAAAGCGTCCTGC

411;GTCGCATTGCATTCATCCATCAGC

412;TAAACCAACAAACGCTGAATAGCA

421;ACGCGATTCCAACGTGAGAGTGTC

422;TCTAATCGGTCGTCAGTCATAGTG

431;CAGCAATCTTGAACACATTATCAT

432;GCATTGGGTCATCCTTAATACCTT

441;GGGTAATTATATCACGAAAATAGT

442;AAGAACCATACGACCAATACTCAT

451;TCCTTAAGAGGGCGTTTGCGACCC

452;ATTAGCCTCAGCAGCCAGCTTGCG

461;GCGTAACCCTGATAGCAGTCGGCG

462;CAGGCACACAAAAATAGTCTTCTC

471;AAAACCATTTTTCGTCTTAGCTGT

472;GACGGCCACCCTTCGGGGCGGTGG

481;GTTATTAATAAAGTGCACCGCATG

482;GTAGGAAGTGTCCGCATATCAAGT

491;CACATTGTAGCATTGTAGGGTCAA

492;CCAAAATTGCCAATTCATCCATTA

4101;GTAACAGATGGCGGCGATTGCGTA

4102;TTGCAAGCTATTTAACTACAAACT

4111;ACGTCAGAAGCAGCCTCATAAGGC

4112;ACTGTAACTATGGCCGTCAACATA

511;CCATGAAAAATATCAAAACAGCTT

512;GTATCGGCCCACACCAGAAGCAGC

521;CGACATTACCGTCTTTCCAGAAAT

522;AATACCATCAGCTTTAGAAATATC

531;TAGCGCCAATATGAGATAGACAAA

532;TTATTTCCAGAGCCATACCGCTGA

541;TTGCTGATTTGGGAGGGTGTCAAT

542;GCATGAAAACATACAAGAACTAAG

551;AGCACTAACCTTGCGACCTCCAAG

552;TAAAAAAGGTCATTTCTTTGATTT

561;GTAAAATACAGAAGGGTAATAAGA

562;TAATCAGCGTGACATTCTGACCAG

571;GCTTGAGTAAGCATTTACGCTCAA

572;GCCTCGATGGCGCATAATCTCGGA

581;GTTGCTTGCAAGCCTCAATAGCAG

582;AAGAGTAGAAATGCCAGAAAGATT

591;CCATAATAGACGCAACGCATTGGG

592;GAAGCCAAGCGAGCAGTAGACTCC

5101;ATAAGCAAGATGCGGTTATCCATC

5102;TCTCTTCCAAGAGCTTGCATCTCA

5111;ATATACCTGGTCTTTCATACGAAA

5112;CGCCCTGCGTATTCTGGCGTGAAG

611;ATTAGAGCCTTGAATGCATCAGGG

612;GGCGGCCTGCAGATTTAATACCAG

621;ATGCCTACCATAGCACCAGAAACA

622;CTTTACCAGCTTTAGCAGTATTGT

631;GCAAGCACATCACCTTGTACCTTC

632;CCTGCAACGAATGCCACCGGAGGC

641;GACCGCCTTATCAGAAACGGCAGA

642;ACCAAATCAAGCAACTCCAAACAA

651;TGGCGCCACCAGCAAGCTTGCCAC

652;GCGGCAGAAGCAGAAGCAATACCG

661;AGCACCAATCACGAGTATCCTTTC

662;TGCAGCAGCAAGATAAACATAAAT

671;TTAAGTGGCTGGAGACCATTAAGC

672;CTCCCAAGAAATAATCTCTTTAAT

681;TCAGCGAAAGAGGAAGCATCAGCA

682;CGTCAACCATACCAGCACCAATCC

691;TAGTAGCGGTAAAGTTTGATTCTC

692;GCTCTTTTAGACCAAACCATGAAA

6101;AACGTTATGATTGTCCAGTTGCAT

6102;TCGGCAATCTCTTTCTTGCCCGGC

6111;AAGGACGTCAATAGTCAGTCTCAT

6112;TCTTTTTGACACAGTCCTTGACGG

S5. Unmodified square DNA origami staples

1 TTCAGGGATAGCAAG

2 GAACCGCCACCCTCAGCCCTTATT

3 TAGTACCGCCACCCTCAAAATCAC

4 CGGAATAGGTGTATCACGCCTCCC

5 GTGCCGTCGAGAGGGTCCACCCTC

6 TAGCGGGGTTTTGCTCACCAGAAC

7 AGGCTGAGACTCCTCATGACAGGAGGTTGAGGCAGGTC

8 CATGAAAGTATTAAG

9 ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATT

10 AGTTTTGCCCATCTTTTCATAATCAGAACCGCCACCCTCA

11 AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTT

12 TATCATAAGCCACCCTCAGAACCGTGATATAAGTATAGCC

13 AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAA

14 CCACATTCGAGCCGCCGCCAGCATAGAGAAGGATTAGGAT

15 AACCTATTATTCTGA

16 TATAAACAGTTAATGCCAAATAAA

17 AACGGGGTCAGTGCCTGCGCAGTC

18 GATGATACAGGAGTGTGTCATACAT

19 AAACGGGTAAAATACGAAAGAGGC

20 ACTAAAGACTTTTTCACTTTGACC

21 CGAGGGTAGCAACGGCACAAAGTACAACGGAGATTTGT

22 AAGACAGCATCGGAA

23 GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGG

24 AAAACGAAAAAGCCAGAATGGAAATGAGTAACAGTGCCCG

25 TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTT

26 ATGCGATTGCACCAACCTAAAACGTAATGCCACTACGAAG

27 TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATT

28 AGAACGAGTTATACCAAGCGCGAATACAGAGGCTTTGAGG

29 GTCACCCTCAGCAGC

30 TGCAGGGAGTTAAAGGATCCGCGA

31 ACGCATAACCGATATAACGAGGCG

32 AGTTGCGCCGACAATGGAACTGAC

33 GAGGTGAATTTCTTAAAGTTTATT

34 CTTTAATTGTATCGGTTATGGTTT

35 AAAATCTCCAAAAAAAACATTCAACCGATTGAGGGAGG

36 AATTTTTTCACGTTG

37 TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATC

38 TACCCAAAATGTTACTTAGCCGGATTCGGTCGCTGAGGCT

39 AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCC

40 AGACCAGGAAAGAGGACAGATGAAACAGCTTGATACCGAT

41 GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTC

42 AAATACATCAAAGACAAAAGGGCGAGGCTCCAAAAGGAGC

43 AAGGAATTGCGAATA

44 TTCAGCGGAGTGAGAACATTAAAG

45 GTATGGGATTTTGCTAGAGCCATT

46 CGTCTTTCCAGACGTTCCAGTAGC

47 CTCATAGTTAGCGTAAAACGTCAC

48 ACTACAACGCCTGTAGCGTAATCA

49 TACCGTAACACTGAGTTTAGCGTCAGACTGTAGCGCGT

50 CAATAGGAACCCATG

51 GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTA

52 GGAATACCTCACCGTCACCGACTTAACAACTTTCAACAGT

53 CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCT

54 AATCAAAACATTAGCAAGGCCGGACGATCTAAAGTTTTGT

55 TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCC

56 TCATAAATAGAATCAAGTTTGCCTTTCGTCACCAGTACAA

57 AGCGTTTGCAGAGGGGGTAATAGTATTCGAGC

58 CGGAACCAATAGCGAGAGGCTTTTAAACTCCAACAGGTCAATAAGAGG

59 TCAGAGCCCCCTCGTTTACCAGACTAAACCAAGTACCGCATTCCAAGA

60 AGAGCCACTACGAGGCATAGTAAGAAGCCGTTTTTATTTTACCAATCA

61 CACCACCAAACTAATGCAGATACAACCGCGCCCAATAGCAAATATCCC

62 TCCTCATTCTAACGGAACAACATTTCTAAGAA

63 TCTGAATTTTGGGAAGAAAAATCTCGACTTGCGGGAGGTTCATGTTCA

64 GGCTTTTTTAAGAACTGGCTCATAGATTAGTTGCTATTTAGTAATTC

65 AAAAGAATACTTTAATCATTGTGATTTATCCTGAATCTTATAGAACCC

66 CCCAGCGATAGTAAATTGGGCTTGTCTTTCCAGAGCCTAAAGCCTTTA

67 CCTGCTCCTCAACGTAACAAAGCTTTATCCCA

68 CAGACGGTTCTTGACAAGAACCGGTTTAACGTCAAAAATGCAGAGCAT

69 CAACTTTGCGCATAGGCTGGCTGACAGAGAGAATAACATACAAAGAAT

70 TTGTCACAAAGACACCACGGAATATTAGACGGGAGAATTAGCATTAAC

71 ACCAGCGCACATAAAGGTGGCAACAAAGTCAGAGGGTAATAAAAGGTG

72 GTGAATTACAAAAGAACTGGCATGAATTGAGT

73 TGGGAATTAAACCGAGGAAACGCAACAATGAAATAGCAATTTAGATAC

74 ACCATTACTAAGCAGATAGCCGAACCCTTTTTAAGAAAAGAATTCTGC

75 CAATGAAAGTTCAGAAAACGAGAAGACTATTATAGTCAGAGGAAGTTT

76 GTAGCGACATTCATTGAATCCCCCTCAAAAAGATTAAGAGTGTTTTAA

77 TTCATCAGTTGAGATTAAGGCT

78 AGGCTTGCCCTGACGATAAACA

79 ACGCAGTATGTTAGCAAGAGAT

80 ATAGCGTCCAATACTGCAAATA

81 GTTTTAAAAATGTTTAGACTGG

82 TTCAAAGCTTAATTGCTGAATAT

83 CGGTATATTACAGGTAGAAAGA

84 CGCGAGGCTCAACAATAGATAAG

85 TATTATGCTCATTCAGTGAATA

86 ATCCAAATACATTATGACCCTGT

87 CACAAGATTAAGACTCCTTATT

88 TAAGCCCATTTAGCTATATTTTC

89 CTTAGAGCGAACCAGACCGGAAGCGCAAAAGA

90 TCATTTTTACCGGAATCATAATTAATCAACAT

91 ACGGGTATTAGTATCATATGCGTTATTCGCGTCTGGCCTTTGGTGCCG

92 ATAATCGGGTATAAAGCCAACGCTTTTTTTAACCAATAGGTTATCATC

93 ATCCTAATTTGAGAATCGCCATATTTAACA

94 CTGAACAAGAAAAATAGCAAATCAGATATAGTAGGAATA

95 CCTGTTTAGTTTTAGCGAACCTCCACGTTAAT

96 GCTAATGCCATTTTCGAGCCAGTATATTTAAATTGTAAACTCCTGATT

97 TGTCCAGATACCGACAAAAGGTAAAGCCCCAAAAACAGGAGGAAGGGT

98 TCATATATAAGATTCAAAAGGGTGCAATCATATGTACCCCTTGCACGT

99 TTTCAACGGTCAAATCACCATCAATATGAT

100 TACTTTTGCGGGAGATTTGCCAGTTACAAAAGAAACACC

101 TACCAAAAAAGAAACGATTTTTTGATATTCAT

102 AAAGCTAAATGCCGGAGAGGGTAGTCATTGCCTGAGAGTCCGTCAGAT

103 TAGCAAAAGATAGCTTAGATTAAGTCCTTGAAAACATAGCACATCGGG

104 ATCCAATAATAGTGAATTTATCAAAATCGTCGCTATTAATTTGCTTTG

105 GCATCAATGACTACCTTTTTAACCTCCGGC

106 TTGGGGCGCGAGCTGTGAGCGCTAATATCAGAACGTAGA

107 ATAACCTGATAATAAGAGCAAGAAATAATAAC

108 ATTTCGCAAAATGCTGATGCAAATTTACCTTTTTTAATGGTTCAATTA

109 GAACGAGTGAACGCGAGAAAACTTAAAATTAATTACATTTCAAACATC

110 CATTCCATGTTAATTTCATCTTCTACCGTAATGGGATAGGTGCATCTG

111 ATATGCAATTTGAAATACCGACCGTGTGAT

112 TGCTGTAGCTCAACAGAAGCCCGAAAGACTTCGGAATCG

113 AAGGCGTTAAATAAGAATAAACGCGGATGG

114 AGCCTGTTTTAATTGCTCCTTTTGGGATTAGAGAGTACCTGACGATAA

115 TCTTACCACTGTCTTTCCTTATCACTCATCGAGAACAAGCAGCAACAC

116 GGGCTTAATTACGAGCATGTAGAACATCGTAGGAATCATTTAACGCCA

117 CAACATGTAATTTAGGCAGAGGAGAACGCG

118 ATATAAAGCGACGACAATAAACAATTGAAGCCTTAAATCATATACCAG

119 TGTAGGTATTTAAATGCAATGCCTTGCACCCAGCTACAATATTACCTT

120 CGGAGACACAAGGATAAAAATTTTCCAACGCTAACGAGCGAGATGGTT

121 AACCGTTCTAGCTGATAAATTAATCGGTTG

122 GAGAGATCTTAAGCAATAAAGCCTAAAATAGCAGCCTTTACCTTCATC

123 AAGAGTCAAATCATACAGGCAAGGAAAACAGGGAAGCGCACGGTGTA
C

124 GTCTGAGATCTACTAATAGTAGTAACTGAACACCCTGAACATATAAAA

125 GTTGGGTTATATAACTATATGTAATGGTCA

126 AAGACAAAAGATTTAGTTTGACCAAGCTATCTTACCGAAGCAAAGTTA

127 ATATTTTAATAACAGTTGATTCCCATCAGGTCTTTACCCTTGACCATA

128 TTTAATGGCTAAAGTACGGTGTCTAGCAAAGCGGATTGCATCAAATGC

129 TAAATGTGTCGCACTCCAGCCAGCCGCTATTACGCCAGC

130 AATTCGCATTAAATTTCAATTC

131 ATCGATGAACGGTAATAGATTT

132 AATATATGTGAGTGAAGAGGCG

133 TCGGATTCTCCGTGGGATCGGC

134 GGAAGAAGCGAGTAACAACCCG

135 GAAACCAGCTGTTGGGAAGGGCGATAACAACTAATAGATTAGGCGAAA

136 ATATTCCTACCAGAAGGAGCGGAAAATACATTTGAGGATTTAGAAG

137 GATGATGGTTGTTAAATCAGCTCACAACAGTA

138 ATATAAGTTAATATTTTGTTAA

139 GTTTGGATGTAACATTATCATTT

140 TAGAACCTTTGCCCGAACGTTATTACTCGTATTAAATCCTATTGCCCT

141 AAAACAGAACGAGCCGGAAGCATACTAACTCACATTAATTGCGTTG

142 AATTGCGTCGTAAAACTAGCATGTAGAAAGGC

143 GTTTAATGGAGCAAACAAGAGA

144 GAATATACAATTGTTATCCGCTC

145 AGAAACAACGTAATCATGGTCATAAAACCTGTCGTGCCAGAGGCGGTT

146 AATACCAATCTAGAGGATCCCCGGAAATGAAAAATCTAAAGCATCA

147 ATCGCGCATAACCTTGCTTCTGTAAATCATAG

148 ATTCATAAACAGTACATAAATC

149 CCTGAGCACCAGTGCCAAGCTTG

150 AAGAAAACGTTTTCCCAGTCACGACTCAATCAATATCTGGGTCAGTAT

151 CCAGTTTGGCTGCAAGGCGATTAACAGTTGAAAGGAATTGAGGAAG

152 ACGACAGTAACAAACGGCGGATTGGACCTAAA

153 GGCCTCTTTTTCCGGCACCGCTTCCCTGTAGCCAGCTTTCCTAGAAAA

154 CTGCGCAAGCAAAGCGCCATTCGCAACGCCATCAAAAATAATACAAAT

155 CGGAACAAAGAAACCGATTATCA

156 AAGTTTGATATACTTCTGAATAATAGATTGTATAAGCAAAATAAGAGA

157 AGCCTGGGACCATATCAAAATTATGGTTGATAATCAGAAAGAGTAATG

158 AATTCCACACAACATAATAAAGA

159 CTGTGTGAAGTAACAGTACCTTTTTACAAAGGCTATCAGGCTATTTTT

160 CTCGAATTTAACGGATTCGCCTGATAATTTTCCCTTAGAAACGCTGAG

161 TGCCTGCAGGTCGACGTTACAAA

162 AACGACGGAAAGAAGATGATGAAAAACAATTTCATTTGAACCAATCGC

163 ACGCCAGGGGGCGCATCGTAACCGTCACGTTGGTGTAGATTTTCAAAT

164 GCGAAAGGGGGATGTAGGGGACG

165 TCTAAAATATCTTTAGGAGCACTCGGTGCG

166 AGACTTTACAAACAATTCGACAAATTTTAA

167 CACTGCCCGCTTTCCAGTCGGGGCTGTTTC

168 GCTGAACCTCAAATATCAAACCCGTTGTAA

169 ATCCTGTTGGAACAAGAGTCCACTATTAAAGA

170 GCAGCAAGCGGTCCACTCCAAC

171 TCACCGCCGAAAAACCGTCTATCAGCTATTAGTCTTTAATAGACGGGCA

172 ACAGCTGGTGCCTAATGAGTGAGAAGTGTAA

173 TTTCTTTTCACCAGTGGCGCGA

174 TGCGTATTCTAAAACATCGCCATTAAAAATAC

175 GCTGAGAGCCAGCAGCCCACCA

176 TAACACCGAAACAGAGGTGAGGCGGCCCGAGA

177 ATCGGCAAAATCCCTTAGTGTT

178 CAGTTTTGATGGTGGTTCCGAA

179 ACGTGGACGCTGGTTTGCCCCAGCAGAGCCGTCAATAGATCATTCAGG

180 AAGGGCTGGCCCTGAGAGAGTT

181 ATAGCCGGGCGCCAGGGTGGTT

182 CGAACGAAGCCAACGCGCGGGGAGCTGCATTAATGAATCGGTACCGAG

183 AAGATACCTGCAACAGTGCCAC

184 TAGGGTTGATAAATCAAAAGAATATCAGTTGGCAAATCAAGTTGGGTA

S6. Square origami modified staples and bridges that hybridize with ΦX 174 scaffolds to make 3 by 3 super-structures

Modified staples for each triangle origami

21101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTCTTCGGCG

21102;AATCTTTTGAACCGCCACCCTCAGCCCTTATT

21105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGGCAGAT

T

21106;TTAAATTTCGGAATAGGTGTATCACGCCTCCC

21109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAACTGGAA

A

21110;GGTGGCGATAGCGGGGTTTTGCTCACCAGAAC

21201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGGGAAGCC

21202;GCAGGAGATATAAACAGTTAATGCCAAATAAA

21205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTCCTCAGCA

21206;ACGAATCAGATGATACAGGAGTGTGTCATACAT

21209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTACGCGGCG

21210;AACAGGGTACTAAAGACTTTTTCACTTTGACC

21301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCGAATCTCT

21302;GAAAACGATGCAGGGAGTTAAAGGATCCGCGA

21305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCAGGAACA

A

21306;ATGTTTATAGTTGCGCCGACAATGGAACTGAC

21309;GAAACGCAATCAATAGAAAATTCATTATCAGCTTGCTTTCAACGACGT

21310;ACATCATACTTTAATTGTATCGGTTATGGTTT

31101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTACGCTGCA

31102;TTGGTCAGGAACCGCCACCCTCAGCCCTTATT

31105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTATAATGTC

31106;GTCGTCATCGGAATAGGTGTATCACGCCTCCC

31109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAGAGCAGT

C

31110;GGCAGCAATAGCGGGGTTTTGCTCACCAGAAC

31201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGTCGGTACG

31202;GCTTTAAATATAAACAGTTAATGCCAAATAAA

31205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTACAAATGC

31206;TATCAGGGGATGATACAGGAGTGTGTCATACAT

31209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTATAACCAG

31210;GAGAGGAGACTAAAGACTTTTTCACTTTGACC

32401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTATAGCAAGG

32402;AAAGACGGTTCAGCGGAGTGAGAACATTAAAG

32405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTGCCAGCGA

32406;AATGGTAACGTCTTTCCAGACGTTCCAGTAGC

32409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCAGATGGGA

32410;CGCTCGGCACTACAACGCCTGTAGCGTAATCA

32101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTCCCCTGCA

32102;ACCTACATGAACCGCCACCCTCAGCCCTTATT

32105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGTACCTCG

32106;CCAGGGCGCGGAATAGGTGTATCACGCCTCCC

32109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAACATCACTC

32110;TTGACGCATAGCGGGGTTTTGCTCACCAGAAC

32201;GATTGGCCTTGATATTCACAAACCCCTGCCTATTTCGGGCAAGGTA

32202;CGGCTTTATATAAACAGTTAATGCCAAATAAA

32205;TCAGGACGTACCGTTCCAGTAAGCACTGGTAATAAGTTTTCGTAAATT

32206;GAGACAGGGATGATACAGGAGTGTGTCATACAT

32209;TAATTTCAACACTAAAACACTCATTGAGGAAGTTTCCATTGCAATGAC

32210;ACAGGAGCACTAAAGACTTTTTCACTTTGACC

33401;GTAAATATTGACGGAAATTATTTAGAAAGGAACAACTAGTTACTCG

33402;ATCTTCGGTTCAGCGGAGTGAGAACATTAAAG

33405;CCAGAAGGAGAGCCAGCAAAATCAAGTAAATGAATTTTCTTTAATAGA

33406;AAACGTACCGTCTTTCCAGACGTTCCAGTAGC

33409;TTTAAACACCATCGATAGCAGCACCATTCCACAGACAGCCACCTATTA

33410;GGACTCAGACTACAACGCCTGTAGCGTAATCA

33101;ATCGGCATTTTCGGTCATAGCCAGCCACCACCCTCATTGAACAAAA

33102;ACCAGTCCGAACCGCCACCCTCAGCCCTTATT

33105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTCTCCTCAT

33106;TGACAGAACGGAATAGGTGTATCACGCCTCCC

33109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAGAGCTTCT

33110;AGGTCGAATAGCGGGGTTTTGCTCACCAGAAC

23301;TCGCCTGATAAATTGTGTCGAACCGCTTTTGCGGGATCATATCCGA

23302;GTCATGGATGCAGGGAGTTAAAGGATCCGCGA

23305;AAGAGTAACAATCATAAGGGAACCACAACAACCATCGCCCTCATTTTT

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23105;AAACCAAAGAGCCACCACCGGAACCCGTACTCAGGAGGTTGGCCACA

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23106;AAAGCGTCCGGAATAGGTGTATCACGCCTCCC

23109;AAAGGAATCACCCTCAGAGCCGCCAGTACCAGGCGGATAAAACCATA

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23110;AGCTATTTTAGCGGGGTTTTGCTCACCAGAAC

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1106;GCTGGAGACATGGCGACCATTCAA

1107;CATCATAGAACATAAATCACCTCA

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1114;CATCACCTGAAACAACCTGATTAG

S7. Unmodified hexagonal DNA origami staples

1 TGATGATACAGGAGT

2 TTACCGTTCCAGTAAGCACCATTA

3 TAAAGCCAGAATGGAACCAATGAA

4 GCCTTGATATTCACAAAGTAGCGA

5 TTGACAGGAGGTTGAGCAGACTGT

6 GAGCCGCCGCCAGCA

7 AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTT

8 ATCTTGACAAGGCCGGAAACGTCAAGCGCAGTCTCTGAAT

9 GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCAT

10 GAAAGAGGAGTTTGCCTTTAGCGTGCAGGTCAGACGATTG

11 AAAGCTAAAATAAGAGAATATAAACCAACTTT

12 CACCAGAACCACCAC

13 GCCACCCTCAGAGCCAGCCATCTT

14 CCGCCTCCCTCAGAGCAGAGCCAC

15 CACGCATAACCGATATGCCGCTTT

16 TAGTTGCGCCGACAATGAAAGACA

17 ACAGCTTGATACCGA

18 TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGC

19 AATCCGCGCAAAATCACCGGAACCCGCCACCCTCAGAACC

20 GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGC

21 ATTATACCCGTCACCCTCAGCAGCGACAACAACCATCGCC

22 CGAGGTGAATTTCTT

23 CCTTTAATTGTATCGGACTTTTTC

24 GAAAATCTCCAAAAAATCAAAAAT

25 AAAGGAATTGCGAATAAATAACAT

26 TTTCAGCGGAGTGAGAGGAGAATT

27 AACAACTTTCAACAG

28 CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTT

29 GTAATGCCGTTTCCATTAAACGGGAAGGCTCCAAAAGGAG

30 TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTT

31 ATAAACAGGGAAGCGCATTAGACGATAGAAAGGAACAACT

32 TGTATGGGATTTTGC

33 TCGTCTTTCCAGACGTGAGAGATA

34 CCTCATAGTTAGCGTAAATAATAA

35 AACTACAACGCCTGTATAGCTATC

36 GTACCGTAACACTGAGGTAAGCAG

37 CCAATAGGAACCCAT

38 TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTC

39 TTGCACCCGAATTGAGTTAAGCCCACGATCTAAAGTTTTG

40 GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGC

41 GACGATAAGCCCTTTTTAAGAAAATTTCGTCACCAGTACA

42 TTTCAGGGATAGCAA

43 AGAACCGCCACCCTCACGGAATAC

44 TTAGTACCGCCACCCTCTCCTTAT

45 CCGGAATAGGTGTATCAAAATACA

46 AGTGCCGTCGAGAGGGAGAAACGC

47 AGTACCAGGCGGATA

48 AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCAT

49 AACTAATGACTGGCATGATTAAGACAGAACCGCCACCCTC

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51 CTAACGGAGGTGGCAACATATAAATTGATATAAGTATAGC

52 TTAGCGGGGTTTTGC

53 GAGGCTGAGACTCCTCATATGGTT

54 GAACCTATTATTCTGAGACATTCA

55 GTATAAACAGTTAATGTATTGACG

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57 ACTGGTAATAAGTTT

58 TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGA

59 ACCGATTGTAATTTCAACTTTAATAATAAGGCGTTAAATAGACGCTGA

60 ATTACCTTCCAAAGACAAAAGGGCAACATGAAAGTATTAA

61 AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCG

62 GAAACACCTCATTAAAGGTGAATTTTGAGTAACAGTGCCC

63 CCATTAGCAAGAACCGGATATTCATCAACAGTAGGGCTTACAAGGATA

64 ACCATCGAGCTGGCTGACCTTCATTTTAACAACGCCAACAATACTTTT

65 CAGAATCAACAGATGAACGGTGTAGCATTTTCGAGCCAGTATCGGTTG

66 AGCGCGTTTTCATCGGCAT

67 CAATCATAAGGGAACCGAACTGAGTACCGACAAAAGGTAAG

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75 TCATTGCCAGCCTTTATTTCAACGATTGAGAATCGCCATACAAGAGTA

76 ATCGATGAACATTATGACCCTGTATGTAATTTAGGCAGAGCAGACCAG

77 TTTGCCCGAACGTTATTAA

78 AATACATTTGAGGATTTAGAAGTTTAAATCC

79 GGCGGTCAGTATTAACACCGGGCGCCAGGGTGGT

80 GCCAGCAGGCCAACGCGCGGGGAGAGGCGGTT

81 CTTGCTGAAAACCTGTCGTGCCAGCTGCATTA

82 TGCGTATTGCCTGCAACAGTGCCATGTACCCCGGTTGATACTATCAGG

83 ATGAATCGCAAATGAAAAATCTAAACGGTAATCGTAAAACACAAGAGA

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88 GCATCGGAACGAGGGTAGC

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90 ATTCTGTCCAGACGACGACTTAGCCGGAACGAGGCGCAGACG

91 AGGCAAGGCAAAGAATTAGCAAA

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93 GCGAGCTGTGATTATCAGATGATGACGCCAGGGTTTTCCCAAGCTTGC

94 TATTTTCACATCCTAATTTACGAGCCCCAGCG

95 ATGGTCAATAACCTGTTTAGCTA

96 TTAAAAGTTTGAGTAACAT

97 TATCATTTTAATAGATTAGAGCCGTCAATAG

98 AAAGAAACGCATTAACATCCAATAAGCTAATGCAGAACGCTGTGTCGA

99 CATATTCCAAAAGGTGGCATCAATTAGATAAGTCCTGAACACAACGGA

100 TCAATATAATCCTGATTGT

101 CTGCAAGGCGATTAAGTTGGGTAGCAATTCA

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104 ATGCCTGCACGAGCCGGAAGCATAAAGTGTAA

105 CATTAATTGCAAATCAACAGTTGATAGGAGCACTAACAACTGCGGAAC

106 AGCCTGGGAACGACGGCCAGTGCCAGTCACGACGTTGTAAATTATCAT

107 AATTCCACACAACATAGGTCGACTCTAGAGGATC

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109 GAAAATAGGATTTTTTGTTTAACGACTCATCGAGAACAAGATAACAGT

110 AAAAACAGCCATATTATTTATCCCTCATCGTAGGAATCATCTAAAGTA

111 AACTGAACACCCTGAACAA

112 TCTTTCCAGAGCCTAATTTGCCAAAGCAAATCAGATATAGAA

113 TCGGCTGTCTTTCCTTATCCCTAAAACGAAAGAGGCAAAAGA

114 TTTGACCATTAGATACATTTCGC

115 TGATTCCCCAAAATTATTTGCACGAAGGGCGATCGGTGCGTAGCAATA

116 CGGTGTCTAAATTGCGTAGATTTTCCATTCGCCATTCAGGCTTGCCTG

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123 ACGTCAGATGAATATACAG

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125 CGGGTACCGAGCTCGAATTAATTGTTATCCGCTC

126 TGGTCATAGGCCTCTTCGCTATTATTAGAACC

127 CTTCTTTGCGCAAATTAACCGTTGGCTGTTTCCTGTGTGACGTAATCA

128 AGTAGAAGTGAGGCCACCGAGTAAAAGAGTCT

129 GTCCATCAATTAGTAATAACATCACTGCGCAACTGTTGGGTAAAACAG

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134 ATAGCCGAACAAAGTTACC

135 GCAACACTATCATAACCCTCGTTCAATACTGCGGAATCGTCA

136 CTTATCCGGTATTCTAAGATGAATCTTACCAACGCTAACGAG

137 CTTAGAGCTTAATTGCTGAATAT

138 TCCTTTTGATTGCTTTGAATACCAACGACAGTATCGGCCTGCAACAGG

139 ACAGGTCAAGAGGCGAATTATTCACGTAACCGTGCATCTGATTTTGAC

140 CCGGAAGCTAGACTGGATAGCGTCTACCAGAC

141 TTCGAGCTTCAAAGCGAACCAGA

142 ACAGTACCTTTTACATCGG

143 GAGAAACACAGCCAGCTTTCCGGCACCGCTT

144 TTCGCCTGATAAGAGGTCATTTTTCGAACCTCCCGACTTGTTGCTATT

145 AATCGCGCGGATTAGAGAGTACCTAGTTTTGCCAGAGGGGAGGCTTTT

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152 CAAAGGGCTCATGGAAATACCTACCCAGTTTGAGGGGACGAGTTACAA

153 GAACAAGAGTCCACTGTCTGAAATGGATTATTTA

154 CCAAAAGACAGATACATAACGCCATCAAATGCTTTAAACAGAAGCCCG

155 TACGCAGTTTGAGATTTAGGAATATGACCATAAATCAAAAAGCAAAGC

156 TACATAAAACAACATTATTACAGGTCCAATCGCAAGACAATAAATGCT

157 AAAGACACCACGGAATAAG

158 TGGGAAGAAAAATCTACGTTAATTTTTCAAATATATTTTAGT

159 AATATTCATTGAATCCCCCAAAGGAATTACGAGGCATAGTAA

160 AAAGACTTCAAATATCGCGTTTT

161 GGATTGCATCATTTGAATTACCTTACAACCCGTCGGATTCAGGGACAT

162 GATGCAAAACATAAATCAATATATCAGCTTTCATCAACATTCTGACCT

163 ACTATATGAGAACGCGAGAAAACTAAAACGAA

164 TCCGGCTTAGGTTGGGTTATATA

165 GAAACAAACATCAAGAAAA

166 CAAAATTAGCGGATTGACCGTAATGGGATAG

167 TAACAATTTCAAAAAGATTAAGAGGTTCAGAAAACGAGAACCACATTC

168 GAAACAGTGACTATTATAGTCAGAATCAGGTCTTTACCCTTAGAAAGA

169 ATAACCTTGCTTCTGTAAA

170 TTCGCGTCTGGCCTTCCTGTAGCGTGAGTGA

171 TTGGCAGATTCACCAGTCAAGTGTTGTTCCAGTT

172 TCTGGCCAATAAATCAAAAGAATAGCCCGAGA

173 GAAAGCGTTGATGGTGGTTCCGAAATCGGCAA

174 TAGGGTTGCACGACCAGTAATAAATCCGTGGGAACAAACGATTACATT

175 AATCCCTTACAGAGATAGAACCCTTAAATGTGAGCGAGTATTTTAATG

176 GGCGAAAATCCTGTTAAGAATACGTGGCACAGAC

177 TACCAGCGATGCGATTTTAAGAACATTTAATGGTTTGAAAAAATCATA

178 GAAATTATAGAACGAGTAGTAAATTCATAATTACTAGAAAAAGATTCA

179 CACCGACTTGAGCCATTTG

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181 ATTTCATCTTCTGACCTAATGGCTCATTATACCAGTCAGGAC

182 GGTCTGAGAGACTACCTTTTTAA

183 GAAGAGTCCGATAGCTTAGATTAATTAAATTTTTGTTAAACTGATAGC

184 AAAGGGTGTATGATATTCAACCGTTTGTAAACGTTAATATCCGAACGA

185 TGTAGGTAAAGCCTGTTTAGTATCCCTGACGA

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187 GTCGCTATTAATTAATTTT

188 CCCTTAGACCAATAGGAACGCCATCAAAAAT

189 AAACATAGAATAGTGAATTTATCATACCGACCGTGTGATACATTGTGA

190 ACCATCAAAGAAAGGCCGGAGACAAGAATAAACACCGGAATGGGCTTG

191 ATAAATTAATGCCGGAGAG

192 GATTGTATAAGCAAATATTTAAATCTAGCTG

193 TATTTTTGAATGGCTATTAGCTGGTTTGCCCCAG

194 CCTAAAACTGGCCCTGAGAGAGTTGCAGCAAG

195 ACCACCAGAGACGGGCAACAGCTGATTGCCCT

196 CGGTCCACGTCTTTAATGCGCGAATCAGCTCATTTTTTAAATCCTTGA

197 TCACCGCCATCGCCATTAAAAATATTTGTTAAAATTCGCAGTCAAATC

198 TTCTTTTCACCAGTGCAGAAGATAAAACAGAGGT

S8. Modified staples and bridges for hexagonal origami staple based super-structures.

Modified staples

11302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGAACC
AAA

11303;GGTCGGCACCTTTAATTGTATCGGACTTTTTC

11306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTCTGATTAG

11307;ATCCATCTAAAGGAATTGCGAATAAATAACAT

11310;AACAACTTTCAACAGTTAACCGT

11402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATGTA
GCT

11403;CAGGTGCCTCGTCTTTCCAGACGTGAGAGATA

11406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCTTATCA
G

11407;ATGGCGAGAACTACAACGCCTGTATAGCTATC

11410;CCAATAGGAACCCATAGCAGAAA

12302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTATAGTG
TT

12303;GGGAGCACCCTTTAATTGTATCGGACTTTTTC

12306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTCTCAGTA

12307;CACGAACGAAAGGAATTGCGAATAAATAACAT

12310;AACAACTTTCAACAGATCACCAT

12402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCAAAGA
CAG

12403;TTGATGCGTCGTCTTTCCAGACGTGAGAGATA

12406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCAGGGTT

A

12407;GAATGGCAAACTACAACGCCTGTATAGCTATC

12410;CCAATAGGAACCCATATTGTTAT

12502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCCAC

CGGA

12503;CCTCCAAAAGAACCGCCACCCTCACGGAATAC

12506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTAAGCAATA

12507;CAAACATACCGGAATAGGTGTATCAAAATACA

12510;AGTACCAGGCGGATAATCTCTTT

12602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACGCGG

CAT

12603;TAGACCAAGAGGCTGAGACTCCTCATATGGTT

12606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCGTACGGG

12607;CACACAGTGTATAAACAGTTAATGTATTGACG

12610;ACTGGTAATAAGTTTCCATTCAA

13402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCGGTCA

ACG

13403;TCCGCATATCGTCTTTCCAGACGTGAGAGATA

13406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCAGCTGTA

C

13407;AAAATACTAACTACAACGCCTGTATAGCTATC

13410;CCAATAGGAACCCATCGACCCTC

13502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCACG

AAAA

13503;TGGGATTAAGAACCGCCACCCTCACGGAATAC

13506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCGTGAGAG

13507;CCAACCATCCGGAATAGGTGTATCAAAATACA

13510;AGTACCAGGCGGATACGCTGAAT

13602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGATGGAG

GCC

13603;ACTCATCCGAGGCTGAGACTCCTCATATGGTT

13606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGATCGCGAA

13607;TTCAGCAGGTATAAACAGTTAATGTATTGACG

13610;ACTGGTAATAAGTTTTCGTTCTC

21102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCTTCG

GCG

21103;AATCTTTTTTACCGTTCCAGTAAGCACCATTA

21106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGGCAGATT

21107;TTAAATTTGCCTTGATATTCACAAAGTAGCGA

21110;GAGCCGCCGCCAGCAACTGGAAA

21202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCAAGTAC
GC

21203;AGAAGGCGGCCACCCTCAGAGCCAGCCATCTT

21206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTGATAAGC

21207;GGCGCATACACGCATAACCGATATGCCGCTTT

21210;ACAGCTTGATACCGATCTTAGAC

21302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTCATAGA
AA

21303;GTTGCCATCCTTTAATTGTATCGGACTTTTTC

21306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTGTCAAAGC

21307;TACTGAATAAAGGAATTGCGAATAAATAACAT

21310;AACAACTTTCAACAGGCGCAAGA

21402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCAAAGA
AAC

21403;ATAGGTCTTCGTCTTTCCAGACGTGAGAGATA

21406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGTTTGGTC

21407;TAGCCAGAAACTACAACGCCTGTATAGCTATC

21410;CCAATAGGAACCCATGACGGTTG

22102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCCTTC
AAG

22103;TTAGCCATTTACCGTTCCAGTAAGCACCATTA

22106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGGGATTGA

22107;CACAAGCCGCCTTGATATTCACAAAGTAGCGA

22110;GAGCCGCCGCCAGCAAAAGTCAA

22202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCTAATAA
GA

22203;CCTCCAAGGCCACCCTCAGAGCCAGCCATCTT

22206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGTGTCAAT

22207;TAGACAAACACGCATAACCGATATGCCGCTTT

22210;ACAGCTTGATACCGACCAGAAAT

22302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTTCAATA
CC

22303;ACACCAGACCTTTAATTGTATCGGACTTTTTC

22306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTTGCAGTA

22307;AGCCATACAAAGGAATTGCGAATAAATAACAT

22310;AACAACTTTCAACAGAACCTCAG

22402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATTTGG
TC

22403;CCAGCCGTTCGTCTTTCCAGACGTGAGAGATA

22406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCCGGAAAC
C

22407;GATTGGTGAACTACAACGCCTGTATAGCTATC

22410;CCAATAGGAACCCATCTCCTTCT

22502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATGCAT
ATAC

22503;TGGCGTGAAGAACCGCCACCCTCACGGAATAC

22506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTGAGTCTCA

22507;TCTCTTTCCCGGAATAGGTGTATCAAAATACA

22510;AGTACCAGGCGGATATTGATTCT

22602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGAGAGGA

AGC

22603;TCCCAAGCGAGGCTGAGACTCCTCATATGGTT

22606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCACGAGTA

22607;CGGCAGACGTATAAACAGTTAATGTATTGACG

22610;ACTGGTAATAAGTTTATCAGAAA

23402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCATTTAA

TT

23403;TAATTCCTTCGTCTTTCCAGACGTGAGAGATA

23406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCAATATCC

G

23407;CGTCATGGAACTACAACGCCTGTATAGCTATC

23410;CCAATAGGAACCCATATCATTTT

23502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATGATT

TGTC

23503;CCAAAACGAGAACCGCCACCCTCACGGAATAC

23506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCATCTCTC

23507;CAATATCTCCGGAATAGGTGTATCAAAATACA

23510;AGTACCAGGCGGATAGTAAGTTG

23602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGATCATT

GTG

23603;AGTTGCGGGAGGCTGAGACTCCTCATATGGTT

23606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGTAGCGACA

23607;GTTGTTCCGTATAAACAGTTAATGTATTGACG

23610;ACTGGTAATAAGTTTTCCATATC

23102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCATAG

AAA

23103;TGGTAGCTTTACCGTTCCAGTAAGCACCATTA

23106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATCAACCAAC

23107;GTCCTGCGGCCTTGATATTCACAAAGTAGCGA

23110;GAGCCGCCGCCAGCATAAGGCCA

31102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCATGA

AGT

31103;AGTATGCATTACCGTTCCAGTAAGCACCATTA

31106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTCAATAGA

31107;ATTTGGCGGCCTTGATATTCACAAAGTAGCGA

31110;GAGCCGCCGCCAGCATCCAAATG

31202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCATAACG

AG

31203;CTCATTAGGCCACCCTCAGAGCCAGCCATCTT

31206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGCTTTAAA

31207;TTCAAATACACGCATAACCGATATGCCGCTTT

31210;ACAGCTTGATACCGATATCAGGG

31302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGTCAAT

AT

31303;AGTCGGGACCTTTAATTGTATCGGACTTTTTC

31306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTTAATCCA

31307;TGACGATGAAAGGAATTGCGAATAAATAACAT

31310;AACAACTTTCAACAGAGTCAATA

32602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACAACG

GCG

32603;CGCCAGCGGAGGCTGAGACTCCTCATATGGTT

32606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGACCAATCT

32607;AAGATGGGGTATAAACAGTTAATGTATTGACG

32610;ACTGGTAATAAGTTTTGAATATT

32102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTGCCGA

AGC

32103;GTTGACCATTACCGTTCCAGTAAGCACCATTA

32106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGCCTTTAG

32107;CGGACGACGCCTTGATATTCACAAAGTAGCGA

32110;GAGCCGCCGCCAGCAGACATTAC

32202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCACGCAC
GT

32203;AAGAACGTGCCACCCTCAGAGCCAGCCATCTT

32206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGCGAACAA

32207;GGACGCTCCACGCATAACCGATATGCCGCTTT

32210;ACAGCTTGATACCGACGCCTTCC

32302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGACGG
GAT

32303;GACGGCAGCCTTTAATTGTATCGGACTTTTTC

32306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTATCCCAC

32307;TAAACGCAAAAGGAATTGCGAATAAATAACAT

32310;AACAACTTTCAACAGCAGTAGCA

33602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGAGGCAG
AAG

33603;AGAGGCCAGAGGCTGAGACTCCTCATATGGTT

33606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGACTTGACT

33607;TTAGTGGTGTATAAACAGTTAATGTATTGACG

33610;ACTGGTAATAAGTTTCTCTTTTA

33102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTTGAAC
AAA

33103;AACCAGTCTTACCGTTCCAGTAAGCACCATTA

33106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTCTCCTCA

33107;TTGACAGAGCCTTGATATTCACAAAGTAGCGA

33110;GAGCCGCCGCCAGCAAGAGCTTC

Bridges

1101;CCCCTCAGCGGCAAAACGCTTCGCTTGGTCAA

1102;ACCTACCGATTAAAATTTTTACCG

1103;TTATAACCCATGATTAAACTCCTA

1104;AAATAAAAGTCTGAAATCACACTC

1105;ATCACGAAGTCATGATTTTGAATT

1106;AAAAAAAGTGAATCGCGAGTGGTC

1107;GCGATAAACAGAAGTGAGAACCAG

1108;GAAGAAGCTGGAGTAACGGTCACA

1109;AACCTGACTATTCCACCTGTAAAA

1110;TTAGGTGTTGCAACAACTGAACGG

1111;CACTGGTCAAATATAACGTTGACG

2201;AATAACCTAATCATGGTGGCGAAT

2202;GTTCTTGCTGGCTGGAGACAAATA

2203;AATCACCTCACTTAAGAAATCACC

2204;GTTCCTGAATGAATGGAATAGCAC

2205;CCGCCAGCGAAGCCTTCAAGAAGG

2206;AGGAGAAACCACCAGCAAGAGCAG

2207;CAATTTAGACATGGCGCATACGAA

2208;ACGATACCACTGACCCTTTGACCG

2209;GGCGGCTTTCAGCAATCTTAAACT

2210;GAATCACCCACATCACCTTGAATG

2301;CGGCAGAAAACGGAAAACATCCTT

2302;TTTCACGCCCAAATCAAGCAACTT

2303;TTGCCACCAAGTCCAAGGCGGCAA

2304;ACAAAACAGGGTCGCCTTTATCAG

2305;TCCTTTCCAGCAATATCGGTATAA

2306;ACCTTTAGGCAGCAGCAAGATAAT

2307;ATTAAGCTCAGGAAATCGTTAAGG

2308;CTCTTTAGTCGCAGTACAGCACGC

2309;ATCAGCACGGCGGAAAACGAACAA

2310;GTAAACATGTCAACCATACCAGCA

1201;TTTTTGAGTGCCATGCTCAGGAAC

1202;GCGGCACAGGAGGAAGCGGAGCAG

1203;AGAAAGCTCAGTCTCAGAATGTTT

1204;GTTGAACACGACCAGAAAGTCGTC

1205;TGTGGTAGAAACTGGCCTAACGAC

1206;AGTTCCATTTGCAGACCCATAATG

1207;AATTAGCATAAGCAGCCAACATCA

1208;TGCCCAGAGATTAGAGTCTTGGTC

1209;AATCACGTCGCATGACAAGTAAAG

1210;TCAGCGTCCATCATGGTAACGCTG

1211;CCAAATGAAGAAATAAATAAGAGGTTTTACCT

2401;CAAATCCGGGCAGCAACGGAAACC

2402;CATCATCTTTTTAGTAAGCTCTTT

2403;TGATTGTCCAGTTGCATGATTAAG

2404;GGTTAGCCTCGGTACGCTCGGCAA

2405;TTTTGCATGTCAGGCATCCACGGC

2406;ATAGTTGTCCAGCAATCTCTTTTT

2407;AGTCGCCGACTGAATGTATAGATA

2408;ACCCTGAAACAAATGCTCGTATTC

2409;CTGGTCTTTTAGGGATTTTATTGG

2410;TTAATCGTAAGCATCTCATTTTGT

2501;AGACATAACAAGAAAAGCGGCATG

2502;AACCAGTAACGCTCGGCGCCAGTT

2503;AAAGGTCATGCGGCATGTGTTAAC

2504;GAGGAGTGGCATTAACAGGAAGCC

2505;GACCAGCAACCATCCTTCATGAAC

2506;CTGTTCACAAATGGTAATAAGACG

2507;ATAACCGGAGTAGTTGCATAAACG

2508;AGGGACATAAAAAGTAGAAGGAGT

2509;TCCATCTCAAAATGTCTACAGTAG

2510;GCAAGGCCGAAAGACGGAGAGCGC

3201;GTTGATAATATCCTCAAGTAAGGG

3202;CCCTGCAACAACGCGAGCAGTAGA

3203;TTTTCCATAATAGACGTTAAAATT

3204;CCTACATACCAAAGACCTTGGAAA

3205;TGCTGTTGGAGCGCCTTTACGCTT

3206;TACCTCGCATTTGGCGCATAATCT

3207;TTGAGCTTGAGTAAGCAACGGCTG

3208;CAGGGCGAGCGCCAGAAATACTGA

3209;ATTGGTAAACGTTTTTTACCTTTA

3210;ATCACTCCGCGAGTCATTTCTTTG

4401;GATTAAGCCCGCACGTAATTTTTG

4402;TTTCTTCTGTCGTAACCCAGCTTG

4403;GGTTGAACGGCGTCGCGCGTCAGT

4404;CAGTGTTTCCTGCGCGTTCTGCTT

4405;TTTTTGCGTACACGCAAGGTAAAC

4406;TTCAGCGGTTCCCAGCCTCAATCT

4407;TCGGCTACAGTAACTTCTTTAACC

4408;GACGCCATTAATAATGTTGCGCCG

4409;GTCACAGGTTTTCCGTAAATTCAG

4410;ATGATGAGCGCATAAATTTGAGCA

4501;AAATGTCAAGGCCGTTTGAATGTT

4502;GAACATAACAGATAGTAATCCACG

4503;TGAACAGCATCGGACTTAAGCAAT

4504;CAATAAACTCAACAGGCTTACCTA

4505;CATGATTTAGCAGGAAAGCGAGGG

4506;AAAGTCCATACGGATTGTTCAGTA

4507;AAGCGGTCTGGAAACGGCGTACCA

4508;AGCCTCAACGCAGCGAAGCTTAAT

4509;CCTGAATGCGAGCACGAGAGCGGT

4510;ATCCAAACCGGTTAAATCCAAAAC

4511;AAATCGAAATCATCTTTTTGTTACTCGTCAGA

5201;TATCGAAGAAGAGAATCTCTACCA

5202;ATGTGACTCAGGTTGGATACGCCA

5203;AAGCGATAAAACTCTGCATATCTA

5204;CTTGACGAACGTGCCAAACTTCTG

5205;AAAGTGTTAGCATATTAAGCCACT

5206;TCCAACGCTTTTCGACTCATCAGA

5207;GCTTTATCAAGATAATGTCAGTTT

5208;ATCGTTAGTTGATGGCAGCAGTAG

5209;CGTAAACAGAAAGGTCGCAAAGTA

5210;TCGAGCTGCCAGCAGTCCACTTCG

5211;ATTTTCTCATTTTCCGCGCAAGGATAGGTCGA

4301;CACTAACCTCCGTGGACAGATTTG

4302;AGCATTTTGCTGATGAACTAAGTC

4303;CGCTGATTCTGCGTTTCATCCCGA

4304;CTCATTCTGATTCTGAATGAGAAG

4305;GCGCCAATACAGCTTCTTGGGAAG

4306;GCTTGGTTACATTAGAAATATCCT

4307;AGCAGCATCAGTGACGTTTAGTGA

4308;ATTCTTTAGCTCCTAGTATCAACC

4309;ATGAAAAAACCTTTAGCAGCAAGG

4310;TGACTTTTATCGGCAACAGCTTTA

5101;GGCAGCAATTAACGTATTTAGCCA

5102;CCAACAGCTGAATCATTAGCCTTG

5103;GATAGCAGTCGGCGTGCATATAAC

5104;TTAAGCGGCTCACCTTGGCACACA

5105;CATACTCATAGCATCAACAGGCCA

5106;CAGAACGTAATGAAGACGGCCATT

5107;AAGTGCACCGCATGGAGAAAAAGC

5108;TGTAGCGAACTGCGATAGGAAGTG

5109;CTACCTGTGGGCATACTGTAACCA

5110;CGTATTTTCGACGACCAAAATTAG

5111;GCGGCGATTGCGTACCGCAAGCTATTTAACTG

4201;TGTTCCAAACCATACGACCAATAT

4202;TAGTCACGCAGCTTTACCGTCTTT

4203;TTAGAGCCAATACCATCAAAGCAT

4204;TCATAAAACGCCTCTATTATTTCC

4205;CCTGACGGATCGGTCGTCAGCCAA

4206;TGTCAAAAACATACAATTGGGAGG

4207;ATTTGGAGGCATGAAAACGATAAA

4208;CAGCATGAGCCTGTCGTAAAAAAG

4209;ACGAACCACATTGCATTCATCAAA

4210;AGCAAAGCGTGACATTCAGAAGGG

4101;TATCGAACCTACGCGATTTCATAG

4102;TCCAGCAAGGCCGTCAACATACAT

4103;TCAGAAGCAGCCTTATTCTTGAAC

4104;TTAATACCTTTCTTTTAAACTCAT

4105;ACAGATACTGGGGTAATTATACTC

4106;TATCCTTAAATTCATCCATTAACT

4107;ATTGTAGCATTGTGCCAGAGGGCG

4108;CCAGCTTGCGGCAAAACAAGTTGG

4109;ATTAATATCTGCGTAACCGTCTTC

4110;TAAAAACCTTCGGGGCGGTGGTCT

3101;AATAATCAAACGCCCTGCATACGA

3102;AATCTCTTGAGCCTCGATACGCTC

3103;TCAATAGCAGGTTTAACCAAGAGC

3104;GTTATCCATCTGCTTAAGAAATGC

3105;GAAAGAGTTGGAAGCCAAGCATTG

3106;GGAACATTCTAGGGGCGGCCTCAT

3107;AGCACCAGAAACAAAAAGAGCCTT

3108;GATTTAATACCAGCATTACCAGCT

3109;AAGTCCTTCACCCATGCCTACAGT

3110;CGGTAGCAGCCAGCCTGCAACGTA

2101;CAAACTATTTCAGCGAAACCAATC

2102;TTAGTAGCACCACCATTACCAGCA

2103;GAATGCAATGAAGAAAGGTAAAGT

2104;ACCATGAAACCAACATACAGATGT

2105;CGGCGTTGAAACGTTATTGCCCGG

2106;GAAGGACGCACCAACAGAAACAAC

2107;TCAAAAGCAATATCAGTCAATAGT

2108;CCTTGACGGTATAATAAAATTTAG

2109;CAGGCAAAACCACCATCATGGCGA

2110;AGGATAAAGAAGAAGACTCAAAGC

2111;GAGGGTAGTCGGAACCCATCATAGGCAGTCGG

S9. Unmodified diamond shaped DNA origami staples

1 CCAATTCTGCGAACG

2 CTGGAAGTTTCATTCCTAAAATGT

3 CATGTTTTAAATATGCGCGGAATC

4 GCTTAATTGCTGAATACTCAAATG

5 TGATAAGAGGTCATTTATGACCATAAATCAAAAA

6 TTTAATTGCTCCTTT

7 AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTC

8 CACGTTGGGATAGCGTCCAATACTAACTAAAGTACGGTGT

9 ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAA

1 ACATTAAATGTGAGCGAGTAAAGTTCAGAAAACGAGATTGCGGATGGCT

0 TAGA

1 CAGGATTAGAGAGTA

1

1 GCGAACCAGACCGGAAGAAGCAAA

2

1 TTCAAATATCGCGTTTAGGAAGCC

3

1 AATATGATATTCAACCAGCTATTT

4

1 TGAGAAAGGCCGGAGAGGTCATTGCCTGAGAGTC

5

1 AAAGATTCAAAAGGG

6

1 AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGT

7

1 GCCATCAACATCAAAAAGATTAAGTAATTCGAGCTTCAAA

8

1 TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAAT

9

2 AATTGTAAACGTTAATATTTTTCTACAAAGGCTATCACAGTCAAATCACC

0 ATC

2 CTGAGTAATGTGTAG

1

2 TTTAGAACCCTCATATAATCGTAA

2

2 GAAGCCTTTATTTCAAATACCAGT

3

2 AAACATTATGACCCTGCGTTAATA

4

2 CTCAGAGCATAAAGCTTTACAGGTAGAAAGATTC

5

2 ATTAAGCAATAAAGC

6

2 GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGC

7

2 ATAATCAGTGTCAATCATATGTACCGCAAGGATAAAAATT

8

2 TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGA

9

3 CTTGAGATGGTTTAATTTCAATAACGGAACAACATTAAAATCGGTTGTAC

0 CAA

3 GGCAAAGAATTAGCA

1

3 TAGCATTAACATCCAAAACTAATG

2

3 TGAAAAGGTGGCATCATACGAGGC

3

3 TGTTTAGCTATATTTTCCCTCGTT

4

3 CATTAGATACATTTCGATAGCGAGAGGCTTTTGC

5

3	TAGATTTAGTTTGAC
6	
3	CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAA
7	
3	GAATAAGGTAACGCCAAAAGGAATATTCTACTAATAGTAG
8	
3	CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGC
9	
4	GGGACGACGACAGTATCGGCCGACGATAAAAACCAAACAAATGGTCAAT
0	AACC
4	TTAGACTGTGTAGATGGGCGCATCTGGGAAGGGCGATCGGAAAGGGGG
1	
4	GTCATAAACGGATTGACCGTAATGCATTAAACGGGTAAAATTCATGAG
2	
4	CTTTAAACCAACCCGTCGGATTCTGAAGGCACCAACCTAAAACGAAAG
3	
4	ATTCAGGCTGCGCAACTGTGTAACCGTGCATCTGCCAGTTTG
4	
4	ATGTGCTGAACCATCGCCCACGCAGGTTCCACAGCATTCAGAACGTGGA
5	
4	GAAGTTTCTCGCTGAGGCTTGCAGTGCCCCAGCAGGCGAAGCGTA
6	
4	ACAGAGGCTTTGAGGACTAAAGACTTTTACGTAATGCCACTACCCGTGGG

