## Supporting Information

## Low-entropy lattices engineered through bridged DNA origami frames

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## Materials

M13mp18 DNA was purchased from Bayou Biolabs, America. All short oligonucleotides were purchased from Sangon Biotech Co. Ltd (Shanghai, China). 10 nm AuNPs were purchased from Ted Pella Inc. Carbon-coated copper grids were purchased from Beijing Zhongjingkeyi Technology Co. Ltd (Beijing, China).

## Design and synthesis of DNA origami frames

Octahedron, cube, hexagonal bipyramid and elongated octahedron DNA origami frames were designed by caDNAno software (downloaded from http://cadnano.org/). In the design, each edge of these frames was composed of a six-helix bundle. For the octahedral and cubic frames, the length of all the edges is 88 base pairs. For each hexagonal bipyramid, the bottom edges of the hexagonal pyramid are 46 base pairs in length, and the length of side edges was 67 base pairs. For an elongated octahedral frame, the length of four bottom edges is 88 base pairs that is equal to the octahedron's, and its side edges are 109 base pairs in length.

DNA origami frames were folded by mixing 10 nM M13mp18 scaffold DNA, 100 nM of each designed staple oligonucleotide (including a certain number of capture DNAs for encaging 10 nm AuNPs inside) in a buffer solution containing 12.5 mM magnesium acetate, 1 mM EDTA and 40 mM tris acetate with a pH around 8.3. The mixed solution was then cooled by a gradient according to the annealing procedure below:
$1.90^{\circ} \mathrm{C} \quad 25 \mathrm{sec}$
$2.90{ }^{\circ} \mathrm{C} \sim 85^{\circ} \mathrm{C} \quad-0.1^{\circ} \mathrm{C} / 5 \mathrm{sec}$
$3.85{ }^{\circ} \mathrm{C} \sim 65^{\circ} \mathrm{C} \quad-0.1^{\circ} \mathrm{C} / 30 \mathrm{sec}$
$4.65^{\circ} \mathrm{C} \sim 40^{\circ} \mathrm{C}-0.1^{\circ} \mathrm{C} / 4 \mathrm{~min}$
$5.40{ }^{\circ} \mathrm{C} \sim 32{ }^{\circ} \mathrm{C}-0.1^{\circ} \mathrm{C} / 2 \mathrm{~min}$
$6.32{ }^{\circ} \mathrm{C} \sim 20^{\circ} \mathrm{C}-0.1^{\circ} \mathrm{C} / 1 \mathrm{~min}$
7. Hold at $20^{\circ} \mathrm{C}$

Prepared DNA origami frames were stored at room temperature.

## DNA functionalization of gold nanoparticles

$200 \mu \mathrm{M}$ of 3 '-thiolated oligonucleotides aqueous solution were incubated with tris-(2carboxyethyl) phosphine (TCEP) in a ratio of 1:100 (DNA: TCEP). The mixed solution was kept in an ice bath for 1.5 hours, and then purified using a size exclusion column (G-25, GE Healthcare) to remove redundant TCEP. Treated thiolated oligonucleotides were mixed with 10 nm spherical gold nanoparticles with a ratio of $300: 1$, followed by buffering the solution to obtain 10 mM phosphate buffer ( pH 7 ) after 1.5 hours. In the subsequent salt-aging process, 2

M NaCl solution was slowly added into the solution in five steps to reach a final NaCl concentration of 0.3 M . The solution was aged at room temperature for 18 hours. Excess oligonucleotides were then removed by centrifuging ( $20,000 \mathrm{rcf}, 1 \mathrm{~h}$ ) the solution 4 times and resuspending with the washing buffer containing 0.1 M NaCl and 10 mM phosphate. The concentration of AuNPs was measured by UV-vis spectrometer and calculated with LambertBeer law.