7 A

4 ACAATGACAACCAAGGCGATTAAGTT

8

4 ATATTCGGATTACGCCAGCTGGCGTGCGGGCCTCTTCGCTGGATAGGT

9

5 GGAGTTAAAGGCCGC

0

5 GAGTCCACTATTAACGAAATCGGCAAAATCCC

1

5 CCTGTAGACAGCCCTCATAGTTAAATCCTGTTTGATGGTTAACCGAT

2

5 GCGGATTGAAATAATTCGCGTCTGCACTCATCTTTGACCCAAAGACAG

3

5 CGAAAGACGCTCATTTTTTAACCAGCGCGAAACAAAGTACTGAGTGAG

4

5 TTGAGAGAGTTAAAATTCGCATTAATCGCCTGATAAATTGTGTCGAAA

5

5 GCAAAAGAATACACTAAAAGCCTTCCTGTAGCCAGCTTTCAT

6

5 CATCGGAAGTCACCCTCAGCAGCGGTTGCGTCGTCAGTACAAACTACAA

7

5 CTAACTCACAGTCGGGAAACCTGTCTGATTGCCCTTCACCAAAT

8

5 ATAAAGTGTAAAGCCTGGGGTGCCTAAAACGGAGATTTGTATCAATTTTT
9 G
6 TTTGCGGGATCCGAGGGTAGCAACGG
0
6 CCGCTTTCCATTAATTGCGTTGCGCCAGCGATTATACCAAATAGGAAC
1
6 CGTGCCAGCTGCATT
2
6 CGATCTAAAGTTTTAGCAAGCGGTCCACGCTG
3
6 TCGTCACCTTTCCAGACGTTAGTGCCTGGCCCTGAGAGACTCACTGC
4
6 AACTAGCAAAAAGCCCCAAAAACACTTAGCCGGAACGAGGCTCACAAT
5
6 CAGGACGTTAAGAACTGGCTCATTTAAGGGAACCGAACTGCATAGCTG
6
6 AAACGAACCTTTAATCATTGTGAAGACAGATGAACGGTGTACAGACCA
7
6 CGCGACCTGCTCCATGTTAGGAAGATTGTATAAGCAAATATT
8
6 TCCACACAAACGCGCGGGGAGAGGCTTTTATTTTTACCGTAACACTGAG
9
7 TTTCCTGTGAAAATCTCCAAAAAAATAATTTTTTCACGTTCAGTT

0

7 TACCGAGCTCGAATTCGTAATCATGGTACCAACTTTGAAAGAGTTACCTT

1 A

7 ATGAATCGGCCACATACGAGCCGGAA

2

7 GTATTGGGGTGAAATTGTTATCCGCGCAGACGGTCAATCACCCGGTTG

3

7 AAGGCTCCAAAAGGA

4

7 ATTTTCTGTATGGGCACCAGTGAGACGGGCAA

5

7 GTCTATCAGCTAAACAACTTTCAACGCCAGGGTGGTTTTTCGGTTTGC

6

7 CAGATACACTTGCCCTGACGAGAATCATCAAGAGTAATCTATGCCTGC

7

7 ATAGTAAGACGTAACAAAGCTGCTTTCATTACCCAAATCACGTTGTAA

8

7 TACCAGACTCAGGAAGATCGCACTGGAAACCAGGCAAAGCGCCATTCG

9

8 CGCATAGGCTGGCTGACCTACACCAGAACGAGTAGTAAATTG

0

8 AGGTCGACATCGGTTTATCAGCTTAGGAATAGAACAAAGGGCGAAAAAC

1

8 AACGACGGTCTTAAACAGCTTGATTAAATCAAAAGAATAGGAAC
2

8 GTAACGCCAGGGTTTTCCCAGTCACGACACCGCTTCTGGTGCCCCAGCCA
3 G

8 CCTTTAATTGTTCTAGAGGATCCCCG
4

8 GGTGAATTCCAGTGCCAAGCTTGCTGACAAGAACCGGATACATTCAGT
5

8 ACCGATAGTTGCGCC
6

8 CAGCGGAGTGAGAACAACTAAAGGAATTGCGA
7

8 CCAACGTGTGTTGTTCCAGTTTGCCCGAGATAGGGTTGAGCTTTCGA
8

S10. Modified staples and bridges for mixed super-structure

Modified staples for hexagonal DNA origami

31H

31H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACTTC
GGCG

31H603;AATCTTTTGAGGCTGAGACTCCTCATATGGTT

31H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGGGCAGAT
T

31H607;TTAAATTTGTATAAACAGTTAATGTATTGACG

31H610;ACTGGTAATAAGTTTACTGGAAA

31H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTAAGT
ACGC

31H103;AGAAGGCGTTACCGTTCCAGTAAGCACCATTA

31H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATTGATAAG
C

31H107;GGCGCATAGCCTTGATATTCACAAAGTAGCGA

31H110;GAGCCGCCGCCAGCATCTTAGAC

31H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCCATAG
AAA

31H203;GTTGCCATGCCACCCTCAGAGCCAGCCATCTT

31H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCGTCAAAG
C

31H207;TACTGAATCACGCATAACCGATATGCCGCTTT

31H210;ACAGCTTGATACCGAGCGCAAGA

32

32H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCTG
TTGAA

32H503;GCCTAACGAGAACCGCCACCCTCACGGAATAC

32H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTGATGCCC

A

32H507;ACAAGTAACCGGAATAGGTGTATCAAAATACA

32H510;AGTACCAGGCGGATACTCCAAAT

32H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACATG

AAGT

32H603;AGTATGCAGAGGCTGAGACTCCTCATATGGTT

32H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGTCAATAG

A

32H607;ATTTGGCGGTATAAACAGTTAATGTATTGACG

32H610;ACTGGTAATAAGTTTTCCAAATG

32H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTATAA

CGAG

32H103;CTCATTAGTTACCGTTCCAGTAAGCACCATTA

32H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATGCTTTAA

A

32H107;TTCAAATAGCCTTGATATTCACAAAGTAGCGA

32H110;GAGCCGCCGCCAGCATATCAGGG

32H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCGTCAA

TAT

32H203;AGTCGGGAGCCACCCTCAGAGCCAGCCATCTT

32H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTTAATCC
A

32H207;TGACGATGCACGCATAACCGATATGCCGCTTT

32H210;ACAGCTTGATACCGAAGTCAATA

33H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATAGA
CGGAG

33H503;ATCTCGAAAGAACCGCCACCCTCACGGAATAC

33H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTTGGTAAT
A

33H507;CAGCAAGGCCGGAATAGGTGTATCAAAATACA

33H510;AGTACCAGGCGGATACTCGGCGC

33H602;TATTTTGTCACAATCAATAGAAAATTCAAGAGAAGGATTAGGACCTC
AAGT

33H603;TGCAATTAGAGGCTGAGACTCCTCATATGGTT

33H606;AGATGGTTAGGGAGGGAAGGTAAACCCCCTGCCTATTTCGCGCCTTT
A

33H607;CTCGCAACGTATAAACAGTTAATGTATTGACG

33H610;ACTGGTAATAAGTTTTTTTTTAC

33H102;AATTAGAGCCAGCAAAATCACCAGTAGCGTCATACATGGCTTTCACG
TAAT

33H103;CTTCTGCGTTACCGTTCCAGTAAGCACCATTA

33H106;GCGCATAGTAGCAGCACCGTAATCACAAATAAATCCTCATACGCAAG
G

33H107;AGCGGCTTGCCTTGATATTCACAAAGTAGCGA

33H110;GAGCCGCCGCCAGCATCCGTAAA

13H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTCATAG
AAA

13H303;TGGTAGCTCCTTTAATTGTATCGGACTTTTTC

13H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTCAACCAA
C

13H307;GTCCTGCGAAAGGAATTGCGAATAAATAACAT

13H310;AACAACTTTCAACAGTAAGGCCA

13H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCGGCG
ATTG

13H403;AATTAGGGTCGTCTTTCCAGACGTGAGAGATA

13H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGTGCAC
CG

13H407;GCCATTAGAACTACAACGCCTGTATAGCTATC

13H410;CCAATAGGAACCCATTAGCAGTC

13H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATCCT
CGGCA

13H503;CAATATCAAGAACCGCCACCCTCACGGAATAC

13H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTATAAAAC
G

13H507;AGCCAACGCCGGAATAGGTGTATCAAAATACA

13H510;AGTACCAGGCGGATAGCATGAGC

12H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCTGGAG
GCC

12H203;ACTCATCCGCCACCCTCAGAGCCAGCCATCTT

12H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCATCGCGA
A

12H207;TTCAGCAGCACGCATAACCGATATGCCGCTTT

12H210;ACAGCTTGATACCGATCGTTCTC

12H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTGGCG
GTGG

12H303;TATCAAGTCCTTTAATTGTATCGGACTTTTTC

12H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTATCCATTA

12H307;TACAAACTAAAGGAATTGCGAATAAATAACAT

12H310;AACAACTTTCAACAGTCAACATA

12H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCCCTG
CATA

12H403;CTTCCAAGTCGTCTTTCCAGACGTGAGAGATA

12H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGCCAAG
CA

12H407;AGTAGAAAAACTACAACGCCTGTATAGCTATC

12H410;CCAATAGGAACCCATTCGATACG

12H502;AAGGAAACCGAGGAAACGCAATAATAAGAGCCACCACCCTCATATT
CAGAA

12H503;CCATAAAAAGAACCGCCACCCTCACGGAATAC

12H506;TTCATCAGATGTTAGCAAACGTAGACCGTACTCAGGAGGTCAATTGG
G

12H507;CGGTTATTCCGGAATAGGTGTATCAAAATACA

12H510;AGTACCAGGCGGATATTACCGTC

11H202;TCGGTCATAGCCCCCTTATTAGCGTTTCCACCCTCAGAGCCGCGGCAA
CAG

11H203;AAAAATATGCCACCCTCAGAGCCAGCCATCTT

11H206;GATTTGTATTGCAGGGAGTTAAAGATTCGGTCGCTGAGGCTTAGAAA
T

11H207;CCAATATGCACGCATAACCGATATGCCGCTTT

11H210;ACAGCTTGATACCGAGATGAACT

11H302;CGGCTACAGAGGCTTTGAGGACTAAAGTTTATCAGCTTGCTTTAGTCA
TTT

11H303;GGTAAAATCCTTTAATTGTATCGGACTTTTTC

11H306;TAAGAAACCAGCCTTTACAGAGAGATAATTTTTTCACGTTTGGCGCAT

11H307;TGTTGCTTAAAGGAATTGCGAATAAATAACAT

11H310;AACAACTTTCAACAGCGCGAGCA

11H402;TCAGAGGGTAATTGAGCGCTAATATCATAGTAAATGAATTTTCCATCT
CAT

11H403;GTCTTTCGTCGTCTTTCCAGACGTGAGAGATA

11H406;GCAAAAGAAACAATGAAATAGCAAGCATTCCACAGACAGCGCAATC

TC

11H407;TGCATCTCAACTACAACGCCTGTATAGCTATC

11H410;CCAATAGGAACCCATTAGTAAGC

Modified staples for diamond shaped DNA origami

21P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCAGCA

CGCT

21P303;AGGAAATGTTTAGAACCCTCATATAATCGTAA

21P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGATTATCAGC

21P307;AGTCCAACAAACATTATGACCCTGCGTTAATA

21P310;ATTAAGCAATAAAGCTGCCAGCC

21P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAATGT

AGCT

21P403;CAGGTGCCTAGCATTAACATCCAAAACTAATG

21P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCCTTATCAG

21P407;ATGGCGAGTGTTTAGCTATATTTTCCCTCGTT

21P410;TAGATTTAGTTTGACAGCAGAAA

22P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTAGCTT

TAG

22P203;AAAACTAGGCGAACCAGACCGGAAGAAGCAAA

22P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATCCTTGAAT

22P207;GCATCACCAATATGATATTCAACCAGCTATTT

22P210;AAAGATTCAAAAGGGCATCACCT

22P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCACCG
CCTC

22P303;GGCGCCACTTTAGAACCCTCATATAATCGTAA

22P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGAGCACCAA
A

22P307;TAAGTGGCAAACATTATGACCCTGCGTTAATA

22P310;ATTAAGCAATAAAGCCAGCGAAA

22P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAACCA
AACC

22P403;CGTTATTGTAGCATTAACATCCAAAACTAATG

22P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCACAGTCC
T

22P407;ACCATCATTGTTTAGCTATATTTTCCCTCGTT

22P410;TAGATTTAGTTTGACGTCGGGAG

22P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCAGCG
AACC

22P103;TAGGGTCGCTGGAAGTTTCATTCCTAAAATGT

22P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAAAACCTGAT

22P107;TGTATCCAGCTTAATTGCTGAATACTCAAATG

22P110;TTTAATTGCTCCTTTGCATTAAC

24P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCAAGC
AATG

24P103;CAACAGGACTGGAAGTTTCATTCCTAAAATGT

24P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAACGTACCAT

24P107;GCAGCGACGCTTAATTGCTGAATACTCAAATG

24P110;TTTAATTGCTCCTTTTTGTTACT

24P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTGTTGG

ATT

24P203;GATTTGTCGCGAACCAGACCGGAAGAAGCAAA

24P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATCATTCTGA

24P207;GGGAAGTAAATATGATATTCAACCAGCTATTT

24P210;AAAGATTCAAAAGGGTCTTTAGC

23P402;CAGTTGAGATTTAGGAATACCACATTCTAAATCATACAGGCAAAATC

CAAA

23P403;TGAGCTTATAGCATTAACATCCAAAACTAATG

23P406;CTTTCCGGAGCAACACTATCATAACATTTGGGGCGCGAGCTTGTTCAG

23P407;TTCTTACCTGTTTAGCTATATTTTCCCTCGTT

23P410;TAGATTTAGTTTGACGTAATCCA

23P102;AAGAAGTTTTGCCAGAGGGGGTAATAGATATAACAGTTGATTCATCT

CTAC

23P103;CTCATATCCTGGAAGTTTCATTCCTAAAATGT

23P106;ACAAACGGTATTCATTGAATCCCCTAATGCTGTAGCTCAATTAAGCCA

23P107;GCGTCAGTGCTTAATTGCTGAATACTCAAATG

23P110;TTTAATTGCTCCTTTTCGCAAAG

23P202;AGGTCTTTACCCTGACTATTATAGTCAGCAAACTCCAACAGGTAATTT

TCT

23P203;TCCACTTCGCGAACCAGACCGGAAGAAGCAAA

23P206;TTAAATCATAATGCCGGAGAGGGTGTTCTAGCTGATAAATTGCTTTAT

23P207;CTCATCAGAATATGATATTCAACCAGCTATTT

23P210;AAAGATTCAAAAGGGGAAGCGAT

23P302;GAGCAAACAAGAGAATCGATGAACGGTATTTTAAATGCAATGCTCAT

TTTT

23P303;ATTTGAGCTTTAGAACCCTCATATAATCGTAA

23P306;TGCGATTTTGGGAAGAAAAATCTATAATACTTTTGCGGGAGTCGGCTA

23P307;CCTCAATCAAACATTATGACCCTGCGTTAATA

23P310;ATTAAGCAATAAAGCTGGTTGAA

Bridges

3101;CCCCTCAGCGGCAAAACGCTTCGCTTGGTCAA

3102;ACCTACCGATTAAAATTTTTACCG

3103;TTATAACCCATGATTAAACTCCTA

3104;AAATAAAAGTCTGAAATCACACTC

3105;ATCACGAAGTCATGATTTTGAATT

3106;AAAAAAAGTGAATCGCGAGTGGTC

3107;GCGATAAACAGAAGTGAGAACCAG

3108;GAAGAAGCTGGAGTAACGGTCACA

3109;AACCTGACTATTCCACCTGTAAAA

3110;TTAGGTGTTGCAACAACTGAACGG

3111;CACTGGTCAAATATAACGTTGACG

3201;CGTCAAACAATCATGGTGGCGAAT

3202;GTTCTTGCAAAACCACCATTACCA

3203;TCTGAATGCAATGAAGAAATCACC

3204;GTTCCTGAATGAATGGTTGACAGA

3205;TAGCGGCGGAAGCCTTCAAGAAGG

3206;AGGAGAAACAGCACCAACAGAAAC

3207;GCATCAAAAGCAATATCATACGAA

3208;ACGATACCACTGACCCAAAAAATT

3209;AAACAGGCTCAGCAATCTTAAACT

3210;GAATCACCACCGAAGAAGACTCAA

4101;GAAGAAATAACGGAAAACATCCTT

4102;TTTCACGCTCATAAGAGGTTTTAC

4103;AGGACGGTTGTCAGCGGGCGGCAA

4104;ACAAAACAGGGTCGCCAGCGCATG

4105;GAGATTAGAGCAATATCGGTATAA

4106;ACCTTTAGATCAACATCATAGCCA

4107;ACGTTTGGTCAGTTCCCGTTAAGG

4108;CTCTTTAGTCGCAGTAGAAAACTG

4109;CACGACCAGGCGGAAAACGAACAA

4110;GTAAACATCAGAATGTTTATAGGT

4111;ACAAAGAAACGCGGCAAGTGCCATGCTCAGGA

3301;GGTAGTCGCATCATGGTAACGCTG

3302;AATCACGTATAAACATCATAGGCA

3303;GGCGACCATTCAAAGGTCTTGGTC

3304;AATTAGCATAAGCAGCTAATAACC

3305;TGACGGTATTGCAGACCCATAATG

3306;TGTGGTAGGGACGTCAATAGTCAC

3307;CCCGGCGTACGGGGAAAAGTCGTC

3308;AGAAAGCTCAGTCTCAAACATAAA

3309;ATGAAACCGGAGGAAGCGGAGCAG

3310;TTTTTGAGGTAGCGGTAAAGTTAG

3401;TAAGAGCTGGCAGCAACGGAAACC

3402;CATCATCTAGTTGATGGCGAAAGG

3403;TTTTGACAGAATCGTTTGATTAAG

3404;GGTTAGCCTCGGTACGCATCCAAC

3405;CTTCTCCTGTCAGGCATCCACGGC

3406;ATAGTTGTGAACGTGCCAAGCATA

3407;TAAACCAGTCCTTGACTATAGATA

3408;ACCCTGAAACAAATGCAAATGTGA

3409;CATGAACATTAGGGATTTTATTGG

3410;TTAATCGTAAATGTCAACAAGAGA

4201;CAGTTTGACAAGAAAAGCGGCATG

4202;AACCAGTAGGTCATGCGGCATACG

4203;AAGCCAAGATGGGAAAGTGTTAAC

4204;GAGGAGTGGCATTAACAATCTGAC

4205;AGACGACCACCATCCTTCATGAAC

4206;CTGTTCACACCGGAGTAGTTGAAA

4207;GGAGTCGCCAGCGATACATAAACG

4208;AGGGACATAAAAAGTACGGCGTCC

4209;AGCGCCAAAAAATGTCTACAGTAG

4210;GCAAGGCCACGACGCAATGGAGAA

3501;CGCTCTTTATTAGACATAATTTAT

3502;AAGGGGCCGCATCGGACTCAGATA

3503;TATTAGTGGTTGAACAGAAGCCCC

3504;AAATTGTTGACCACCTCTCATGAT

3505;TAACTTGAACATACCAAAGACGAG

3506;CGCTTGCCTCTGGAAACGTACGGA

3507;ATAGAGGCCAAAGCGGTTTAGTAC

3508;GGCTGCGGACGACCAGAGCCTGAA

3509;ACGGCAGAGGCGAGCGCCAGAACG

3510;CTTTAGACAAATCATCTTCGGTTA

3601;CGTCAGAATACATCACTCCTTCCG

3602;TTTTGACGAGTAGCAATCCAAACT

3603;GAGCACGAGAGCGGTCCACGTTTT

3604;TCAGTAAGAACGTCAGGCCTCAAC

3605;AAACGCAATGTTTCCTGCGCGTAC

3606;TAAACGCGATCCCACAAAGTCCAG

3607;GCAGGAAAGCGAGGGTAACAATTC

3608;TAACCGGACGCTCGACAATAAACT

3609;ACGGCAGCGCCATTAATAATGTTT

3610;TTCAGCGCACGGGATGAACATAAT

3611;GGCCGTTTGAATGTTGCTTCCATGATGAGACA

2401;CATATCACGCGCAAGGATAGGTCG

2402;CATTTTCCAGCAGCCTTATGGCCG

2403;CATCACGAACGTCAGAGCCAGCAG

2404;GATTTAATTCGTAAACGTAACAGA

2405;ACTTCTCAAAGCAGTAGTAATTCC

2406;CAAGATAAAGCATTGTGCCAATTC

2407;TGGGGGAGCACATTGTTTTTTCGA

2408;AAATATCCGAAAGTGTGTTATTAA

2409;TCTATAGTTAACTTCTGCGTCATG

2410;AAAACTCTTTTTCGTCCCCTTCGG

2501;GGCGTGTGAGGTTGGATACGCCAA

2502;ATCGAAGCCACACAAAAATACTGA

2503;CTGTACCATACTCAGGGCGCATAA

2504;AGATTTGTCGTCACAGTGAAGACG

2505;CATGGAAAGTTGCGCCGCCAAAAC

2506;CAGTAACTGAAGTGTCCGCATAAA

2507;TCAACGCTACCTGTAGTTTCCCAG

2508;TCATCTCTCTTTTTGCACGACCAA

2509;CGTACCCGGTTCTGCTTCAATATC

2510;CGGCGTCGAAGCTATTTAACTGGC

2601;CGTATTTTTAACCCAGCTTGGTAA

2602;AAGCACTCGGGCATACTGTAACCA

2603;TGTAGCGAACTGCGATCGTGGACA

2604;ATTGTGAGCATTTTCAGAAAAAGC

2605;CAGAACGTTCCCGAAGTTGCGGCT

2606;TTCTGAACTAGCATCAACAGGCCA

2607;TTAAGCGGCTCACCTTAGCTTCTT

2608;GCGACAGCTTGGTTTTCATATAAC

2609;CCAACAGCTAGTGAGTTGTTCCAT

2610;TCCTAGACTTAACGTATTTAGCCA

2611;CATATCTGACTTTTTGCTTTAGCAGCAAGGTC

1201;TAAAAACCTCATTAGCCTTGCGAC

1202;GCAAGAACCTGCGTAACCGTCTTC

1203;CCAGCTTGCGGCAAAACATACGAC

1204;CGAAAATAGTCACGCAAGAGGGCG

1205;TATCCTTAAAGCATTGGGATTATC

1206;CCTCTAATTGGGGTAATTATACTC

1207;TTAATACCTTTCTTTTCGGTCGTC

1208;TGAGAGTGTCAAAAACTCTTGAAC

1209;TCCAGCAAGATAAACCAACCATCA

1210;CTGTCGCACTACGCGATTTCATAG

1211;CTGAATAGCAAAGCCTTTGCATTCATCAAACG

2301;CCAATCCGTTATCGAACTCAACGC

2302;CGAAAAGACTTTAATAACCTGATT

2303;TGGAGACAAATAATCTCAGAATCT

2304;AGCTTGATGCGGTTATACCTCACT

2305;CATAAATCCCATCTGCTTATGGAA

2306;TTGGGGATAATACCGCCAGCAATA

2307;CAGCAAGAGCAGAAGCTGAGAAAG

2308;TGCCACAAGCCTCAATTTAGACAT

2309;CAAACAATAGCAGGTTTAAGAGCC

2310;CTCAAAGTCGGAGGCGGCTTTTTG

1101;AAGTCAACAAATAATCAGCGTGAC

1102;GGGTAATATGATTCTGCGTTTGCT

1103;AGAAGAGCCATACCGCAGAACGAA

1104;AAGCCTCCAAGATTTGCAGTAGCG

1105;ATCCTTTGGAGGCATGAAAACATA

1106;AGGGTGTCAGCATCAGTGACGACA

1107;CAACCACACCAGAAGCAATCCTGA

1108;TCCTAGACAAATTAGAATACCATG

1109;CTTTATCAGCCAATACCATCAGCT

1110;TTTCCAGAAATTGTTCCAAGTATC

2201;TGAATGCCCAGCACTAACCTTGCG

2202;CTTTGATTTTATCGGTAGCAAGCA

2203;CATGCCTACAGTATTGTGGTCATT

2204;ACTGACCAGCCGTTTGTAATACCA

2205;GGCAGATTAGCTTGAGTAAGCATT

2206;AATCTCGGGTTAGGAACATTAGAG

2207;GGGCGGCCTCATCAGGAAACCTGC

2208;GGAAAGATTGGTGTTTCCAGAAAC

2209;CCATAGCATCCATAATAGACGCAA

2210;GTAGACTCCAAGAAGTCCTTTACC

2101;TGCAACGTTCTGTTGATAAGCAAG

2102;TTTGTGCATCAGAAACGGCAGAAG

2103;CAAATCAAGCAACTTATATACCTG

2104;TATTCTGGCGTGAAGTTGCCACCA

2105;GGCAGACTCGCCGACTGAATGCCA

2106;TTTTTGAGACGAGTATCCTTTCCT

2107;CAGCAGCAAGATAATCTCTCATTT

2108;GGCAATCTCTTTCTGATTAAGCTC

2109;CCCAAGCATTGTCCAGTTGCATTT

2110;TCTTTTTGAGGAAGCATCAGCACC

2111;TCAACCATACCAGCAGATTCTCAAATCCGGCG

APPENDIX C

SUPPLEMENTAL INFORMATION FOR CHAPTER 4

Supplemental Information

Encapsulation of Gold Nanoparticles in a DNA Origami Cage

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Materials:

All unmodified helper strands were purchased from Integrated DNA Technologies, Inc. (www.idtdna.com) in 96-well plates, suspended in ultrapure water and used without further purification. All 3' thiol-modified DNA strands were also purchased from IDTDNA and purified using denaturing PAGE gel electrophoresis. Tris(carboxyethyl) phosphine hydrochloride (TCEP) was purchased from Sigma-Aldrich, USA. Bis (p-sulfonatophenyl) phenylphosphine dihydrate dipotassium salt (BSPP) was purchased from Strem Chemicals Inc. Colloidal solutions of 5nm, 10nm and 15nm AuNPs were purchased from Ted Pella Inc.

Experimental Methods:

Phosphination and concentration of AuNPs. AuNPs (5, 10 and 15 nm, Ted Pella Inc.) were stabilized with absorption of BSPP. BSPP (15 mg) was added to the

colloidal nanoparticle solution (50 mL) and the mixture was shaken overnight at room temperature. Sodium chloride (solid) was slowly added to the mixture and stirred until the color changed from deep burgundy to light purple. The resulting mixture was centrifuged at 3000 rpm for 30 min and the supernant was carefully removed with a pipette. AuNPs were then resuspended in 1 mL solution of BSPP (2.5 mM). The concentration of the AuNPs was estimated by the optical absorbance at 520 nm. Phosphine coating increases the negative charge on the particle surface and therefore stabilizes the AuNPs in high electrolyte concentrations at high particle density.

Preparation of AuNP-DNA conjugates. The disulfide bond in the thiol modified oligonucleotides was reduced to a monothiol using TCEP (20mM, 1h) in water. The oligonucleotides were purified using size exclusion columns (G-25, GE Healthcare) to remove the small molecules. Monothiol modified oligonucleotides and phosphinated AuNPs were then combined (DNA to AuNP molar ratio of more than 200:1) in 0.5×TBE buffer (89 mM Tris, 89 mM boric acid, 2 mM EDTA, pH 8.0) containing 50 mM NaCl for 40 hours at room temperature to ensure the AuNPs were fully covered by thiolated DNA. AuNP-DNA conjugates were washed with 0.5×TBE buffer in Microcon (100kDa, Millipore, Billerica, MA) columns to remove the excess oligonucleotides. The concentration of these AuNP-DNA conjugates was estimated from the optical absorbance at 520 nm. Freshly prepared AuNPs, fully covered by DNA strands, did not precipitate in the buffer (5 mM Tris + 1 mM EDTA, 16mM $MgCl_2$), which is preferred for the formation of DNA origami. This high salt resistance property of fully covered AuNPs makes it possible to assemble them on the DNA origami template.

Self-assembly of DNA origami template. Cage origami was designed by caDNAno software (http://cadnano.com/), using single stranded M13mp18 DNA (7249nt, New England Biolab.) as the scaffold, and the generated helper strands (sequences are shown after Fig. S12. A molar ratio of 1:10 between the long, viral ssDNA and the short, unmodified helper strands (unpurified) was used. The modified helper strands that hybridize with the thiolated DNA strands on AuNP-DNA conjugates were used in 1:1 ratios to that of the viral DNA (5 nM). DNA origami was assembled in 5 mM Tris + 1 mM EDTA, 16 mM $MgCl_2$, pH 8.0 buffer, and cooled slowly from 80℃ to room temperature. DNA origami was then mixed with AuNP-DNA conjugates with 1:2.5 ratios and annealed from 40℃ to room temperature.

Purification of origami-AuNPs complexes. The annealed product of the DNA origami and AuNPs reaction was loaded in a 1.5% Ethidium Bromide stained agarose gel (running buffer 1×TAEMg^{2+}, loading buffer 60% glycerol, 15 V/cm). Selected bands were cut out and the DNA Origami-AuNPs complexes were extracted from the gel with Freeze-Squeeze columns (Bio-Rad) at 4℃.

TEM characterization of origami-AuNPs complexes. The TEM samples were prepared by placing 2 uL of the sample solution on a carbon-coated grid (400 meshes, Ted Pella). Before depositing the sample, the grids were prepared by negative glow discharge using an Emitch K100X machine. After 1 min, excess sample was wicked from the grid using filter paper. To remove the excess salt, the grid was washed with a drop of water and excess water was wicked away using filter paper. The grid was treated with a drop of 0.7% uranyl formate solution and excess solution was wicked away using filter paper. Again the grid was treated with a second drop of uranyl formate solution for 10

seconds, and the excess solution was removed uisng filter paper. To evaporate any additional solution, the grid was kept at room temperature. TEM studies were conducted by using a Philips CM12 transmission electron microscope, operated at 80 kV in the bright field mode.

Cryo-EM imaging and tomogram reconstruction: Sample (DNA cage with 3 capture strands encapsulating a 5 nm AuNP inside) was prepared and frozen on C-flat CF-2/0.5-4C grids (Protochips) using an FEI Vitrobot. Tomograms were acquired using Leginon software (S1) on a Tecnai F20 Twin transmission electron microscope operating at 120kV, with a nominal magnification of x50,000 and a defocus value of -2μm. Tomograms were reconstructed from a total of 62 sequential 2° tilts, going to +/- 60° with a total dose of ~200e^{-}Å^{-2} applied over the course of the tilt series. Images were recorded with a Gatan 4K-by-4K-pixel charge-coupled device (CCD) camera. Tomograms were reconstructed using Tomogrophy components (S3-S5) in the Appion software package (S2) and post-processing was done with the IMOD software package (S5).

Supplemental references:

Figure S1. 0.7% agarose gel of DNA origami cage structure. Lane 1: M13 strands; lane 2: cage origami annealed in 5 mM Tris + 1 mM EDTA, 16mM $MgCl_2$ buffer cooling slowly from 80℃ over 37h.

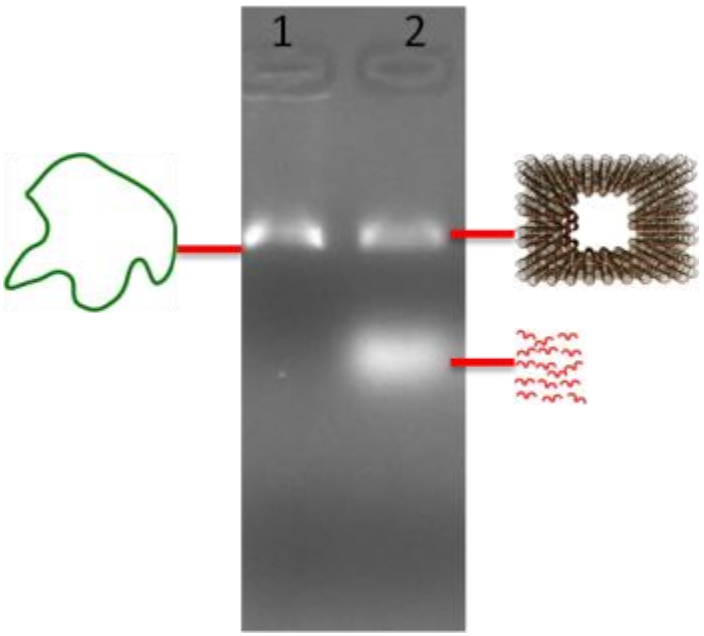
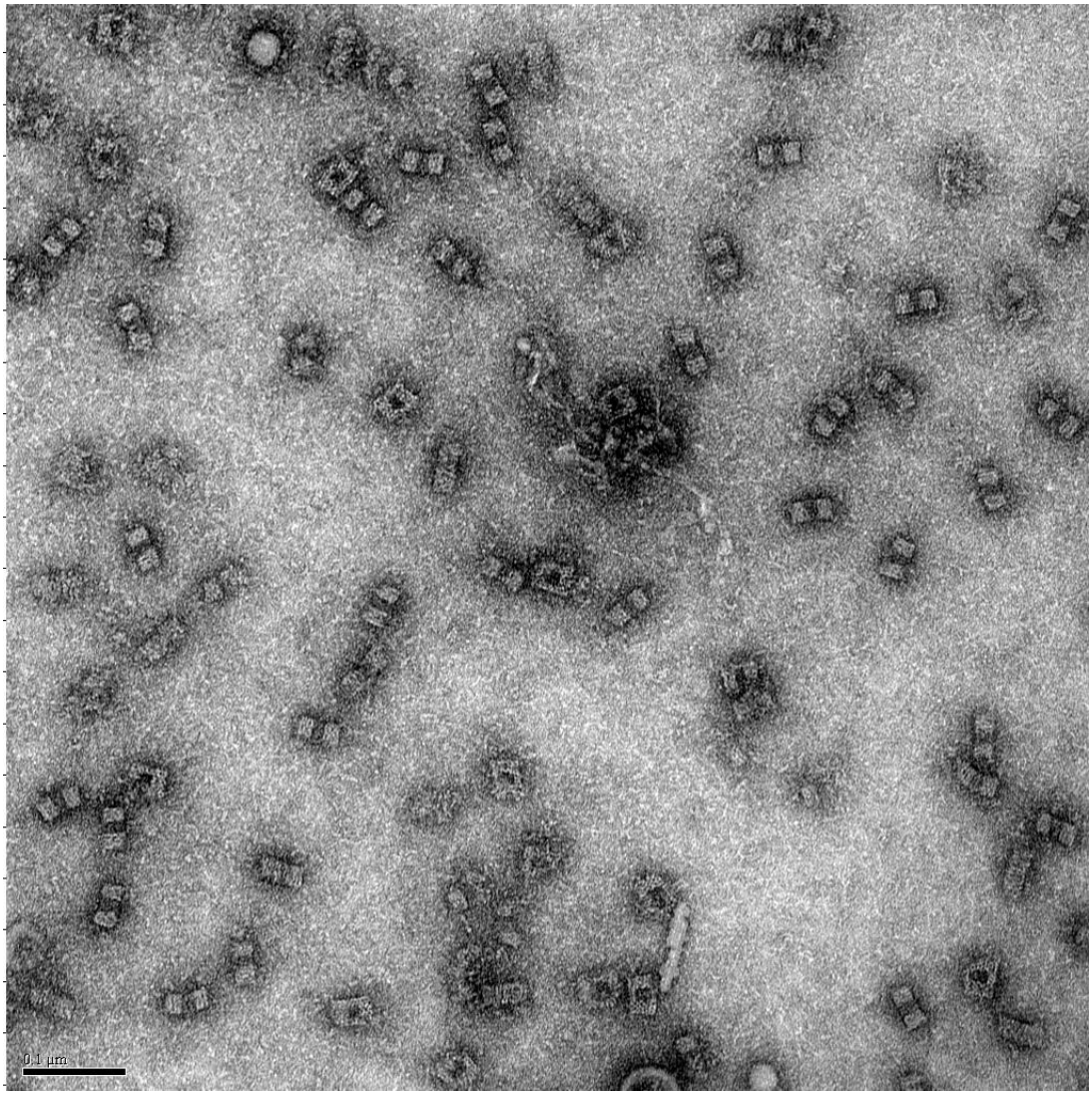
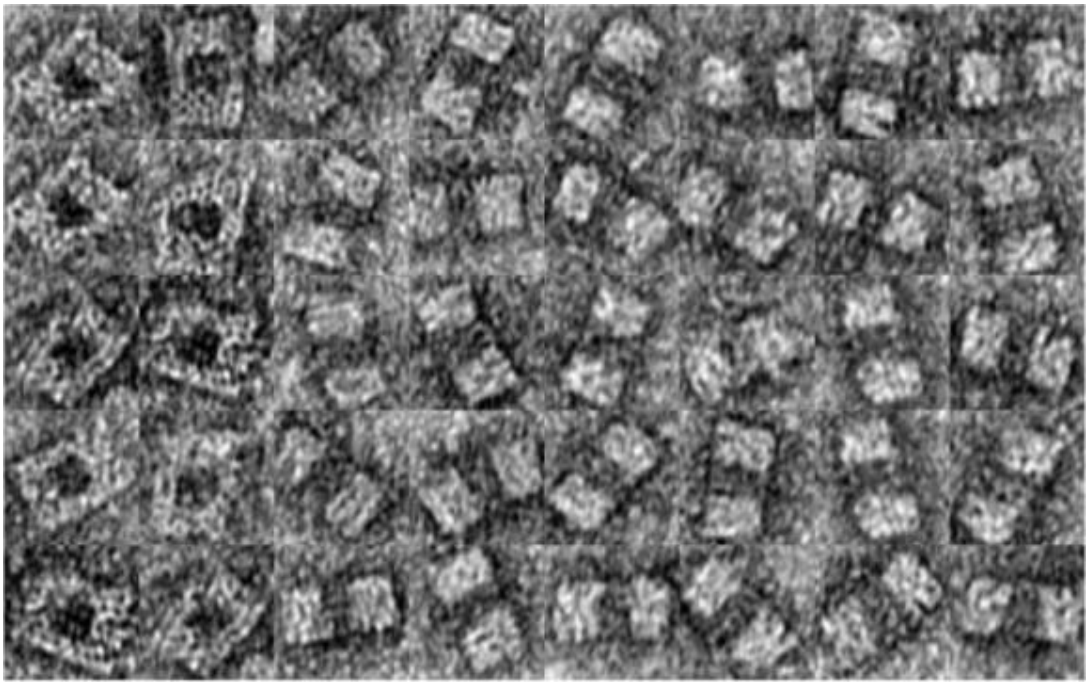


Figure S2. TEM images of DNA origami cages (scale bar: 100nm).



Zoom-out TEM image of the DNA origami cage structure



Zoom-in TEM images of the DNA origami cage structure

Figure S3. 1.5% Agarose gel of the DNA origami cage and cage with AuNPs. Lane 1: M13; lane 2: DNA origami cage; lane 3: DNA origami cage conjugated with AuNPs; lane 4: AuNPs only.

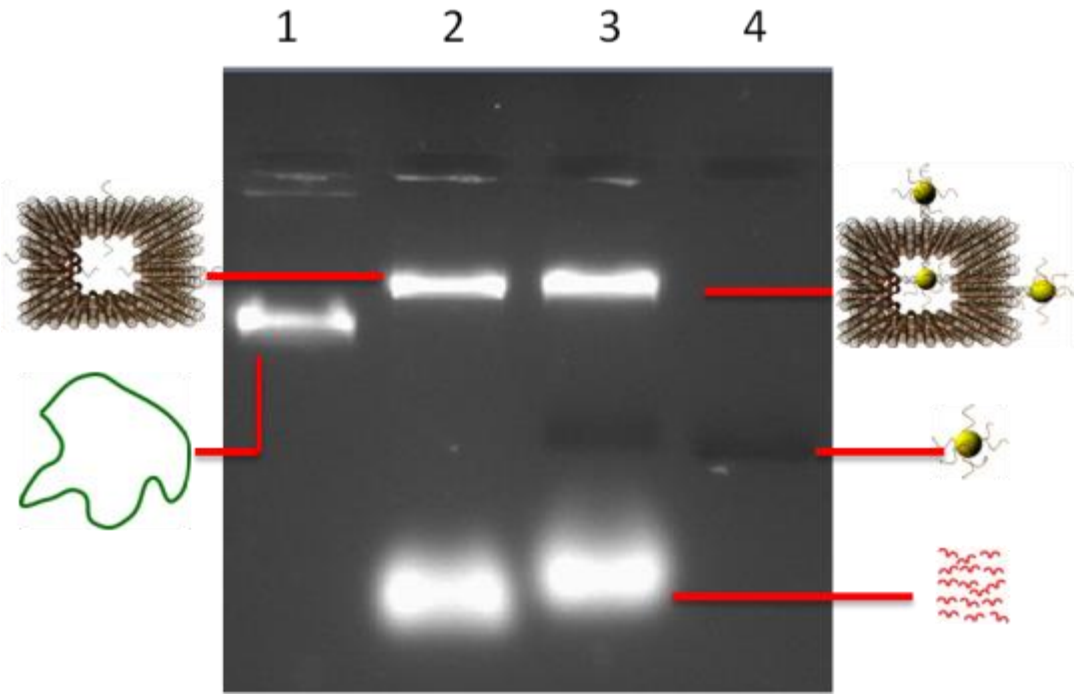
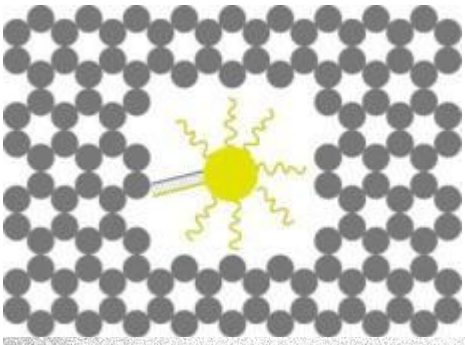
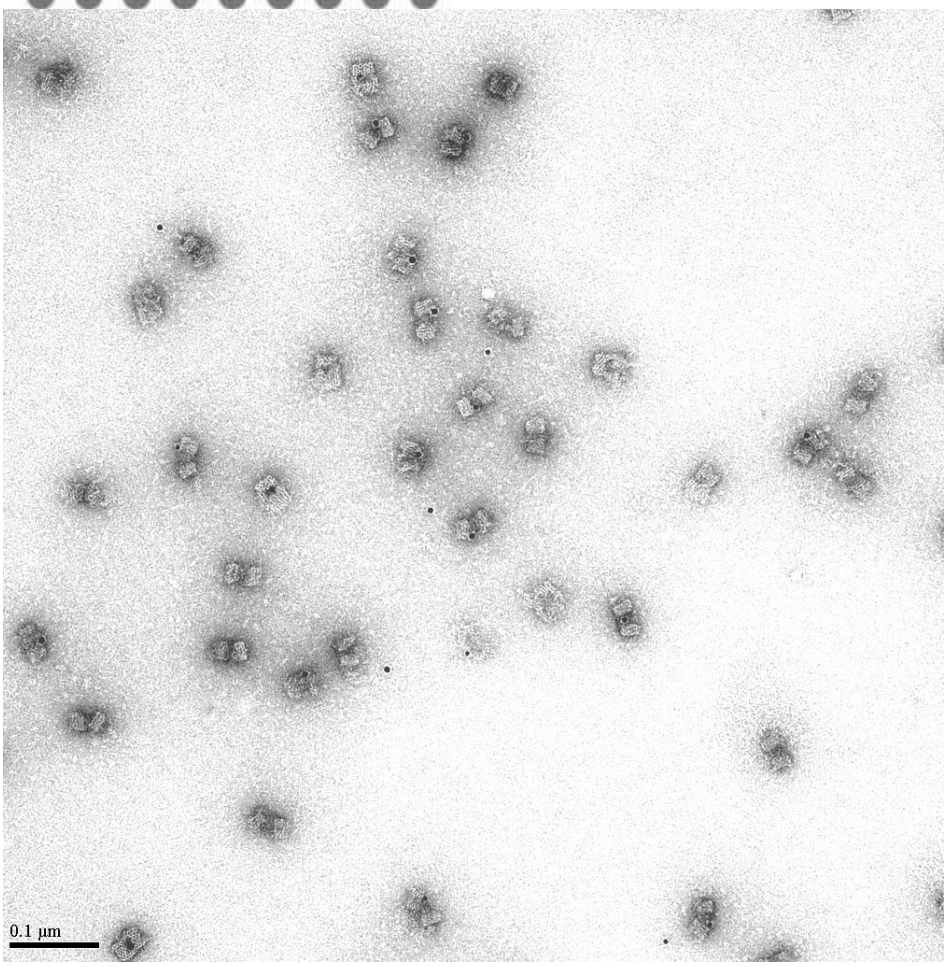
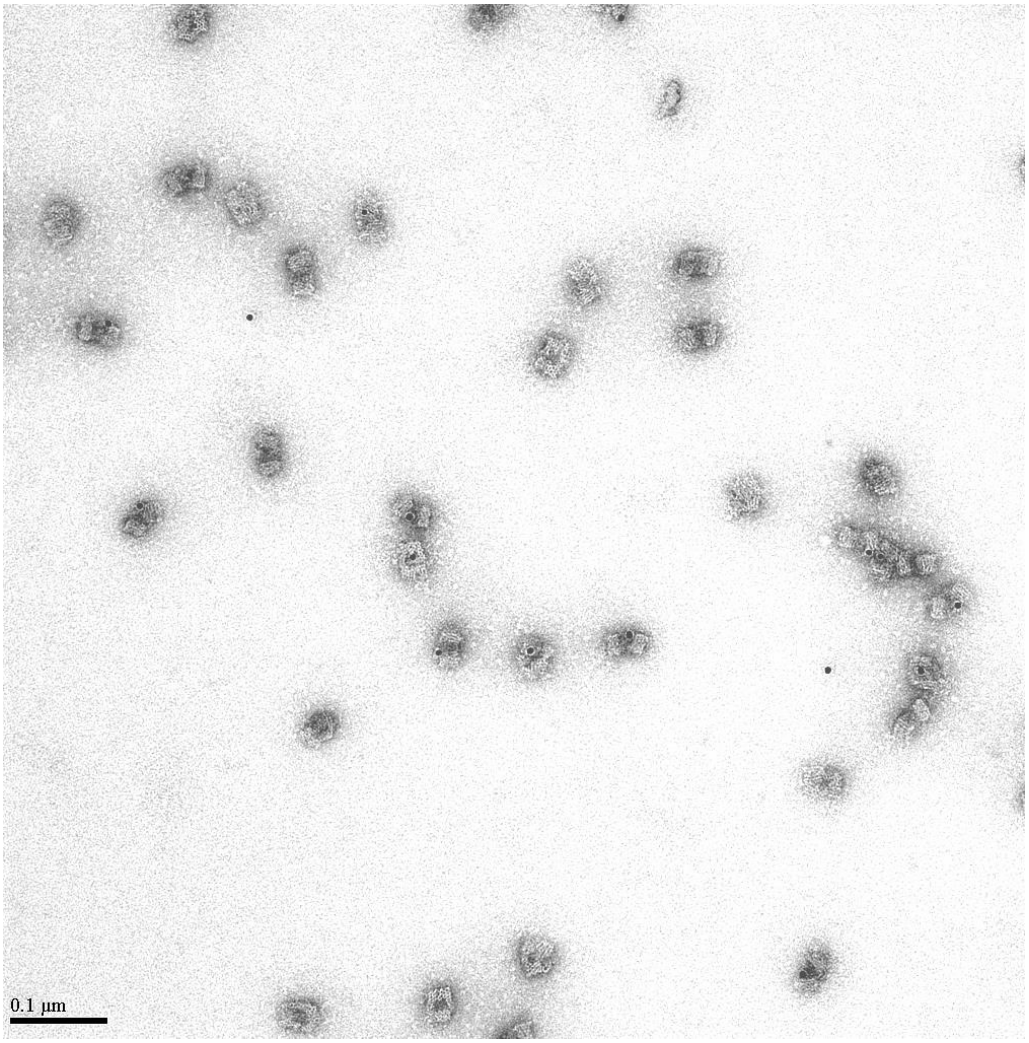


Figure S4. Zoom out and zoom in TEM images of DNA cages containing one 5nm AuNP inside the cage through hybridization with one capture strand. The yield is ~36.2%, from the zoom-out image.

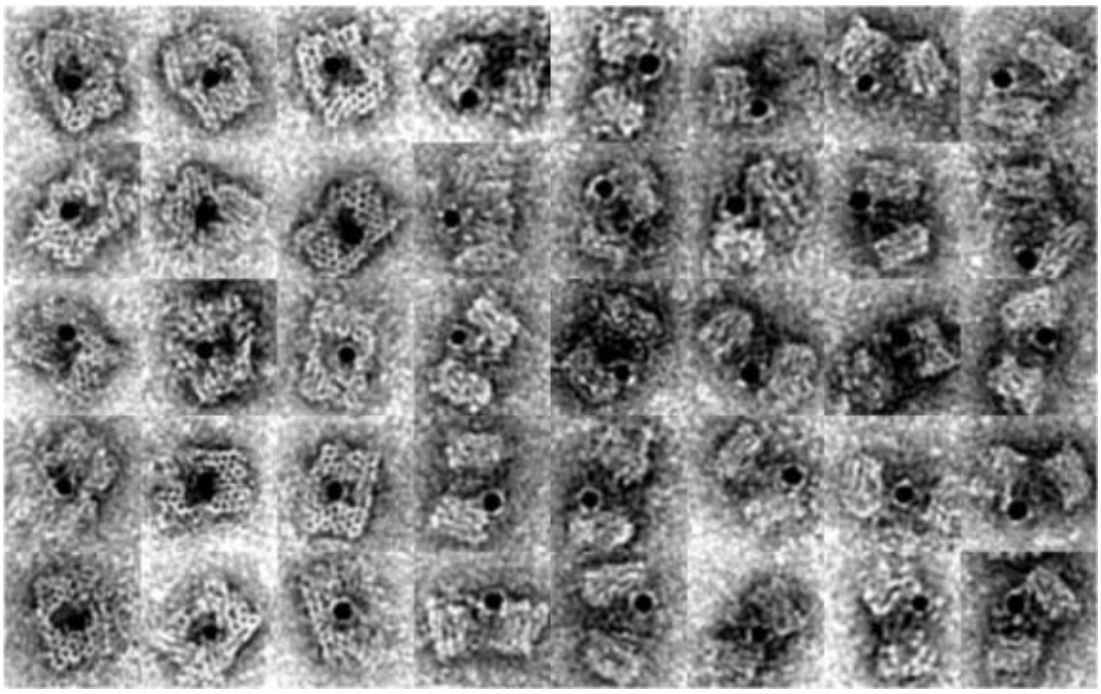




Zoom-out TEM image of the DNA origami cage structure

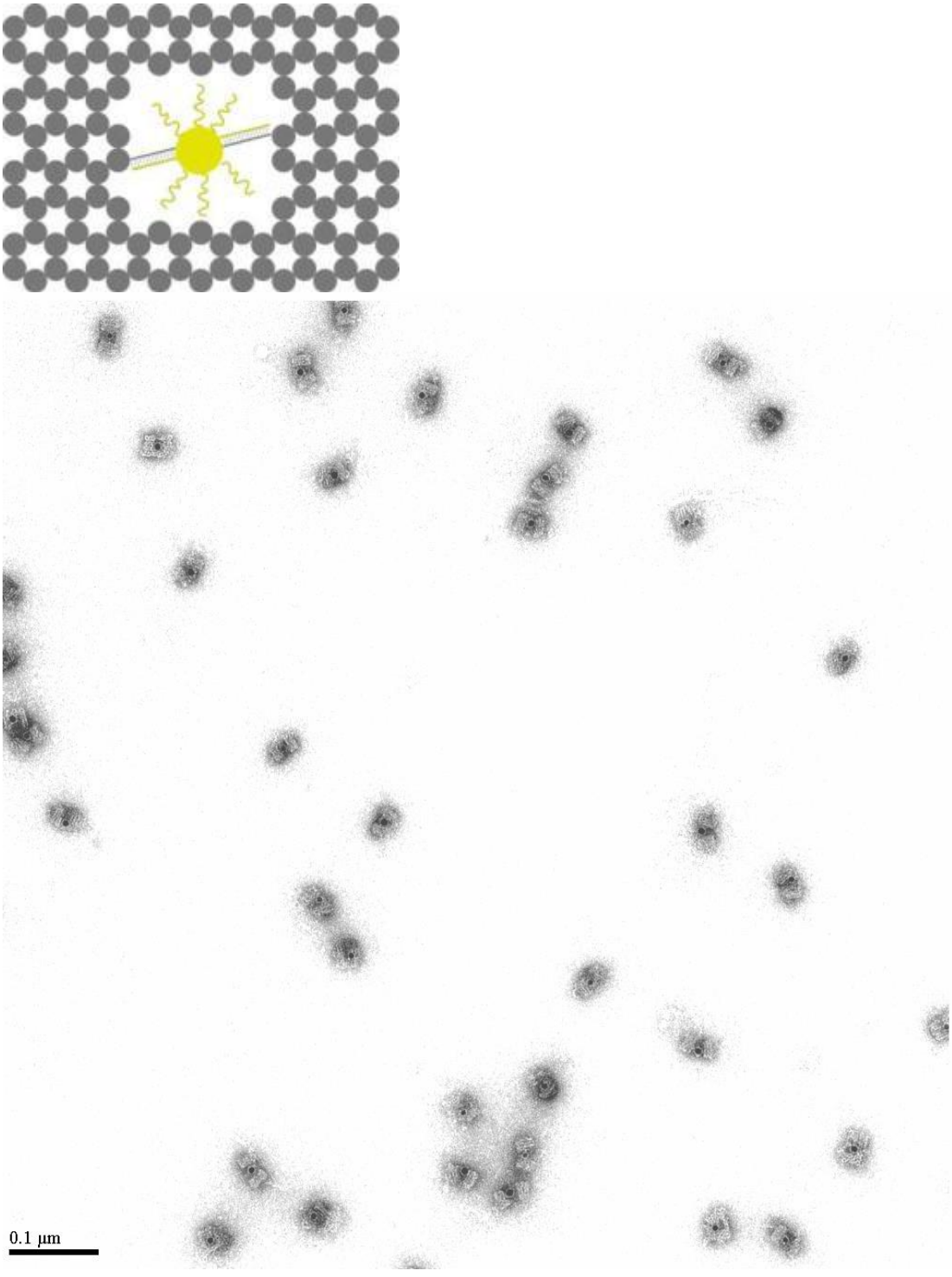


Zoom-out TEM image of the DNA origami cage structure

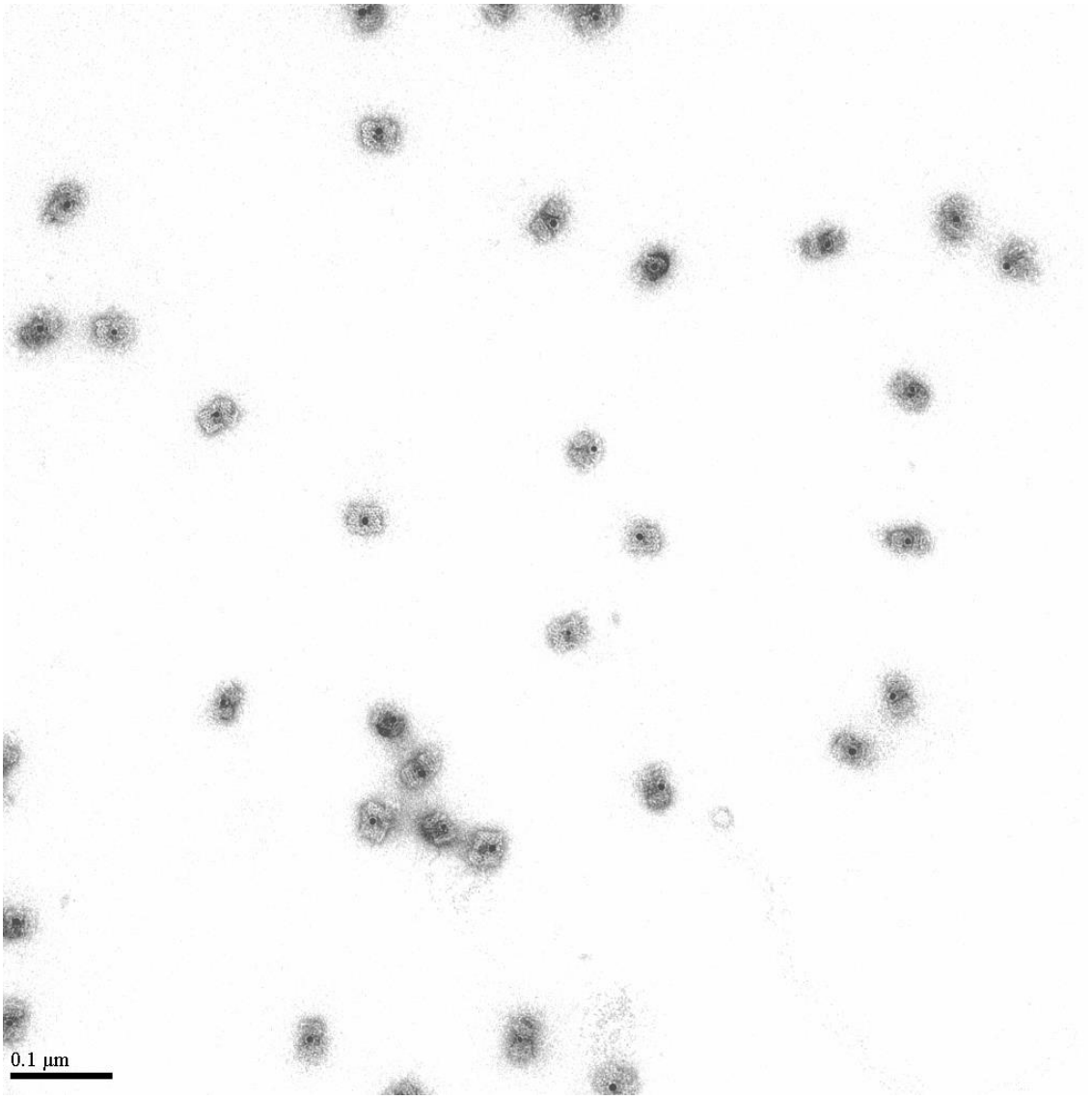


Zoom-in TEM images of the DNA origami cage structure

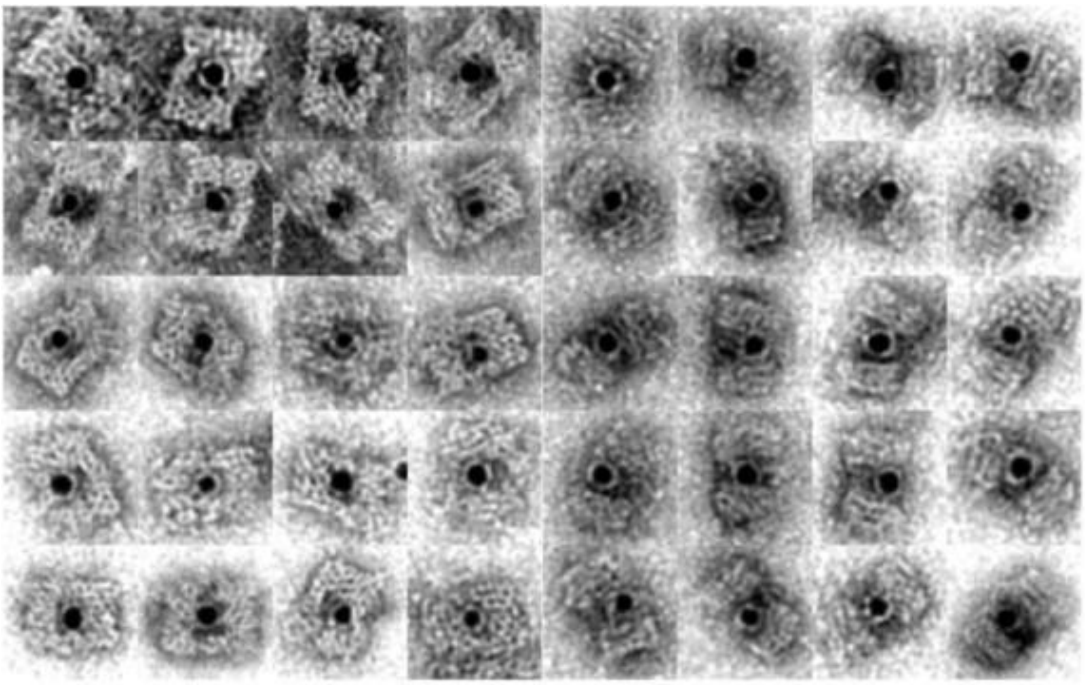
Figure S5. Zoom out and zoom in TEM images for cage containing one 5nm AuNP through hybridization with 2 capture strands. The yield is ~97.9%.



Zoom-out TEM image of the DNA origami cage structure

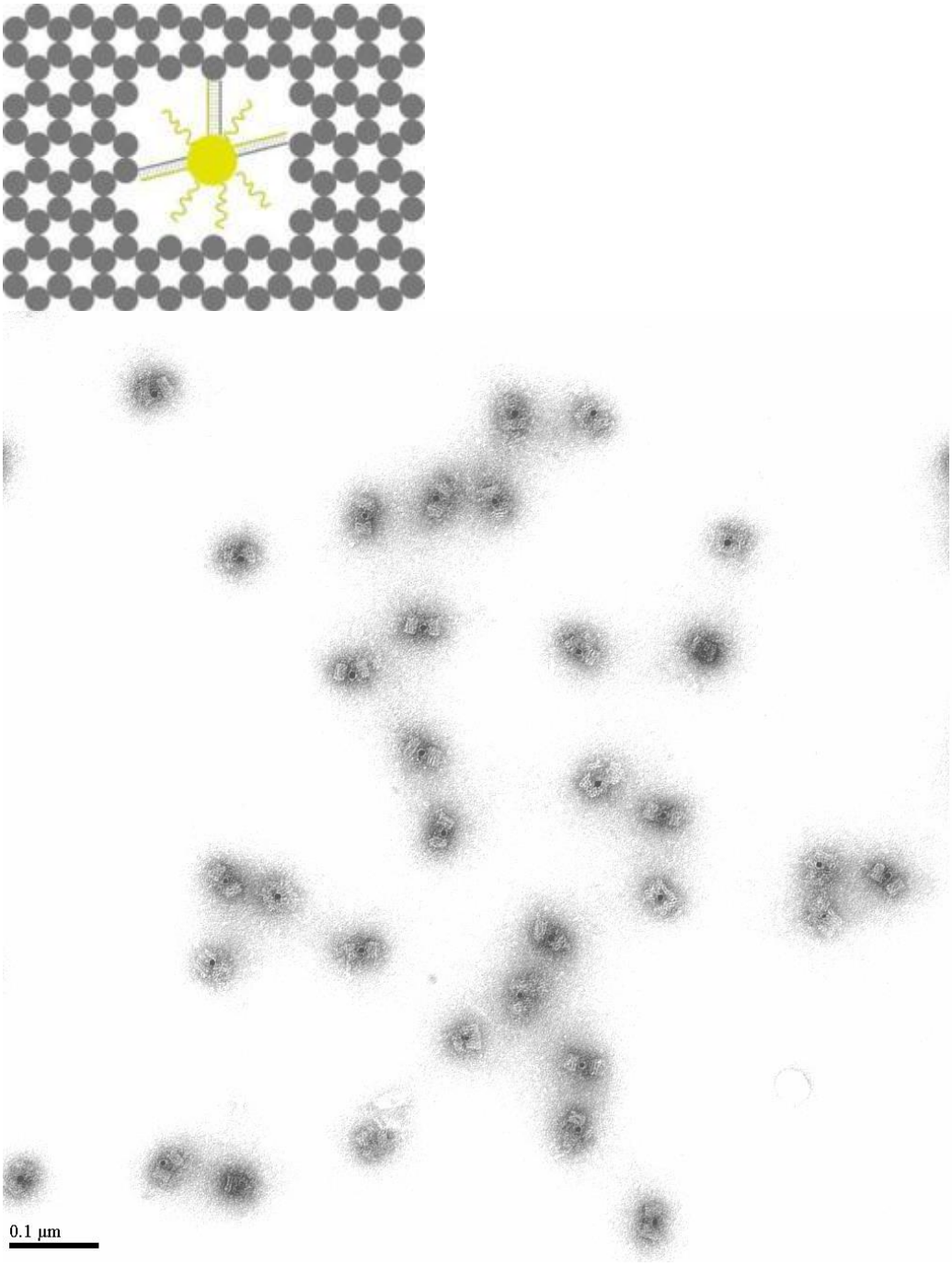


Zoom-out TEM image of the DNA origami cage structure

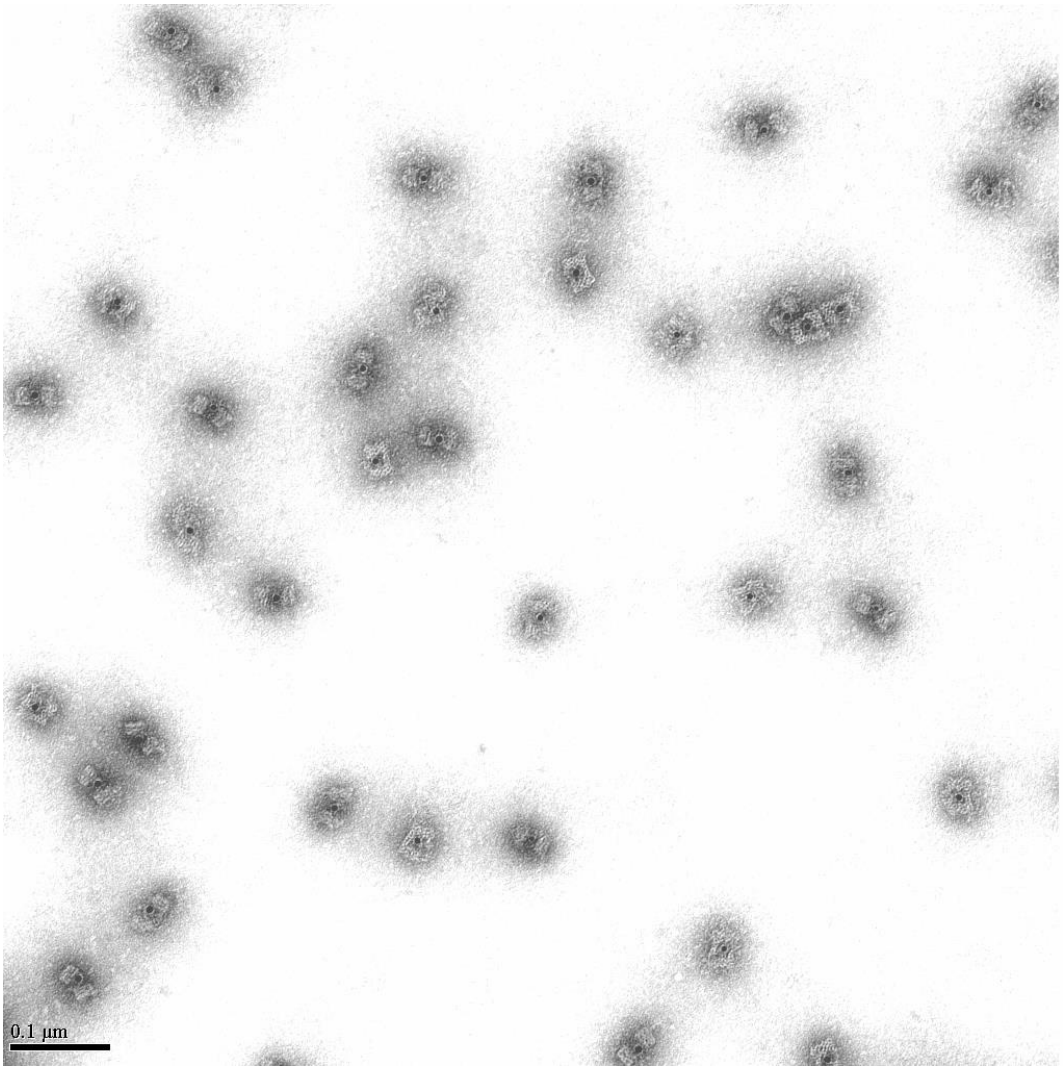


Zoom-in TEM images of the DNA origami cage structure

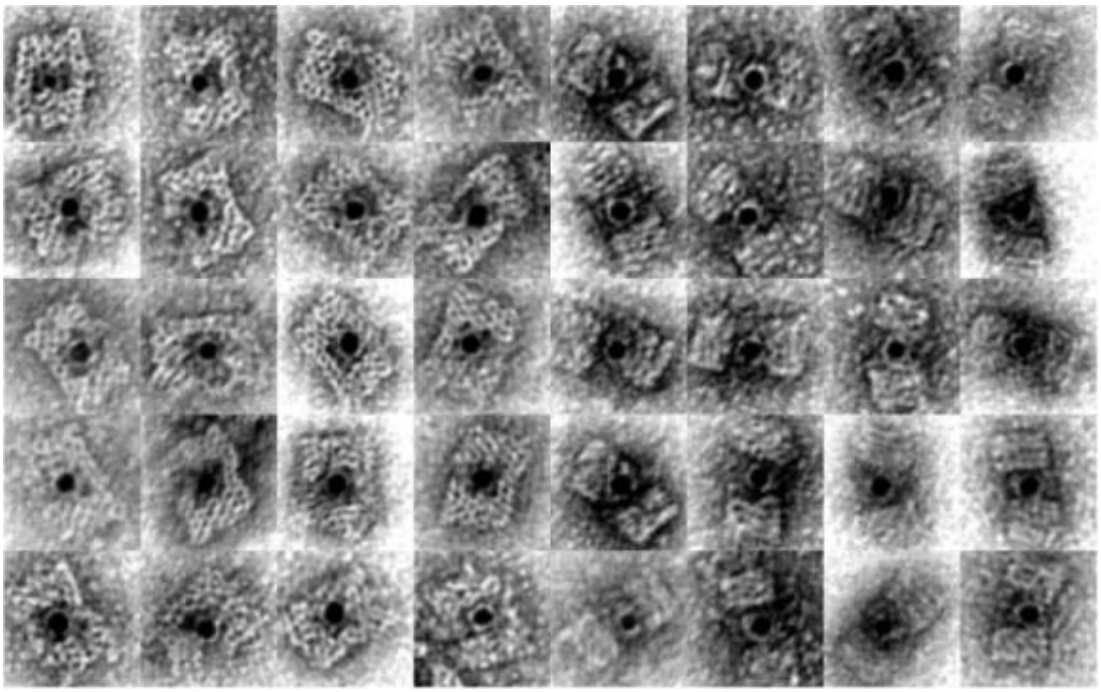
Figure S6. Zoom out and zoom in TEM images for cage containing one 5nm AuNP through hybridization with 3 capture strands. The yield is ~96.9%.



Zoom-out TEM image of the DNA origami cage structure

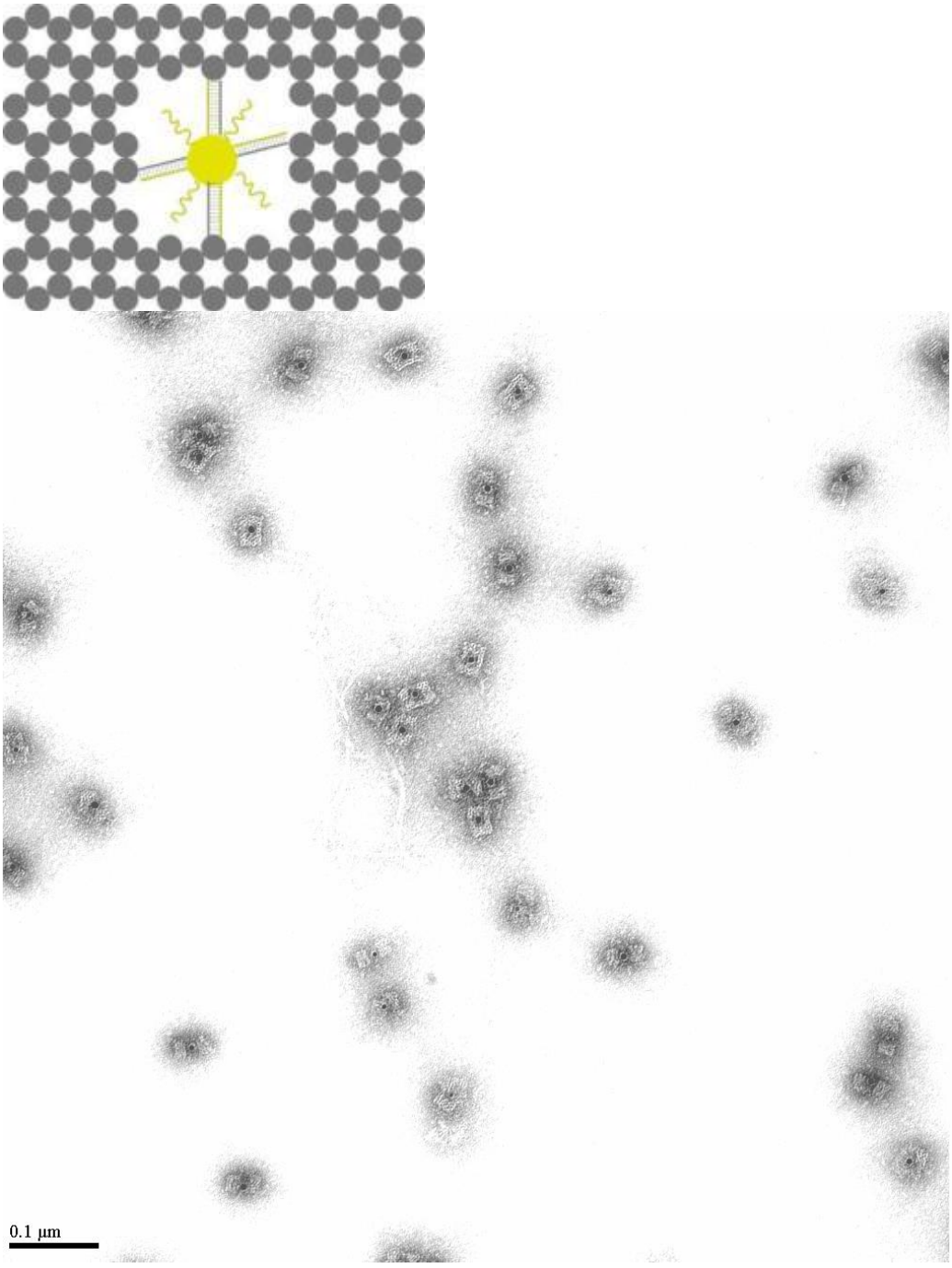


Zoom-out TEM image of the DNA origami cage structure

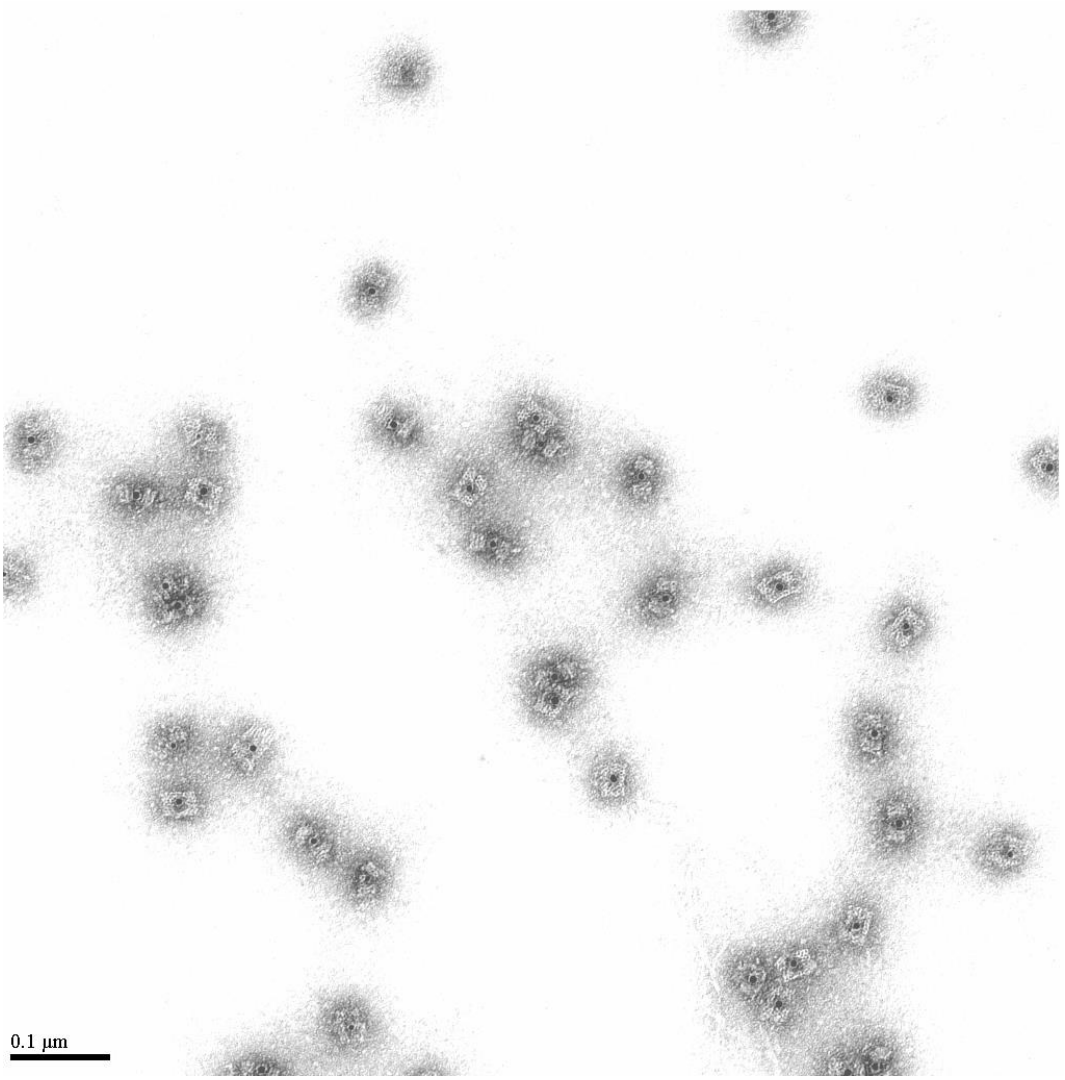


Zoom-in TEM images of the DNA origami cage structure

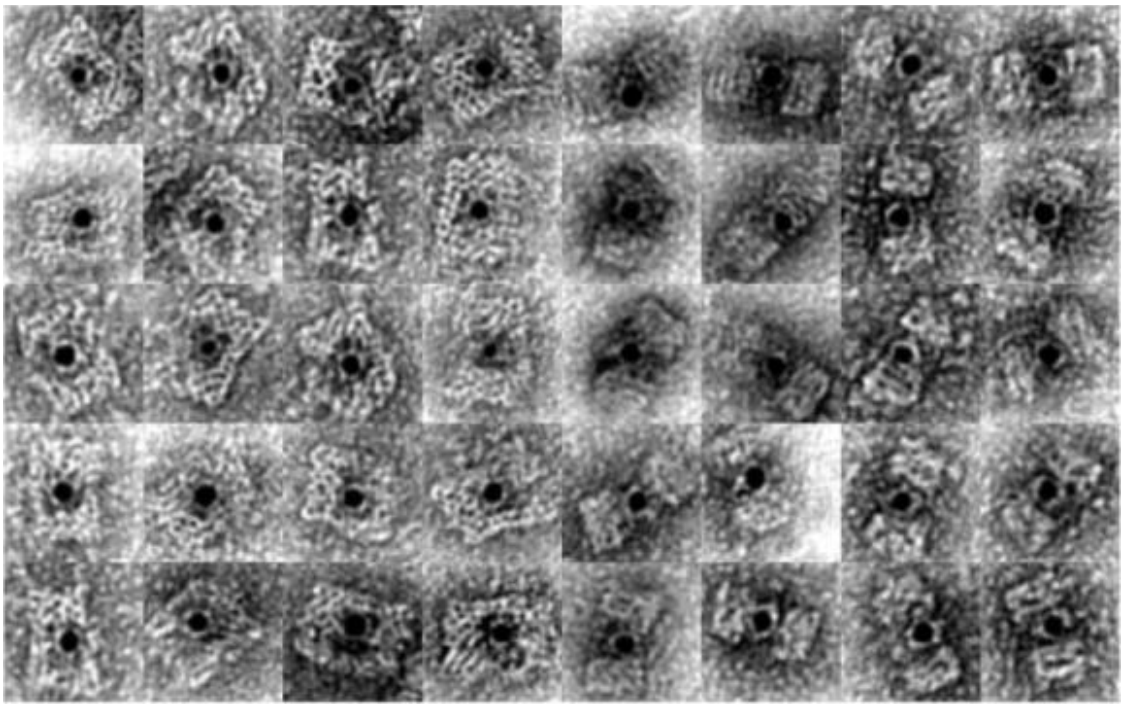
Figure S7. Zoom out and zoom in TEM images for DNA cage containing one 5nm AuNP inside through hybridization with 4 capture strands. The yield is ~99.5%



Zoom-out TEM image of the DNA origami cage structure

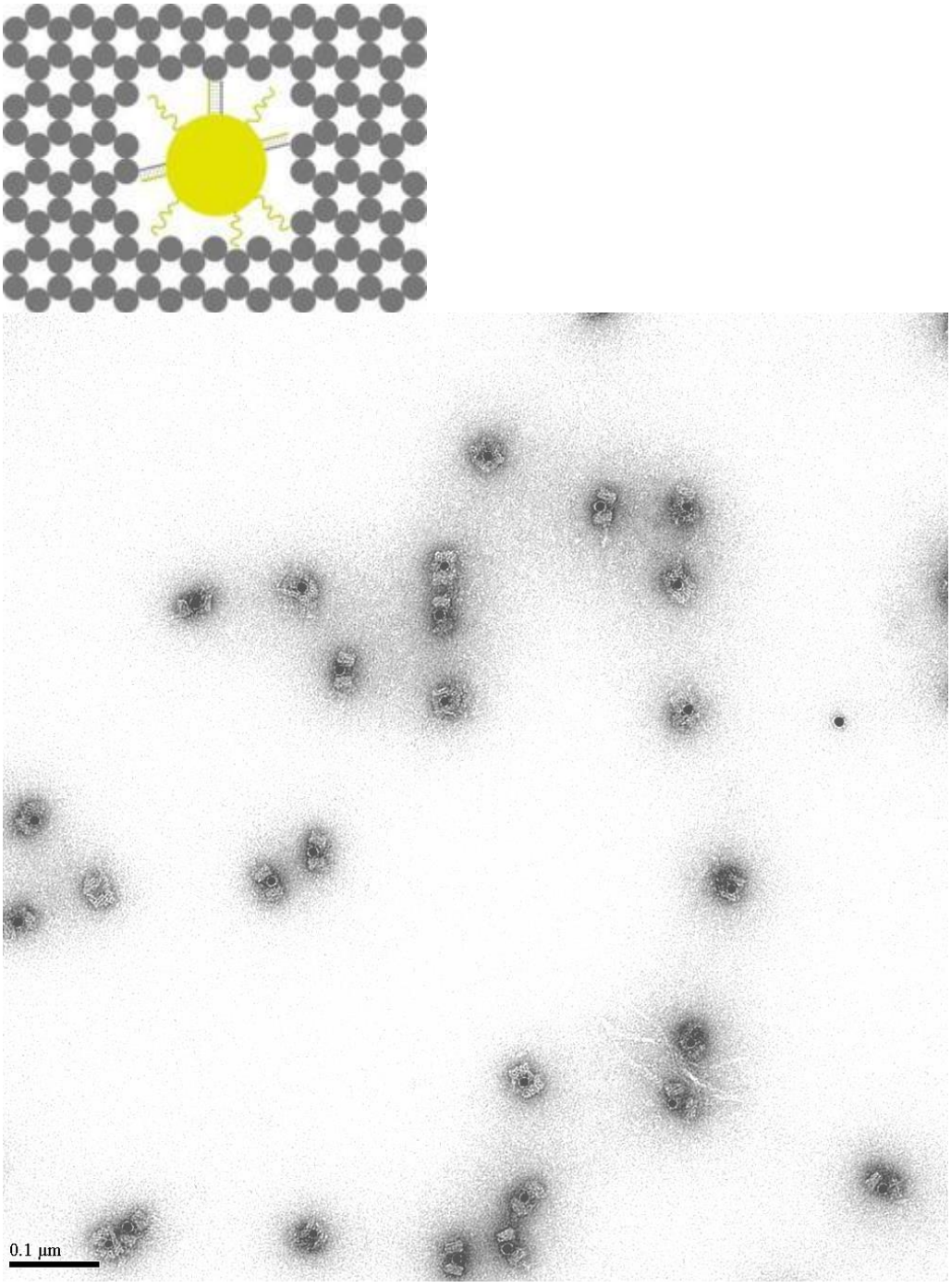


Zoom-out TEM image of the DNA origami cage structure

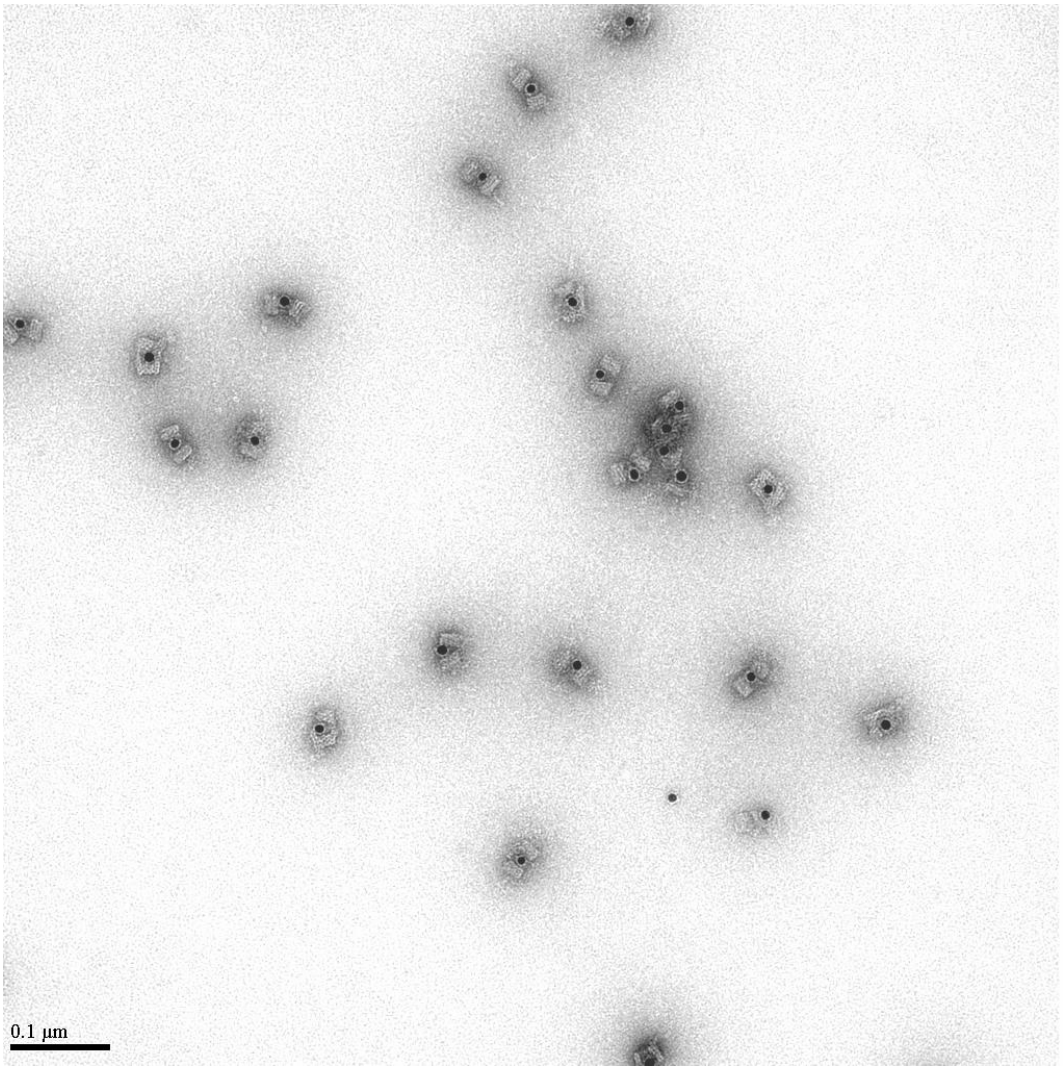


Zoom-in TEM images of the DNA origami cage structure

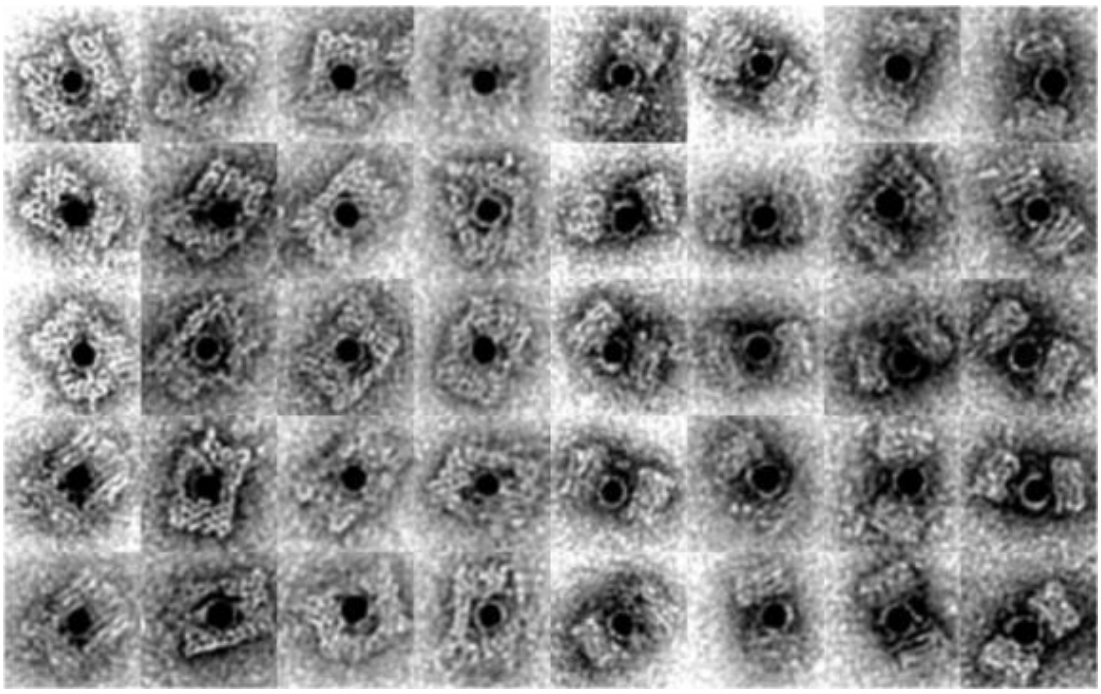
Figure S8. TEM images of cage containing one 10 nm AuNP inside through hybridization with 3 capture strands with ~92.7% yield.