## Encaging AuNPs inside DNA origami frames for conjugated monomers

In order to insert AuNPs inside the DNA origami frames, functionalized AuNPs and prepared DNA origami frames were mixed at a ratio of $1.2: 1$. The mixed solution was then cooling from $50^{\circ} \mathrm{C}$ to $20^{\circ} \mathrm{C}$ at a rate of $0.6^{\circ} \mathrm{C} \mathrm{h}^{-1}$ to obtain a high yield.

## Fabrication of 3D lattices and 2D planar structures

According to the design of each system, corresponding bridging DNA strands and functionalized AuNPs were added into the prepared DNA origami frame solution. The molar ratio between the frames, bridged DNA strands and AuNPs was 1:1:1.2. To reduce the effect of dilution, a few of 125 mM magnesium acetate solution was added to adjust the magnesium salt concentration to original 12.5 mM . The mixed solution was then slowly cooled by a gradient according to the annealing procedure below:

1. $20^{\circ} \mathrm{C} \sim 50^{\circ} \mathrm{C}+1^{\circ} \mathrm{C} / \mathrm{min}$
$2.50{ }^{\circ} \mathrm{C} \sim 20^{\circ} \mathrm{C}-0.2^{\circ} \mathrm{C} / 1 \mathrm{~h}$
2. Hold at $20^{\circ} \mathrm{C}$

This procedure was repeated another two times to produce the final sample. Prepared 3D lattices and 2D planar structures were stored at $4{ }^{\circ} \mathrm{C}$.

## Silicification of DNA frameworks

The supernatant of the prepared 3D lattice solution was pipetted out slowly without disturbing bottom aggregates, followed by buffering with a solution containing 7.0 mM magnesium acetate, 1 mM EDTA and 40 mM tris acetate to remove free staple DNAs and AuNPs. $0.79 \mu \mathrm{~L}$ of $10 \%(\mathrm{v} / \mathrm{v})$ N-trimethoxylsilylpropyl-N,N,N-trimethylammonium chloride (TMAPS) methanol solution was then mixed with the lattice solution and shaken at $20^{\circ} \mathrm{C}$ for 20 min . Subsequently, $0.90 \mu \mathrm{~L} 10 \%(\mathrm{v} / \mathrm{v})$ tetraethoxysilane (TEOS) methanol solution was added and kept shaking at $20{ }^{\circ} \mathrm{C}$ for $30 \mathrm{~min} .{ }^{1}$ After the shaking, the solution was allowed to stand for about 12 hours. The supernatant of the final solution was pipetted out and the aggregates were washed slowly with ultrapure water for several times.

## TEM sample preparation and imaging

The sample solution of $5 \mu \mathrm{~L}$ was dropped onto a glow-discharged carbon-coated grid and deposited for 4 minutes. The droplet was then wicked away by a piece of filter paper along the edge of the grid. $5 \mu \mathrm{~L}$ of $2 \%$ ( $\mathrm{w} / \mathrm{v}$ ) uranyl acetate aqueous solution was then dropped onto the carbon-coated grid. After staining for 8 seconds, the excess staining solution was wicked away in the same manner and dried in the air. The negative-stained sample was imaged by a JEM2800 TEM operating at 200 kV .

## SEM of siliconized samples

The silicon slice, as the SEM substrate, was carefully cleaned with ethanol and water in advance. $6 \mu \mathrm{~L}$ siliconized sample solution was dropped onto the silicon slice and dried under an infrared light. The sample was then imaged on the Zeiss Ultra Plus FE-SEM.

## SAXS experimental methods

The SAXS measurements were conducted at the beamline BL19U2 at Shanghai Synchrotron Radiation Facility (SSRF). $50 \mu \mathrm{~L}$ of the sample solution was transferred to a glass capillary with an inner diameter of 1 mm . The capillary was sealed with wax to maintain the liquid phase and the aggregates sedimentated at its bottom. The 2D scattering data were collected on a Dectris Pilatus 2 M pixel-array detector with 12 keV (wavelength $\lambda=0.932 \AA$ ) incident X-rays.