Zoom-out TEM image of the DNA origami cage structure

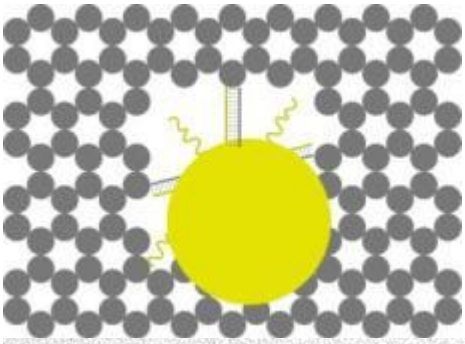


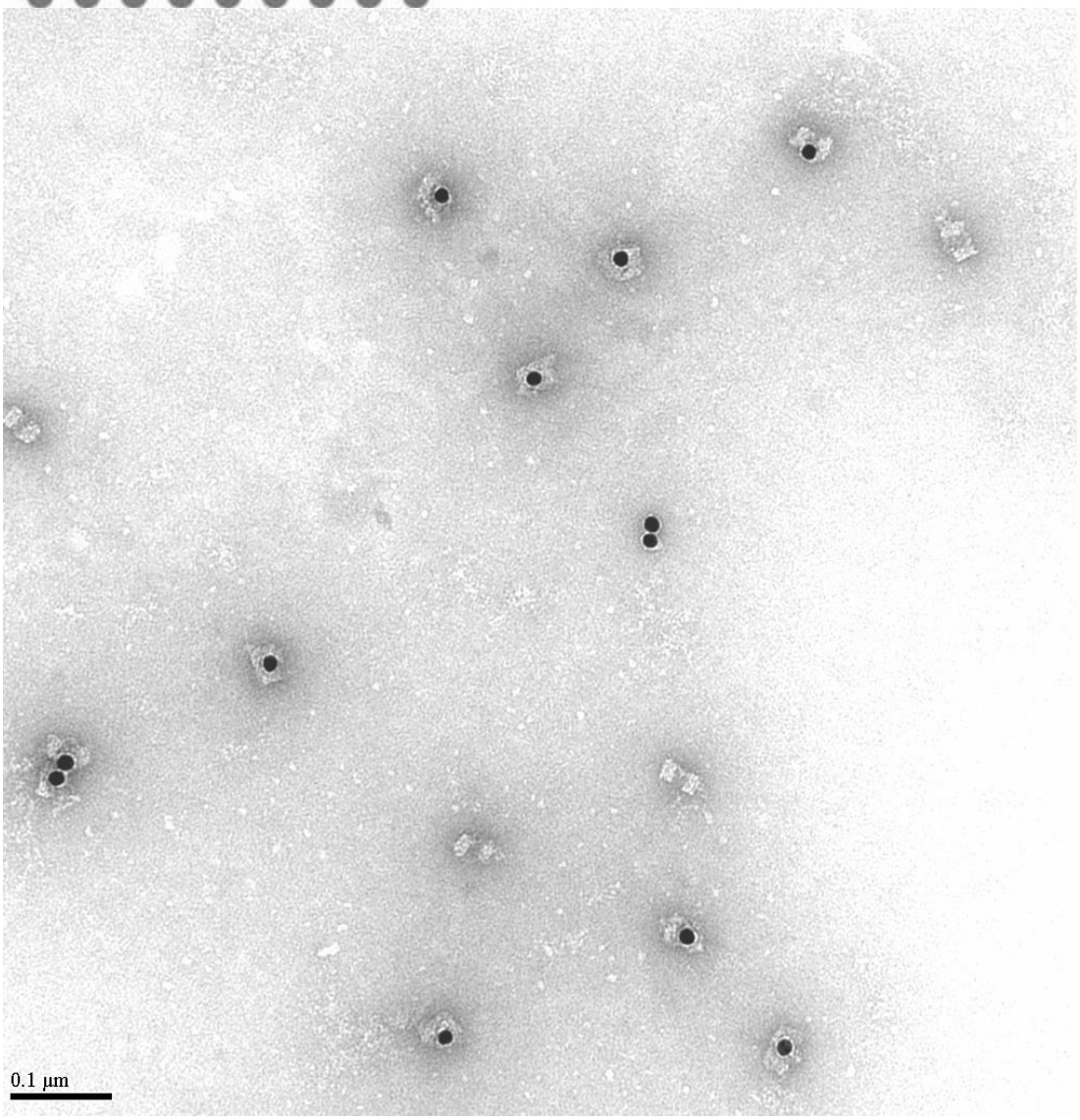
Zoom-out TEM image of the DNA origami cage structure



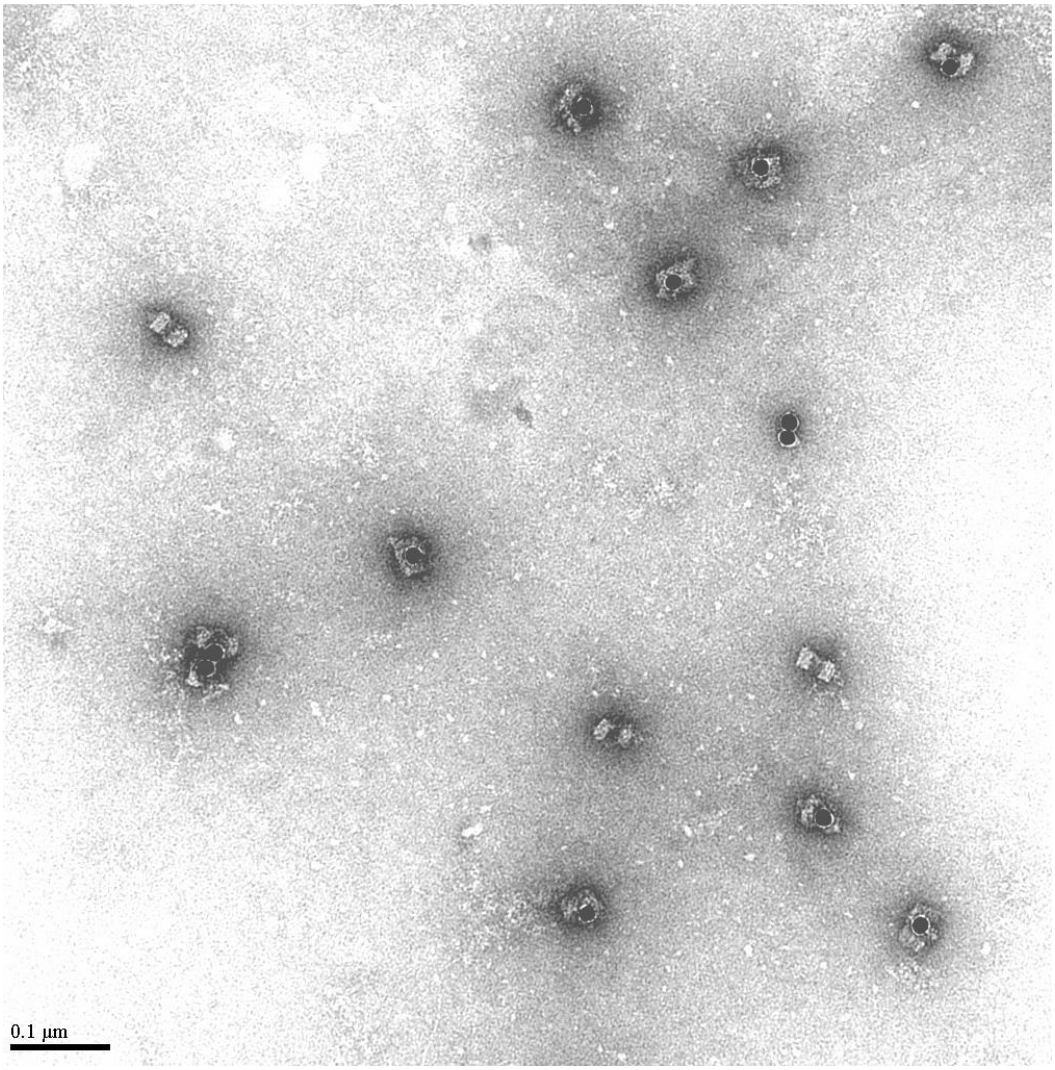
Zoom-in TEM images of the DNA origami cage structure

Figure S9. TEM images of DNA cage with one 15 nm AuNP inside through hybridization with three capture strands. The yield is ~67.8%.

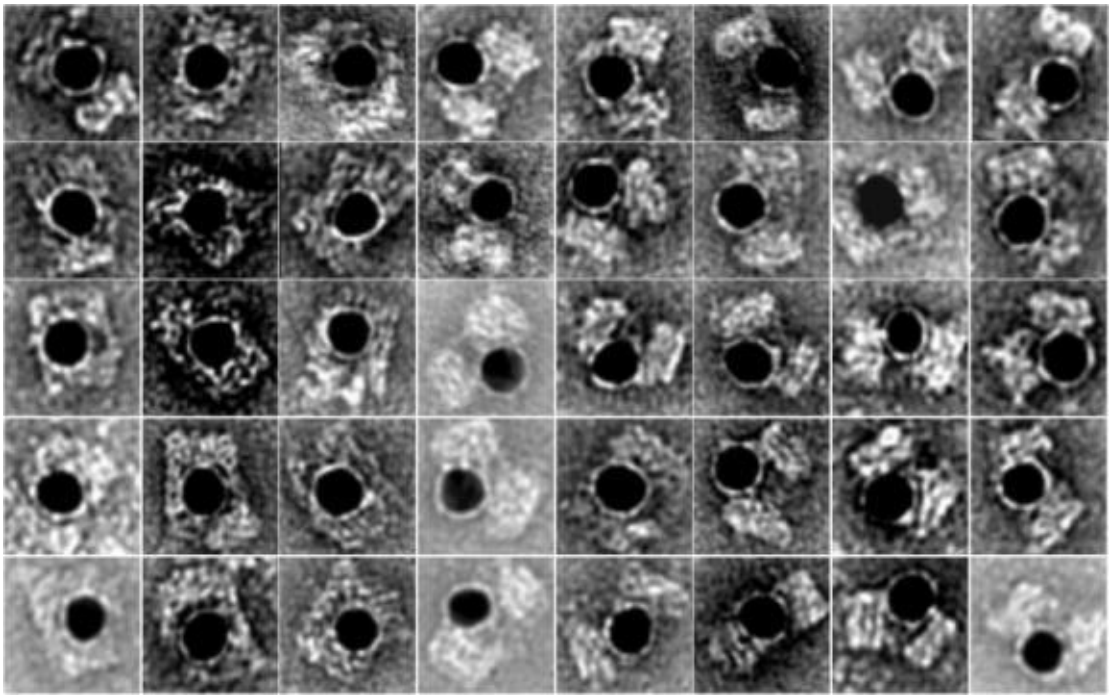




Zoom-out TEM image of the DNA origami cage structure

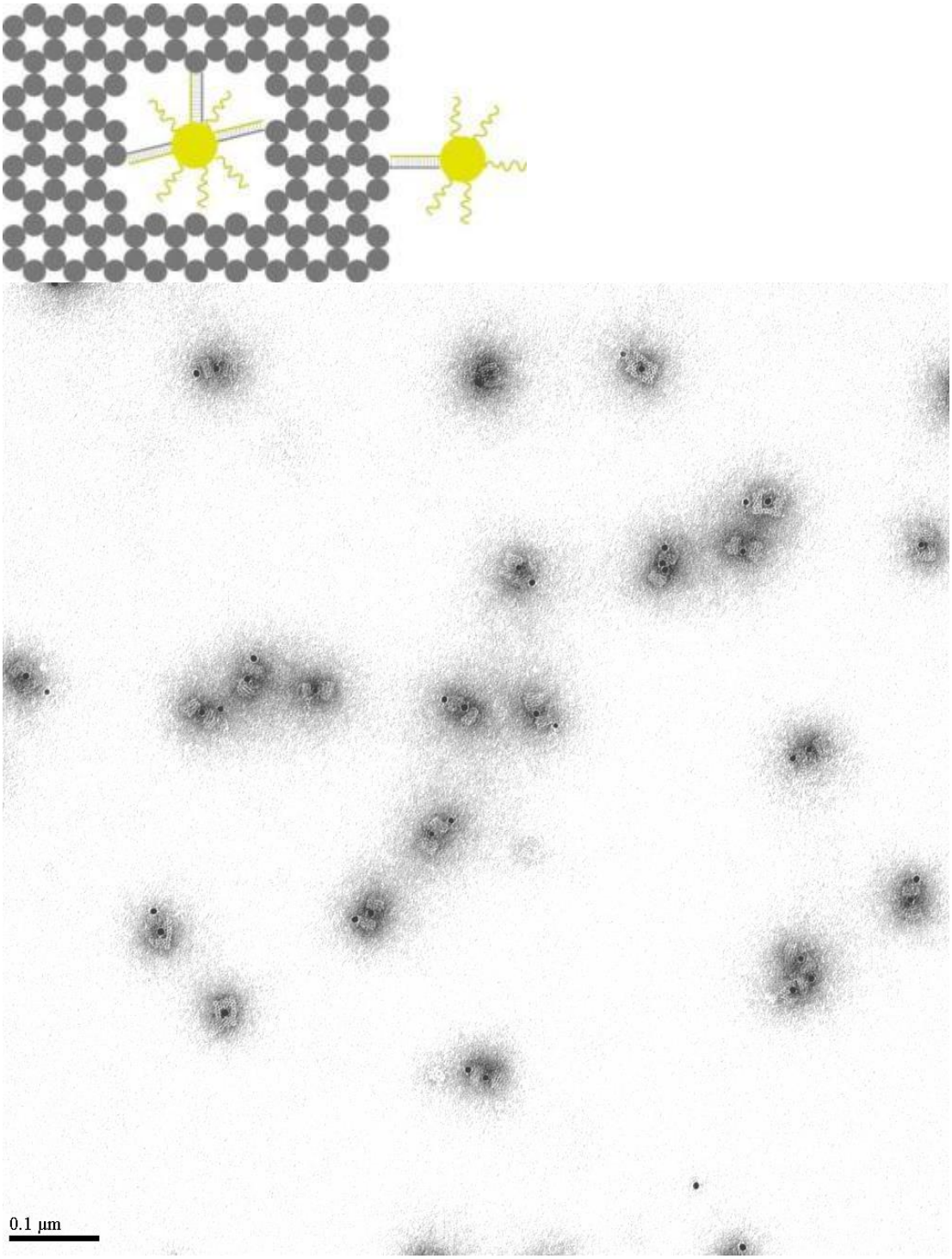


Zoom-out TEM image of the DNA origami cage structure

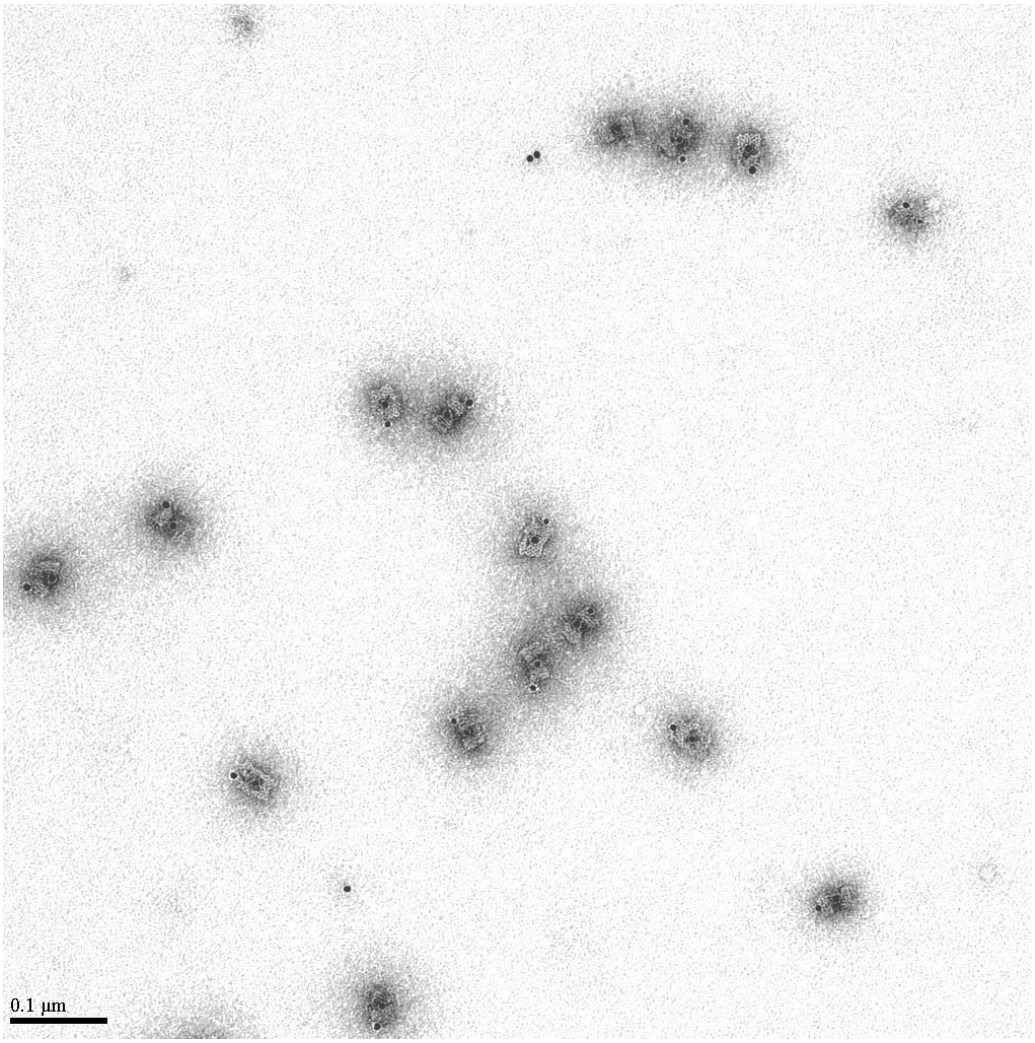


Zoom-in TEM images of the DNA origami cage structure

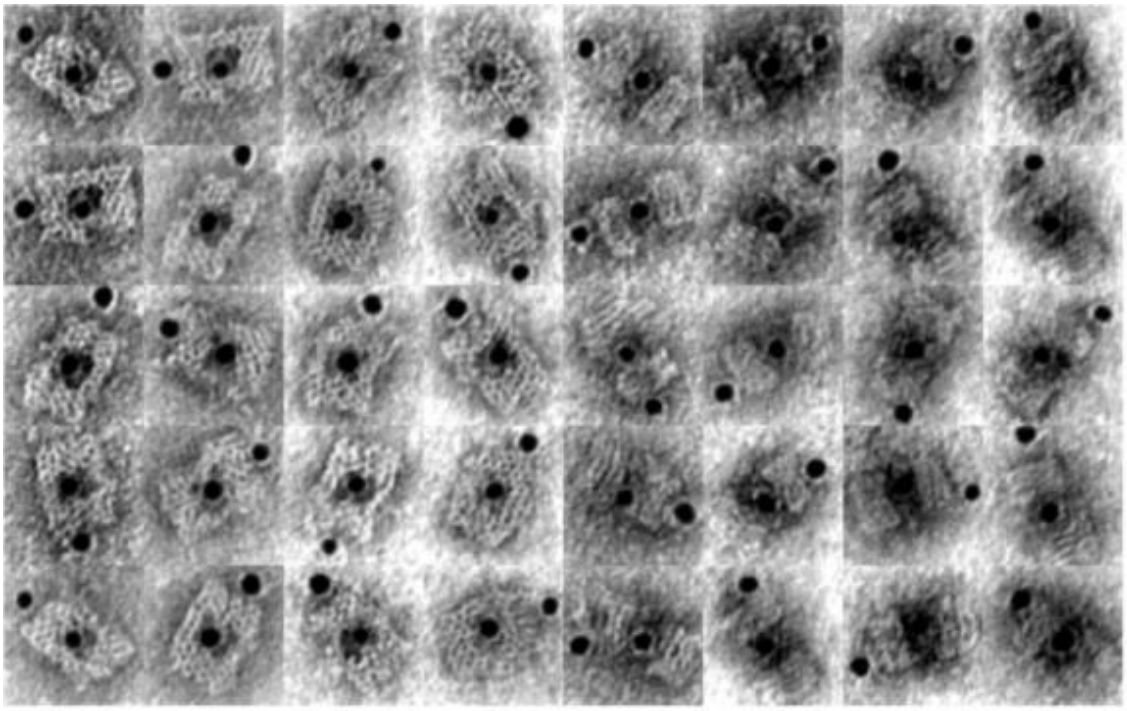
Figure S10. TEM images of DNA cage with one 5 nm AuNP inside and one 5 nm AuNP outside. The yield is ~85.1%.



Zoom-out TEM image of the DNA origami cage structure

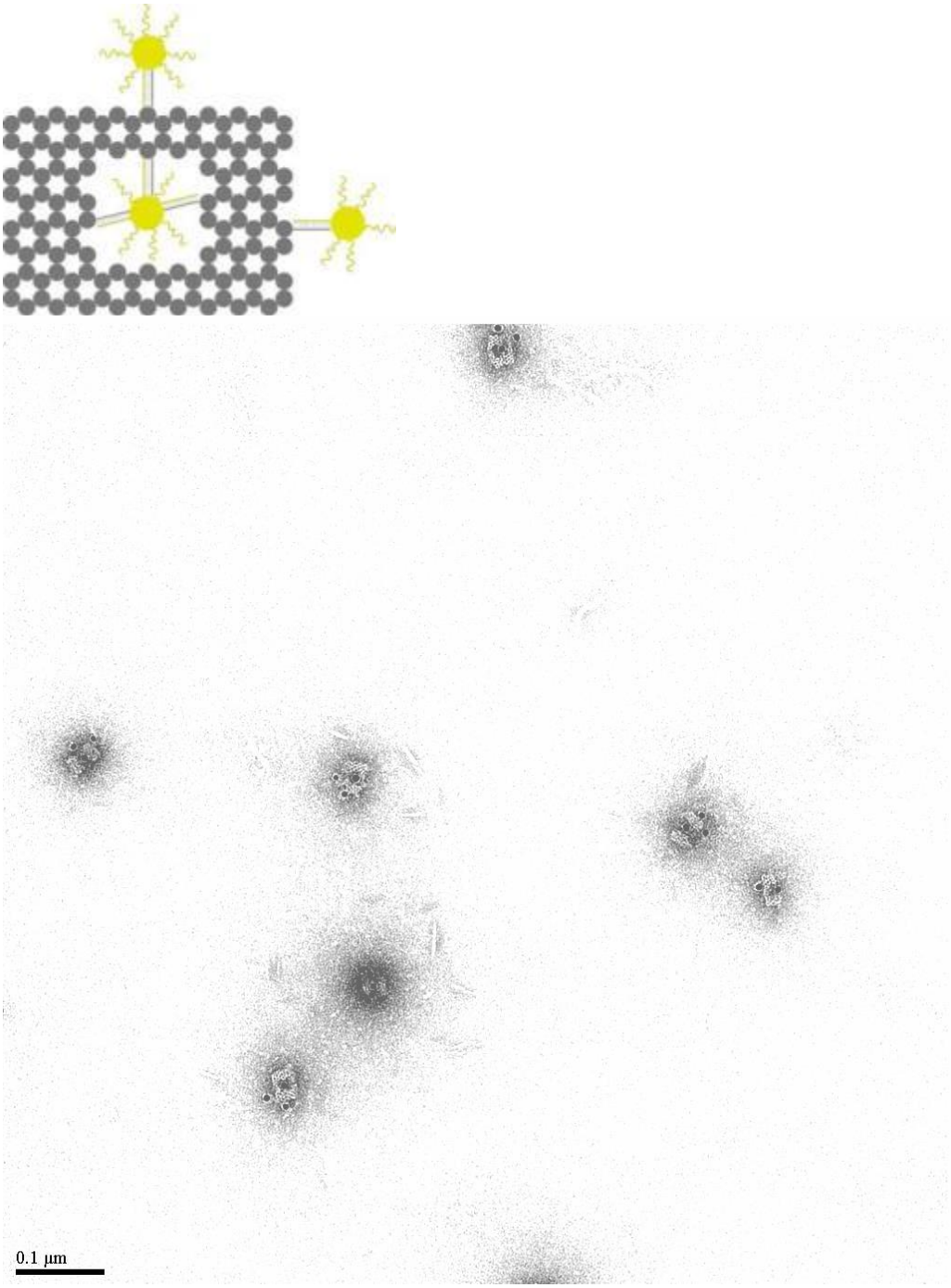


Zoom-out TEM image of the DNA origami cage structure

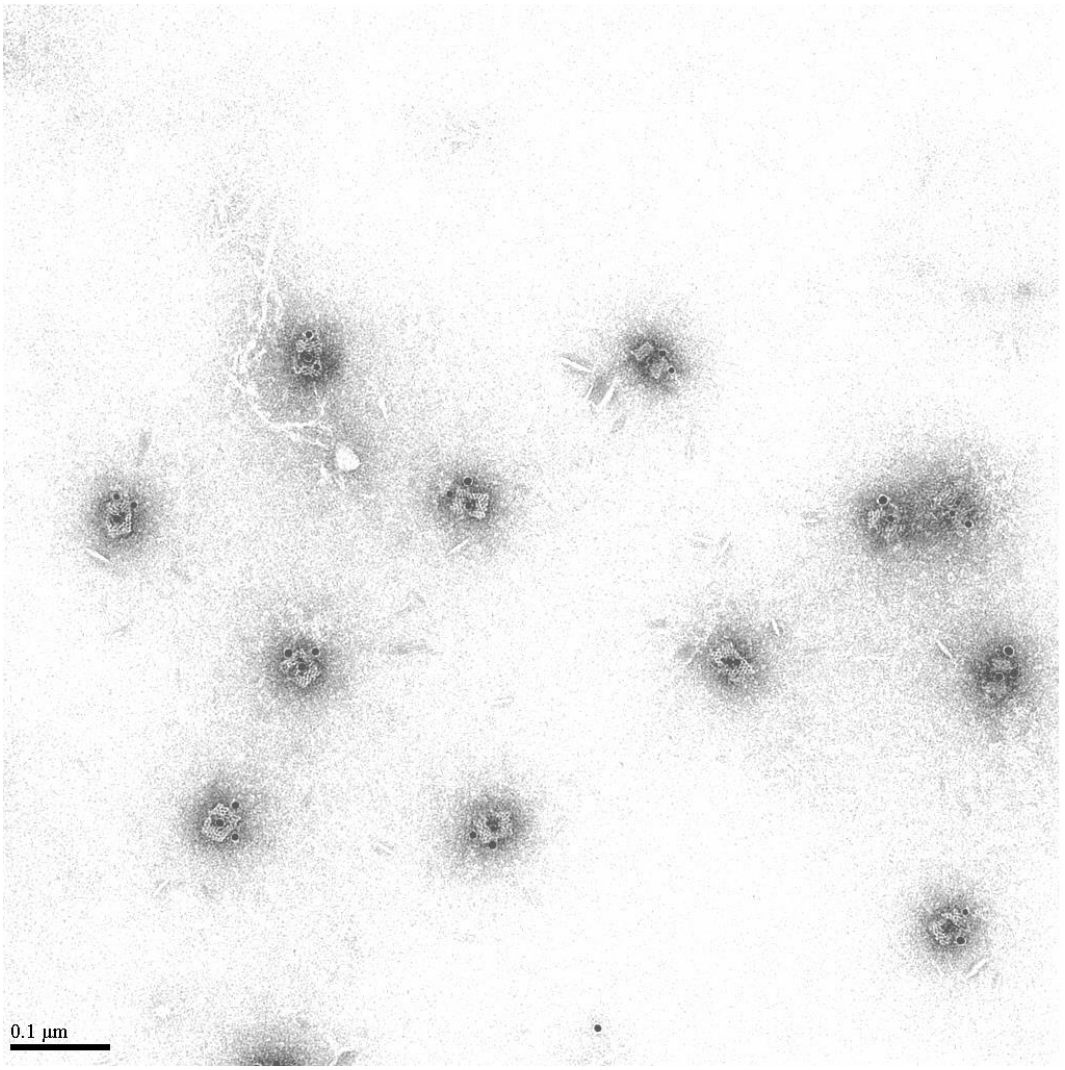


Zoom-in TEM images of the DNA origami cage structure

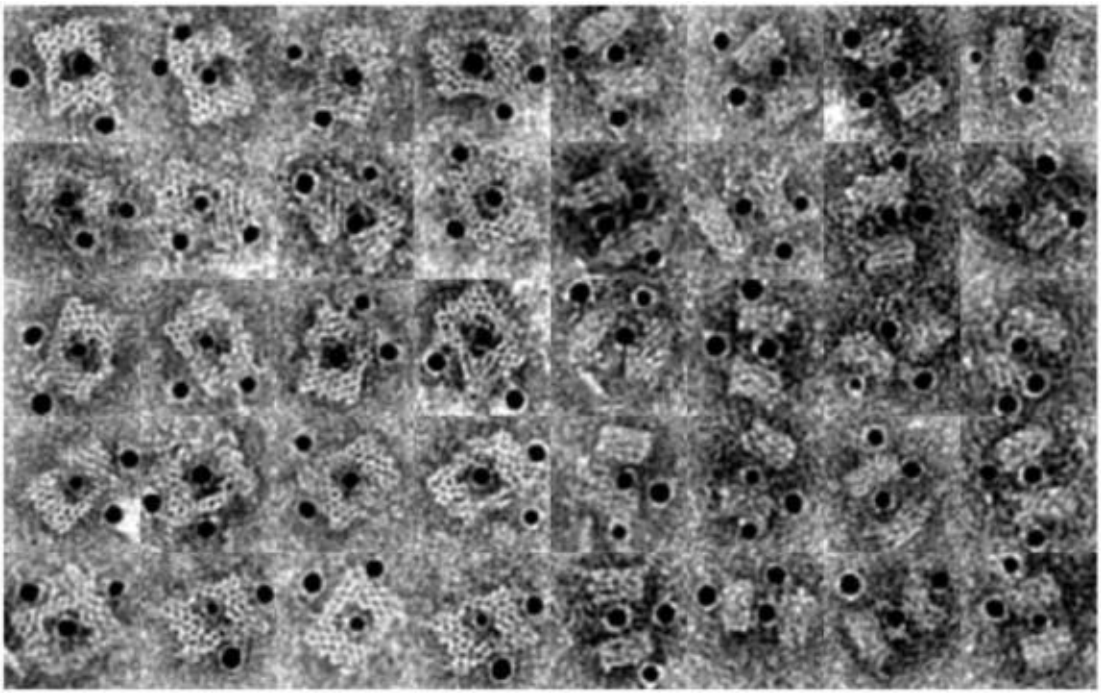
Figure S11. Zoom out and zoom in TEM images of cage with one 5 nm AuNP inside and two 5 nm AuNPs outside, forming 90° angle. The yield is ~80.0%.



Zoom-out TEM image of the DNA origami cage structure

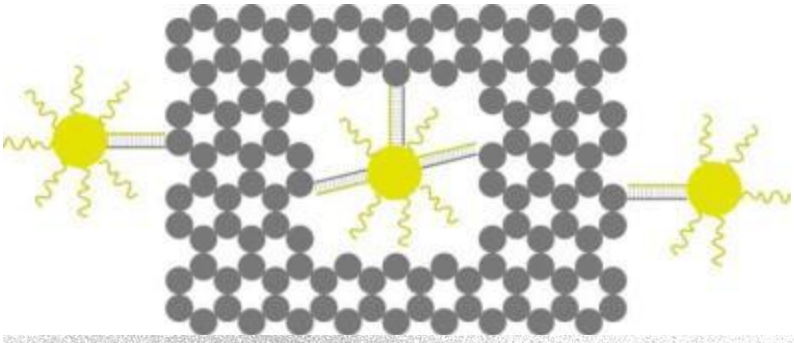


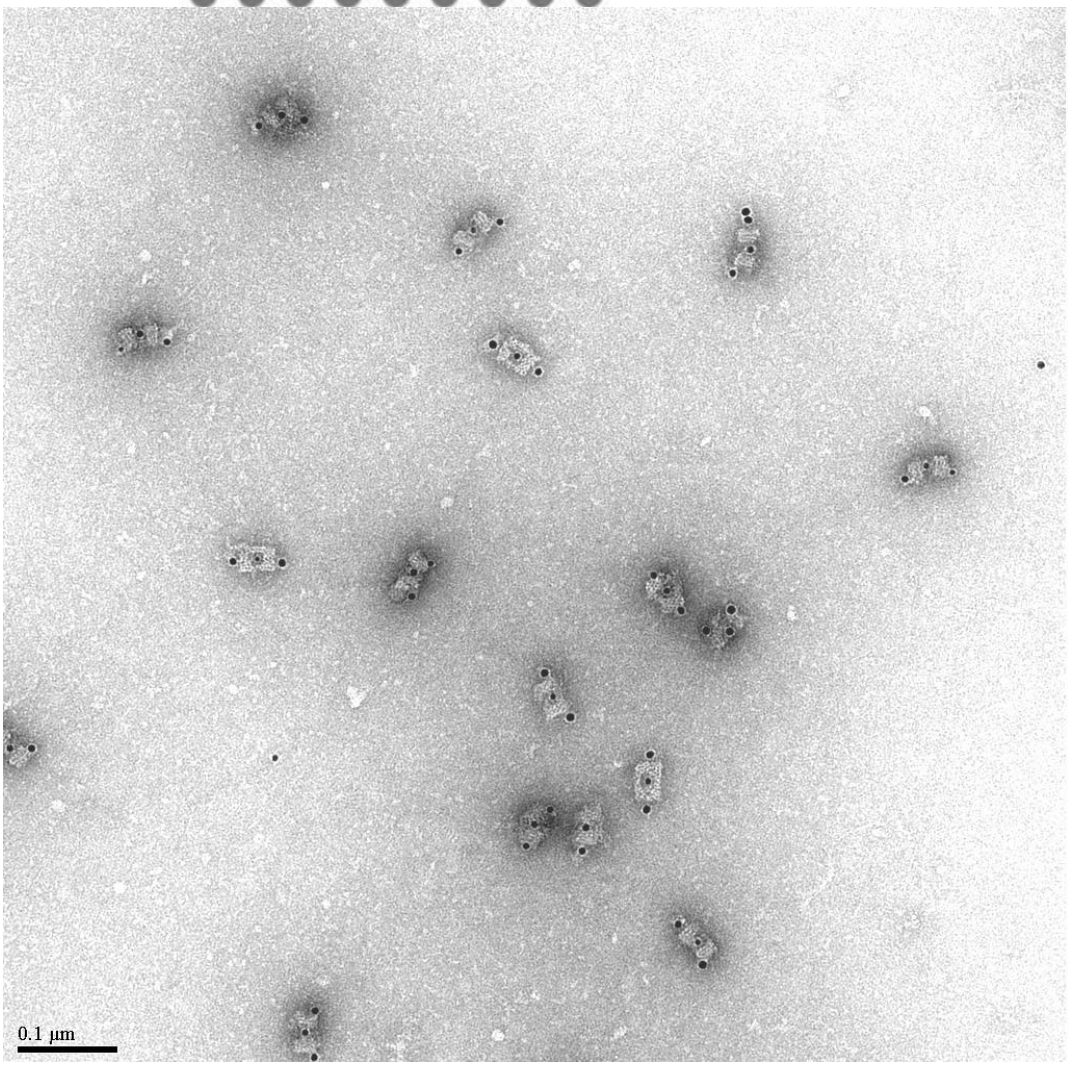
Zoom-out TEM image of the DNA origami cage structure



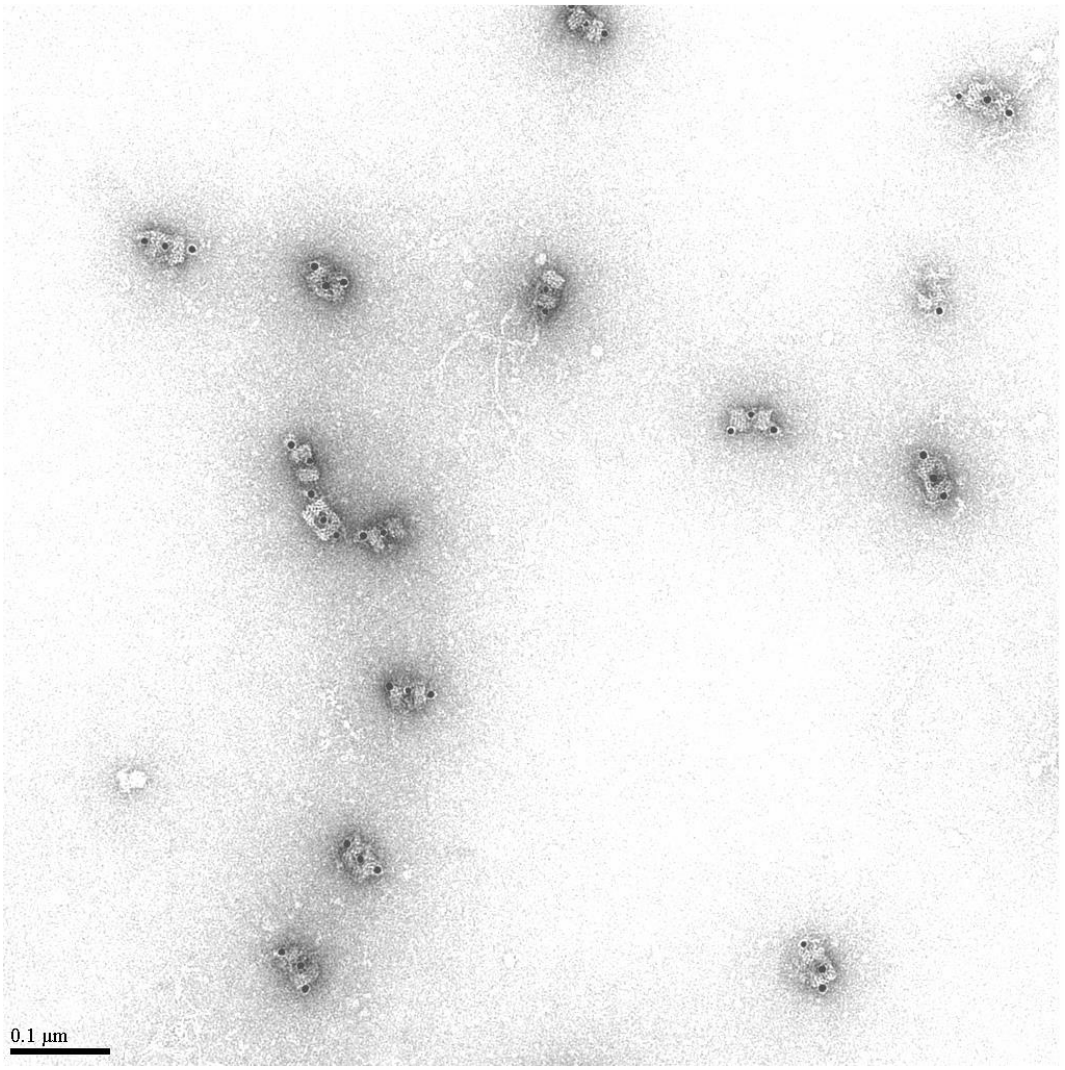
Zoom-in TEM images of the DNA origami cage structure

Figure S12. Zoom out and zoom in TEM images of DNA cage with one 5 nm AuNP inside and two 5 nm AuNPs outside forming 180° angle. The yield is ~84.3%.

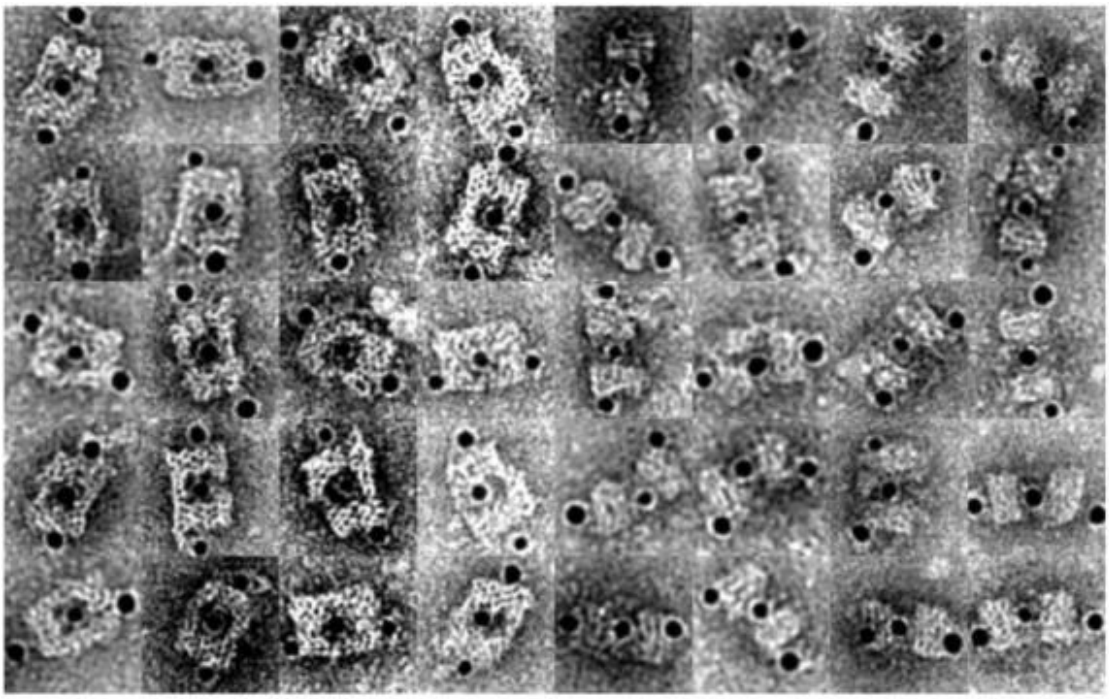




Zoom-out TEM image of the DNA origami cage structure

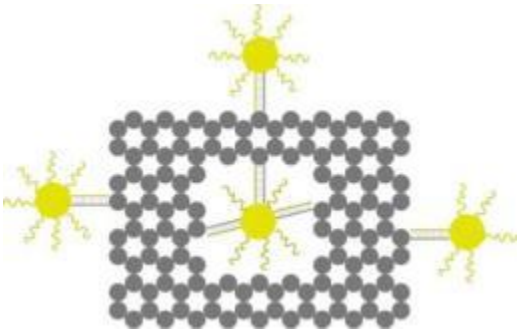


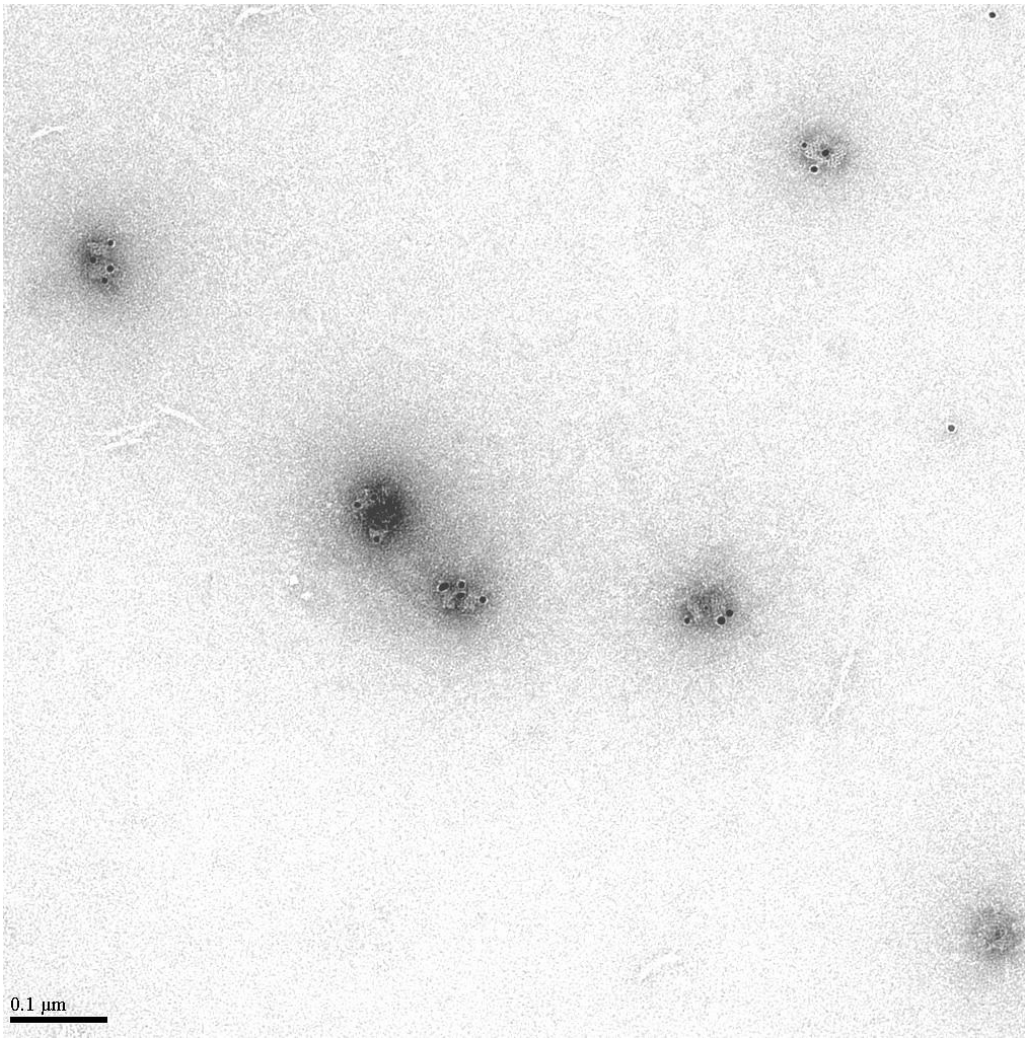
Zoom-out TEM image of the DNA origami cage structure



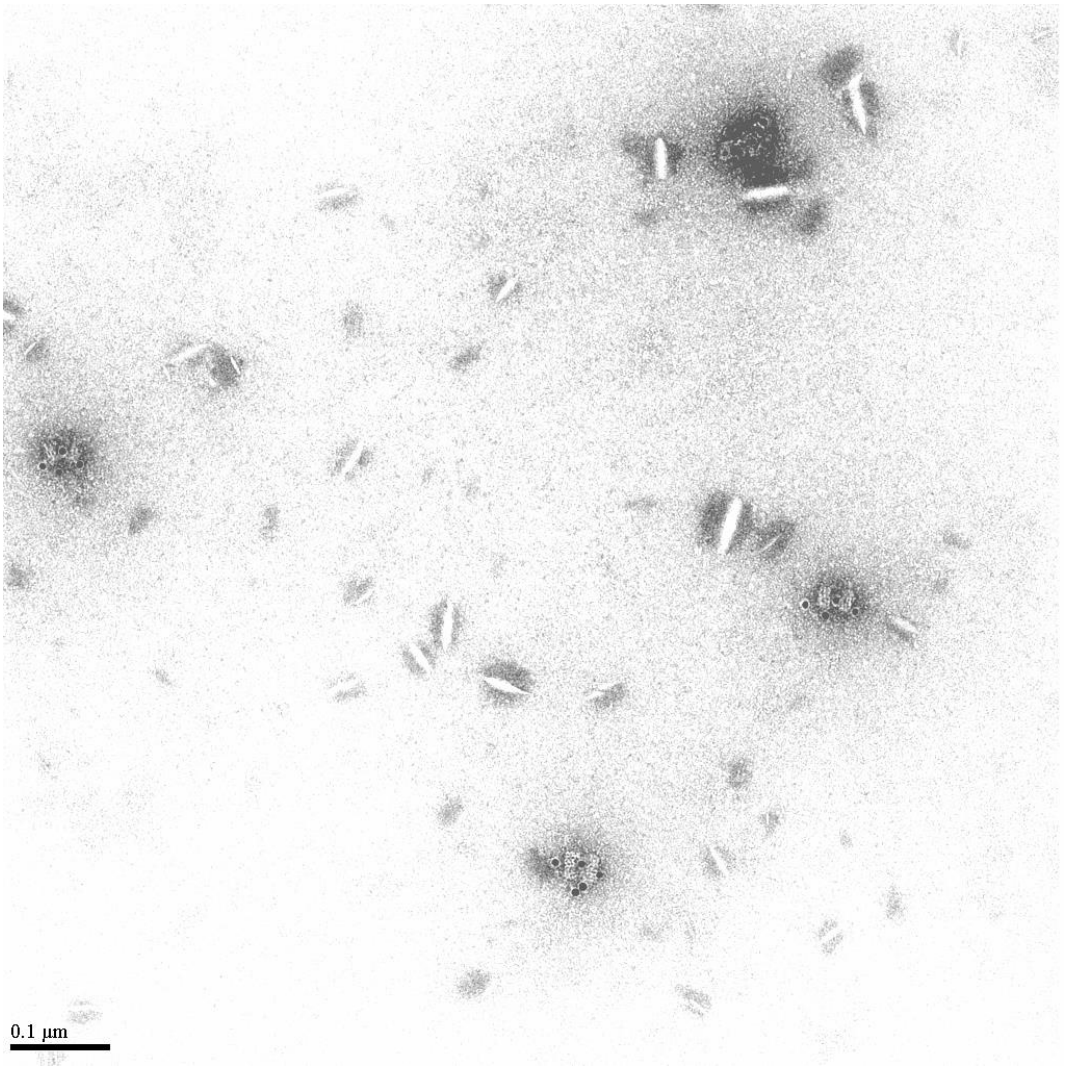
Zoom-in TEM images of the DNA origami cage structure

Figure S13. Zoom out and zoom in TEM images of DNA cage with one 5 nm AuNP inside and three 5 nm AuNPs outside. The yield is ~36.7%.

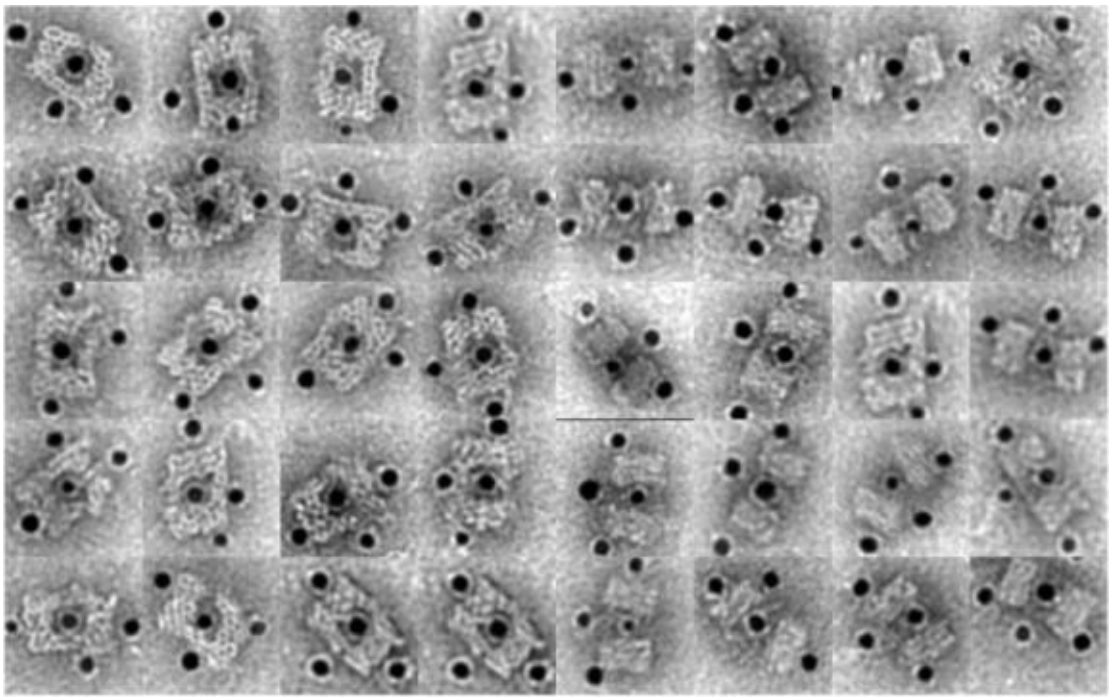




Zoom-out TEM image of the DNA origami cage structure

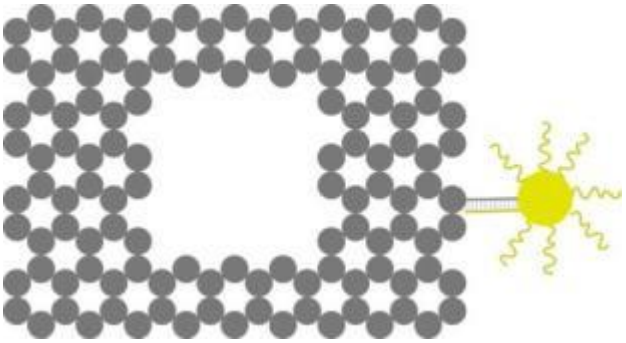


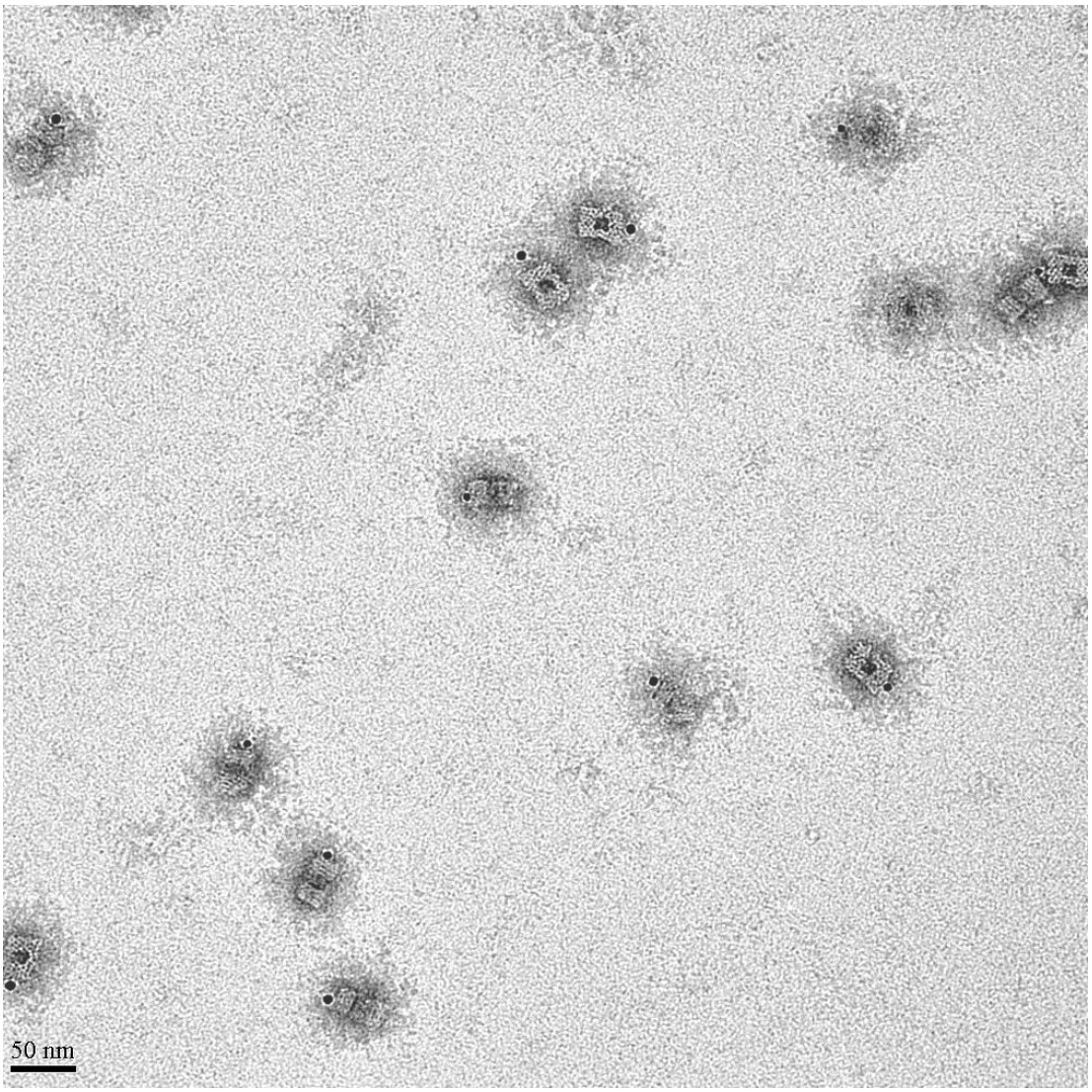
Zoom-out TEM image of the DNA origami cage structure



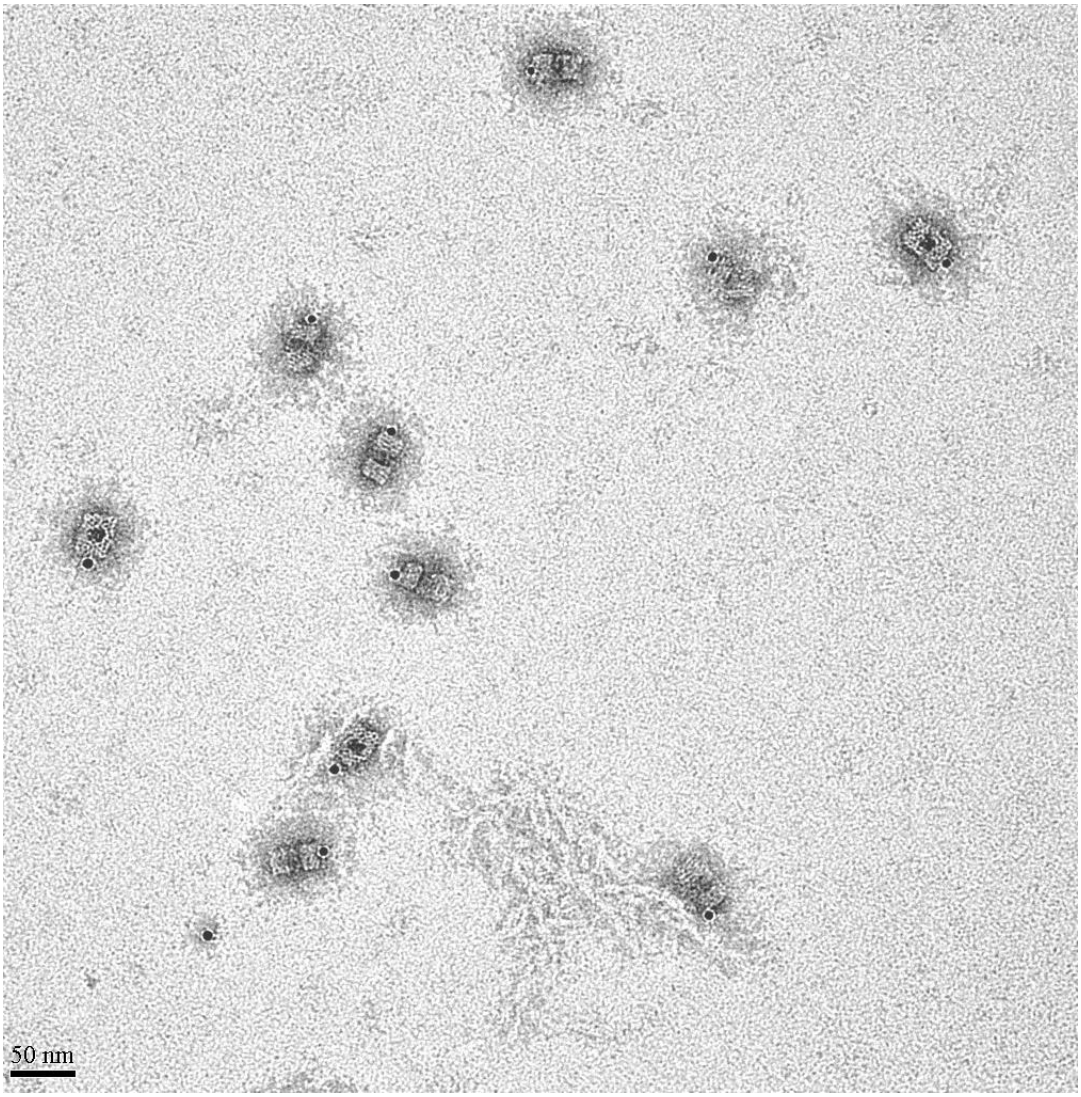
Zoom-in TEM images of the DNA origami cage structure

Figure S14. TEM images of cage with one 5 nm AuNP outside, through hybridization with one capture strand. They yield is ~93%.

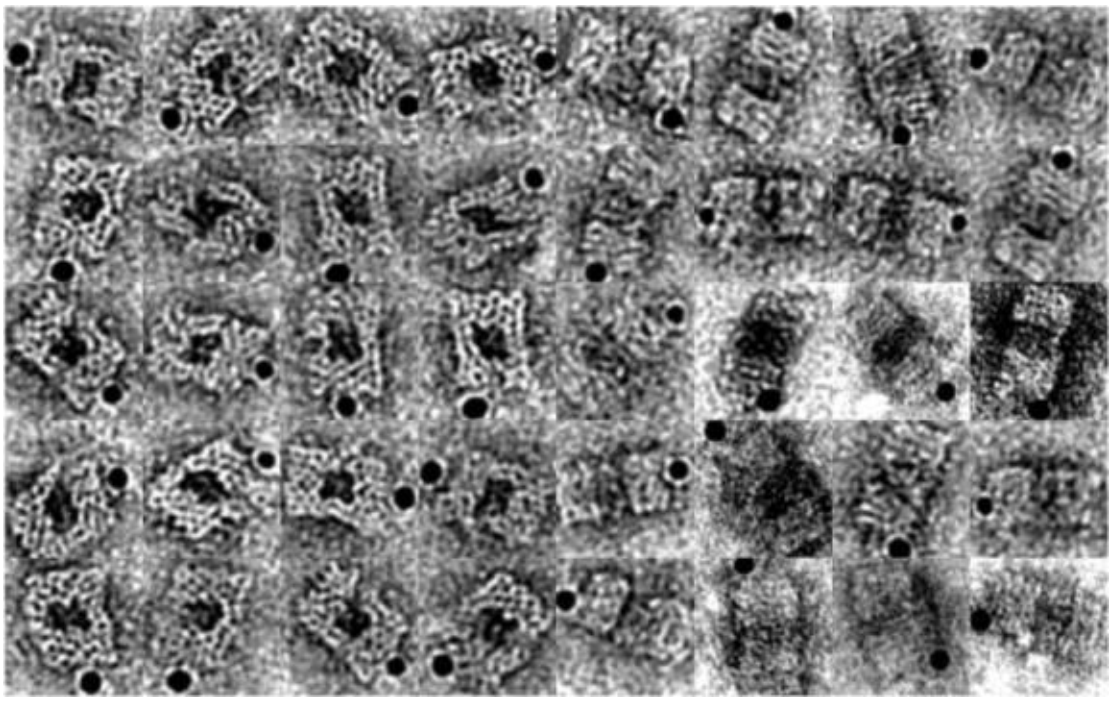




Zoom-out TEM image of the DNA origami cage structure

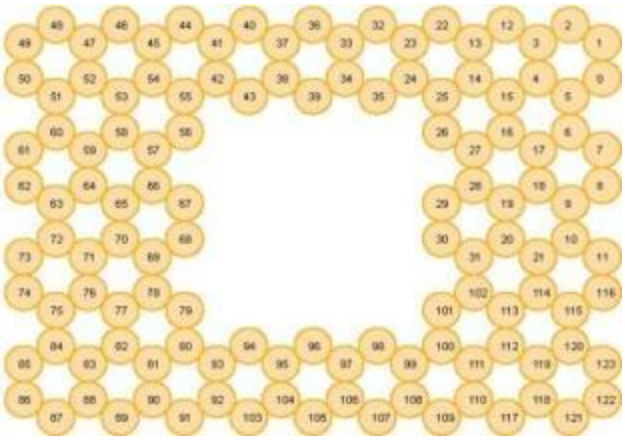


Zoom-out TEM image of the DNA origami cage structure



Zoom-in TEM images of the DNA origami cage structure

Figure S17. Design schematic of the DNA origami cage.



Sequence of staple strands containing A_{15} probes for hybridization with the DNA (T_{15}) on the AuNPs:

3 inside probes:

Probe from helix #29: AAAAAAAAAAAAAATTTCCTTGAAAACAGTCAATA

Probe from helix #39:

AAAAAAAAAAAAAAAGTCCAGAACAAATTCTTACATATTACTAGAAAAAGA

AATCCA

Probe from helix #68:

AAAAAAAAAAAAAAACAATAGAAAGGGCGACATTAACTGT

3 outside probes:

Probe from helix #11:

TTCACTAACTTTCATGAGGCTGTCACCCGGCGAAAAAAAAAAAAAAAAAA

Probe from helix #36:

AAAAAAAAAAAAAAAGATCGGTGCGGGCGTCAACTGTTGGGAAGG

Probe from helix #62:

AAAAAAAAAAAAAAACAGGTCATTGCCAAGAGAGGGATTTATCACCGTCAA

AAATCACCAAGCAATAAAGCAAACATTTAGCTATGCTG

Sequences of thiolated strands that coated the AuNPs. Two thiolated strands are used:

AuNPs that linked with probe from helix #11 were covered with 5'-SH-TTTTTTTTTTTTTTT-3'

AuNPs that linked with probes from other helices were covered with 5'-TTTTTTTTTTTTTTT-SH-3'

Sequences of unmodified staple strands:

1 TGGCAGGTCGACTCTAGGCCAAGCCAGACGTTGTAAAACGTT

2 CCTGATTCAAAGGGCGAAATGGGCAAGAGTCCACTATTAAAGAACGTTT

3 AGCTTTTGCGGAGAAGATAGCGATAGCTTAGATTT

4 GATAATATCTAAAGGAACATTAATGTCGGGATGTGTGAAATTGTT

5 AATCGCGGATTGCTCAAATGAACAGTGCGCGGTCAGTATTAACATT

6 TGAAATATCTAACCTCATAATTGCGCCTAATAAGCATAAAGTGTAAATT

7 GCAGAAAAATAATATCCCATT

8 ATAGGAGAATATTTTACAGAGAGACGCGAGGGAAGGCTTATCCGGTAT
T

9 CGAGTAACCGTCACGTTGGTGTAGATTT

10 AATCCAGGCCTAATTTGCCAGAACGAGCTTTTATCCTGAATCTTTT

11 CAGCCCATGAAATAAGAAACGAGATTAGCGGGAGGTTTTGAAGCTT

12 AGAGAAATAAAGGTCATAAAGATTCAAAAGGGTGAGAAAGTT

13 TACAATCGTAGCAAACAAGAGAATCGTT

14 TTTGTACCAACTCAGAGCATAAAGCTTT

15 TACCCCTGTACAAGGATTACACCATCAATATGATATTT

16 TTAAGATTTAGTTTGACCATTAGATACATTT

17 TCTTTCATTCCAACTAATGTAGCTAGAGCTTAAGAGGTCATTTTTGCTT

18 GGTCAGTTAAACAGTTCATTGAATCCCCCTTT

19 GCCTATTAGCGTCCTAATAGTAAAATGTTTTT

20 GAGACTCGCTTTTGACGATAAAAACCAAAATT

21 AACACATTATGTTAATAAAACGAACTTT

22 TTCACTAACTTTCATGAGGCTGTCACCCGGCGAAAATCCTGTTTGATTT

23 TTTGTAACACCCTCATAGTTTCAGGGATAGCAAGCCTT

24 TGTTTCCAACCTGTCTCACATAATATCACCAGCAGTTGAATATACC

25 ATACGAGCCGGGAGTGAGAGGTGAGCACGCTGGAAATTGTACA

26 GCGTATTCCAGCTGTTGAGGACTCAATCGCAAAAGGTTACAA

27 TAAATCATCCAGTTTGGAAGCGCCAGGGAGCTGATTATCTAATAGA

28 TATTTGCAGAAGATAAAACAGCTCGAACGAACCACTTGCATGCCC

29 GATTATACATTAAAAATACAACGAACCGTCTATCAATCA

30 GCCTGATGAATAACAATTTTCCTTGAAAACAGTCAATA

31 CGAATAGATAGTGAGTGTTTGAATTACCTTTTTACATTACAAACATACC

32 GTAATATATTTGGTTTGTTAATTGATTTAGGTGAACAATGTAGAAAGAT

33 TTTAATCATAACCGACCGGTAAAGGGCATTTAAACCAAATCA

34 ATCGCAGCCAGGTTGGGTTATACCTACCATATCAGAAGTTTG

35 TGGCAGGTCGACTCTAGGCCAAGCCAGACGTTGTAAAACGTT

36 CCTGATTCAAAGGGCGAAATGGGCAAGAGTCCACTATTAAAGAACGTTT

37 AGCTTTTGCGGAGAAGATAGCGATAGCTTAGATTT

38 GATAATATCTAAAGGAACATTAATGTCGGGATGTGTGAAATTGTT

39 AATCGCGGATTGCTCAAATGAACAGTGCGCGGTCAGTATTAACATT

40 TGAAATATCTAACCTCATAATTGCGCCTAATAAGCATAAAGTGTAAATT

41 GCAGAAAAATAATATCCCATT

42 ATAGGAGAATATTTTACAGAGAGACGCGAGGGAAGGCTTATCCGGTAT
T

43 CGAGTAACCGTCACGTTGGTGTAGATTT

44 AATCCAGGCCTAATTTGCCAGAACGAGCTTTTATCCTGAATCTTTT

45 CAGCCCATGAAATAAGAAACGAGATTAGCGGGAGGTTTTGAAGCTT

46 AGAGAAATAAAGGTCATAAAGATTCAAAAGGGTGAGAAAGTT

47 TACAATCGTAGCAAACAAGAGAATCGTT

48 TTTGTACCAACTCAGAGCATAAAGCTTT

49 TACCCCTGTACAAGGATTACACCATCAATATGATATTT

50 TTAAGATTTAGTTTGACCATTAGATACATTT

51 TCTTTCATTCCAACTAATGTAGCTAGAGCTTAAGAGGTCATTTTTGCTT

52 GGTCAGTTAAACAGTTCATTGAATCCCCCTTT

53 GGATTAGCAATATAAAAAGCGCTACCTGAACTTAGACGATCGGCTACG
A

54 ACCGTCAAAAATCACCAAGCAATAAAGCAAACATTTAGCTATGCTG

55 CATCGTATAGCACCATTACCAAGCCAGCCCGACTTAATACCC

56 TTCTGCCGCCTCCCTCAGCCACCACCCTCATTCAAAGCAGAGGAA

57 CTGTAGCAAGACAAAAATTCAAGTTTATTTTGTCAGGCAACAACGT

58 CCACCACCACCGGAATCCAAAAAGGGTCTTTACCCTGATCCATAA

59 GAGTCTTTTCATAGCCCCCTTATTGCTCAGA

60 AGAGAGCCGCTTGCCTTTAGCGTAAGATAGCAGCACCGATTATTCGGAG

61 CGCCACCCAGGAGGTTGCTCCTTTTGATAATTGCTCATCCAAATTC

62 CAGACGAGCATTGAAGAACCAATGAAAC

63 GCTATAATGCAGTACGGATTTGGGCAATAACATTTTTAGTAA

64 GCCCGAAATTGCATTGGAAGTGCGAACGAGTAGCGAACGAGA

65 ATCAAAAACCAGGCGCATAGGCAGATGATGCTCATCCAGAAC

66 ATGACTTCGTAACAAATCGTCATAAATATTCAGAATTTG

67 GATGCCAGAGGGGGAATACTGCGGAAGCACGGTGTATCATAA

68 AGTTTGTGCAGACGGTCGAAATCCGCGACATCGCCACCTTATAGGACGT

69 AATTGGGCTTAGAAACATCAGTGAAAATCAAGACAAGACAAT

70 ACTAAGGAATAACTAATGTTGAGAAATATATATACATTAATA

71 TGGGATAAAACACTCATCTCATGATACCGATAGCATAATTTT

72 GGTTTGCTTCTTAAAAGTTTGACACAACTCGTCCTAAA

73 GGGAACCACGAGGCAGTAAATCATTGTGAAGTTTACCAGACGCAAAAG
A

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76 AATTCATGAGTACAAACGCCTGGCGGGCAACTGGTTTTGCGGTTT

77 CCGACAATATTCGGTATTAAAATCGGCAAAATCCCCCCAGCATCAGCAG

78 GACTTTTACGTAATTTCATCAGCAGATACAAGAAAAATCTACTACA

79 CGAAAGAAGGCTTTGAGGAGCACAG

80 CCCTCAAGACGGAATAGGTGTAAAAGAAGGCACCAGTAA

81 AAATCTCGCGTAACGATCTAAAGACAGCTGAGTTTCGTCACCCTAA

82 TTGGTGAGAAGCTACAGCAGCATCCCACGCTGGTTTGCCTTCACCAATT

83 ACAAATGAATAACAGCTGCTTGCTACCAGTCGCGATTTCTTT

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85 TTTAGGGTTGAGTGTTGTAAAGAATAAGG

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3

10 TTCCGCTTTTGCGGGATCTGCAGGGACCGATATGAC

4

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5

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2
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3
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4
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5
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6
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6

19 TTGGAGATTTGTATCCTGCTCCATGTTT

7

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8

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20 TTACAACTAAACTCAGAACCGCCTT

5

20 TTGGGATTTTGAGTACAAACTACTT

6

20 TTAACGCCTGTAGCATTCCACAGTTTTGTCGTCTT

7

Reference

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APPENDIX D

SUPPLEMENTAL INFORMATION FOR CHAPTER 5

Supplemental Information

DNA Origami Templated Self-assembly of Discrete Length Single Wall Carbon Nanotubes

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Experimental Materials and Methods

Materials: All helper strands were purchased from Integrated Technologies, Inc. (www.IDTDNA.com) in the form of 96-well plates normalized to 100 uM. M13 viral DNA and ΦX 174 DNA was purchased from New England Biolabs, Inc. (NEB, Catalog number: #N4040S and N3023S). Single walled carbon nanotubes were purchased from Southern Nanotechnology. Size exclusion HPLC columns were purchased from Sepax Int.

DNA Origami assembly: Each individual DNA origami structure was assembled in a one-step annealing reaction by mixing M13 and helper strands in 1:5 ratio in 1× TAE-Mg^{2+} buffer (20mM Tris, pH 8.0, 2mM EDTA, 12.5 mM $MgCl_2$). The final concentration of M13 and assembled structures was 10 nM; the final concentration of helpers was 50 nM, with a final volume of 100 µL. The oligo mixtures were cooled from 90°C to 70°C over the course of 90 min, and then further cooled from 70°C to 4°C over 620 min.

Carbon nanotube preparation and separation: 0.1 mg of SWNTs were added to 150 µL of 50 µM single stranded DNA label, and sonicated in an ice bath at 9W for 3h. The resulting solution was centrifuged at 13000 rpm for 60 min and the supernatant was collected. The SWNT solution was injected into an HPLC system with three columns

arranged in series (2000A, 1000A and 300A) and run in TBS-NaCl buffer at a speed 0.2mL/min. Specific fractions were collected for use in subsequent experiments. The separated SWNT solution was incubated for 48 hours with the single stranded DNA linker in a 1:10 ratio, and a100KD Amicon filter was used to remove excess linker strand.

DNA Origami and SWNT assembly: Assembled DNA origami (500 pM) was mixed with an excess of purified SWNT, incubated in 1×TAE-Mg^{2+} buffer for 30 min at room temperature, and subsequently imaged.

AFM imaging: The samples (2 µL) were deposited on freshly cleaved mica (Ted Pella, Inc.) and left to adsorb for 3 min. Buffer (1×TAE-Mg^{2+}, 400 µL) was added to the liquid cell and the sample was scanned in a tapping mode on a Pico-Plus AFM (Molecular Imaging, Agilent Technologies) with NP-S tips (Veeco, Inc.).

TEM imaging: TEM samples were prepared by placing 2 µL of the sample solution on a carbon-coated grid (400 meshes, Ted Pella). Before depositing the sample, the grids were prepared by negative glow discharge using an Emitch K100X. After 1 min, excess sample was wicked from the grid using filter paper. To remove the excess salt, the grid was washed with a drop of water and excess water was wicked away using filter paper. The grid was treated with a drop of 0.7% uranyl formate solution and the excess solution was wicked away using filter paper. Again the grid was treated with a second drop of uranyl formate solution for 10 seconds, and the excess solution was removed using filter paper. To evaporate any additional solution, the grid was kept at room temperature. TEM studies were conducted with a Philips CM12 transmission electron microscope, operated at 80 kV in bright field mode.

Figure S1. HPLC profile of the separation of DNA wrapped SWNT by SEC columns arranged in series (2000, 1000 and 300), monitored by UV absorbance at 260nm.

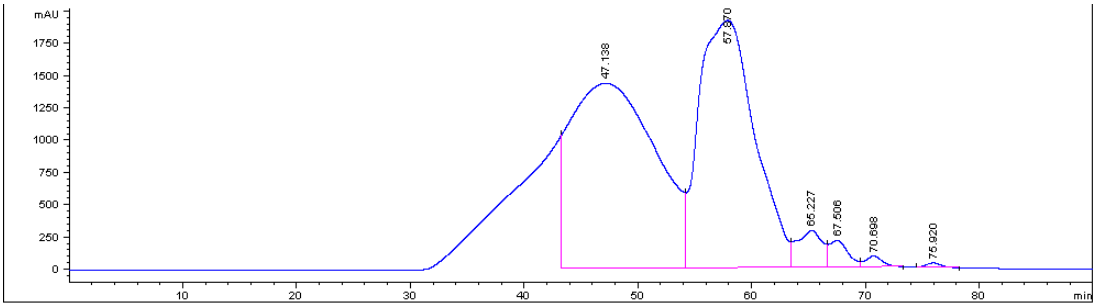


Figure S2. AFM image of a single DNA labeled SWNT attached to a DNA origami structure through hybridization of a random sequence probe. (image size 5um×5um)

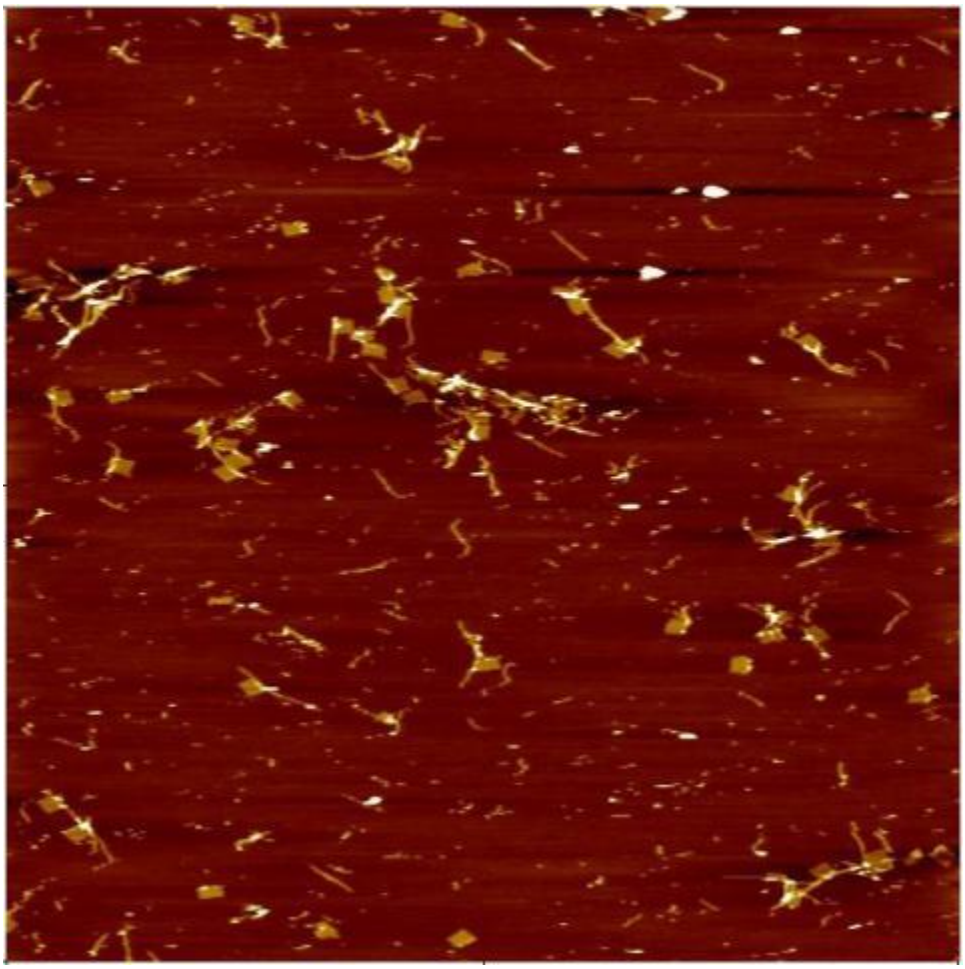


Figure S3. AFM image of a single DNA labeled SWNT attached to a DNA origami structure through hybridization of a poly T probe. (image size 5um×5um)

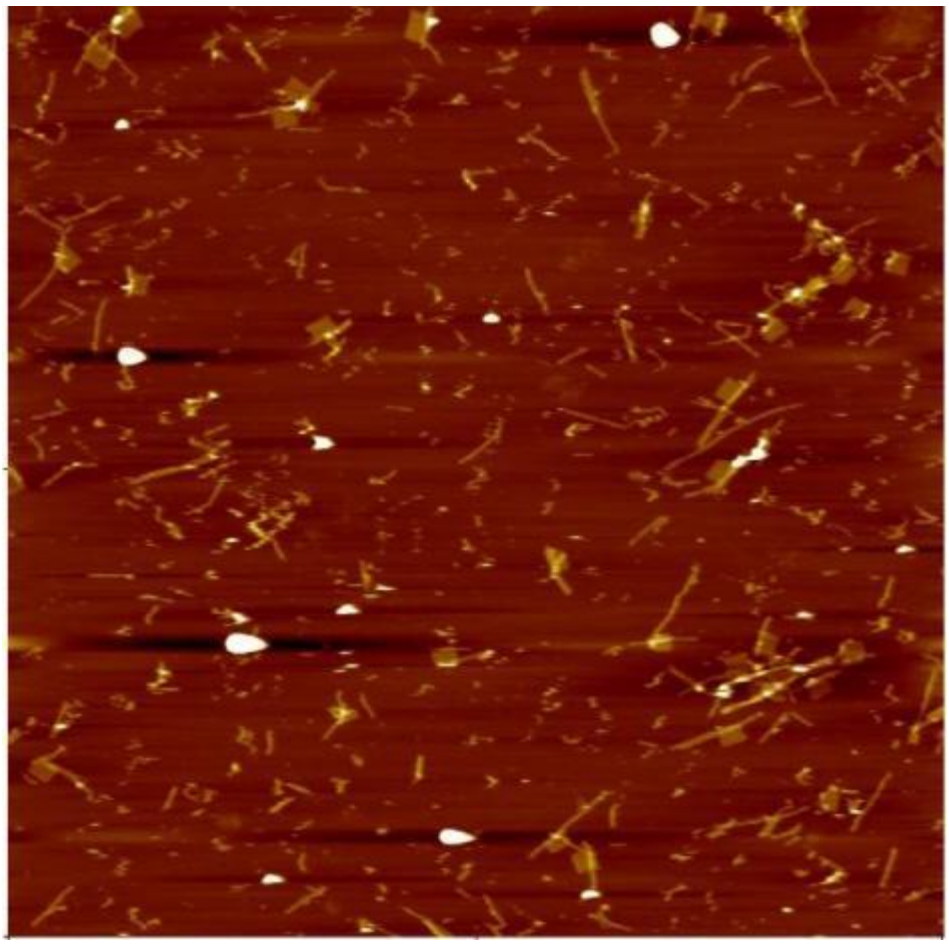
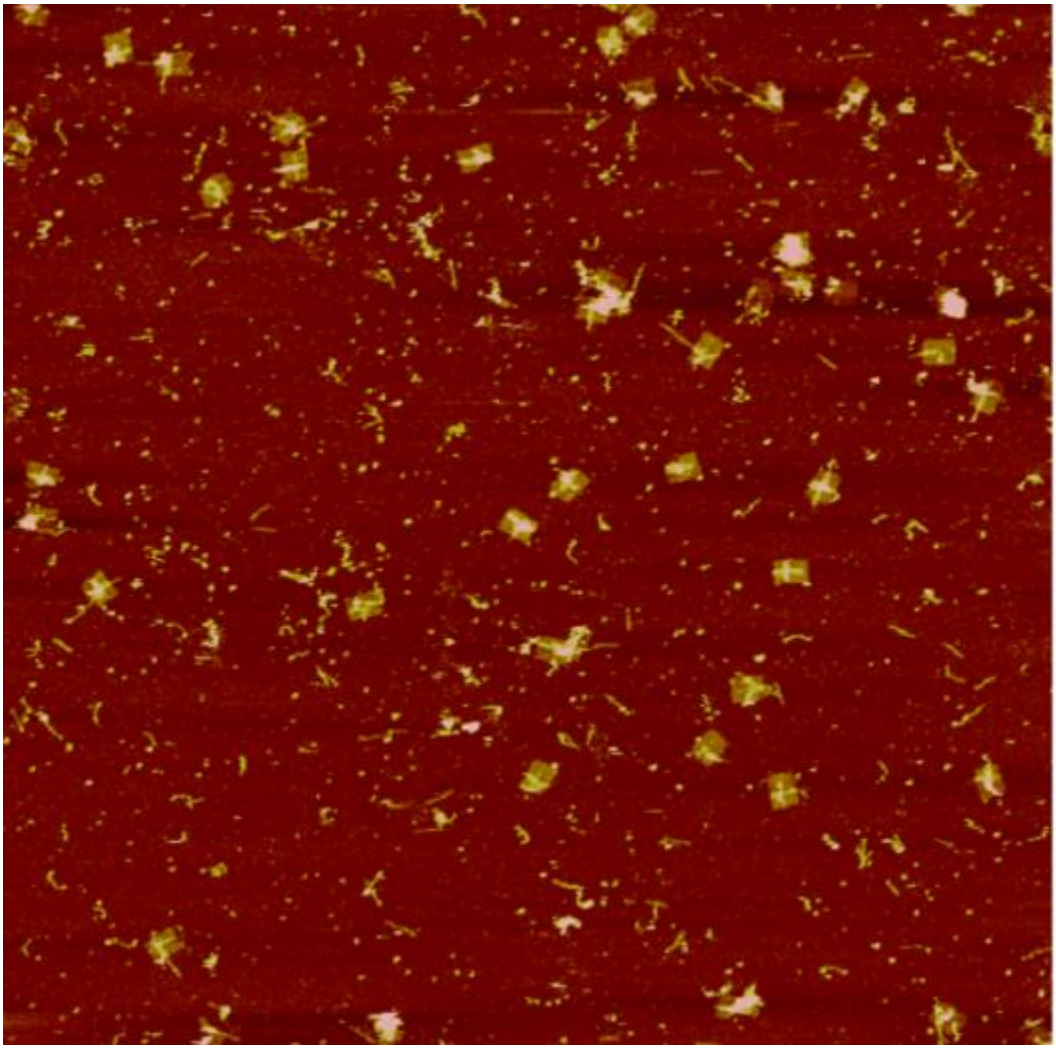


Figure S4. AFM images of two SWNTs (150 nm long) assembled on rectangular DNA origami. (3um×3um)



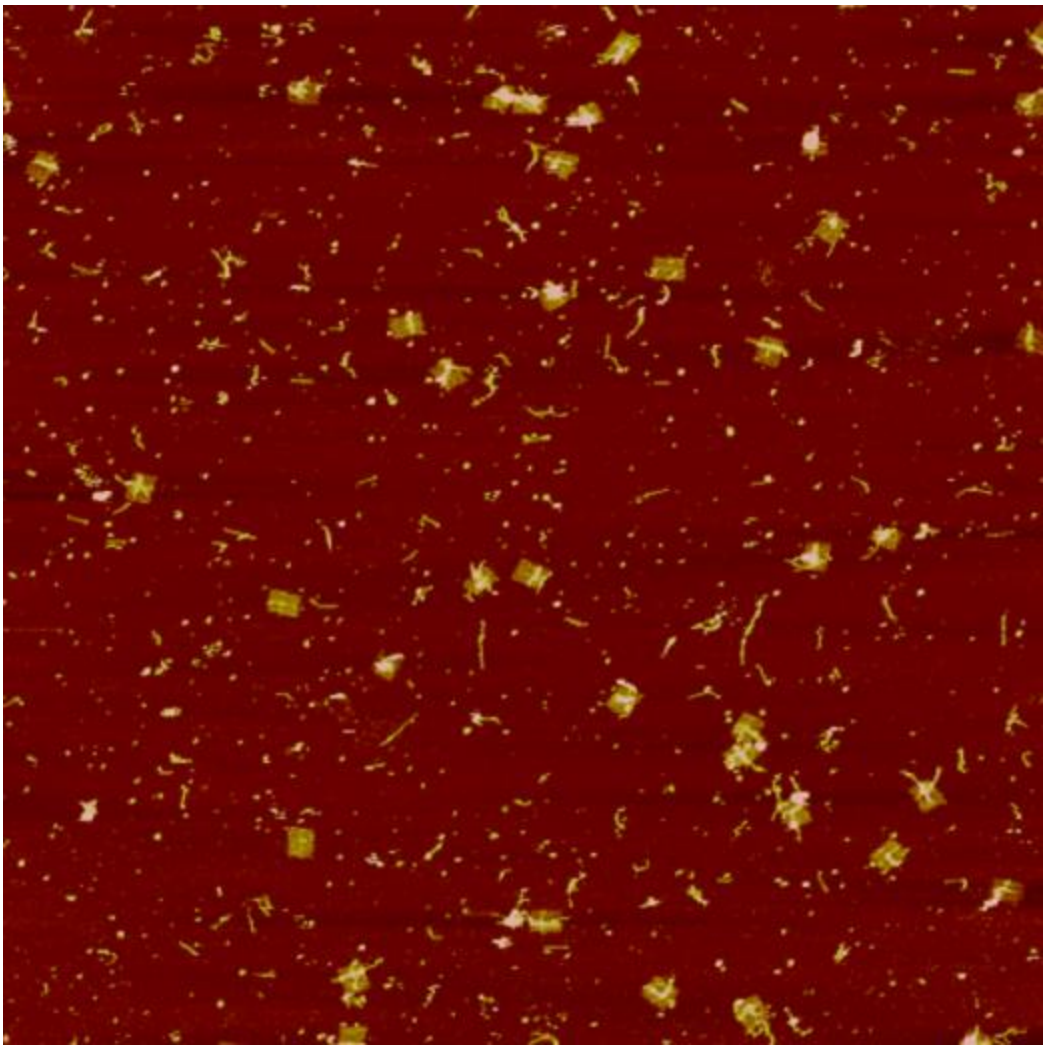


Figure S5. AFM images of two SWNTs (200 nm long) assembled on rectangular DNA origami. (5um×5um)

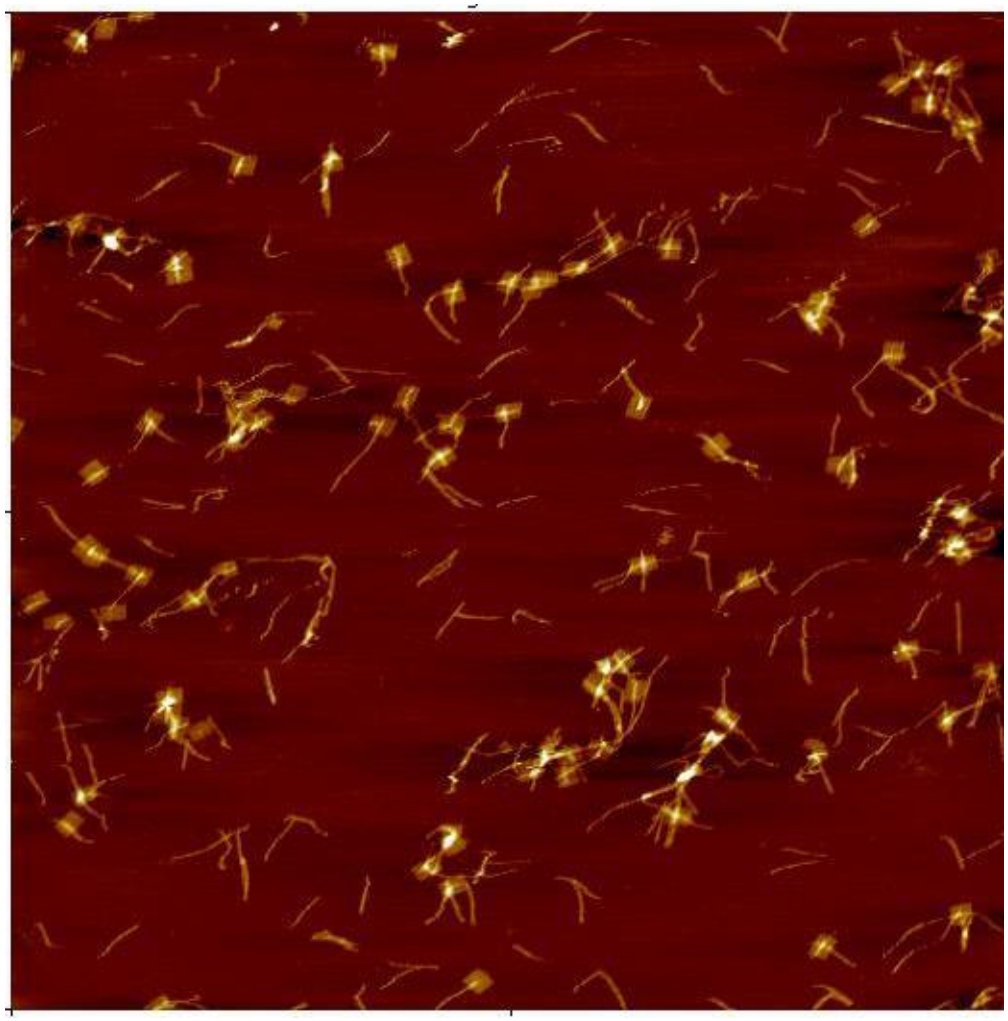


Figure S6. AFM images of two SWNTs (350 nm long) assembled on rectangular DNA origami. (5um×5um)

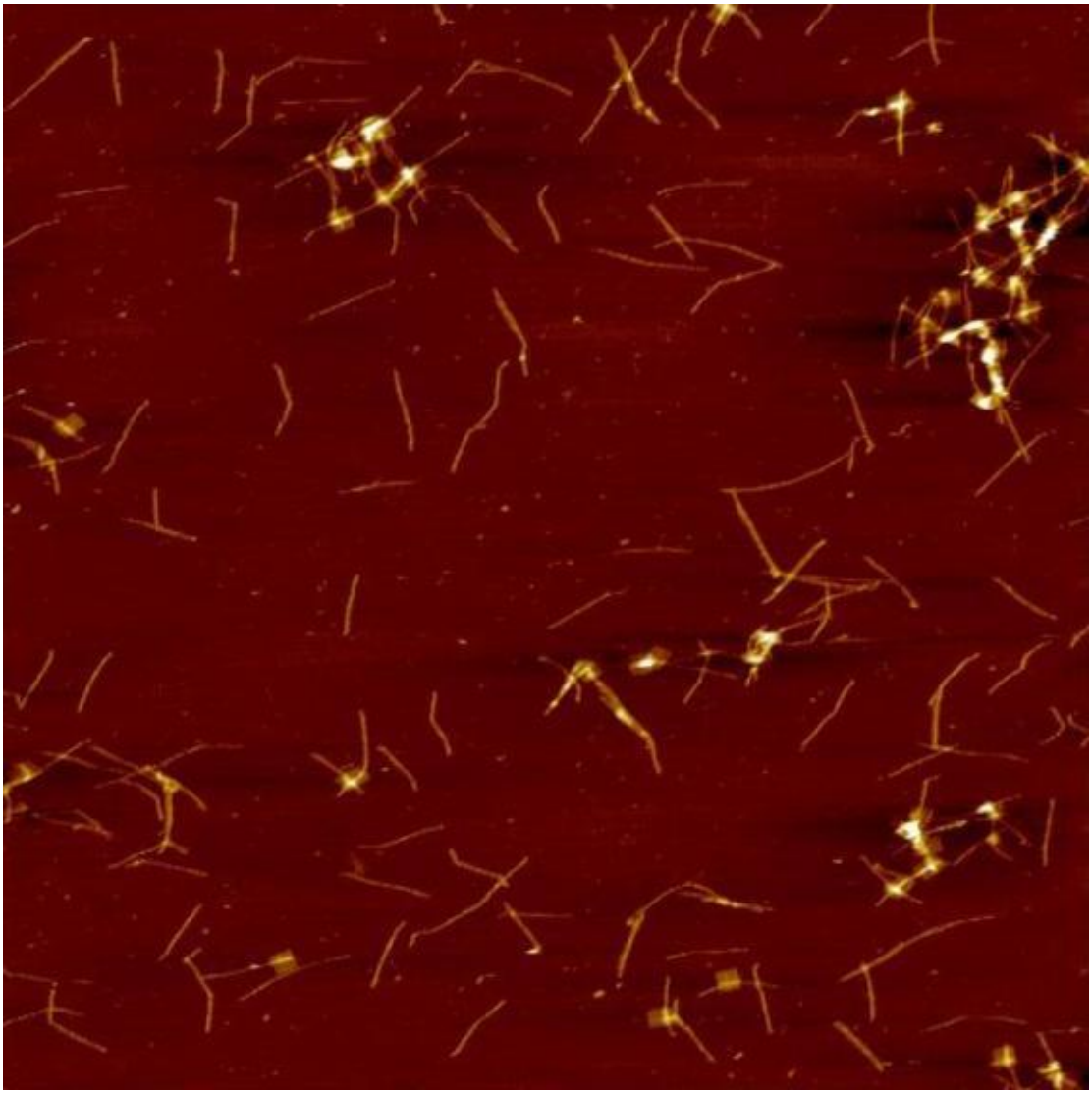


Figure S7. AFM images of two SWNTs (450 nm long) assembled on rectangular DNA origami. (5um×5um)

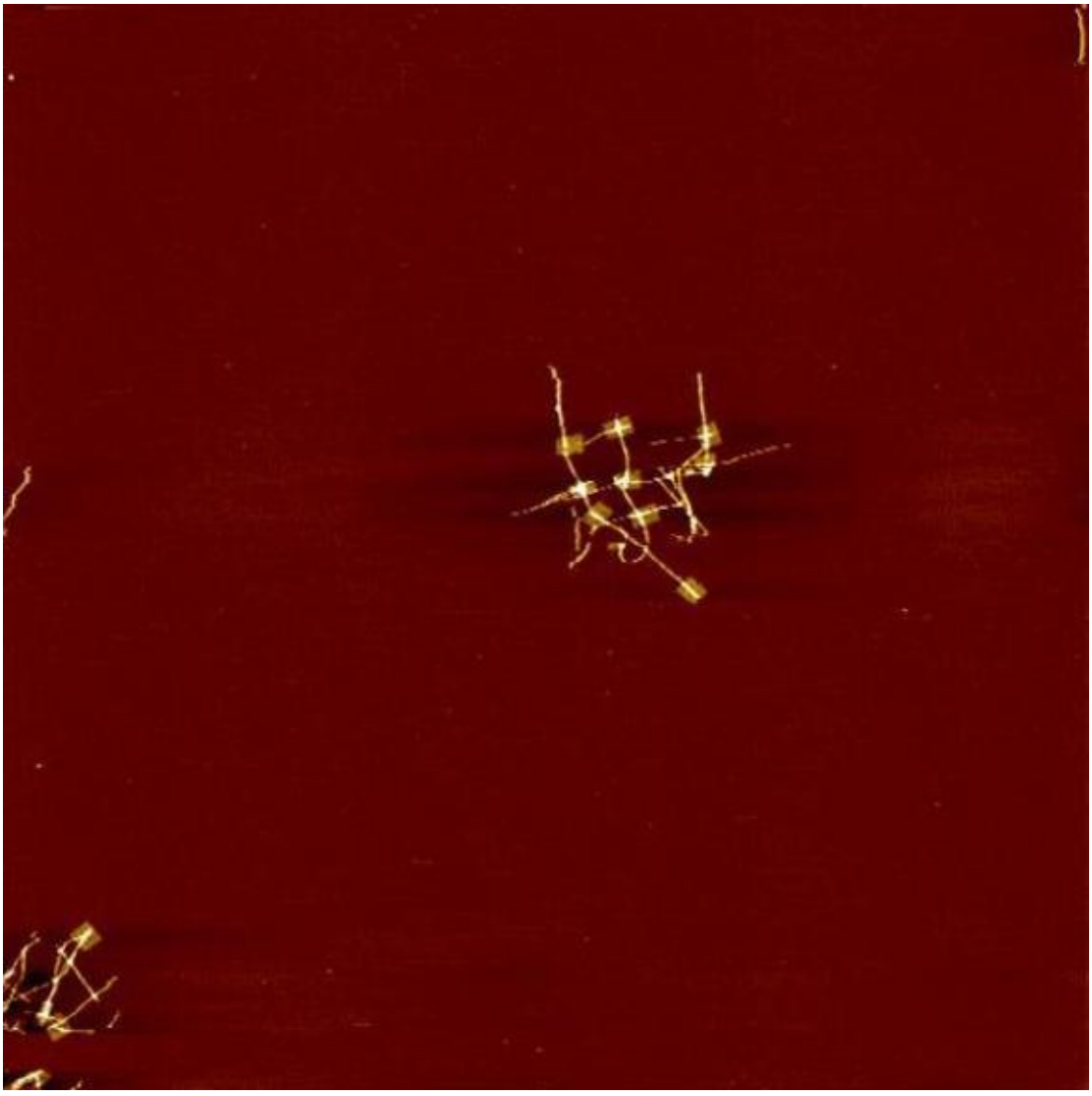
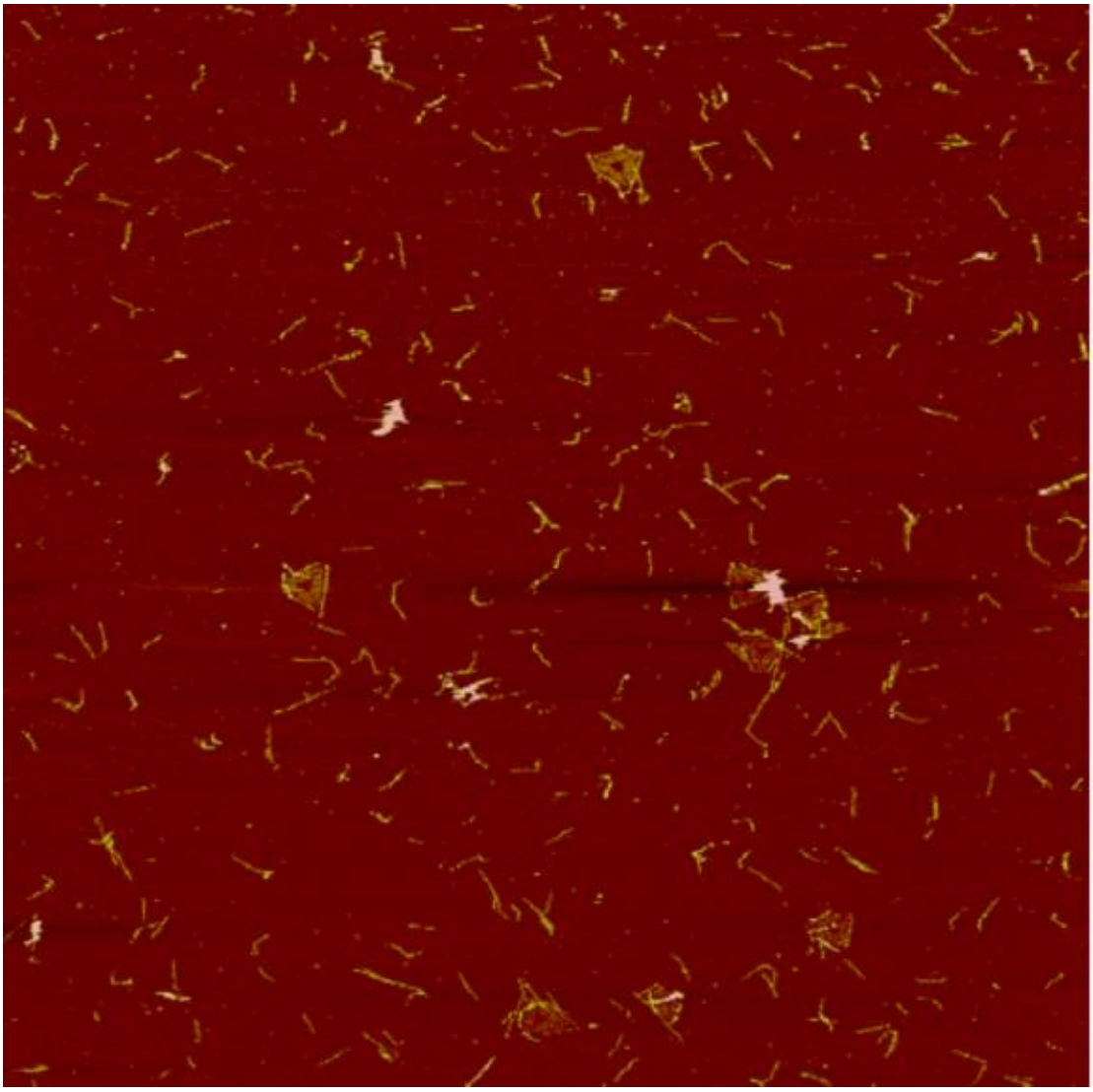


Figure S8. AFM images of three SWNTs assembled on triangular DNA origami.