Area images were integrated into a 1D $\mathrm{I}(q)$ scattering curve according to the function $\boldsymbol{q}=$ $4 \frac{\pi}{\lambda} \boldsymbol{\operatorname { s i n }}\left(\frac{\theta}{2}\right)$ of the scattering vector $q$, where $\theta$ is the scattering angle. ${ }^{2}$ The structure factor $\mathrm{S}(q)$ was obtained by dividing $\mathrm{I}(q)$ by the corresponding particle form factor $\mathrm{P}(q)$.

## The geometric models for polyhedral DNA origami frames

The polyhedral DNA origami frame geometric models are shown in Figure S2, and described using $d_{1}, d_{2}, L_{1}, L_{2}, L_{3}$ and $L_{4}$ as the width and length of the polyhedral edges. The exact values are calculated based on the following constants: the helix width of DNA is 2.0 nm and the distance between adjacent base pairs is 0.34 nm . Stereo modeling shows the simplified frame geometry accurate to each double helix (represented by the cylinder). Potential deformations are not involved in these models.

## Close-packed models and bridge pattern models for 3D lattices

According to the pre-designed arrangements of polyhedral frames, we constructed a series of close-packed 3D lattice models with no gaps (Figures S15-S17 and S34). Considering the
steric hindrance caused by adjacent structures, the vertices of DNA origami frames just touch each other. At bridged junctions, both the octahedral and cubic frames are illustrated with a pair of vertices as shown in Figures S6 and S8. Due to the difference in crystal growth directions, the hexagonal bipyramid and binary systems exhibit two non-identical crystallographic axis directions respectively (Figures S7 and S31). The lattice parameter values of these models calculated according to the space analytic geometry are as follows:

Geometric constants involved:

$$
\begin{aligned}
& d_{1}=5.5 \mathrm{~nm} ; d_{2}=6.0 \mathrm{~nm} ; \\
& L_{1}=29.9 \mathrm{~nm} ; L_{2}=22.8 \mathrm{~nm} ; L_{3}=15.7 \mathrm{~nm} ; L_{4}=37.1 \mathrm{~nm}
\end{aligned}
$$

Octahedron model:

$$
a=b=c=\sqrt{2}\left(L_{1}+d_{1}\right)=50.1 \mathrm{~nm}
$$

Cube model:

$$
a=b=c=2\left(L_{1}+\frac{d_{2}}{2}\right)=65.8 \mathrm{~nm}
$$

Hexagonal bipyramid model:

$$
\begin{gathered}
a=b=2\left(L_{3}+d_{1}\right)=42.4 \mathrm{~nm} \\
c=2 \sqrt{L_{2}^{2}-L_{3}^{2}}+\sqrt{2} d_{2}=41.6 \mathrm{~nm}
\end{gathered}
$$

Binary system model:

$$
\begin{gathered}
a=b=\sqrt{2}\left(L_{1}+d_{1}\right)=50.1 \mathrm{~nm} \\
c=\frac{\sqrt{2}\left(L_{1}+d_{1}\right)}{2}+\sqrt{\left(L_{4}+d_{1}\right)^{2}-\left(\frac{\sqrt{2}\left(L_{1}+d_{1}\right)}{2}\right)^{2}}=59.4 \mathrm{~nm}
\end{gathered}
$$

## SAXS model fitting and lattice parameter calculation

The theoretical scattering data of the lattice structures was calculated by using PowderCell software. For the simple cubic and body-centered cubic lattices with defined structural parameters, we calibrated the first SAXS peak $\left(q_{1}\right)$ of the experimental data with the first peak in theoretical spectrums to compare the peak positions and the intensity ratio. We then calculated the experimental lattice parameters in cubic lattices ( $\boldsymbol{a}=\boldsymbol{b}=\boldsymbol{c}$ ) based on the peak position of $q_{1}$. The three lattice parameters of the simple hexagonal and tetragonal structures are not equal $(\boldsymbol{a}=\boldsymbol{b} \neq \boldsymbol{c})$. We first calculated their experimental values using the first two SAXS peaks ( $q_{1}$ and $q_{2}$ ), and then performed the calibration. The lattice parameter values calculated from the experimental data are as follows:

Simple cubic lattice, octahedron:

$$
a=b=c=\frac{2 \pi}{q_{1}}=50.0 \mathrm{~nm}\left(q_{1}=0.1258 \mathrm{~nm}^{-1}\right)
$$

Body-centered cubic lattice, cube:

$$
a=b=c=\frac{2 \sqrt{2} \pi}{q_{1}}=65.9 \mathrm{~nm}\left(q_{1}=0.1349 \mathrm{~nm}^{-1}\right)
$$

Simple hexagonal lattice, hexagonal bipyramid:

$$
\begin{gathered}
a=b=\frac{4 \sqrt{3} \pi}{3 q_{2}}=43.0 \mathrm{~nm}\left(q_{2}=0.1687 \mathrm{~nm}^{-1}\right) \\
c=\frac{2 \pi}{q_{1}}=42.1 \mathrm{~nm}\left(q_{1}=0.1494 \mathrm{~nm}^{-1}\right)
\end{gathered}
$$

Simple tetragonal lattice, binary system:

$$
\begin{gathered}
a=b=\frac{2 \pi}{q_{2}}=50.0 \mathrm{~nm}\left(q_{2}=0.1258 \mathrm{~nm}^{-1}\right) \\
c=\frac{2 \pi}{q_{1}}=58.4 \mathrm{~nm}\left(q_{1}=0.1076 \mathrm{~nm}^{-1}\right)
\end{gathered}
$$

## DNA Sequences

a. Staple strands of octahedral DNA origami frame

Oct-staple-1 TGTAGCATTCCAACGTTAGTAAATGAAGTGCCGCGCCACCCT
Oct-staple-2 CTTAAACAGCTTATATATTCGGTCGCTTGATGGGGAACAAGA
Oct-staple-3 AATAGCAATAGCACCAGAAGGAAACCTAAAGCCACTGGTAAT
Oct-staple-4 AGCTTTCATCAACGGATTGACCGTAAAATCGTATAATATTTT
Oct-staple-5 CTTCATCAAGAGAAATCAACGTAACAGAGATTTGTCAATCAT
Oct-staple-6 AAAGATTCATCAGGAATTACGAGGCATGCTCATCCTTATGCG
Oct-staple-7 ATAAATCATACATAAATCGGTTGTACTGTGCTGGCATGCCTG
Oct-staple-8 CAACGCTCAACAGCAGAGGCATTTTCAATCCAATGATAAATA
Oct-staple-9 AAACGAAAGAGGGCGAAACAAAGTACTGACTATATTCGAGCT
Oct-staple-10 AGAGCCTAATTTGATTTTTTGTTTAAATCCTGAAATAAAGAA
Oct-staple-11 GACAGGAGGTTGAAACAAATAAATCCGCCCCCTCCGCCACCC
Oct-staple-12 TCATATGGTTTACGATTGAGGGAGGGAAACGCAATACATACA
Oct-staple-13 GGTAGCTATTTTAGAGAATCGATGAAAACATTAAATGTGTAG
Oct-staple-14 GAAACATGAAAGCTCAGTACCAGGCGAAAAATGCTGAACAAA
Oct-staple-15 ATCAAAATCATATATGTAAATGCTGAACAAACACTTGCTTCT
Oct-staple-16 AACGGGTATTAAGGAATCATTACCGCCAGTAATTCAACAATA
Oct-staple-17 ACTGTTGGGAAGCAGCTGGCGAAAGGATAGGTCAAGATCGCA
Oct-staple-18 CAGAATCAAGTTTCGGCATTTTCGGTTAAATATATCACCAGT
Oct-staple-19 GCTCACAATTCCGTGAGCTAACTCACTGGAAGTAATGGTCAA