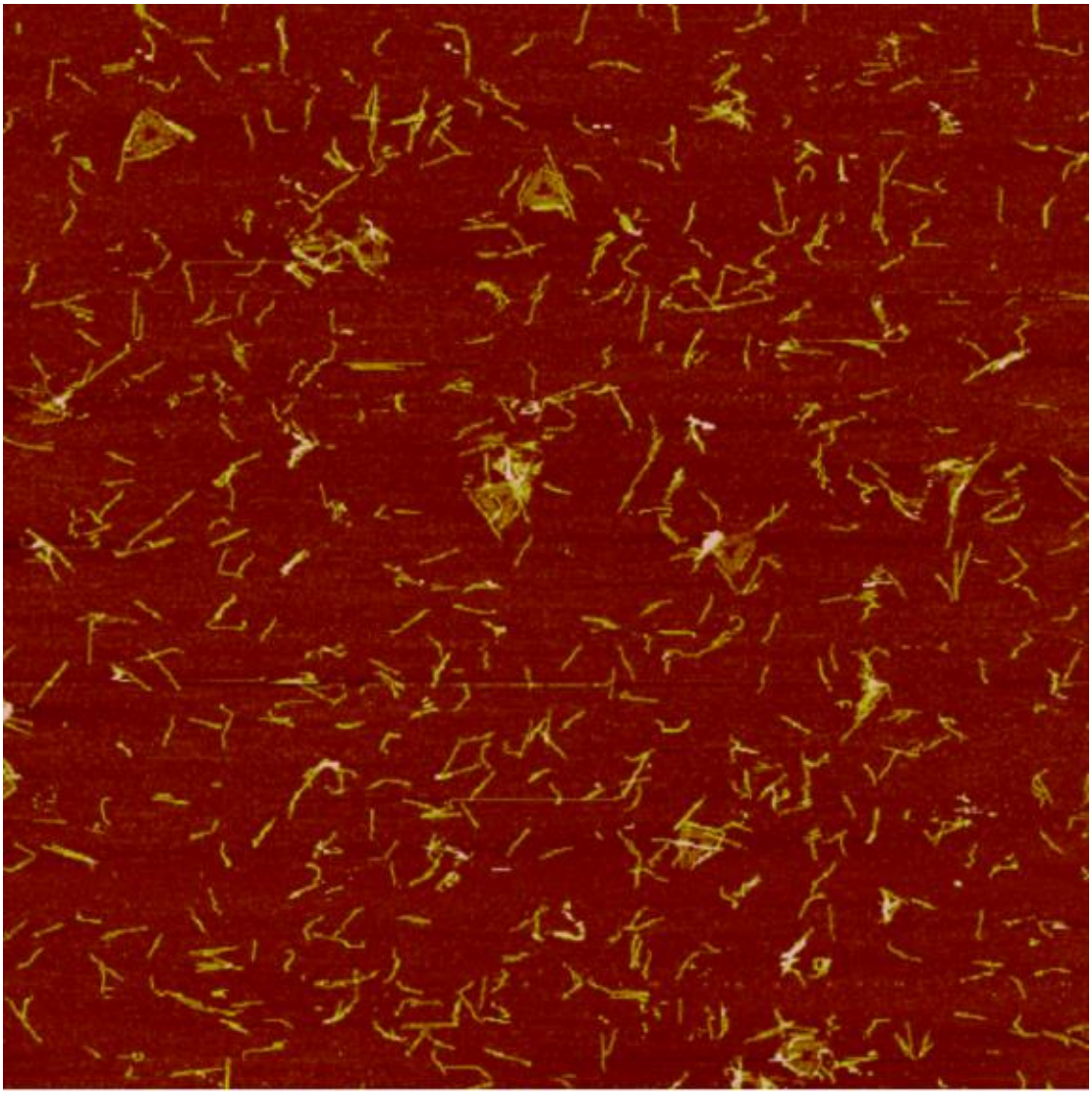
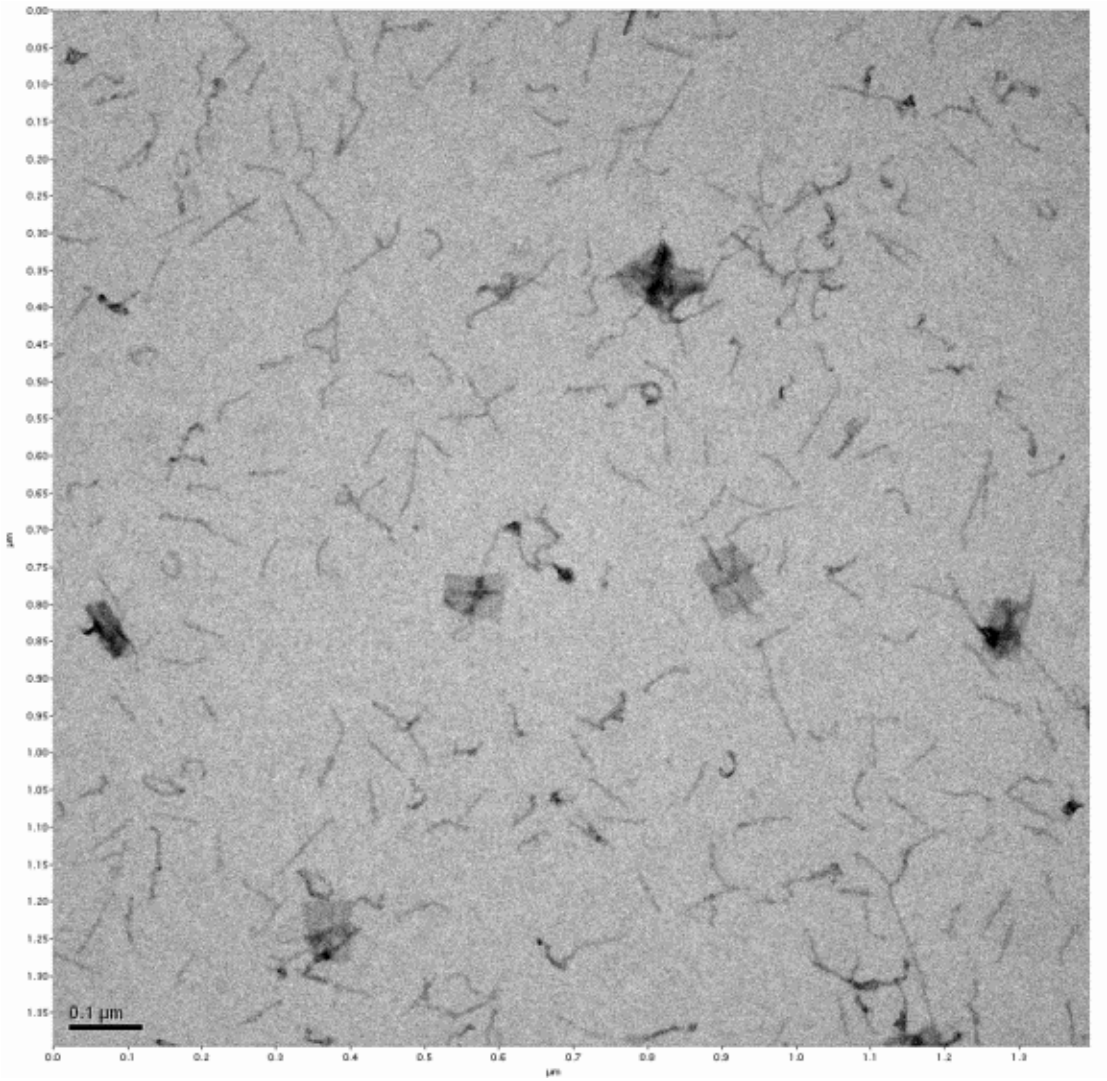


Figure S9. TEM images of two SWNTs assembled on rectangular DNA origami.



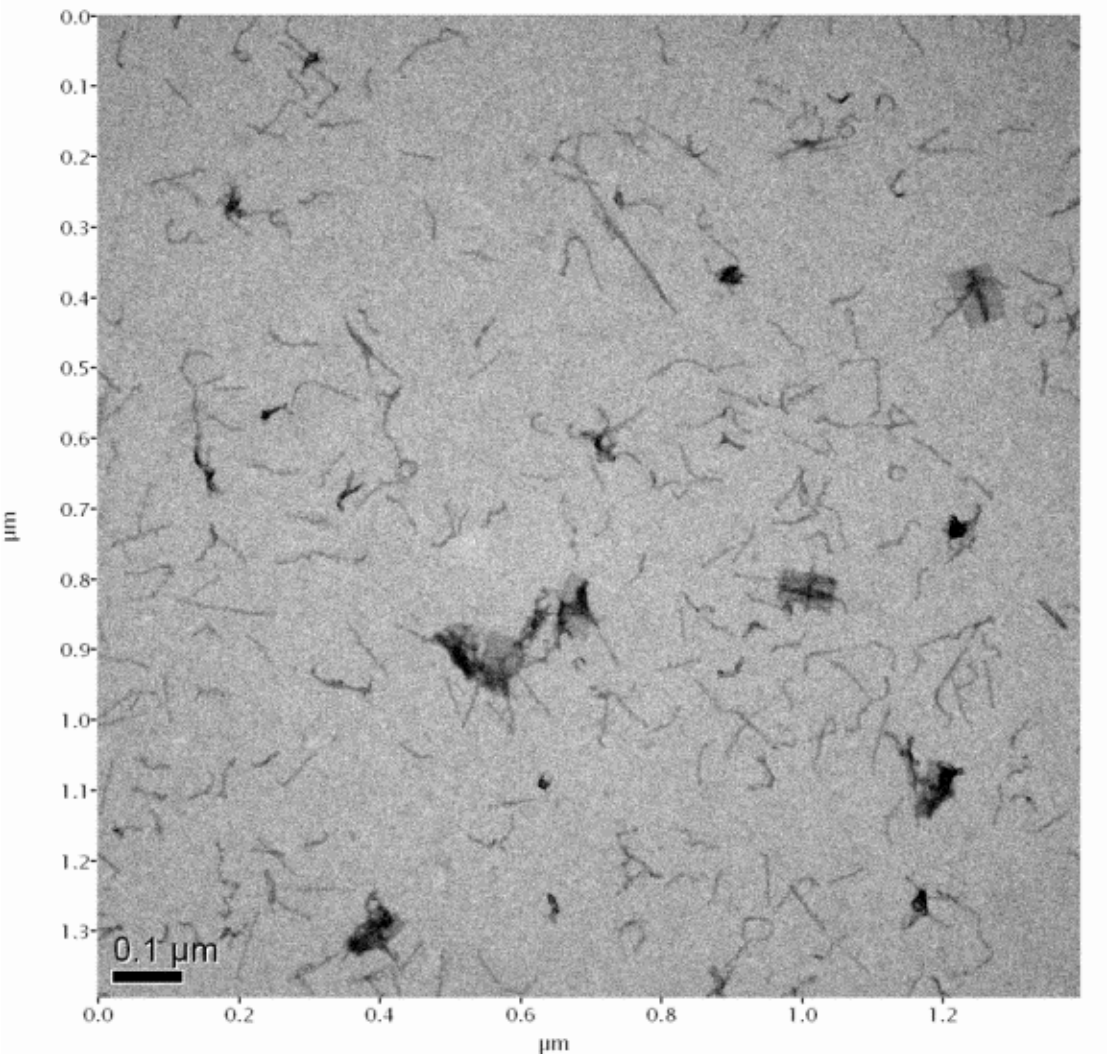
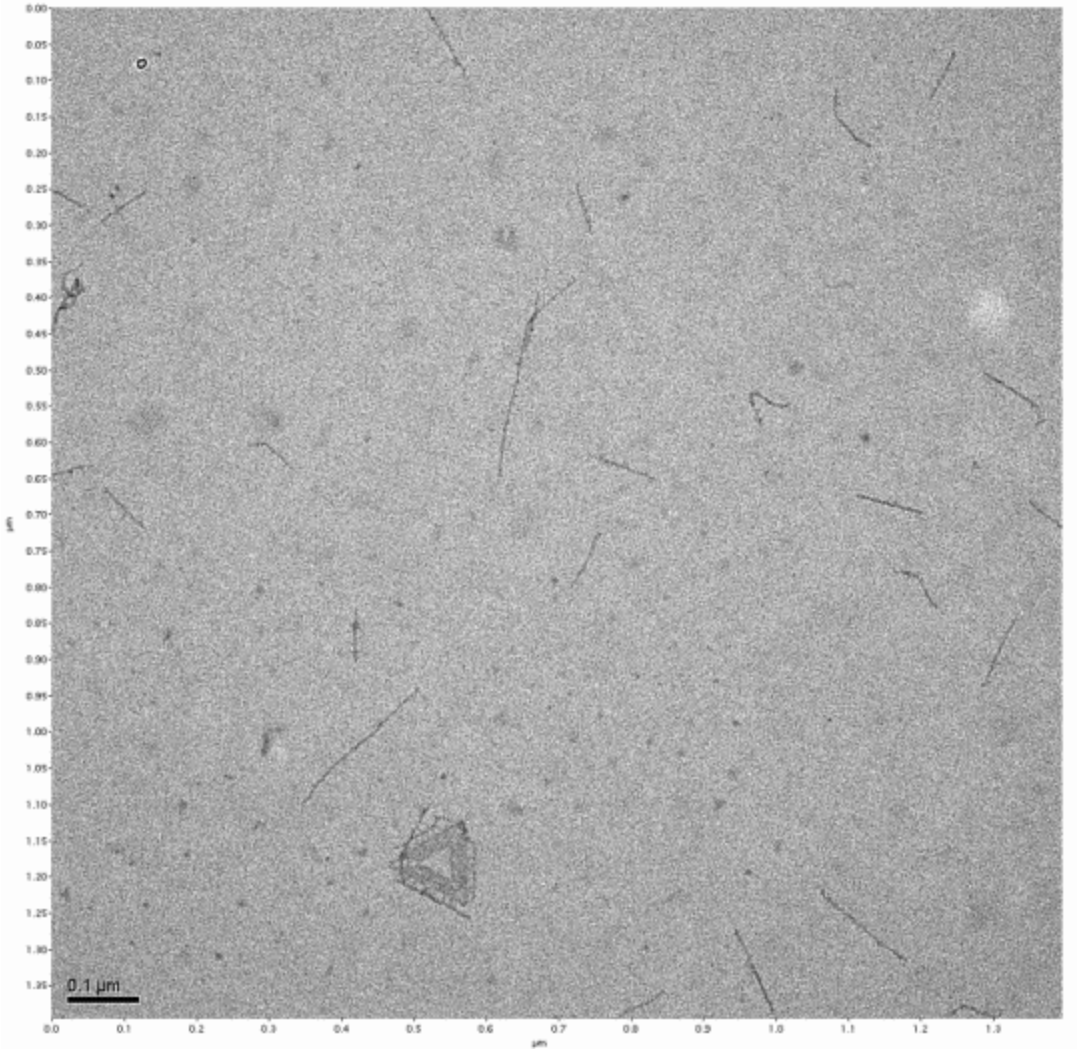
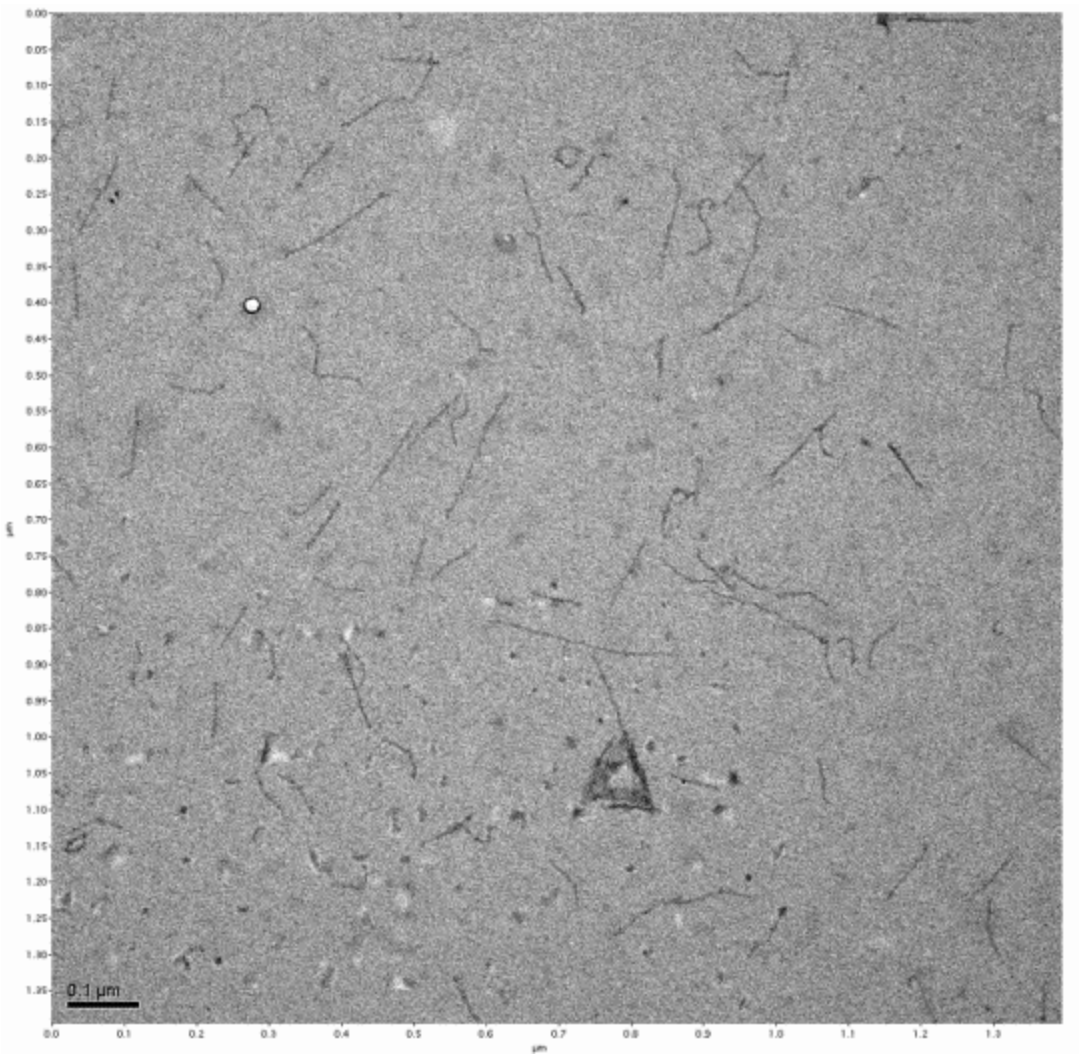

0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
1.2
1.3
µm
0.1 µm
0.0
0.2
0.4
0.6
0.8
1.0
1.2
µm

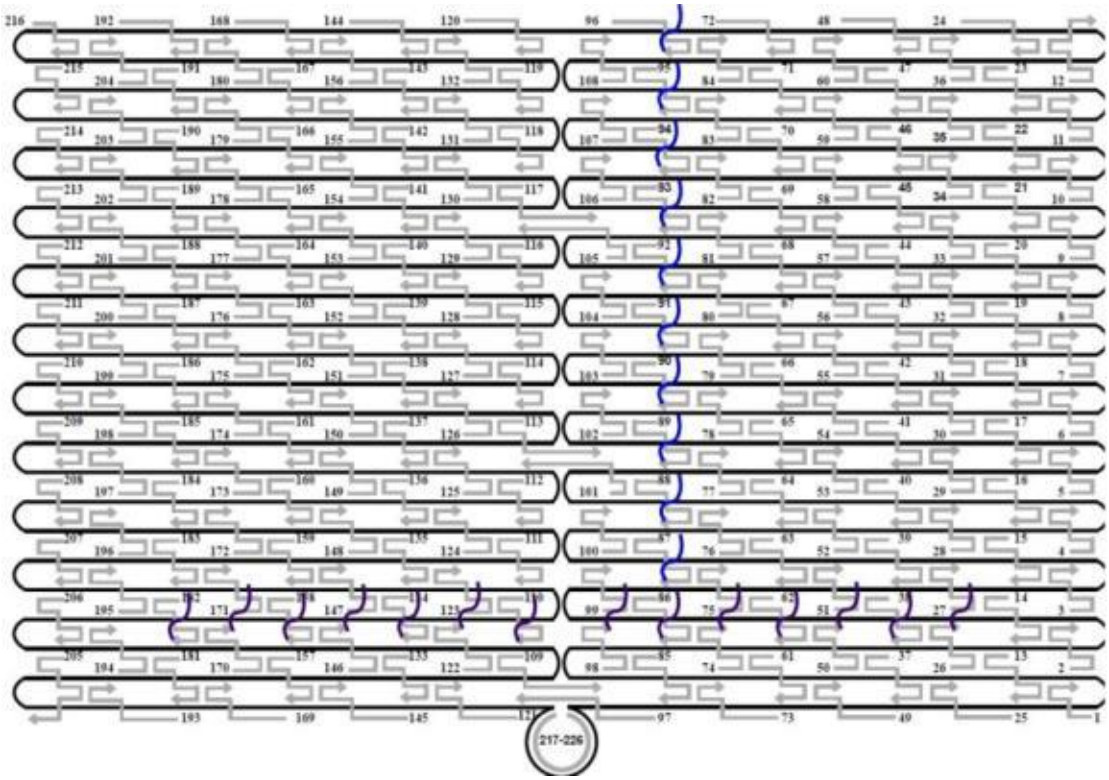
Figure S10. TEM images of three SWNTs assembled on triangular DNA origami.




0.1 µm

DNA sequences:

rectangular DNA origami



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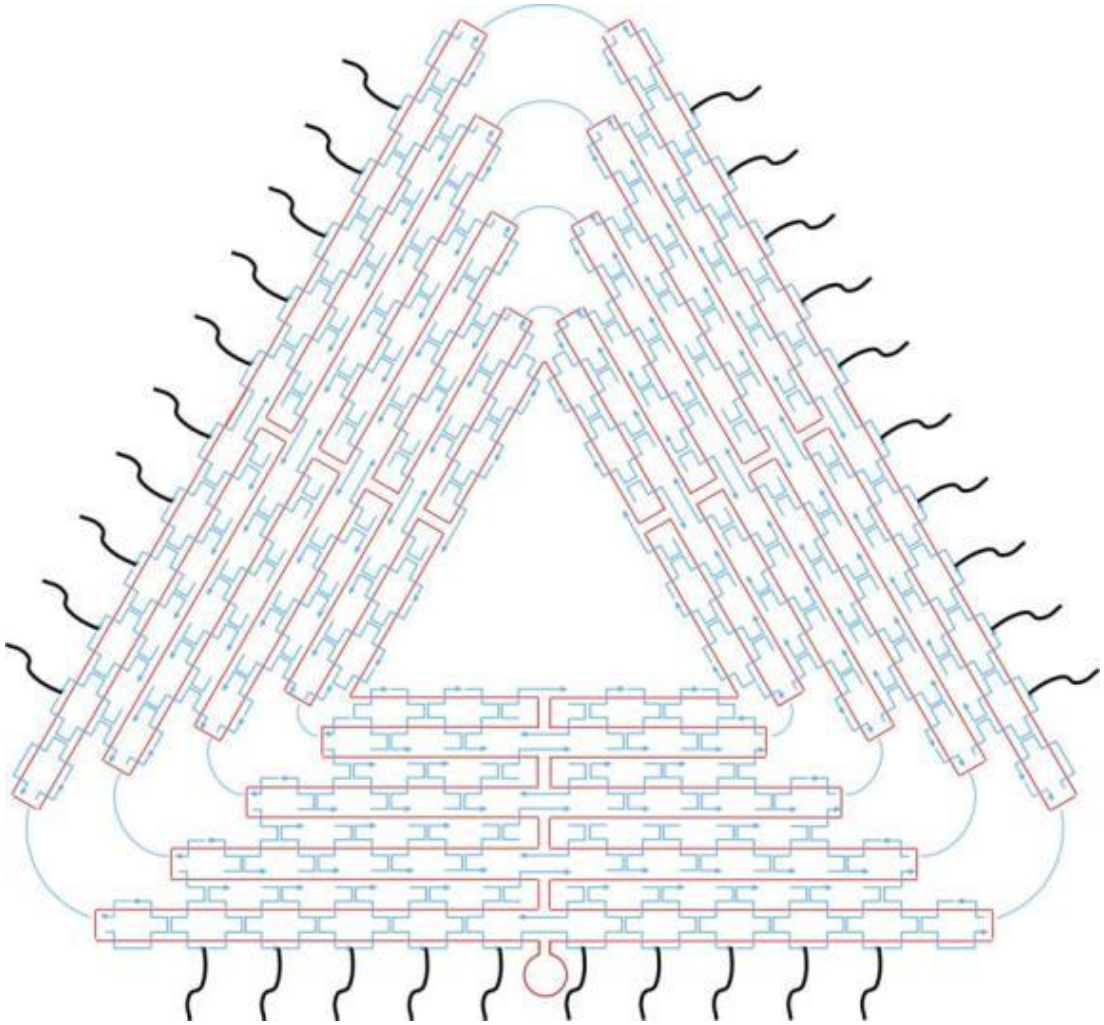
Triangular DNA Origami



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C01, TCGGGAGATATACAGTAACAGTACAAATAATT,

C02, CCTGATTAAAGGAGCGGAATTATCTCGGCCTC,

C03, GCAAATCACCTCAATCAATATCTGCAGGTCGA,

C04, CGACCAGTACATTGGCAGATTCACCTGATTGC,

C05, TGGCAATTTTTAACGTCAGATGAAAACAATAACGGATTCG,

C06, AAGGAATTACAAAGAAACCACCAGTCAGATGA,

C07, GGACATTCACCTCAAATATCAAACACAGTTGA,

C08, TTGACGAGCACGTATACTGAAATGGATTATTTAATAAAAG,

C09, CCTGATTGCTTTGAATTGCGTAGATTTTCAGGCATCAATA,

C10, TAATCCTGATTATCATTTTGCGGAGAGGAAGG,

C11, TTATCTAAAGCATCACCTTGCTGATGGCCAAC,

C12, AGAGATAGTTTGACGCTCAATCGTACGTGCTTTCCTCGTT,

C13, GATTATACACAGAAATAAAGAAATACCAAGTTACAAAATC,

C14, TAGGAGCATAAAAGTTTGAGTAACATTGTTTG,

C15, TGACCTGACAAATGAAAAATCTAAAATATCTT,

C16, AGAATCAGAGCGGGAGATGGAAATACCTACATAACCCTTC,

C17, GCGCAGAGGCGAATTAATTATTTGCACGTAAATTCTGAAT,

C18, AATGGAAGCGAACGTTATTAATTTCTAACAAC,

C19, TAATAGATCGCTGAGAGCCAGCAGAAGCGTAA,

C20, GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGA,

C21, TCAATAGATATTAAATCCTTTGCCGGTTAGAACCT,

C22, CAATATTTGCCTGCAACAGTGCCATAGAGCCG,

C23, TTAAAGGGATTTTAGATACCGCCAGCCATTGCGGCACAGA,

C24, ACAATTCGACAACTCGTAATACAT,

C25, TTGAGGATGGTCAGTATTAACACCTTGAATGG,

C26, CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCA,

C27, CGCGAACTAAAACAGAGGTGAGGCTTAGAAGTATT,

C28, GAATCCTGAGAAGTGTATCGGCCTTGCTGGTACTTTAATG,

C29, ACCACCAGCAGAAGATGATAGCCC,

C30, TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAG,

C31, GCCACCGAGTAAAAGAACATCACTTGCCTGAGCGCCATTAAAA,

C32, TCTTTGATTAGTAATAGTCTGTCCATCACGCAAATTAACCGTT,

C33, CGCGTCTGATAGGAACGCCATCAACTTTTACA,

C34, AGGAAGATGGGGACGACGACAGTAATCATATT,

C35, CTCTAGAGCAAGCTTGCATGCCTGGTCAGTTG,

C36, CCTTCACCGTGAGACGGGCAACAGCAGTCACA,

C37, CGAGAAAGGAAGGGAAGCGTACTATGGTTGCT,

C38, GCTCATTTTTTAACCAGCCTTCCTGTAGCCAGGCATCTGC,

C39, CAGTTTGACGCACTCCAGCCAGCTAAACGACG,

C40, GCCAGTGCGATCCCCGGGTACCGAGTTTTTCT,

C41, TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGG,

C42, GTAACCGTCTTTCATCAACATTAAAATTTTTGTTAAATCA,

C43, ACGTTGTATTCCGGCACCGCTTCTGGCGCATC,

C44, CCAGGGTGGCTCGAATTCGTAATCCAGTCACG,

C45, TAGAGCTTGACGGGGAGTTGCAGCAAGCGGTCATTGGGCG,

C46, GTTAAAATTCGCATTAATGTGAGCGAGTAACACACGTTGG,

C47, TGTAGATGGGTGCCGGAAACCAGGAACGCCAG,

C48, GGTTTTCCATGGTCATAGCTGTTTGAGAGGCG,

C49, GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATT,

C50, GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTT,

C51, AGTTGGGTCAAAGCGCCATTCGCCCCGTAATG,

C52, CGCGCGGGCCTGTGTGAAATTGTTGGCGATTA,

C53, CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAA,

C54, CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATG,

C55, TGCTGCAAATCCGCTCACAATTCCCAGCTGCA,

C56, TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCA,

C57, TGGCGAAATGTTGGGAAGGGCGAT,

C58, TGTCGTGCACACAACATACGAGCCACGCCAGC,

C59, CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACC,

C60, TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCT,

C61, TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAAT,

C62, GCGCTCACAAGCCTGGGGTGCCTA,

C63, CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTT,

C64, AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGG,

C65, ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCC,

Link-A1C, TTAATTAATTT TTT ACCATATCAAA,

Link-A2C, TTAATTTCATC TT AGACTTTACAA,

Link-A3C, CTGTCCAGACG T ATACCGAACGA,

Link-A4C, TCAAGATTAGTGTAGCAATACT,

Link-B1A, TGTAGCATTCC TTT TATAAACAGTT,

Link-B2A, TTTAATTGTAT TT CCACCAGAGCC,

Link-B3A, ACTACGAAGGC T TAGCACCATTA,

Link-B4A, ATAAGGCTTGC AACAAAGTTAC,

Link-C1B, GTGGGAACAAA TTT CTATTTTTGAG,

Link-C2B, CGGTGCGGGCC TT CCAAAAACATT,

Link-C3B, ATGAGTGAGCT T TTAAATATGCA,

Link-C4B, ACTATTAAAGA GGATAGCGTCC,

Loop, GCGCTTAATGCGCCGCTACAGGGC,

CNTA64,ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCATTTT
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CNTA61,GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTTTTTTTTTT
TTTTTTTTTTTT

CNTA56,ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTATTTTTTT
TTTTTTTTTTTT

CNTA49,AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTTTTTTTTTT
TTTTTTTTTTTT

CNTA41,TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAGTTTTTTTT
TTTTTTTTTTTT

CNTA37,AGAGAATAACATAAAAACAGGGAAGCGCATTATTTTTTTTTTTTTTT
TTTTT

CNTA12,CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAATTTTTT
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CNTA20,TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGATTTTTTT
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CNTA26,CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATATTTTTTT
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CNTA30,GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGCTTTTTT
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CNTB64,ACCAACCTAAAAAATCAACGTAACAAATAAATTGGGCTTGAGATTT
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CNTB61,AAAACACTTAATCTTGACAAGAACTTAATCATTGTGAATTTTTTTTTT
TTTTTTTTTTTT

CNTB56,CCAAGCGCAGGCGCATAGGCTGGCAGAACTGGCTCATTATTTTTTTT
TTTTTTTTTTTTT

CNTB49,TATCATCGTTGAAAGAGGACAGATGGAAGAAAAATCTACGTTTTTTT
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CNTB41,CGACCTGCGGTCAATCATAAGGGAACGGAACAACATTATTTTTTTTT
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CNTB37,ACAGGTAGAAAGATTCATCAGTTGAGATTTAGTTTTTTTTTTTTTTTT
TTTT

CNTB12,AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAATTTTTTT
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CNTB20,TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGCTTTTTTTT
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CNTB26,CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGACTTTTTTT
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CNTB30,TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCATTTTTTTT
TTTTTTTTTTTT

CNTC64,AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGGTTTT
TTTTTTTTTTTTTTTT

CNTC61,TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAATTTTTTTT
TTTTTTTTTTTTT

CNTC56,TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCATTTTTTT
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CNTC49,GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATTTTTTTTTT
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CNTC41,TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGGTTTTTTT
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CNTC37,CGAGAAAGGAAGGGAAGCGTACTATGGTTGCTTTTTTTTTTTTTTTTT
TTTT

CNTC12,AGAGATAGTTTGACGCTCAATCGTACGTGCTTTCCTCGTTTTTTTTTT
TTTTTTTTTTT

CNTC20,GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGATTTTTT
TTTTTTTTTTTTT

CNTC26,CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCATTTTTTT
TTTTTTTTTTTT

CNTC30,TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAGTTTTTTT
TTTTTTTTTTTT

APPENDIX E

SUPPLEMENTAL INFORMATION FOR CHAPTER 6

Supplemental Information

DNA Origami Cage Trapping Enzyme: Protection and Boosting Enzyme Activity

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Preparation of Enzyme DNA conjugates

GOx, HRP, G6pD, LDH, MDH are conjugated with SPDP with 1:5, 1:20, 1:3, 1:5, 1:5 ratio respectively. And then SPDP conjugated enzyme mixed with Tcept treated thiolated DNA with 1:10 ratio for 1h. Amicon 30kD filter was used to purify enzyme DNA mixture, with 10×HEPES (1.5M NaCl) and PBS buffer.

Preparation of Enzyme DNA origami complex

DNA Origami was annealed with M13 and 10 times helpers from 80°C to 4°C for 37h, and then enzyme DNA conjugates were mixed with DNA half origami with 1:15 ratio and annealed from 37°C to 4°C for 2h. DNA linkers were added to connect two half cage origami together, incubating at room temperature for 3h.

Enzyme assay

96-well-plate reader was used to measure enzyme activity through the absorbance change. HRP and GOx enzyme activity was monitored with 410nm absorbance. G6pD, LDH and MDH enzyme activity was monitored with 340nm absorbance.

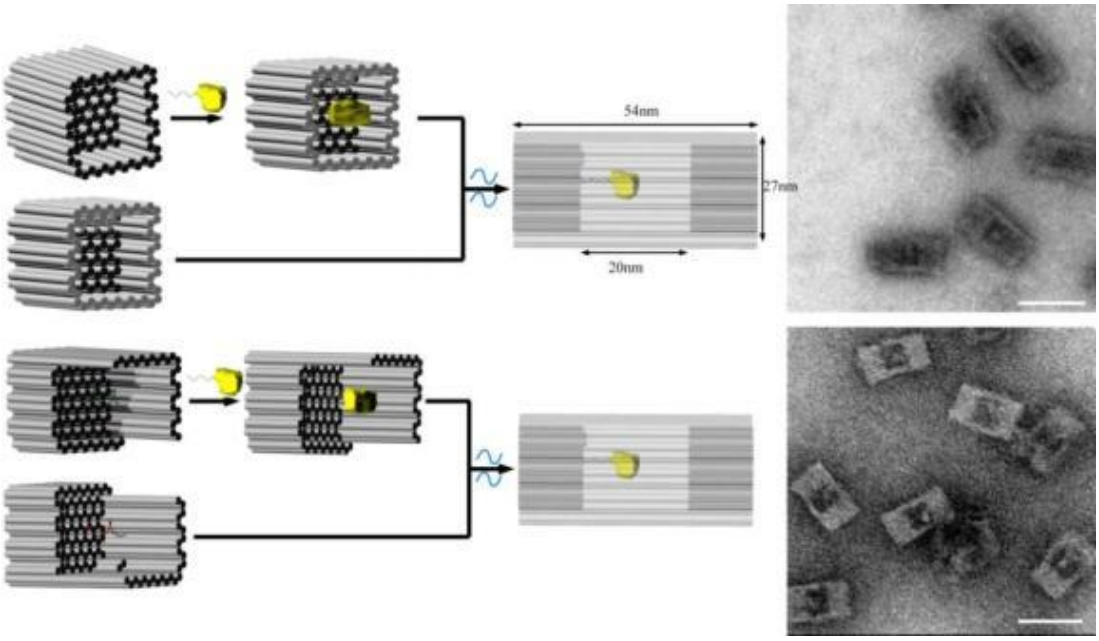


Figure S1. Two different designs for cage structure with different encapsulation yield, assembled with GOx.

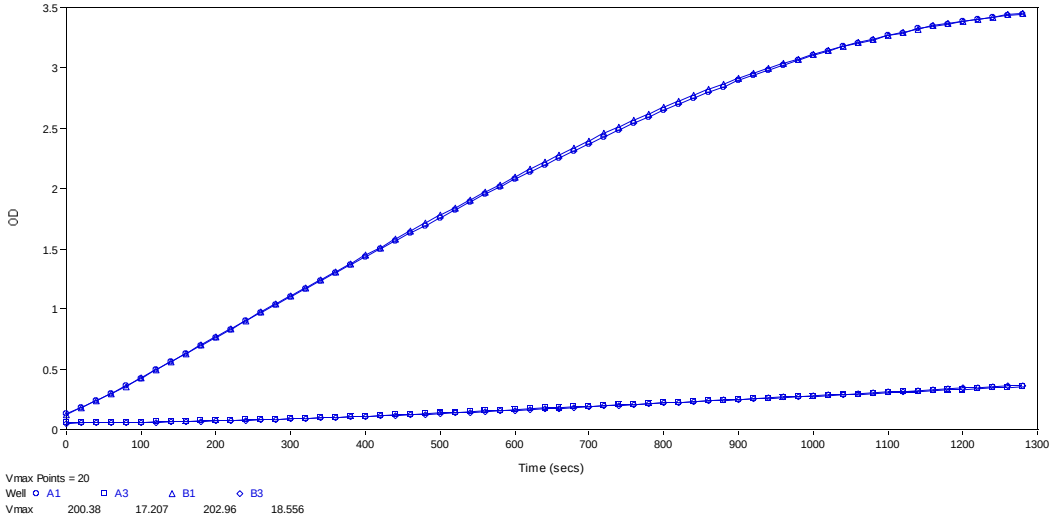


Figure S2. Raw activity for free HRP GOx cascade enzyme and enzymes inside DNA cage.

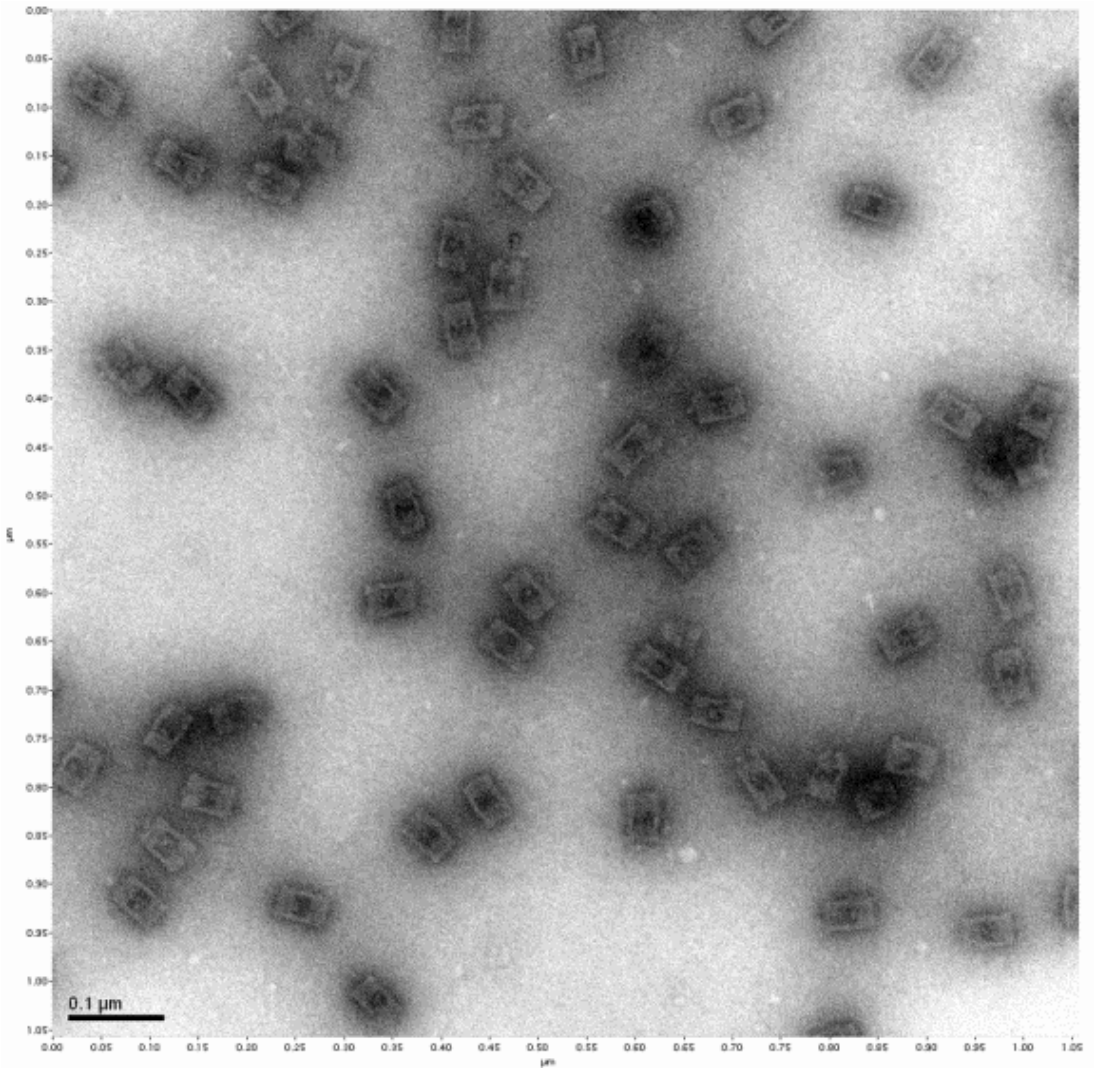


Figure S3. TEM image for HRP GOx cascade enzyme inside DNA cage.

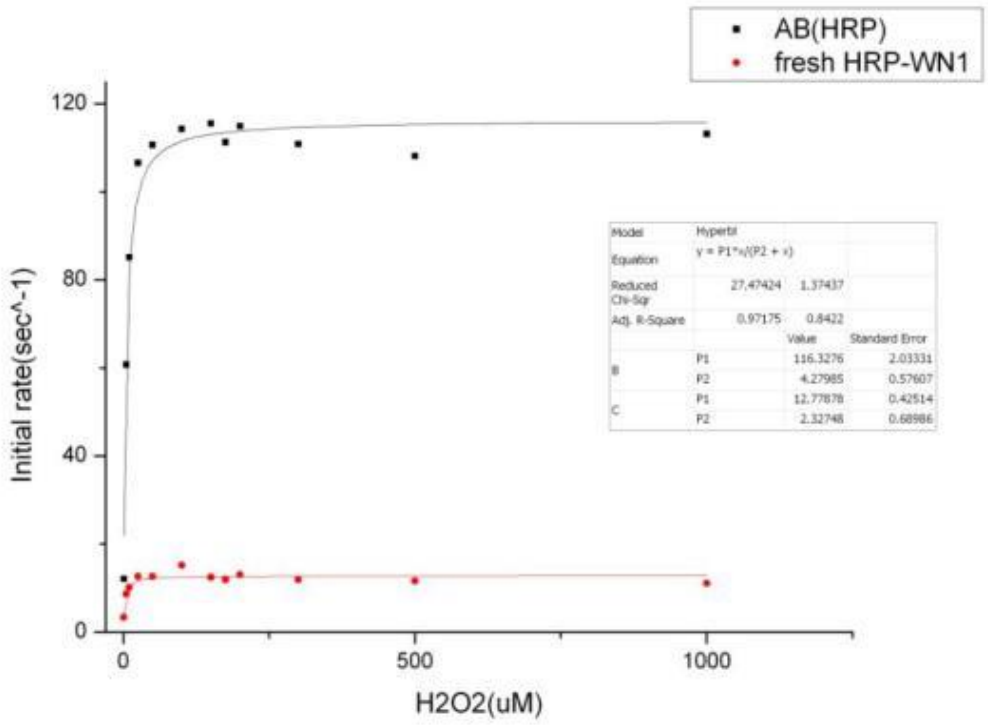


Figure S4. HRP enzyme inside cage Michaelis-Menten curve (against H_2O_2), compared with fresh free HRP enzyme.