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TGATTGCTTTGAGCAAAAGAAGATGAAATAGCAGAGGTTTTG GGCCCTGAGAGAAGCAGGCGAAAATCATTGCGTAGAGGCGGT TTTGCGGATGGCCAACTAAAGTACGGGCTTGCAGCTACAGAG CAAATGCTTTAAAAAATCAGGTCTTTAAGAGCAGCCAGAGGG TTTGCGGAACAATGGCAATTCATCAATCTGTATAATAATTTT GTCACCAGAGCCATGGTGAATTATCACCAATCAGAAAAGCCT GGACAGAGTTACTTTGTCGAAATCCGCGTGTATCACCGTACG CAACATGATTTACGAGCATGGAATAAGTAAGACGACAATAAA AACCAGACGCTACGTTAATAAAACGAACATACCACATTCAGG TGACCTACTAGAAAAAGCCCCAGGCAAAGCAATTTCATCTTC TGCCGGAAGGGGACTCGTAACCGTGCATTATATTTTAGTTCT AGAACCCCAAATCACCATCTGCGGAATCGAATAAAAATTTTT GCTCCATTGTGTACCGTAACACTGAGTTAGTTAGCGTAACCT AGTACCGAATAGGAACCCAAACGGTGTAACCTCAGGAGGTTT CAGTTTGAATGTTTAGTATCATATGCGTAGAATCGCCATAGC AAGATTGTTTTTTAACCAAGAAACCATCGACCCAAAAACAGG TCAGAGCGCCACCACATAATCAAAATCAGAACGAGTAGTATG GATGGTTGGGAAGAAAAATCCACCAGAAATAATTGGGCTTGA CTCCTTAACGTAGAAACCAATCAATAATTCATCGAGAACAGA AGACACCTTACGCAGAACTGGCATGATTTTCTGTCCAGACAA GCCAGCTAGGCGATAGCTTAGATTAAGACCTTTTTAACCTGT CCGACTTATTAGGAACGCCATCAAAAATGAGTAACAACCCCA GTCCAATAGCGAGAACCAGACGACGATATTCAACGCAAGGGA CCAAAATACAATATGATATTCAACCGTTAGGCTATCAGGTAA AACAGTACTTGAAAACATATGAGACGGGTCTTTTTTAATGGA TTTCACCGCATTAAAGTCGGGAAACCTGATTTGAATTACCCA GAGAATAGAGCCTTACCGTCTATCAAATGGAGCGGAATTAGA ATAATTAAATTTAAAAAACTTTTTCAAACTTTTAACAACGCC GCACCCAGCGTTTTTTATCCGGTATTCTAGGCGAATTATTCA GGAAGCGCCCACAAACAGTTAATGCCCCGACTCCTCAAGATA GTTTGCCTATTCACAGGCAGGTCAGACGCCACCACACCACCC CGCGAGCTTAGTTTTTCCCAATTCTGCGCAAGTGTAAAGCCT AGAAGCAACCAAGCCAAAAGAATACACTAATGCCAAAACTCC ATTAAGTATAAAGCGGCAAGGCAAAGAAACTAATAGGGTACC CAGTGCCTACATGGGAATTTACCGTTCCACAAGTAAGCAGAT ATAAGGCGCCAAAAGTTGAGATTTAGGATAACGGACCAGTCA TGCTAAACAGATGAAGAAACCACCAGAATTTAAAAAAAGGCT CAGCCTTGGTTTTGTATTAAGAGGCTGACTGCCTATATCAGA CGGAATAATTCAACCCAGCGCCAAAGACTTATTTTAACGCAA CGCCTGAATTACCCTAATCTTGACAAGACAGACCATGAAAGA