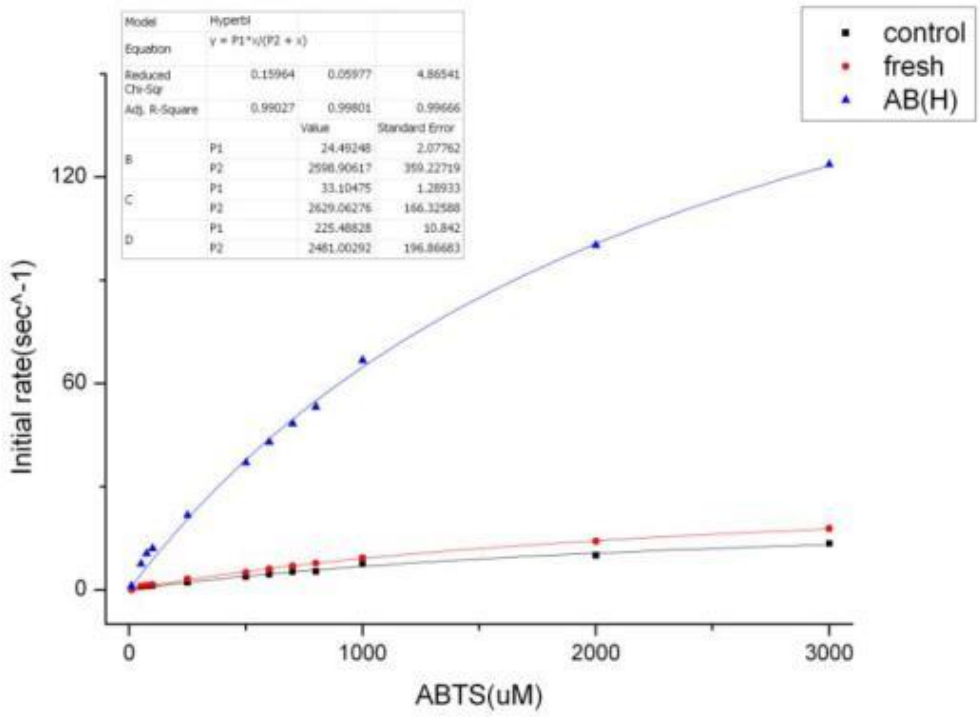


Figure S5. HRP enzyme inside cage Michaelis-Menten curve (against ABTS), compared with fresh free HRP enzyme.

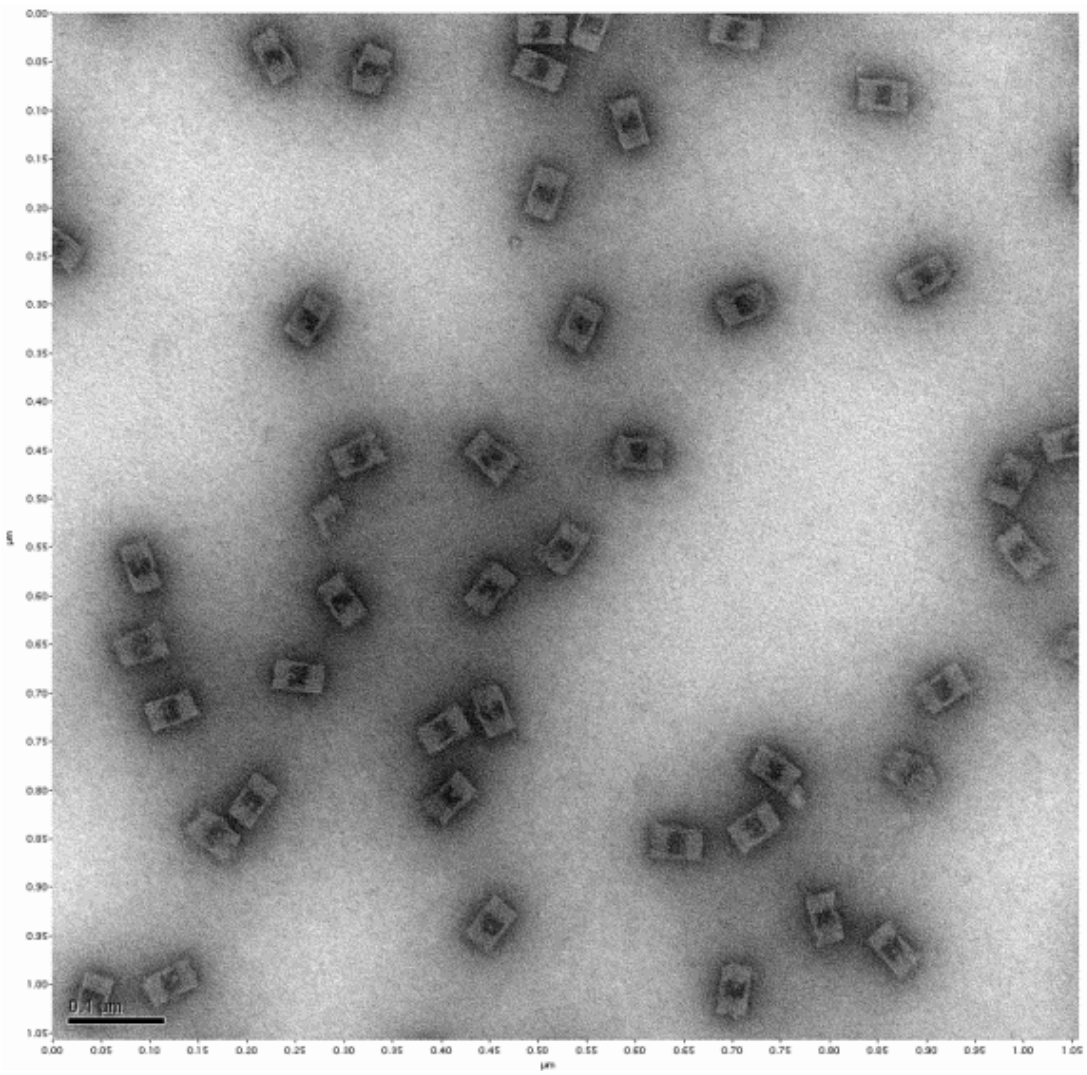


Figure S6. TEM image for purified DNA cage with HRP enzyme inside.

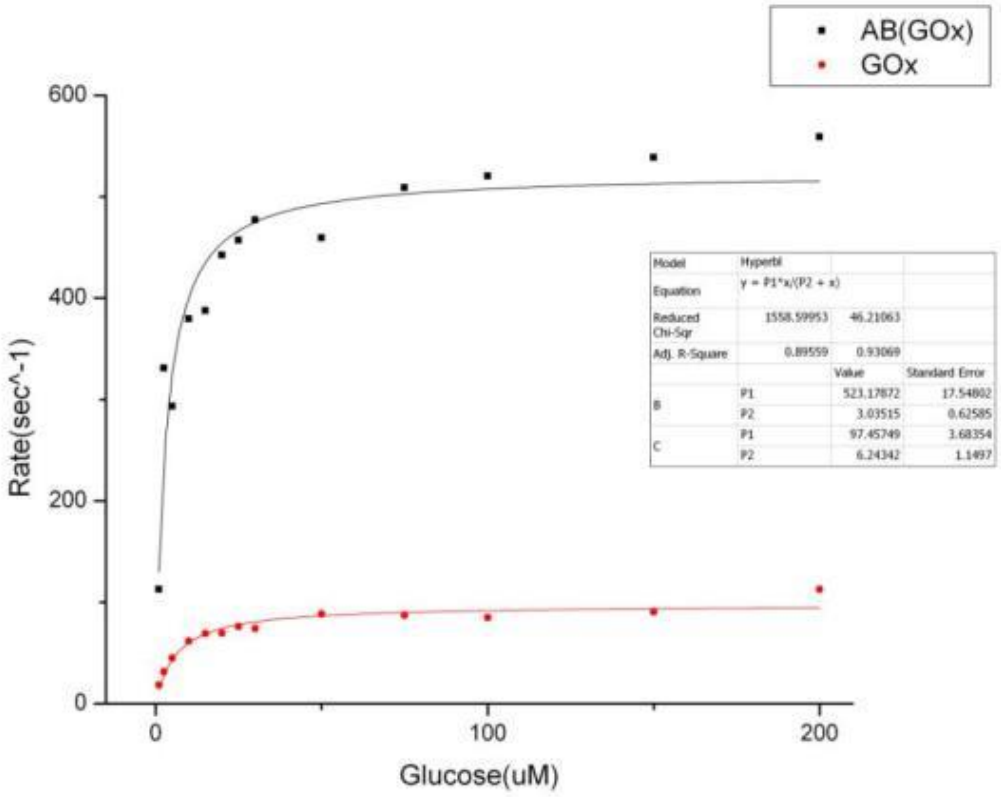

AB(GOx)
GOx
600
400
200
0
Rate(sec^-1)
0
100
200
Glucose(uM)
Model Hyperbl
Equation y = P1*x/(P2 + x)
Reduced Chi-Sqr 1558.59953 46.21063
Adj. R-Square 0.89559 0.93069
Value Standard Error
B P1 523.17872 17.54802
P2 3.03515 0.62585
C P1 97.45749 3.68354
P2 6.24342 1.1497

Figure S7. GOx enzyme inside cage Michaelis-Menten curve (against Glucose), compared with fresh free GOx enzyme.

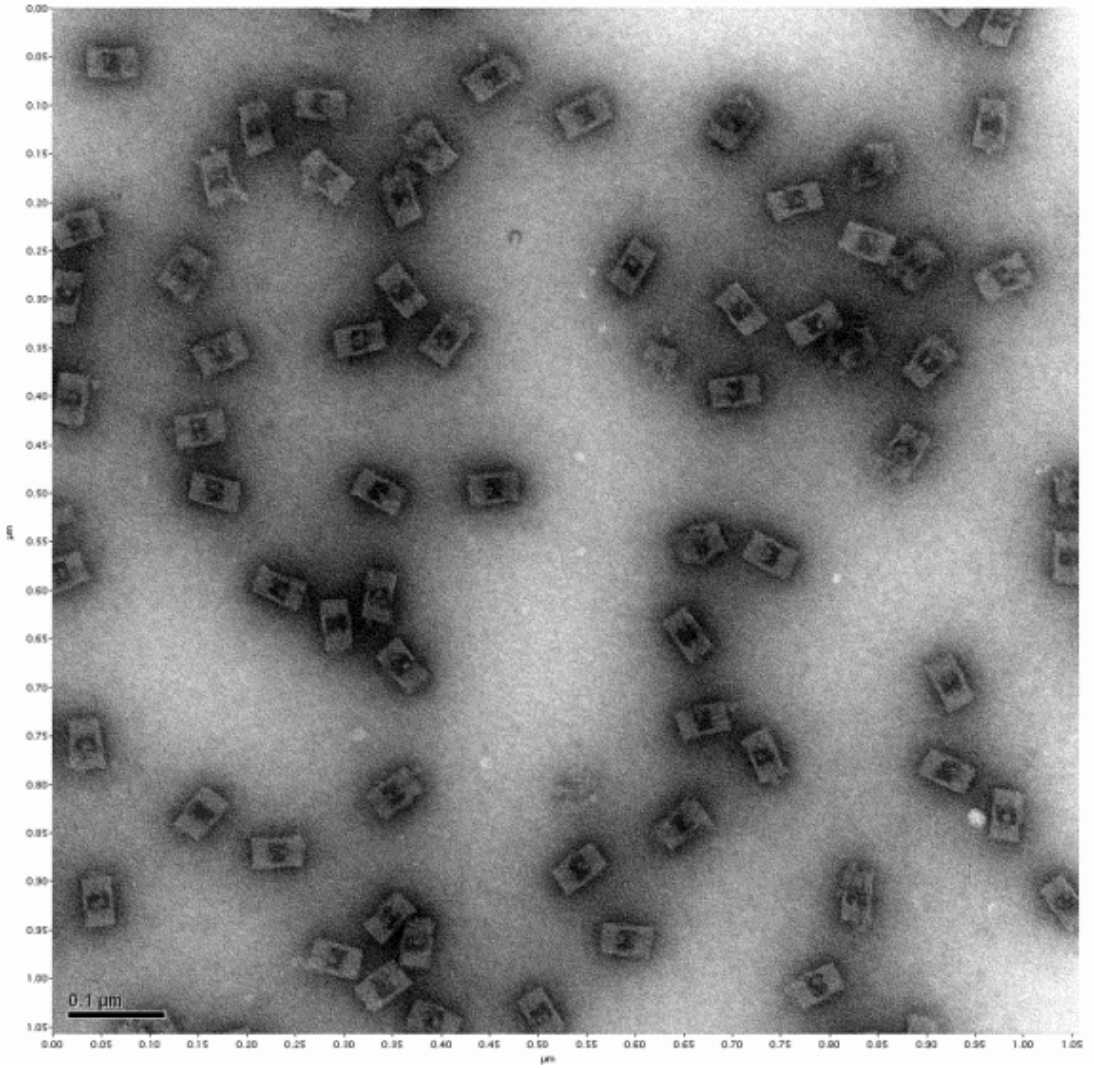


Figure S8. TEM image for purified DNA cage with GOx enzyme inside.

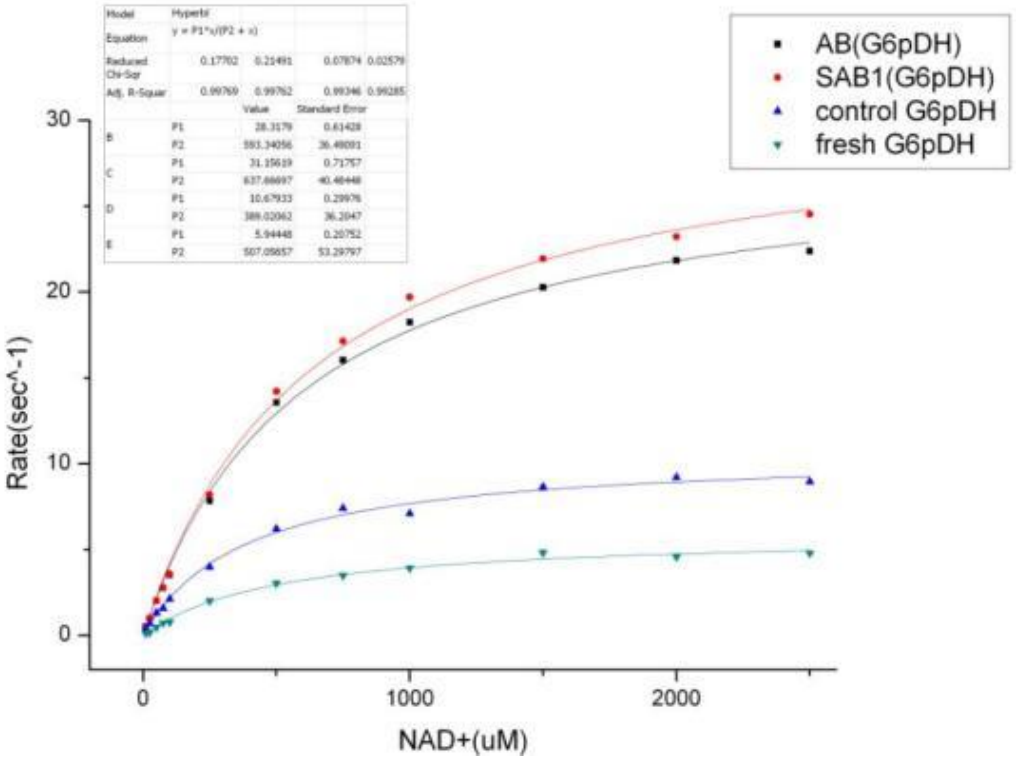


Figure S9. G6pD enzyme inside cage Michaelis-Menten curve (against NAD+), compared with fresh free G6pD enzyme.

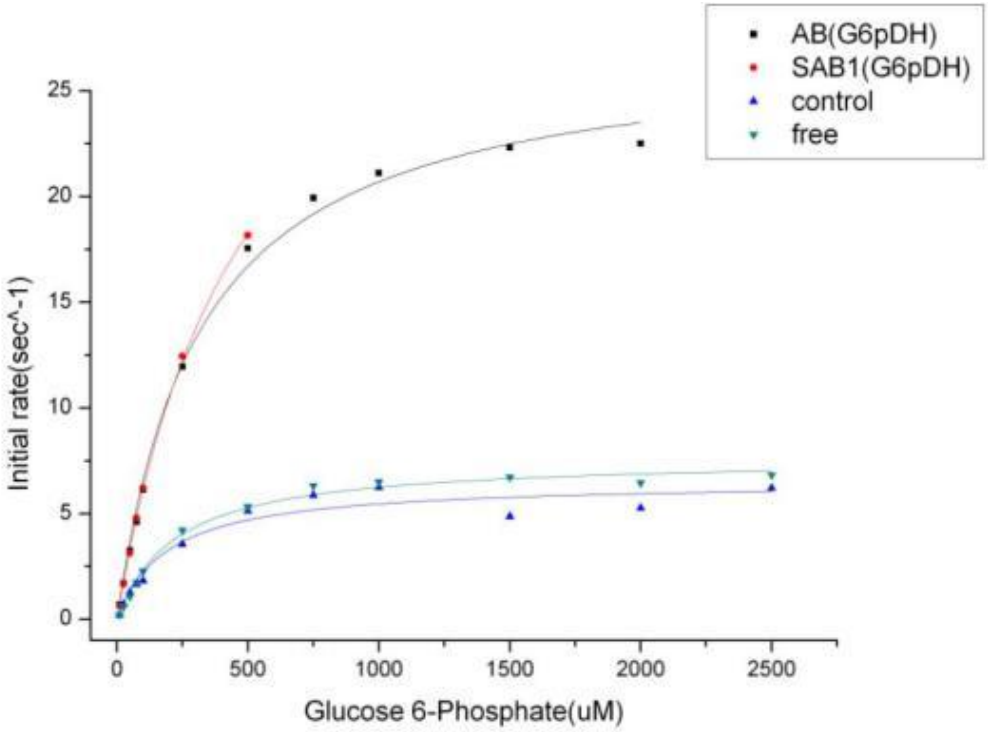


Figure S10. G6pD enzyme inside cage Michaelis-Menten curve (against glucose 6-phosphate), compared with fresh free G6pD enzyme.

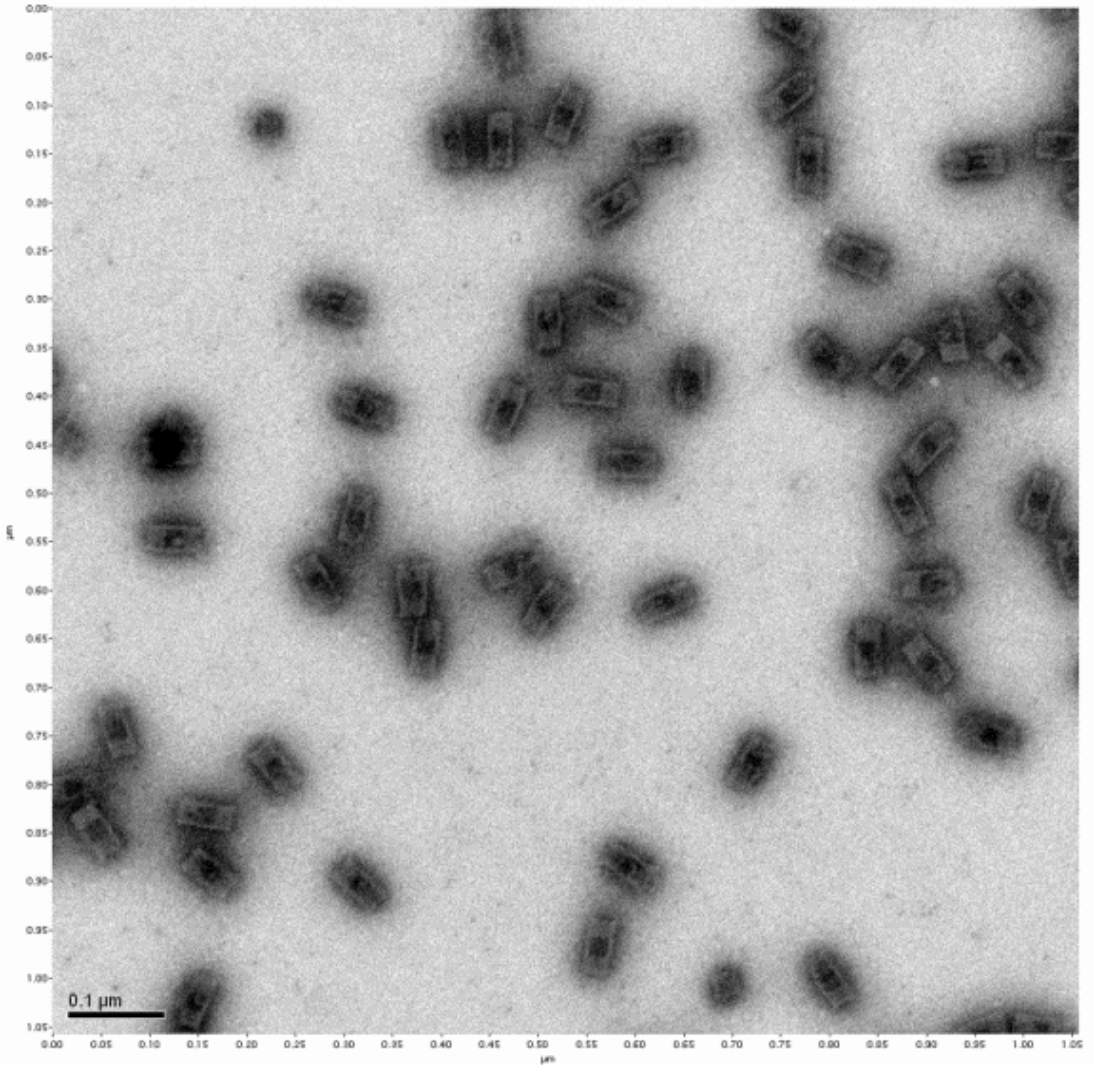
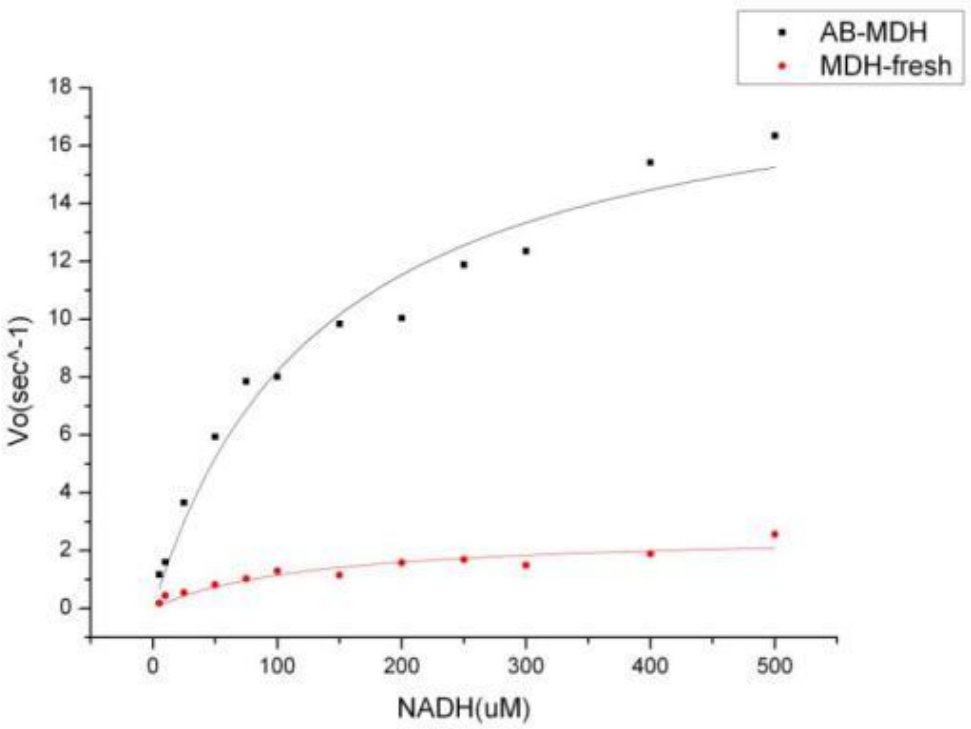
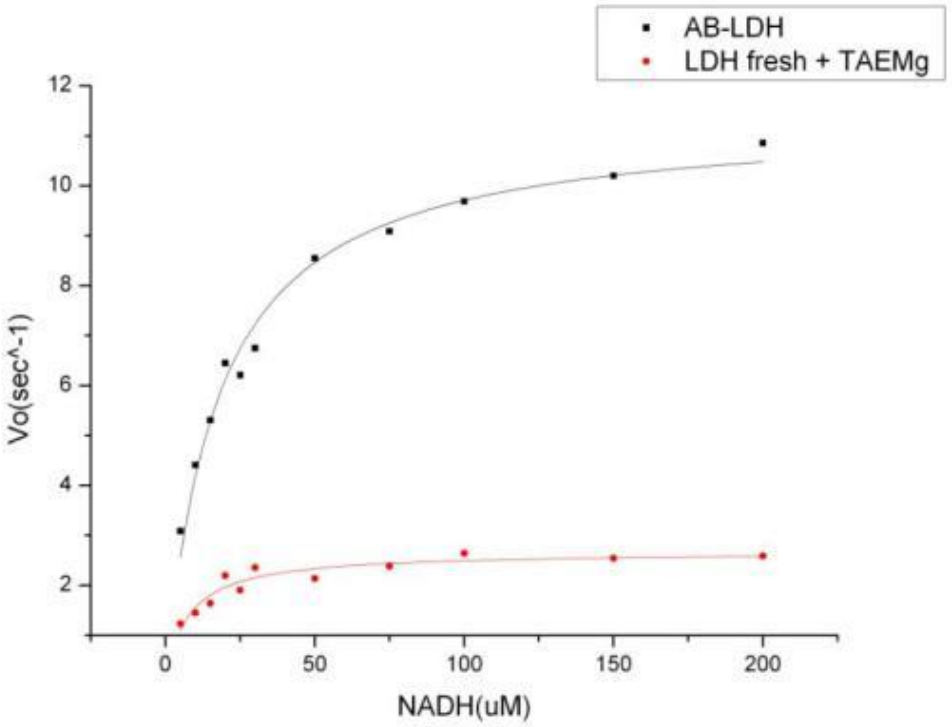


Figure S11. TEM image for purified DNA cage with G6pD enzyme inside.



	Km(uM)	Vmax
AB-MDH	137±26	19.4±1.4
MDH fresh	127±45	2.6±0.3

Figure S12. MDH enzyme inside cage Michaelis-Menten curve (against NADH), compared with fresh free MDH enzyme.



	Km(uM)	Vmax
AB-LDH	17.2±1.5	11.4±0.3
LDH fresh	7.2±1.3	2.7±0.1

Figure S13. LDH enzyme inside cage Michaelis-Menten curve (against NADH), compared with fresh free LDH enzyme.

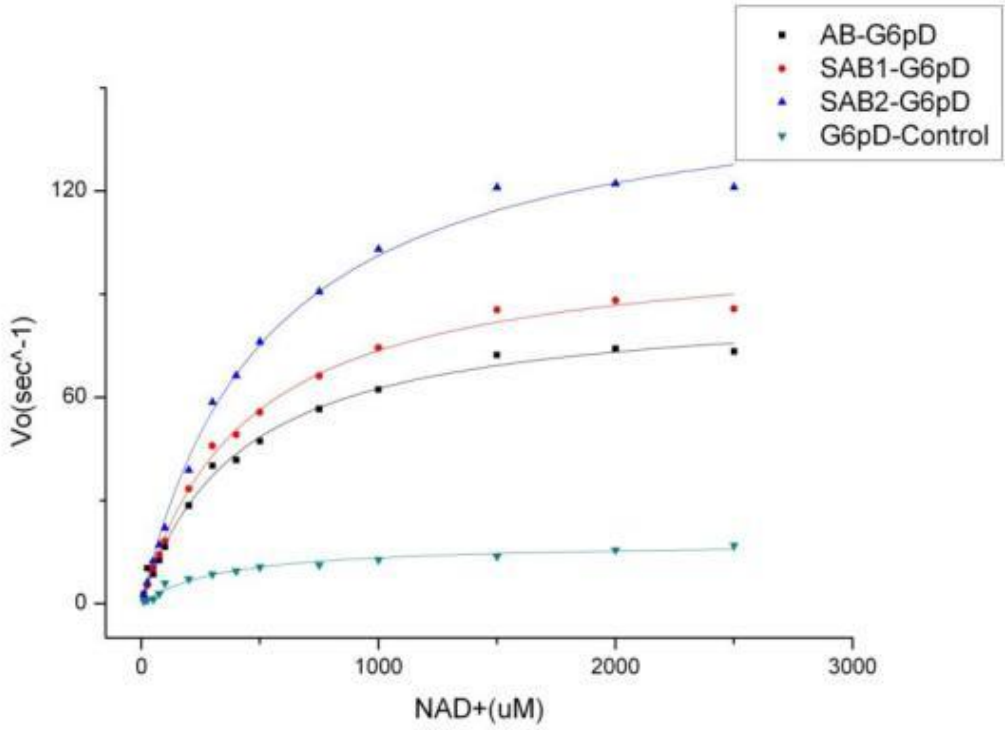


Figure S14. G6pD enzyme inside three different DNA cage Michaelis-Menten curve (against NAD+), compared with fresh free G6pD enzyme.

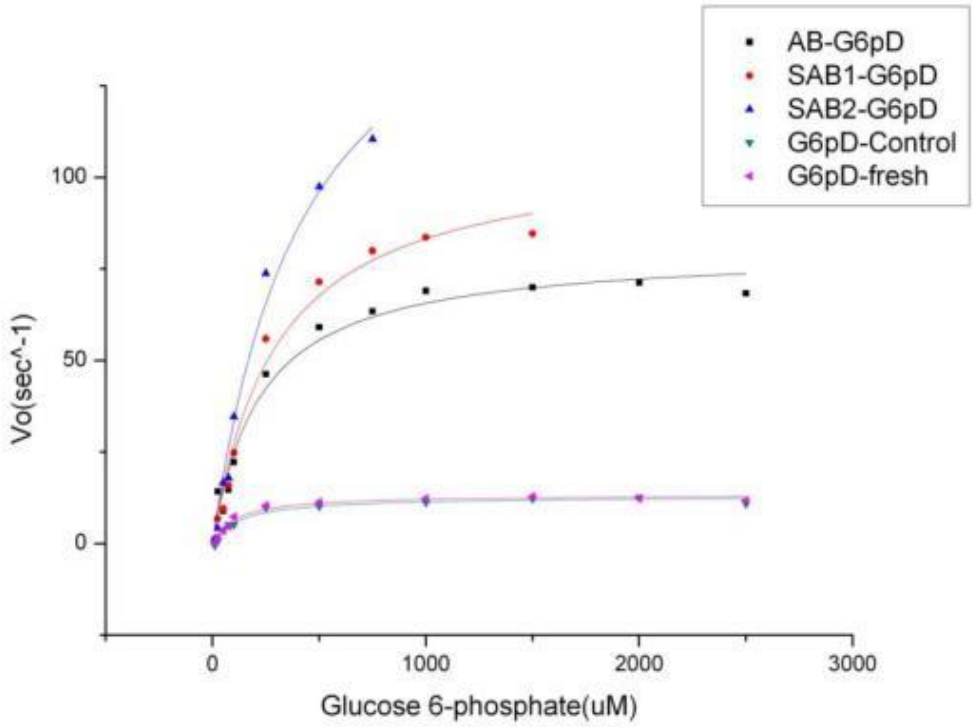


Figure S15. G6pD enzyme inside three different DNA cage Michaelis-Menten curve (against glucose 6-phosphate), compared with fresh free G6pD enzyme.

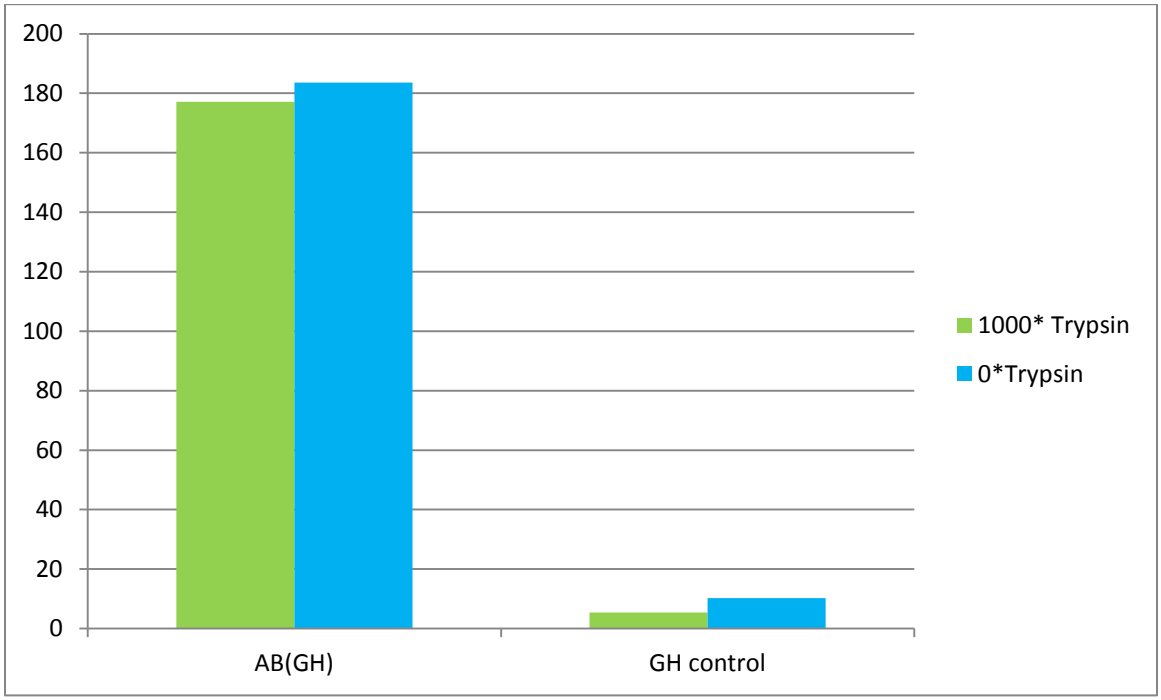


Figure S16. Raw data for Trypsin digestion test.

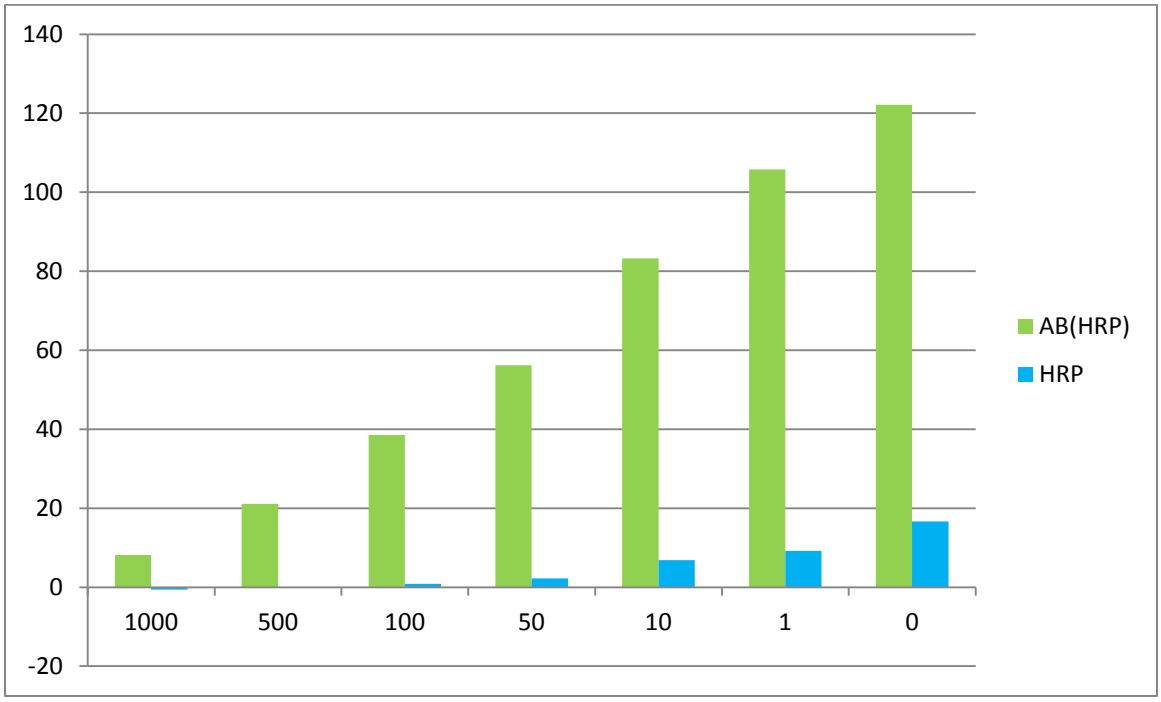


Figure S17. Raw data for BSA protection experiment.

Sequence

AB Cage-Left cage

5[18]	GGTGGAGAGGCGGTTTGCGTTTT
11[18]	CGAGTTGGGTAACGCCAGGTTTT
13[9]	TTTTTCGCCATTCAGG
17[9]	TTTTGCCAGCTTTCATCAACATTCGT
21[9]	TTTTTGGAGCAAACAAGAGAATCGGAAGATTAGC
25[9]	TTTTGGGAGAAGCCTTTATTTCAAAAAGGGACAG
31[5]	GGTGGCATCAATTCATGGGCGCGACCTGTTTGTATAAGCAAATTTT
36[16]	ATATAAAGTAGTAGATGGGCGCTTTT
43[18]	AATCATACTAATAGTAGTAGCATTTT
54[17]	GCTGTCATAGCACCGAGCTCGAATTCGTTTT
55[2]	TTTTTGAGGACTAAAGACTTTCAACACTAAGG
67[18]	CGGTTTTGCTTTGCGCTAGTGAGCTAACTCACATTTT
69[2]	TTTTGAAGGATTAGGATTAGCGGTAGCAACGCGA
83[2]	TTTTAAAAGGGCGACATTCAACCAGGC
95[18]	TGACTAATATGTTTGATGTTTGCCCCAGCAGGCTTTT
97[2]	TTTTAGGCTTATCCGGTATTCTAGTTT
108[20]	CTCAACAAGTATCACATAATTTATTAAAGTTCCAGTTTGGAACATTTT
1[5]	TTTTAGAGTCCACACTAGAAAATT
3[5]	TTTTGAAAATCCTCAGAGAGATTTT
5[5]	TTTTATTGGGCGGAGCCACCATTTT

7[5] TTTTAATTGCGAAACAACTTTT

9[5] TTTTAATCATGGCTCATTCAGTTTT

11[5] TTTTGTTTTCCCAGTCATTTTT

15[9] TTTTATCGTAACCGTGGCAAAGCGCCATTTT

19[9] TTTTATTTAAATTGTGGCCTTCCTGTATTTT

23[9] TTTTGAGACAGTCAAATGCCTGAGAGTCTTTT

27[2] TTTTAGCCTCAGAGCATAAAGCTTAATACTTTTGCTTTT

29[2] TTTTAACATCCAATATTAAGCAATAATTTT

33[2] TTTTAAATGGTCAATAAGCTGAAAATTTT

35[5] TTTTATTCCCAATGATACATTTCGCTTTT

37[2] TTTTAAATATGCAACTAACAGTTGTTTT

39[5] TTTTGCGGATGGCCTCAACATGTTTT

41[2] TTTTGTTTACCAGACGACGATAATAGCAAAAAATCATTGAGAAAG GCCGTTTT

43[2] TTTTACATAACGCCAAATCATAACCCTCTTTT

45[5] TTTTAGAAAGATACTAATGCAGATTTT

47[2] TTTTGGAAGAAAAATCTATTACAGGTTTT

49[5] TTTTGAATTACCTGTCAGGACGTTGTTTT

53[5] TTTTGAATAAGGTAAATTGGGCTTTT

57[2] TTTTCACCCTCAGCAGGCTACAGAGGCTTTT

59[5] TTTTATATTCGGTTTGCGGGATCGTTTT

61[2] TTTTGATACCGATAGTCATAACCGATTTT

63[5] TTTTAATTGTACTTAAACAGCTTTT

65[2] TTTTAATAATTTTTTAAGGAGCCTTTT

67[5] TTTTCAACAGTTAGGAATTGCGAATT

71[2] TTTTCGGAACCTATGACTCCTCAAGATTTT

73[5] TTTTGTCAGTGCCCCCCCTGCCTATTTT

75[2] TTTTCATACATGGCTTTTAACGGGTTTT

77[5] TTTTCATTAAAGCTTCCAGTAAGCGTTTT

79[2] TTTTAGGTTGAGGCAGATAAATCCTTTT

81[5] TTTTCCCTCAGAGAGCATTGACAGGTTTT

85[2] TTAAGTTTATTTTGAGCGCCAAAGACTTTT

87[5] TTTTATACATACAACACCACGGAATTTT

89[2] TTTTGAACTGGCATGAACGTAGAAATTT

91[5] TTTTCAAAGTTACGAATACCCAAAATTTT

93[2] TTTTGCAATAGCTATCATAGCCGAATT

95[5] TTTTAACCCACAAAACAATGAAATATTTT

99[2] TTTTCGAGAACAAGCAATCAGATATAGATTTT

101[5] TTTTAGAAACCAATACCGCACTCATTTTT

103[2] TTTTACGCGCCTGTTTCGAGCATGTTTTT

105[5] TTTTATAAAGTACAGCTAATGCAGATTTT

107[2] TTTTTGAGAATCGCCATAAGAGAATTTTT

109[5] TTTTAGCCTGTTTGTAGGGCTTAATTTTT

1[28] GACTCCAATAAACACCAGGGAAGCGCATAAGTCAGCGGCAAATGC
AGCA

1[77] GAACCATCGTAAAGCACTAAACTTGACG

2[34] TAGGGTTCCGAAATAGGGTAAACAAATC

2[55] GGTCAAAAGAATAGAGGGCGAAAAACCGTAAATAAGAGAATTAA

3[49] ATAAAAGGAACACCCACCACCGG

3[77] GGGAAAGGGGCGCTGGCAAGTCGCTGCGCGTAACCTTGACGA

4[34] AGCGGTCCTTTTCACCCTCAGATTTAGC

4[69] GTAGCTCTTTAGAGTCGGAACATGGCCCACTACGT

6[34] CGGCCAACGCTTTCTTTTCTGAATGGCT

6[48] CTGCATTGACGGGCAGAGAGTATCCCTT

6[76] GCACGTAAGCTAAACAGGAGGTTTTATAATCAGTGGTAAAAG

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12[69] GAAATATTGGTAATGAAGAACACACCGA

12[76] ATCGTCTATTTACACAGAGATAGCGCAC

13[21] CTGCGCACGATTAACGTTGTACCCGGGTTGTTTCCCCTAATGCACT

13[42] CGATCGGAAAGGGGGCCAAGC

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101[155] GGCGCACGAAACATGACCCCTAATGCCGTTTCCATTAAACGGGTTTT

AB-Linker

1[97] TTTTTAAACACTATTT

3[108] GGTATAAATCAAAAGAATAATCGGCAAAATCCCTGA

5[108] CCTGCCCCAGCAGGCGAAGCGGTCCACGCTGGTTGC

7[108] AAGATTGCCCTTCACCGCGAGACGGGCAACAGCTCG

9[108] GCTTGCGTATTGGGCGCCCGCGGGGAGAGGCGGTAA

11[109] AGAAACCTGTCGTGCCACCCGCTTTCCAGTCGGAC

14[105] GGGAGTAACGACCGTG

16[115] TGTTTTGAATGGCTATTAGTGGCACAGACAATATTG

18[115] TGTGAGGCGGTCAGTATTGAAGATAAAACAGAGGCA

20[115] AGAATATCAAACCCTCAAACCTTGCTGAACCTCAGG

22[115] GGTAATAGATTAGAGCCGTAGGAGCACTAACAACGC

24[115] GGCCCGAACGTTATTAATCGTATTAAATCCTTTGCA

26[115] CGTCAGATGATGGCAATTATCATATTCCTGATTAAC

28[66] TCGAAATAAAGAAATTGCATTTGCACGTAAAACAGG

41[63] ACCCAATAGGAACGCCACAGCTCATTTTTTAAAG

56[66] ATGCCTGATTGCTTTGAAAAACAATAACGGATTCCA

69[63] TTGAGATCTACAAAGGCTGGGTAGCTATTTTTGACA

84[66] AATCAAGAAAACAAAATTGATGATGAAACAAACATG

99[63] TATGGCATCAATTCATCGGTTGTACCGG

100[66] GGAATCGTCGCACATAGCGATAGCG

103[63] GTATGGCTTAGAGCCCAATTCTGCT

104[66] GGCTGAGAGACTATAACTATATGAG

107[63] TCACCATAAATCAATTTAATTCGTA

108[66] TGAAATATATTTGGTTTGAAATACC

AB-probes

18[48] GGAACGCATTCGCATGCATCATATTATACATAAGGCCGGAACGAG GCGCAG

33[129] GTTAGGATTCGGCGCCTGACAACATGTTCAGCTA

34[53] ATGACCATAAATCGCCTGATAAAT

48[53] TGTGTCGAAATCCCTCAGAACCGC

49[121] AAAGGTAAAGTAAGAAACAATGAA

51[117] TTTAGGCAGAGGCATTCAACGCCAACATGTAA

61[117] CGAACAAAGTTACCAGAAAGTAAGCAGATAGC

62[53] CACCCTCAGAGCGCAGCACCGTAA

64[57] CCATGTACCGTAACACCAAGCCCAATAGGAAC

75[117] GTAAGCGTCATACATGTGAATTTACCGTTCCA

78[57] CATCGGCATTTTCGGTGACTGTAGCGCGTTTT

79[117] ACAGGAGGTTGAGGCAGCCGCCGCCAGCATTG

SAB1-left half cage

0[55] TTGCTTTGACGAGCACGTA

0[79] GCCGCTACAGGGCGCGTGGTCAAT

1[37] TAACGTGCTTTCAATTCTACCACCGAGTAAAAGTT

1[72] AACCTGTTTAGCTAGCTTAGTTTGACCATTAG

1[104] AGGGCGCTGAACGTGGCGAGAAAGGGGAGCCCCCGATTTAGGTCGAGG

2[55] GGTGGCATCCTCGTTAGAATCAAATACTATGG

2[87] GAAATATTTTCATTTGAGTACGGTGCTGAATA

3[37] ATAGTAGTAGCCTAAATCGAAACTATC

3[72] GCAAGGCAAAGAAGGAGCTTAATTGTCTGGAA

4[55] GCATAAAGATTAACATCATGAGTCTGTCCATCAGCAAAATCAC

4[87] ATCTTAGCAAAATTAACAGGATTAATTCGAGC

4[103] TGCCGTAAGTCTATCAGTGAACCATTGGAACAAGAGTCCAAAAGAATA

5[37] GTACCAAAAACAAAATTTTAATACCTA

5[72] GGGAACGTCAAAGGGCGCGTTTTAGAGAGTAC

6[55] CAAGGATAATTATGACCCGTGCTGGTAATATCGCGCAGTCTCT

6[87] GAACGTGGACTCCAGATAGTCAGACGAGAATG

7[37] AACCCTCATATAGGCCGGAGAGGGGGTGCTTTTGCTATTCGGTTATT

7[72] TGTGGCAAAATCCCTTTCAGAAAAAGCAAAGC

7[104] GCCCGAGAGCAGGCGAAAATCCTGAGAGAGTTGCAGCAAGTTTTTCTT

8[55] GGTGAGAAATTTTAAACAGTGACGCTCAATCGGGGATAGCAAG

8[79] AAATCGTAAGCGTCCACCAGACGA

9[37] AGTCAAATCACCTATTTTTTATTTTTGATGTCAATCATAT

9[72] TAGGCCCTTCACCGCCCTCGTTTAATACTGCG

10[55] GAGGGTAGCATCAATAAGCGAGAGAATAGTAA

10[79] TGATTCTGCTAATGCAGAGAATCGGAAGATTGTATTAACTCACATTAA

10[103] TTCACCAGGCGGGGAGAGGCGGTTTGCGTATTTCCAGTCG

11[37] AGATCTACAAAGGCTATCAAAACTAGCAATATTTA

11[72] TCTGGAGCAAAAATCGGCCAACGCTGAGACGGGCAACAGC

12[63] TAATCGTAGGTCATTGATGCCGGA

13[35] GTACCCCGGTTGATAATCAGAATATTTTGAGATGCGA

13[96] TTGCGTTGGTCGTGCCAGCTGCATTAATGCAAGATACATAACAACA

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14[63] AAACGTTAAAAGCCCCTTCATCAGTTGAGGGCCGC

14[95] CTAATGAGTGAGCAAGAGTCAGGAGGTTTAAT

15[35] TAAATTTTTGTTAAATCAGCTTAATTCGCTTGGTAAC

15[80] GTTATCCGCATAGCTGGCTTGCCCTCTTGACA

16[63] ATCAAAAACATTTTTTGTGAATTACCTTAAGAAGC

17[35] GTAGCCAGCTTTCATCAACATTCCGTGGGCCGAACTGCGCAGACG

ACG

17[80] TGCCAAGCACGACGTTAACGGTGTGACCTGCT

17[96] CTGCAGGTAATTCGTAATCATGGTCTCACAATTCCACACATGGGGT

GC

18[63] TCGGATTCTAAATGTGTACCCAAATCAACCTGCGG

19[35] TTGACCGTAATGGGATAGGTCCATCTGCCGACCCCCA

20[63] TAACCGTGACGTTGGTGAACGAGGACCAACTT

20[95] TGGGAAGGAGCTGGCGAAAGGGGGCAGGGTTTTCCCAGTCTTGCA

TGC

21[35] GACGACAGTATCGGCCTCAGGAAGATCGCACTCCAGCGCGCATCG

21[88] CTTCTGGTGCCGGAAAGCAACTGT

44[71] ATACATTTGCAACTAAGGGCGCGATCATACAG

45[88] GTTTCATTGAGTAGATGAAAGGAGCCGCCGCGCTTAATGC

46[71] TAATGCTGCAACAGGTGCAATAAAACTTTTGC

47[48] GGCCTGAAGCAAACTCTAGCTCAACCAATAAAGCTGAAAA

47[88] CTTTAATTGGCTTAGAACCCTAAAGAAGGGAA

48[23] CCAGCCATTCACTTGCCCATATTTAAGGCTTACAATAGCACGAATT CA

48[71] TTCAAAGCGACTATTAAGCCTTTACTGAGTAA

49[48] CATTTGTCTTTACCCTGAACCAGACCTGTAATGCCTCAGA

49[88] GGATTGCACAAATATCGAAAAACCAGCACTAA

50[23] TACATTGGTGCAACAGTAATTTTCTTAATTGAAAAGCCAAGAGGAC GA

50[71] ACCATAAAGACTGGATGGTAAAGAAACCGTTC

51[56] AATGTTTATCAAAAATTGCAATGCTTTCAACG

51[88] GAATCGTCTAAACAGTATAAATCACTATTAAA

52[23] AACAGAGAAGTAATAAGGATTATATCGTCGCTAGTGAATATAGCC CTC

52[71] CGATAAAAACATTCAAATAAATTACCTGAGAG

53[56] GGAATACCACCAAAATTGATATTCTTCAAAAG

53[92] CAAATCATAACCTGGCCCTGTTTGATGGTGGTTCCG

54[19] CCCTAATCCTGACAGATGATCTATTGAT

54[31] GCGAACTGTACGTGGCTTCTGGCC

54[43] AGTCCCACCAGCTTAAAATTCGCAT

54[79] ATTACAGGATTATACCCAAATATTGTGAAATT

55[56] TTTTAAGAACTGGCTCTAGAAAGAAAAAACAGATGAACGG

56[31] CGGTCAGTAAAAATACAAGGCCGCTTGCGCAT

56[79] TTCAACTTTGAATAAGTTTCCTGTACGGCCAG

57[56] AAAGCTGCTCATTCAGTAATCATTAACCAATATAAATTGT

58[19] ATCTATCATTTTAATTTTAATAAAAATC

58[31] CCCTCAATAAATGAAACCACCAGATTTTGCGGTTTCTTAA

58[79] AGAACCGGGACAGATGGTAAAACGTCTTCGCT

59[64] TGAAAGAGATATTCATAGCGAGTAGGAACGCC

60[31] AGGTTATCTCAACAGTTAAAGACTGCGGAACAGTATGCGT

60[79] CCATGTTACGAAACAATGCGGGCCCAGCTTTCCGGCACCG

61[24] GTCAACACCTACGAAGTTTTCATGTTTTTCAC

61[56] GCGATTATACCAAGCGCTTAGCCGGTAGATGGACAACCCG

62[23] AATACATTATTCGACAGCACCAACAAGATTGCTTTGAATATCATTT
CA

62[40] GGCAAAAGAATATAGAT

64[50] TTGGTAAAATACGTT

66[50] CTACAGAGGCTTCCATTAAGTCAATCATCATCTTTAGTTTGAGGGG
AC

67[8] TTGTAACATTGGTTT

67[40] GGTAGCAAAACCTCAATAAGGGAAAACAAACGGCGGA

68[50] GAAAGACAGCATCGGAAAAAATCTAAAAGGTGAGG

70[50] TGAGGCTTGCACCCTCAGCTAAAACAGGCATCACCGTCTGGCCTTC
CT

71[32] AACCGATAAAAAGAAGACAGACAAGAG

72[44] GACAACAACCATCGCCCATTTAAGGGACAGGATTATT

73[24] ACCGATAGCCGTAACAATTACCCT

74[23] ACAGCCCATATATGTGTAATGGAAAGTGAATT

74[44] CTTTCGAGGTGAAGATCGTCAGGGAGTTACGAACGAATTTAATGC

75[24] GAAATTCGACCTTTTTCTGAGTTTTTTAGTAC

76[23] AGATTTTCATTTAACACATCAAGATTAGGCGG

76[44] GGAGCCTTTAATTAAGACGAG

77[24] TCCAAAAAAGTTTTGTATTTCATTCCCAAATC

78[23] GTTGACAGGAAACAAAATTACCTGTGATGCAA

78[44] TGCGAATAATAATAGGAAGTTTTGAGGACTGAAAGGAATATCAAA

79[24] GCCTGGAATAAACAACCGTCTTTCTTGCTCAG

81[24] TTTCAACATCCATCGCAAGACAAAGTTAATTTTGAAACATCCAAGT CC

82[50] TTTCTGTATGGTTTT

84[50] AGTTAGCGTAAAGTAAATGAAT

86[50] AACGCCTGTAGCATTCATTGTTTATCAGCTTG

89[32] CATTTTCATCTGAAATTTTTGCCAGAC

90[44] GCCACCCTCAGAGCCACCAATGAAAAACGTATTACCG

91[24] AGAACCGCACCAGTATGAAGCCAG

92[23] CGCCACTTCATATGCGTACTAGAAAAAGTACC

92[44] CGTACTCAGGAGGCGTCACCACCCATGTATTGCGCCGACAAT

93[24] TATCAGGAGTACTGGTTTATACAATTGAGGCA

94[23] ATAGGTCTATCATAATCGTTAAATCATCCCTC

95[24] ATAAGTGCAAATAAGGAATAAGTTCCAAAGGT

96[23] TACCAGGTTTTGAAATCATCTTCTTCAACAAT

96[44] GATTAGCGGGGTTCAGACGTTCGATCTAAAAAGGCTCCAAAA

97[24] ATCCATCATATTATTCACCGACCGCTCAGAAC

100[50] TTTCCCTGCCTATTT

102[50] GAGTAACAGTGCCCGTGATCGTCGAGAGGGTT

106[50] GAATTTACCGTTCCAGCTTCACCCTCAGAACC

107[32] AATGGAAACAGAACAACTCATGGATAG

108[44] AAATAAATCCTCATTAAATCGCTGAGTAGTAACCGTT

109[24] TTGGCCTTAGCAAGGCTCCGGGAA

110[23] GGTCAGCAACCGCGCCTTTATTTTAGATTAGT

111[24] GACAACCAAAGCCGTTCGGAAACGATTGACGG

112[23] AAAGTAATACCGCACTCCAAGAACCGCAAATT

113[24] AGAGCCACACTGTAGCCATCGAGAACATTTTG

114[23] CGCCAGTTTTATCATTCAATCAATCCAGTTAC

114[4 CAGAGCCGCCACCTGTATAAACAGTTAATGCC

4]

115[2 AGATACCGCCATCTTTGCGTTTTCCACAATCA

4]

116[2 TGAACAAGGTAGAAACTCATAATCCGCAAACA

3]

118[5 TTTGCCCCCTTATTT

0]

120[5 AGTTTGCCTTTTTTCGGTCATA

0]

122[5 TAGCAGCACCGTAATCAGCGAGCCGCCGCCAG

0]

124[5 CAGTAGCACCAGAAACCATCGA

0]

125[3 TTAGAGCCACGCAAATAAGAACTCGTT

2]

126[4 CACCGACTTGAGCCATTTGGTTTTATAATAAGGGATT

4]

127[2 TTAAAGGTATAATAAGTACCGAAG

4]

128[4 AGGGAAGGTAAATTCACCAATTTACCATTGATATTCACAAAC

4]

130[4 AGACAAAAGGGCGACAAGTAGCGACAGAATCA

4]

132[2 ATAGATAATACAGAGAGTCAAAAAT

3]

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4]

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3]

135[3 AGGTGGCACAAACGTAGACACCACGGAAT

2]

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65[8] TTTTTTGCCCGACTTTAGGAGCACTTTTT

69[8] TTTTTCATATTCCGCCTGCAACAGTTTTT

73[3] TTTTGAAGGGTTAGAACGGCAATTCTTTT

75[3] TTTTTGCACGTAAAACAAATTATCATTTT

77[3] TTTTGATGAATATACAGAAGTTTGATTTT

79[3] TTTTGGGAGAAACAATATAAATCCTTACAAACATGAGGATTTAGA AGTATTTT

83[8] TTTTAAGATGATTACCTTTTACATCTTTT

85[8] TTAATTACAGGTTTAACGTCATTTT

87[8] TTTTTAAATCAATATCAAAATTATT

91[3] TTTTGAAAACATAGCGAACCTTGCTTTTT

93[3] TTTTGAGAAGAGTCAATACAGTACA

95[3] TTTAACCTCCGGCAAACAAAATTTT

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103[8] TTTTACACCGGAGAGAGACTACCTTTTTT

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107[8] TTTTAGTAGGGCCCTTAGAATCCTTTTTT

109[3] TTTTTGTAATTTAGGCACGCTCAACTTTT

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123[8] TTTTGAATCATTTTTTCGAGCCAGTTTTT

127[3] TTTTTTAGCGAACCTCCAGCAAATCTTTT

129[3] TTTTAAGCCTTAAATCACATCGTAGTTTT

131[3] TTTTTGAATCTTACCAAGGGTATTATTTT

133[3] TTTTAGAGCCTAATTTGAATCGGCTACGAGCATAAAAATAATATCC CATTTTT

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46[23] GTAGCAATGAAGTGTTATTCTAAGAGCTATCTAGCAAGAAACAATGAATTTT

47[5] TTTTTAGTAATAACA

50[15] CAGATTCATCTGTAAACTTCTGAATAATGTTTT

51[5] TTTTGTCACACGACCTAGAACCCATCAATATAAA

53[5] TTTTTGACCTGAAAGCGTAAGAAATAG

55[13] TTTTACATCGCCATTATTAACACCTGATTATAGGAGCGGGAAATAAA

57[3] TTTTGCCACGCTGAGAGCCAGCAGCCAAT

59[13] TTTTCAGTTGGCAAATAAAATATACGTTATTACTCGTATACGGATTC

61[3] TTTTAACAACTAATAGATTAGAGCC

63[0] TTTTTTAGACTT

81[0] TTTTCGCAGAGG

99[0] TTTTTTTCAAAT

117[0] TTTTCCTAATTT

128[23] AAATTCTTCACAAGAAAGCGCTAATATCAGAGTTTT

130[23] CACCCAGCAACACCCTCGCATTAGACGGGAGATTTT

135[0] TTTTATAAGAAA

136[14] GAAAATACGATTTTTATTTATCCCAATCCAATTTT

2[122] TTTTGGAAAGCCGGCGGCAAGTGTAGTTTT

4[122] TTTTAAGTTTTTTGGGAGCTTGACGGTTTT

6[122] TTTTGTTGTTCCAGTTCACCCAAATCTTTT

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14[119] TTTTCATAAAGTGTAAAGCCACATACGAGCCGGAAGTTTT

16[119] TTTTCCGGGTACCGAGCTCGCGACTCTAGAGGATCCTTTT

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20[119] TTTTTCGCCATTCAGGCTGCCCAGGCAAAGCGCCATTTTT

56[92] TTTTGAGATCGTTGGTTTT

58[93] TTTTGAGTAATGACGTTTT

60[92] TTTTTCCGCACAGACTTTT

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19[80] ATTACGCCGCGATCGGAGTACAACGGAGATTTT

45[56] TTAAATATCGCAGAGCGGGAGCTAAACAGGAGAAGAAAAGTTTT

54[93] TTTTAACGGAACGC

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4]

134[4 TTTTTAAAAGAAAAAAATCACAGCGTTTGGAACCGCCTCCCT

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136[4 TTTTGTATGTTAG

8]

138[4 TTTTGAACTGGCATGATTAAATTACCAGCGCCAA

8]

140[48] TTTTGAGGAAACGCAATAGAGAACCGATTGAGGG

142[48] TTTTAGATAGCCGAACAACCAGAATTATCACCGT

SAB1-right half cage

22[116] GCGTATTGGGCGCCAGGGTGGTTTTTCTTTTCACCAGCTTGCTTC

23[88] ATCGGCCAGGAAACAGAATTTATCCAGACGAC

24[71] TGTCGAAAATCCTGTTTGATGGTGAAAGAATA

24[116] ATTTGAATTACCTTTTTTAATACGCGCGGCCAGCTGC

25[56] GCCCGAGAAGTCCACTATTAAAGAGTCTATCAGAACCATCGTAAA GCA

25[88] AAACAAAAAAGATGATATTTACGATGAAAATA

26[71] GGAACAAGTAGGGTTGTTCAGCTAAGACGCTG

26[116] TTTCAATTACCTGAGCAAAAGTTAATTACATTCTGTCAAAATCAT

27[88] TACAAAATGCCTGATTTGAGCGCTTCACCGAC

28[55] CTAAATCGGACGGGGAAAGCCGGCAAGGAGCGGGCGCTAGTAAC CACC

28[71] GAGGTGCCACCCAAATGAATAACACAAGAAAA

28[116] GGGAGAAACAATAACGGATTCCGCGCAGAGTCAAAAAGCATGTA G

29[88] GAATATACAGATTTTCAGCAGCACTAAGTTTT

30[71] GAAAGCGAGAACGTGGTTAGAGCCCCCTGAAC

30[116] ACAGAAATAAAGAAATTGCGTAGTAACAGTATCACCGAATATCA
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31[56] ACACCCGCATGGTTGCTTTGACGAGAGCGGGAGCTAAACA

31[88] CTACCATATCTGAATAATTAAGAGAGGAGCGGCCGAACGT

31[104] TATTTGCACGTAAAT

32[71] CGCGTACTCGCGCTTATGAGTAACAACGTCAC

32[116] CCTGATTGTTTGGATTATACTTCAAAATTACTGGTAACGTAATCA

33[64] GGAGGCCGATTAATATCTACAGGG

33[96] ATGGCAATCCACCAGAGCTTATAC

34[79] TCAAGGGATTTTAGACCCTATTATTAGCG

34[124] TCATTTTGCGGAACAAAGAAATCATCAATATAAT

35[64] CCACCGAGTTGTAGCAATACTTCTAAGAACTCAAACTATCCGCCA
GCC

35[96] TATTAATTGTATTAAAGAATCATGAGGAAGTTCAG

36[79] ATTAACCGTAAAAGAGATTAGGATTCTGAAACCAGT

36[124] TTACAAACAATTCGACAACTCTTAAAAGTGACCCCCA

37[96] TACATTTGTAGATTAGCAGAGGCCGCTTTTGCAAT

38[63] ATTGCAACGACGCTCAATCGTCTGTCACACGACCAGTAATCCTTC
TGA

38[79] AATATTACGGCCTTGCAGGAGGTTGAGGGTTG

38[124] TTTAGGAGCACTAACAACTAAAGGATTTAACTAAAGA

39[96] AGGAATTGTCAGTTGGCATTGCTT

40[79] TTCACCAGAAATGGATAACCCATGCCTCAGAG

40[124] AAACCCTCAATCAATATCTGGAGGAAGGTTGCAGGGA

41[64] CCTGAAAGAATGGCTATTAGTCTTCATTAAAAATACCGAACGAAC CAC

41[96] AAGCATCAAGCCAGCACAGCGGAG

42[124] CTGCAACAGTGCCACGCTGAGCCTTGCTGCGGTTTAT

43[80] CAGCAGAAACAGACAATATTTTTGCGTAAGAAAGTTTTGTCTGTA GCA

43[96] AGAGGTGAGGCGGTCAGTATTAACACCGC

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48[143] GGGACGCATAGTAAAACGGTGTCTTGTTTTAAGAAATCCG

49[136] GCATCGTATAGGTCACTTCATTCCGGTAAAGAAATGCAATTCAGT TTG

56[127] GAAATTGTCATGGTCAACCGTGTGATAAA

60[127] CTCACATTTGGGGTGCAAGACAAAGAACG

62[95] ATTAATGATGTAAATCCAATAGTGTACATAAACATCAAGA

62[119] CGGGAAACGAGACTACCTTTTTAATTAGTACC

63[72] AGAAGAGTGTCGCTATTGAATAACTGAGACGGGCAACAGCTGAT TGCC

63[104] AGGTCTGACTGTCGTGGGAGAGGCGGTTT

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65[115] TATATAACTATATGAGGCATTCAACGCCAAAGCCGTTTTTAT

67[115] CGAGAAAACTTTTTATGGCTTAATTGAGAATC

68[135] CGGAGAATTTGTTAAATCCTGTGT

69[115] TTTCATCTTCTGAATTCTTACTTTAGTATAGAACGCGAGGCG

73[109] GAAAAAGCCTGCAGTATAAAGC

75[109] CAACGCTCAACAGTAGTTCACCGCGCCCAATA

77[109] GCCATATTTAATTCGAGCCAGT

79[109] AATAAGAGAATATAAAAGCATCATTCCAAGAA

80[87] GACAATAACCATCCTAGAAACAAATACCAAGT

80[119] GACAAAAGCAATAATCGGCTGTCTTCGAGAAACGATTTTTCCCAC
AAG

81[72] ATAATATCACAACATGAGTGTTGTTCAATATA

81[104] AAACCAATGTAAAGTAATTTAACAATTTC

82[135] TAACACTTAATAAAGCTTTAGGCAGTAAATGC

83[115] CGGGTATTAAACCGTCAAACAGCCATATTATT

83[136] CACTCGAATGTACCAACTCAGAGCATCGATGA

84[135] GAACAAGCACATGTAAGAAGCCTTTCAAGGGT

85[136] AACCTGTTTTGCGGGAAAACATTATCACAAAT

86[135] AATGGATTAACGCAAGTTATACAACCTAAATT

87[136] GGCTTCGAATATTTTAGATAAAAAATTAATGC

88[135] GTATTCTACATATGCGTTCTAAAC

89[115] TTTTAGCGAACCTCCCGAAGTGTTGGTGTTCTCCGTG

91[109] AATCAAGATTAGTTGCGTAAACTGGCATGATT

95[109] TTGCCAGTTACAAAATAGGCTTTTTAAGAAAA

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98[87] GCAGCCTTAGGGTAATGCTTTGAACGTCAGAT

99[72] AAAGTCAGTACAGAGACAAGTTTTTCCAGTTT

99[104] AGAGATAATGTTTAACGGCGAATTATTCA

99[120] AATTGAGTCATAATTATTCATTAAAGAATCAA

100[135] ATTGCGCCTTTAATTCTCCAACAGAAGTACCG

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101[136] AGCTAGTCAAGCAAACGAGCTTCAAGTAGCAT

102[135] CCGAAGCCATTAGAGACTAACGAGATCTCAAT

103[136] GTTCAGAAAAGAGGTCGTACCTTTGCTATCGA

104[135] GCTTTACATACCAACGAATATAATATATAGAA

105[115] GAAACCGAGGAAAAAGACACCGTGGCAACCGCCACCCTCAGA

105[136] TAACGGGAAATTGCTGATTTTTGCATTTCGCA

106[135] CCCAAAAGGCTCAACAGGACTTGC

107[11 AAGACTCCTTATTACGCATAAAGGCGATTAGATGGGC
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111[10 TTATTTTGTCACAATCCATGAACCAGAGCCAC
9]
113[10 GGTTTACCAGCGAGGGAGGGAA
9]
115[10 GGTAAATATTGACGGACAGTCAGACTGTAGCG
9]
116[87] TTGAGCCACCATCGATAGGTTTAAGTTAGAAC
117[72] CAATGAAATTTGGGAACGAGAAAGTTGGGGTC
117[10 GTAGCGACAGGTGAATTACCTTTTACATC
4]
117[12 GTTTGCCTCCTCTTTTGATGATACAAACAAAG
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5]
119[11 CGTTTTCATCGGCCCGGAATT
5]
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6]
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5]
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5]

121[13 GTGAATTAATAGTAAGTAACGCCACAGTCTTA

6]

122[13 TTTAACCGAACCCTCGGAAACGCACGCAATAA

5]

123[11 CACCGGAACCGCCGACGGAGG

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123[13 AGCCGGAGAAATAGCGTTTACCAGCCTCAAAT

6]

124[13 CTCAGAACATATAAAAGGGGTATG

5]

125[11 GCCACCACCCTCAGAGCCTTCGCCAGCTTGGGGATGT

5]

127[10 GCCGCCAGCATTGACAAAGGAGCCTTTCAACTAAA

9]

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9]

129[10 CAGACGATTGGAAAGCCAGGGGATCGTCTTTGAGGGAAGTATTA

9] GACT

131[10 GGAAAGCGCAGTCTCTAACTACAGAGGCACCCTCA

9]

132[11 TACCGTTCTCCATTAATCATCTTTTTGAGTAACATTA

9]

133[109] TAAGCGTCATACATGGGCTTAAAACACACGGGTAA

134[75] GCCTATGCGCCGGAAGGGAA

134[87] AACGGGGTATGAAAGTATGGAAGGTCCTGATTATCAGATG

135[104] CAAGCGCGAGGAGTGT

135[120] TACAACGGAGATTTGTGAATACACCCATGTTATAAGGGAAATTTTCGG

136[103] GCGATGAGACTCCTCAATAGCCCGTCCTTTGCATAGATAA

137[80] ATATAAGTAGAGAAGGTCTGTCCAAATTATCA

137[128] AATACGTAGCAACGGCTGACCAACCAAATAAATCATCATT

138[103] CTTTTTAGGTGTATCACTCATTTTAGCCGTCACAGTTGAA

139[80] CCACCACCCCGTACTCTGGTAATATCACGCAA

139[128] GCAGCGAACCGATATATTCACAAAGTAATCTTTCCCTCAG

140[103] GTTAAGGATAGCAAGCACAGCCCTCAAATCAAAAAATCTA

140[143] ACGCATAAAGACAGCAGTACAGACTTTGAAAGATTGCCCC

141[80] TTCCACAGCCAATAGGTATTTACATCCAGAAC

141[104]	TTTCGAGGTGGGTTT
141[128]	TGATACCGTCCAAAAGAACCGGATTCAGCCAC
142[103]	CAGCTAGTTAGCGTAAAACAGTTTGCAAATGAGATAAAAC
142[143]	AAAAAGGCATAGTTGCCATCAAGACAGGCGCAATTTCAAC
143[66]	GGGATTTTGCTAAACAACTTTCCGATCTAATACGTGGCTTGGCAGA
143[104]	TTTGAGAATAGCCTT
143[128]	GGAATTGCCATTCAGGTCCGGCAC
46[154]	TTTTTCAGGAAGATCGTGCCGGAAACGTAACATTTTTTCACGTTTTTT
50[154]	TTTTCCGTAATGGGAACCGTGCACTAAAGTATGTTTAGACTGGATTTT
54[151]	TTTTCTGGCCTTAAAGGCCGGAGACTTTT
56[151]	TTTTCCAATAGGTGATATTCAACCGTTTT
58[151]	TTTTTAATATTTTTGAGAGATCTACTTTT

60[151] TTTTATTGTATACCTGAGAGTCTGGTTTT

64[156] TTTTAGCAAACAAGAGAATAAAGCTTTTT

66[156] TTTTAAAGGCTATCAGGTGACCCTGTTTT

68[156] TTTTTTCTAGCTGATAATTTTTAGATTTT

70[156] TTTTAGTCAAATCACCAGCCTGAGTTTTT

74[151] TTTTACCCTCATGTAGATTTAGTTTTTTT

76[151] TTTTTAATACTTTAGCTATATTTTCTTTT

78[151] TTTTAAATCGGTAAGGTGGCATCAATTTT

80[148] TTTTCAAGGCAAAGAATTAGCAAAACCTAATCGTAAAACTAGCATGTTTT

82[156] TTTTTTCTACTAATAGTAAGCGAACTTTT

84[156] TTTTATTTGGGGCGCGAAATTGCTCTTTT

86[156] TTTTGACCATTAGATACGGATGGCTTTTT

88[156] TTTTTTCCCAATTCTGCATATGCAATTTT

92[151] TTTTTAGAGCTTATCGTCATAAATATTTT

94[151] TTTTCTTTTGATAACGAGAATGACCTTTT

96[151] TTTTCAGACCGGTTTACCCTGACTATTTT

98[148] TTTTAAGCCCGAAAGACTTCAAATATTCTCCAATAAATCATACAGGTTTT

100[156] TTTTTTATAGTCAGAAGCCACATTCTTTT

102[156] TTTTATAAATCAAAAATAAAGGAATTTTT

104[156]	TTTTTTCATTGAATCCCACGACGATTTTT	
106[156]	TTTTTAGCGTCCAATACTTGCAAAATTTT	
110[151]	TTTTAAAAACCATAGTAAATTGGGCTTTT	
112[151]	TTTTTACGAGGCCCTTATGCGATTTTTTT	
114[151]	TTTTAACTAATGCCAGTCAGGACGTTTTT	
116[148]	TTTTATTATTACAGGTAGAAAGATTTAAATCAAAAAGATTAAGAG GTTTT	
118[156]	TTTTTGGGAAGAAAAATGAACGAGGTTTT	
120[156]	TTTTTAAGAACTGGCTCAGGACAGATTTT	
122[156]	TTTTTTGAGATGGTTTATAGGCTGGTTTT	
124[156]	TTTTCGAGAAACACCAGCCCAAATCTTTT	
128[151]	TTTTCTGACCTTGCCGACAATGACATTTT	
130[15	TTTTTGAACGGTTCGTTTT	

1]

132[15 TTTTCGCAGACGACGAAGGCACCAATTTT

1]

134[14 TTTTAAATTGTGTCGAAATCCGCGATTAACGAACTAACGGAACAA

8] CTTTT

136[15 TTTTCCTAAAACGAAAGAGGCAAAAATCATCGCCTGATTTTT

6]

138[14 TTTTGAACGAGGGTAATGCCACTGTCAATCACTTAGCCGCTACGT

6] TATTTT

44[154] TTTTCAGGCAAAGCG

47[136] GCTGACGACAGTATCGGAAGTTTTAGGCTTGCCCTGATTTT

48[154] TTTTGCCAGTTTGAG

51[136] GGAACAAATAACAACCAGGGTGAGCCTGTAGCCAAAAATAATTC

GCGTTTTT

51[144] CGGCGGATAATGTGTAATATAACAGTTGATTTT

62[148] TTTTTCAATCATATGTACCCCGGTTGATCCAGT

65[136] TGATGTTGAGCAAATACCCCAAAAACAGGAAGTTTT

67[136] AGCTATTTTGTTAAAATTTAAATTGTAAACGTTTTT

69[136] TAATGATAAACGCCATTCAGCTCATTTTTTAATTTT

71[115] TAAGGCGTTAAATAAGAAAAACGTCGGATATTAAATGTGAGCGA

GTTTT

140[15 TTTTACAACCATCGCCC

6]

142[15 TTTTGAAAATCTCCAAA

6]

23[32] TTTTTTGCAGCAAGCGGTCCCCTGGCCCTGAGAGAGTTTT

25[32] TTTTAATCCCTTATAAATCAGTTCCGAAATCGGCAATTTT

27[32] TTTTCAAAGGGCGAAAAACCACGTGGACTCCAACGTTTTT

29[32] TTTTCCCCGATTTAGAGCTTGAACCCTAAAGGGAGCTTTT

31[32] TTTTGCGGTCACGCTGCGCGGGCGCTGGCAAGTGTATTTT

37[40] TTTTTCACTTGCCTGAGTAGTTGATTAGTAATAACATTTT

39[40] TTTTGAAATACCTACATTTTAGGAAAAACGCTCATGTTTT

41[40] TTTTCCAACAGAGATAGAACAAAAGGGACATTCTGGTTTT

43[40] TTTTAGCCCTAAAACATCGCTAATGCGCGAACTGATTTTT

53[114] TTTTTCTAGAGGATCAACGCATGCCTGCAGGTTTT

55[111] TTTTATTCGTAATTATCCGCTTTTT

59[111] TTTTTGTAAAGCCAATTGCGTTTTT

63[58] TTTTAGATTAATGCATTTT

81[59] TTTTCTGAATAAAAATTTT

99[58] TTTTTGAACAAGCAATTTT

117[59] TTTTCCGGAAGTGCCTTTT

135[58] TTTTTCGGAAAGGAACGGCAGTGAGGTTTT

137[67] TTTTGTCGATAGTACTTTT

139[66] TTTTCGCCACTACCGTTTT

141[67] TTTTAACGCCGTCTTTTTT

22[55] CTTCACCGACGCTGGTTTGCCCCAGCAGGGAGTAATTAATTTTCCCTTTT

33[32] TTTTTTCCTCGT

34[47] AATCCTGATAGAATCAGCACGTATAACGTGCTTTTT

35[40] TTTTGAAGTGTTTTTATAATTACGCCAG

45[114] GGGCGACCACCAGAGAAAGGAAAATTGTATAACCTCAAATATCTTTT

47[114] CCAGCTCGTAGAAAATATTTT

49[114] GTTTTCTTGAAGCCTTATTTT

51[114] CCAGTGCATAATTACTATTTT

57[111] TTTTTTCCACACAACATATTTATATTTTAGTTAA

61[111] TTTTTCACTGCCCGCTTTAATGCTTAGGTTGGGT

66[135] CCAATCGCCTAATGAGTTCGCATTAAACGAGCCGGAAGCATTTT

70[135] AAATACCGTAGCTGTTCAGCTTTCATCCCCGGGTACCGAGTTTT

72[127] ACCGGAATCCAAGCTTGACGTTGTAAAACTTTT

90[127] GGGAGGTTCCAGTCACAAGTTGGGTAACGTTTT

108[127] TTAGCAAAGGCGAAAGGGCCTCTTCGCTATTTT

126[127] CAGAACCATCGGTGCGCTGCGCAACTGTTTTTT

SAB1-linker

44[114]	GGGTCCCAATTCTGCGAACCCATATAACAGTTGATAA
46[114]	TTAGGTCATTTTTGCGGATGCTCCTTTTGATAAGACG
48[114]	CCAGAAGCCCGAAAGACTTTCAAAAAGATTAAGAGGG
50[114]	GACTCCCCCTCAAATGCTTATAAATATTCATTGAAGG
52[114]	TCGAGTAAGAGCAACACTAAGGAATTACGAGGCATAC
54[111]	CTCTTAATAAAACGAACTGAAGAAAAATCTACGGA
56[111]	CACGTAGTAAATTGGGCTTAGAAACACCAGAACGAAA
58[111]	TAAGCTGACCTTCATCAACAGGCGCATAGGCTGAG
60[111]	TGCATAAATTGTGTCGAAATTTGTATCATCGCCTGGC
63[40]	AAAACATAGCGATAGCTTTTAGAATCCTTGAAAGA
81[40]	GGACAACAATAGATAAGTCGAACGCGCCTGTTTATGT
99[40]	TAAGACGGGAGAATTAACCAGGGAAGCGCATTAGA
117[40]	CGGATTACCATTAGCAAGGAATCACCAGTAGCACCAA
135[40]	ACATGCCCCCTGCCTATTCGTATAAACAGTTAATA
137[48]	ACGCAGGCGGATAAGTGCCGGGTTTTGCTCAGTACCA
139[48]	CAACGCCACCCTCAGAACCGCCACCCTCAGAACAA
141[48]	AAACACCAGTACAAACTACTAACACTGAGTTTCGTCC
143[48]	TAAATGAATTTTCTGTATTCCAGACGTTAGTAAGC

SAB1-probe

88[50]	CCCAATAGGAAGTACAAACTAC-GGAGGGAGGG
94[44]	GATATAAGTATAGTGACACAGACAGCCCTCAT-GGAGGGAGGG

104[50] CTTTTGATGATGTCAGTGCCTT-GGAGGGAGGG

110[44] CATTGACAGGAGGATTTAAGCGTCATACATGG-GGAGGGAGGG

112[44] GCCACCAGAACCATTAACGGGACAGGAGTATAGGTGTATCAC-GGAGGGAGGG

85[115] TTTCATCGTAGGACGTCTTTCCTGAATCTAAGTTACCAGAAG-CCAGCCAGCC

87[115] GCAAGCAAATCAGGCTTATTTTGCACCCAGCT-CCAGCCAGCC

93[109] ACAATTTTATCCAGAGCCTAAT-CCAGCCAGCC

103[115] GTAAGCAGATAGCTATAATAGAAAATTCATAT-CCAGCCAGCC

109[109] CATACATAAAGACGGAATAAGT-CCAGCCAGCC

SAB2-left half cage

1[16] TTTTCAGTACAAACTACAACCACTGAGTTTCGTCACTTTT

3[16] TTTTAATTTTCTCAGCTTTCCGGCATTTT

5[16] TTTTTCACGTTGGAGATCTTTTT

7[16] TTTTATACCGATAGTTGCGCTTTCTTAAACAGCTTGTTTT

11[13] TTTTCCATTAAACGGCAAGCGCGAAATTTT

12[31] GATTATACGTAAAATATGTTTAGAGTCACCCTGTTAAAGGCCGCTT TTTTTT

13[13] TTTTCAAAGTACAACAACCGAACTGATTTT

14[31] CATAAGGGGGAGATTTAAGAAGTTTTGCCTTTT

15[13] TTTTCCAACTTTGAAAACGTAACAAATTTT

16[31] CCCAAATCAGAGGACACCCTCGTTTACCATTTT

17[13] TTTTGCTGCTCATTCATGCGATTTTATTTT

18[31] ATTACCTTAGTGAATATACGAGGCATAGTTTTT

19[13] TTTTAGAACTGGCTCCGGTTTT

20[39] TAATAAAACGAACTAAATTATACCGATTTAGGAATACTTTT

21[21] TTTTAACAACATTATGCTTCAAATTCAAATAGAGAGTACCTTTATT TT

23[19] TTTTCACATTCAACTAATGAAAAAGATTAAGAGGAATTTT

25[19] TTTTAAGAGCAACACTAGACTATTAAATCAAAATCAACATGTTTTA TTTT

27[19] TTTTGACGACGATAAAAACGACAGTTCAGAAAACGATTTT

29[19] TTTTAGAGGGGGTAATAATAAATATAGCGTCCAGTAGATTTAGTTT TT

31[21] TTTTGATTCATTGAATCCTTTT

33[13] TTTTCCCTCAAATGCTTTAAGGTGTGTCTGGAAGTTTTTT

35[13] TTTTGAATGACCATATAGTCAGAAGCTTTT

37[13] TTTTAAAGCGGATTGCATCAACAGGTCATTTTTGCGTTTT

39[13] TTTTGCCCGAAAGACGCGTTTT

41[21] TTTTAACCAGACCGGACATTATGAAAGCTAATCAACGCAAGGATT TTT

43[19] TTTTATTGCTCCTTTTGCATAAATTAAGCAATAAAGTTTT

45[19] TTTTGATGGCTTAGAGCCCAATAAATACTAATATGAGAAAGGCCG GTTTT

47[19] TTTTAATATGCAACTAAAAACGCGAGCTGAAAAGGTTTTT

49[19] TTTTTCATTCCATATAAGTCAATAAACCATTAGATTT

51[21] TTTTTTGCCTGTTTAGCTTTTT

53[13] TTTTATATTTTCATTTGGGGTCCAATATGATATTCATTTT

55[13] TTTTGGCATCAATTCTCATACAGGCATTTT

57[13] TTTTAGGCAAAGAATTAGCAAGCATATATTTTAAATTTTT

59[13] TTTTCCTCAGAGCAT

61[25] TTTTCCCTGTACATTTTTTCATTAAATCTGGCCTTCCTGTTTTT

63[19] TTTTAAAAATTTTTAGATCCTAAACGTTAATATTTTTTTT

65[19] TTTTGCAATGCCTGAGTAAACAGGAGGTTGATAATTGACCGTAATG TTTT

67[19] TTTTAGACAGTCAAATCTGTACCCCTTTT

69[19] TTTTACCGTTCTAGCTGGAGCAAACATCAGGTCACTC

70[27] TTGAAAAATCTCGCGAATAATAATTTTTTTTT

71[17] TTTTAAAGGCTAAGAGAATCGATTTT

73[13] TTTTTGAACGGTAATCGTAAAACTGCATCTGCCAGTTTTT

76[23] AGATTGTATAATTTT

77[13] TTTTGCAAATATTTAAATTGTTTCCCGTCGGATTCTTTTT

79[13] TTTTGTTAAAATTCG

81[25] TTTTACCAATAGTCGACTCAGTGCCAAGAAATTGTTATCCTTTT

83[19] TTTTAGCCAGCTTTCATATACAGTCACGACGTTGTATTTT

85[19] TTTTCCGTGGGAACAAACAAGGCGAAGCTGGCGAACTCACATTAA TTTTT

87[19] TTTTGGATAGGTCACGTGCTCGGTGCGGGCCTCTTCTTTT

89[19] TTTTTTGAGGGGACGACGCCATTCACGGAAACCCGTATTGGGCGTT TT

90[27] CAGCGTATGGGACAGACGTTAGTAAATGTTTT

91[11] TTTTCCGCTTCTGGTGCGGCTGCGCAACTTTT

93[13] TTTTTGTTGGGAAGGGCGATATTGTCGTGCCAGCTGTTTT

95[13] TTTTGCTATTACGCCTTAAGTTGGGTTTTT

97[13] TTTTAACGCCAGGGTTTTCCAAAGTGTAAAGCCTGGTTTT

99[13] TTTTAAACGACGGCCTAGAGGATCCCCGTTTT

101[11] TTTTGGTACCGAGCTCGAATTCGTACAAAGGGCATTAAAGA

103[19] TTTTGCTCACAATTCCATGTTGTTCAGAATAGC

105[19] TTTTGGTGCCTAATGAGCGAAATCGGAAAATCC

107[19] TTTTTGCGTTGCGCTCAAGCGGTCCCCTGGCCC

]

109[19 TTTTCATTAATGAATCGAGACGGGCAACAGCTGATTTTTT

]

111[21 TTTTCCAGGGTGGTTTTTCTTTTTACCGTAAGCCTGTAG

]

113[13 TTTTGCCCTTCACCGACGCTGGTTTGTTTT

]

115[13 TTTTCCCCAGCAGGCGCAAAATCCCTTTTT

]

117[13 TTTTTATAAATCAAACAGTTTGGAACTTTT

]

119[13 TTTTAAGAGTCCACT

]

121[24 TTTTGAAAAACCGTCTATCATCCAACGTATCATGG

]

0[55] CCAATAGGAACCCATGATAACGTGTTAGAGAGG

1[40] CATTCCACAGTTTTGTTTAAAAATCCATCAGGA

1[72] TCGAGAGGTCAGTACCAGGCGGATTAACAGTG

1[88] AAGTATAGACCCTCAGAGCCACCACCCTCATTTTCAGGGAAAGTG
CCG

2[55] CGATCTAAAGACAGCCAAGGGATTCTTTCCTCGCTTTGAC

3[40] AACAACTTAACAACTAGAACCTACTAAGGAGAG

3[72] CCCGTATAGGGTCAGTGCCTTGAGCACAAACAAATAAATCGATTG GCC

4[55] TAGAAAGGTCAACAGTTTCAGCGGTAGCGTAA

4[87] TTTTAACGAACAGTTAATGCCCCCATTAGCGGGGTTTTGCGTTGAT AT

5[40] AGGCTCCATTGCTTTCATTTTAGTTGAATTCTGC

6[55] TTATCAGCAAAGGAGCAACAGAAACATA

6[71] TTGATATTCGCCTCCCTCAGAGCCGAGCCACCACCGGAACCAGTA GCG

7[40] ACAACAACCTGAGGCTCATTACCGCTTATCC

7[88] CAGAACCGTTGAGGCAGGTCAGACCTCATTAAAGCCAGAAGTAAT AAG

8[55] TTCGGTCGCATCGCCCTAATGGTTTAAT

9[40] AAAGACAGCTTTGAGGCACTACGA

9[72] ACAGAATCATAGCAGCGTGAATTATCACCGTCAAATTATT

10[31] CTTTTTCATGAGGAAGGCGGGATC

10[55] TACAGAGGCATCGGAAATAGAAGGCGCCCAATTTTT

10[87] AACCATCGAAGTTTGCCTTTAGCGAAAATCACCGGAACCAGCCAC CCT

11[48] AGGCACCAAAACACTCGCGTTTTAGCGAA

11[64] CGAAAGAGACCGTAATGCAACGGC

12[63] ATACACTAACCTAAAAAATCAGATCGAGGGTACCGATATA

12[79] CATTAAAGTTTATTTTGTCACAATGACACCACGGAATAAGTACCCA AA

12[95] ATTGACGGACCGACTTGAGCCATTGAAACGTCACCAATGA

13[48] AATTGTGTCGGAACGATTTTGAAGCCTTA

15[48] ACCAGGCGTTGACAAGTATCCTGAATCTT

15[64] GGCTGACCCTCCATGTTACTTAGCCGAAATCCGCGACCTGGCAAA AGA

15[80] AGAACTGGCGCAATAATAACGGAAAGAGCAAGAAACAATGGTTA AGCC

15[96] AGACTCCTATAAAAGAAACGCAAACAATAGAAAATTCATAAGGTA AAT

17[48] GAAACACCTAATTTCATTTCCAGATATTATTTAACG

18[63] AGATGGTTAGAACGAGTAGTAAATTTCATCAAGAGTAATCCATAG GCT

18[79] CAATAATAAAAACAGGGAAGCGCATTAGACGGGAGAATTAAACC CACA

18[95] AGAATTGAAAATAGCAATAGCTATAAGGAAACCGAGGAAACATG ATTA

19[58] GAGAGAAACAGCCAGCCTAATTTGCCAGTT

22[39] TCAGTTGAAGTCAGGACATTGTGA

22[71] ACAAAATAATAACATATGGGCTTG

23[40] CATAAGTCACTTTAATCGTTGGGAAGACTTTACA

24[38] AAGGAATAGGCTTGCATTCATTA

24[60] ACCAACGCTAACGATCCTAAT

25[41] ACAATTTAACCGGATCCTGACGA

26[41] TTTGCACTAAGATGAACGCGGTCAAT

26[60] AATCAAGATTAGTATAATCGG

27[39] TAGCGAAGGGGCGCAGAGTGTACAG

28[37] TTGCAAGTATCATCCCCCCAGC

28[60] CCTCCCGACTTGCCACTCATCCTGTCTTTGTATCATATGCGT

29[42] CGCGAGATCTTTGAGCCTGATA

30[40] GGTATTAAACGTAATGCACTAAAGA

32[51] CATCACCGACCGACCGGAATACGCGAGAATAACTATTTTT

32[66] AGCCGTTTTTAAGCAAGCA

33[56] GAGAACAAGAATAAACTGTGATAAATAAGGCG

36[55] TTACGAGCATAAAGCCAACGC

38[55] TGTTTATCACGCCAACTAATAAGAATTAATTAACCTTGCTCTTTTTT
A

39[52] CGCCAAACAACAAAAGTACCGACAAAAGAGTGAATA

40[39] TAATTCGATACAGGTAGAAAGCCAATCTACGT

42[38] AGGATTATCGCGTTTATAAGTCCTGCAGATA

42[71] GGCATTTTCGAGCCAGATGTAATTTAGGCAGA

43[41] TTTAACAAACAATAGTAATGCAGATCATTCA

44[40] AGAATCAGAAGAAAAATTTTACCCTTCACCAGCT

44[60] TCAACAGTAGGGCACGCTGAGATTTTCCCAAAC

45[39] CTGAATAGTATGTAGAAAATATCCCAGCCGCCAA

46[37] TGTAGCATCAGGTCTTCCAAGAACCAAAA

46[60] TATACAAATTCTTCTTTTTAAAAAATCATTACAAAATTGAG

47[41] CTGTTTACCTTATCAACCAATCATGCTAT

48[40] ACTAGAACGATTAAACCGAATCGTCGTACTAAGAA

48[71] TTTTTTAAATAAGCA

49[39] TTCCCAAATGTAGGAATAAGTACCGGGGGAGGCTT

50[37] GAACGAATACTGCGTGCAGGGACAGCAGCG

50[63] CCTAAATTACGCATAAGTATCGGT

51[52] TTCAAAACTTTTAATTGCGTAGATT

51[56] TTTTTTTTCTTCTGA

54[66] GGTTGGGTTATTTTT

57[56] TTTTAAGAGTCAATA

61[39] TGCGGGTACTCTGTAAATACCAAAAAAGCAAACTCCAATATTGTTC
AGC

61[56] ATGGAAACCTAATAGATTTAGAAGAATCAACACAATCAATATCTG
GTC

62[38] CTTTATTATCGGTTGCTTGAAAAATAGCCATA

63[41] ATCAAGATTAGAATCTCGTCGCTGAACAGGTC

63[52] AAAATTCATTTGTTTGAGGATTAGAGCCAGGAAGGT

64[40] GATGAACTCGATAGCTTATTAACATTTAATTG

64[51] CAAATTTTAAAAAACAATTCCAAACCCTGTTG

65[39] AGGTAAAGTAGGTCTGAAGATTAAGTTAATTG

66[38] AAAAGGGGTAGTAGCGCTGATGCAGTAAAAGC

66[71] GGATTCGCCTGATTGCCGGGAGAAATTCATCA

67[42] AGTACCATGTAAATGAGACTACACCATAATGC

67[52] ACATTTTGAATAGAGCGGAAGCGGAACATCTAAAGCATCAC

68[39] ATATAATCAATCGCAACGCAAATGCAGTTGA

68[60] TTCAGGTTTAACGTACTTCTGATATAATCATTAACACCGCCT

69[39] AATGCCAGATCAAATATGACAAAGACATAATT

70[38] GGTAGCTATACATTTGAGGTGAACGACAATG

70[62] CACGTAACTTTAATTAGTGAGAA

71[52] TCAAAATAATGGGCAGAAGATAAAA

71[56] TTTTTTTAATTATTT

81[39] CATCAATTGGTCAATAGAATCAGCTATACTTT

81[56] TATCTAAATTGACGCT

82[38] TTCGCGTTTTTGTTAGTATTAAAACCACAAAC

82[71] AGTTGGCATATTTT

83[40] AATGTTATGACAACTCATAATACAAATAGAAGC

84[38] GTAACAAGCCCGAACAGCCCCAAAATGTGT

84[60] CTTGCTGAACCTCCAGAGATAGATTCACCTGGTAATATCCAG

85[42] GAAAAAAAGAAACCGTTATTAAAGAAGAT

86[39] CCAGCCGGATCAGAAACAATCATAACCCAGTAAC

86[60] GCAACAGTGCCACAGAATACGGAAC

87[39] GATGGGAGTCTGATTGTACCAGAAGCCAAGATTC

88[37] TAACCGTAGCATGTAGAGTCTGATAAATT

88[60] CAGAGGTGAGGCGACTGATAGTGGCACAGAGTAAAAGAGTCT

89[39] TCGGCCCCAAAGGGTTATTGGATTATCAGATGA

90[38] AGATCGCATTGCCTGAAGGAATTCAAAAAAA

90[52] TTTACGAAACCGATTT

92[55] CCCTAAAAAGGAACGGCAGTGAGGATGCGCCGTAACCACC

96[51] CCTTGATTAGTAACTATCGGCGGCGAACGATTTAGA

101[39] TCATAGGCCTGAAATGGGCCTGCAGGGAACGC

102[37] CTGTGTGCTTGCATGACCAGTACAACATTA

102[60] AACAATATTACCGCACTAAATTTTTGGGG

103[39] TACGAGTGCAGTCACACATTATTTAGAAAAATAA

104[38] GCATAAAGGGACATTATGTGCTGCGGAGCAAAT

105[42] TTCTTTCTGACCTGCTGGCCAAAAAGAGCGA

105[64] TTTTTTTACTTGCCT

106[39] TTGTAGCTAAAGGGGGTTTGAATGTGGTGTA

106[60] GTCCATCACGCAACGCTGGCAAAGCGAAA

107[39 CTTTCCCCGACAATATTAAAGCGTAGCTGAGAG

]

108[38 GAAACCTAGTCTTTACGCCATTCGACAGTA

]

109[39 CGCGGGGACCATCGCCAATGCGCGAGTCCGCATCG

]

109[64 TTTTTTTAATCCTGA

]

110[38 CGGTTTGAGGCAAAGCGTCTTTCTTTTGCTA

]

112[47 GAGCACGTCGCGCTTACCAAGTCGG

]

113[32 TGAGAGAGCACCAGTGGCCAACG

]

114[47 ACACCCGCCGCTAGGGATTAACCG

]

115[32 TGTTTGATTTGCAGCACTGCCCG

]

116[47 GGAGCGGGGGGAAAGCCCTCCGGAA

]

117[32 CCGAGATAGGTGGTTCTGAGCAATAC

]

118[47 GCTTGACGCCGTAAAGCCACTGTTTC

]

119[32 ACGTGGACGGGTTGAGCACAACA

]

0[111] TTTTCACCCTCAGAACCGCCCCCGGAATAGGTGTATTTTT

2[111] TTTTCAAGAGAAGGATTAGGTGCCTATTTCGGAACCTTTT

4[111] TTTTATACAGGAGTGTACTGTGGAAAGCGCAGTCTCTTTT

6[111] TTTTCAGCATTGACAGGAGGCCACCCTCAGAGCCACTTTT

8[111] TTTTCCATCTTTTCATAATCTCAGACTGTAGCGCGTTTTT

10[111 TTTTCAAGGCCGTGGGAATTAGAGCCAGTTTT

]

12[119 TTTTCCGATTGAGGGAGGGATGGTTTACCAGCGCCATTTT

]

14[119 TTTTATAAAGGTGGCAACATTATTACGCAGTATGTTTTTT

]

16[119 TTTTCGAACAAAGTTACCAGCTTACCGAAGCCCTTTTTTT

]

18[119 TTTTCTAATATCAGAGAGATACTGAACACCCTGAACTTTT

]

20[62] TTTTGAAAATAGCAGCAAAATCCAAATAAGAAACGACGACAATTT

TT

40[71] TTTTTCCAGACGATTTTTTGTTTT

80[71] TTTTACTAACAAAGTACATATTTT

82[51] TTTTAAAGCATTGGCACAATCGTCATTGCAACAGGAAAAATTTT

104[71] TTTTGAGTAGAAGAACTCAAATAACATCAGGGAAGAAGTGTAGCTTTT

108[71] GAAGTGTTTTTATAATTACGCCAGCTATGGTTGTTAGAATCAGAGCGGTTTT

110[71] TTTTAACAGGAGGCCGATTACTCATAGTTAGCAAGCTTTT

114[63] TTTTGCTGCGCGCTACAGGGTTTT

118[63] TTTTGAGCCCCCGTGGCGAGTTTT

120[47] TCGAGGTGCGATGGCCCACTACGTTTTT

120[63] TTTTATCAAGTTCGGAACCCTTTT

SAB2-right half cage

1[136] TTTTATTGACGGACCGACTTTTTT

3[136] TTTTTTTGGGAAACCATTAGTTTT

5[136] TTTTCGGAAACGATCAGTAGTTTT

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APPENDIX F

CO-AUTHOR APPROVAL

I verify that the following co-authors have approved of my use of our publications in my dissertation.

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