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ACGCGAGGCTACAACAGTACCTTTTACAAATCGCGCAGAGAA CAGCGAACATTAAAAGAGAGTACCTTTACTGAATATAATGAA GGACGTTTAATTTCGACGAGAAACACCACCACTAATGCAGAT AAAGCGCCAAAGTTTATCTTACCGAAGCCCAATAATGAGTAA GAGCTCGTTGTAAACGCCAGGGTTTTCCAAAGCAATAAAGCC AATTATTGTTTTCATGCCTTTAGCGTCAGATAGCACGGAAAC AAGTTTCAGACAGCCGGGATCGTCACCCTTCTGTAGCTCAAC ACAAAGAAATTTAGGTAGGGCTTAATTGTATACAACGGAATC AACAAAAATAACTAGGTCTGAGAGACTACGCTGAGTTTCCCT CATAACCTAAATCAACAGTTCAGAAAACGTCATAAGGATAGC CACGACGAATTCGTGTGGCATCAATTCTTTAGCAAAATTACG CCTACCAACAGTAATTTTATCCTGAATCAAACAGCCATATGA GATTATAAAGAAACGCCAGTTACAAAATTTACCAACGTCAGA AGTAGATTGAAAAGAATCATGGTCATAGCCGGAAGCATAAGT TAGAATCCATAAATCATTTAACAATTTCTCCCGGCTTAGGTT AAAGGCCAAATATGTTAGAGCTTAATTGATTGCTCCATGAGG CCAAAAGGAAAGGACAACAGTTTCAGCGAATCATCATATTCC GAAATCGATAACCGGATACCGATAGTTGTATCAGCTCCAACG TGAATATTATCAAAATAATGGAAGGGTTAATATTTATCCCAA GAGGAAGCAGGATTCGGGTAAAATACGTAAAACACCCCCCAG GGTTGATTTTCCAGCAGACAGCCCTCATTCGTCACGGGATAG CAAGCCCCCACCCTTAGCCCGGAATAGGACGATCTAAAGTTT TGTAGATATTACGCGGCGATCGGTGCGGGCGCCATCTTCTGG CATCCTATTCAGCTAAAAGGTAAAGTAAAAAGCAAGCCGTTT CAGCTCATATAAGCGTACCCCGGTTGATGTGTCGGATTCTCC CATGTCACAAACGGCATTAAATGTGAGCAATTCGCGTTAAAT AGCGTCACGTATAAGAATTGAGTTAAGCCCTTTTTAAGAAAG TATAAAGCATCGTAACCAAGTACCGCACCGGCTGTAATATCC ATAGCCCGCGAAAATAATTGTATCGGTTCGCCGACAATGAGT AGACAGTTCATATAGGAGAAGCCTTTATAACATTGCCTGAGA AACAGGTCCCGAAATTGCATCAAAAAGATCTTTGATCATCAG ACTGCCCTTGCCCCGTTGCAGCAAGCGGCAACAGCTTTTTCT TCAAAGGGAGATAGCCCTTATAAATCAAGACAACAACCATCG GTAATACGCAAACATGAGAGATCTACAACTAGCTGAGGCCGG GAGATAACATTAGAAGAATAACATAAAAAGGAAGGATTAGGA CAGATATTACCTGAATACCAAGTTACAATCGGGAGCTATTTT CATATAACTAATGAACACAACATACGAGCTGTTTCTTTGGGG ATGTTTTGCTTTTGATCGGAACGAGGGTACTTTTTCTTTTGA GGGGTGCCAGTTGAGACCATTAGATACAATTTTCACTGTGTG CTTCGCTGGGCGCAGACGACAGTATCGGGGCACCGTCGCCAT

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Oct-capture-2

Oct-capture-3

Oct-capture-4

Oct-capture-5

Oct-capture-6

Oct-capture-7

Oct-capture-8

TCAGAGCTGGGTAAACGACGGCCAGTGCGATCCCCGTAGTAG TTAGCGGTACAGAGCGGGAGAATTAACTGCGCTAATTTCGGA GATATTCTAAATTGAGCCGGAACGAGGCCCAACTTGGCGCAT TGTCGTCATAAGTACAGAACCGCCACCCATTTTCACAGTACA CGATTATAAGCGGAGACTTCAAATATCGCGGAAGCCTACGAA AACATGTACGCGAGTGGTTTGAAATACCTAAACACATTCTTA GTCTGGATTTTGCGTTTTAAATGCAATGGTGAGAAATAAATT GCCTTGAATCTTTTCCGGAACCGCCTCCCAGAGCCCAGAGCC CGCTGGTGCTTTCCTGAATCGGCCAACGAGGGTGGTGATTGC TGATTATCAACTTTACAACTAAAGGAATCCAAAAAGTTTGAG ACATAACTTGCCCTAACTTTAATCATTGCATTATAACAACAT GTAGCGCCATTAAATTGGGAATTAGAGCGCAAGGCGCACCGT TTATTTTTACCGACAATGCAGAACGCGCGAAAAATCTTTCCT TTTCAATAGAAGGCAGCGAACCTCCCGATTAGTTGAAACAAT GGGCGACCCCAAAAGTATGTTAGCAAACTAAAAGAGTCACAA AGCCGAAAGTCTCTCTTTTGATGATACAAGTGCCTTAAGAGC GTGGGAAATCATATAAATATTTAAATTGAATTTTTGTCTGGC CCCACGCGCAAAATGGTTGAGTGTTGTTCGTGGACTTGCTTT ATGACCACTCGTTTGGCTTTTGCAAAAGTTAGACTATATTCA TCCAAATCTTCTGAATTATTTGCACGTAGGTTTAACGCTAAC GGGTTATTTAATTACAATATATGTGAGTAATTAATAAGAGTC ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTGGGGTGCCAG TTGAGACCATTAGATACAATTTTCACTGTGTG

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTTCAGAGCTGG GTAAACGACGGCCAGTGCGATCCCCGTAGTAG

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTTTAGCGGTAC AGAGCGGGAGAATTAACTGCGCTAATTTCGGA

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTTGATTATCAA CTTTACAACTAAAGGAATCCAAAAAGTTTGAG ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTGTAGCGCCAT TAAATTGGGAATTAGAGCGCAAGGCGCACCGT ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTAGCCGAAAGT CTCTCTTTTGATGATACAAGTGCCTTAAGAGC

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTGTGGGAAATC ATATAAATATTTAAATTGAATTTTTGTCTGGC

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTCCCACGCGCA AAATGGTTGAGTGTTGTTCGTGGACTTGCTTT

Note: In order to position one gold nanoparticle in the body center of the octahedral frame, 'ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTT' sequence was added in the blue marked staple DNA strands.
b. Bridging strands of octahedral DNA origami frame

Oct-bridge-1 TGTAGCCTTTTGTCAGAGGGTAATTGAGAACACCAAAATAG

Oct-bridge-2
Oct-bridge-3
Oct-bridge-4
Oct-bridge-5
Oct-bridge-6
Oct-bridge-7
Oct-bridge-8
Oct-bridge-9
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Oct-bridge-19
Oct-bridge-20
Oct-bridge-21
Oct-bridge-22
Oct-bridge-23
Oct-bridge-24

CTATTATTCTTTTTGTTAAAATTCGCATTATAAACGTAAACTAG CATTATCATTTTTCAGGTCGACTCTAGAGCAAGCTTCAAGGCG AACATCCATTTTTTCACGTTGAAAATCTTGCGAATGGGATTT AACGCCTTTTGTAAAGATTCAAAAGGCCTGAGTTGACCCT CGGAGAGTTTTCAGAGCCACCACCCTCTCAGAACTCGAGAG GCGCATTTTATTGCGTAGATTTTCAAAACAGATTGTTTG GTCTTTCCTTTTCTCCAGCCAGCTTTCCCCTCAGGACGTTGG TTCGCCTTTTAAGGGAACCGAACTGAGCAGACGGTATCAT GCTGACTTTTAAGCCTTAAATCAAGACTTGCGGAGCAAAT ACAGGTAGTTTTGATAAGTCCTGAACAACTGTTTAAAGAGAA ATTCCAAGTTTTATTTTAAGAACTGGCTTGAATTATCAGTGA GTATAAAGCTTTTGGTAATAGTAAAATGTAAGTTTTACACTAT CCCCCTTTTTAGGCGTTAAATAAGAAGACCGTGTCGCAAG AGTGAATTTTTTTTCAAAGCGAACCAGACCGTTTTATATAGTC CCAACCTATTTTGTAAATCGTCGCTATTGAATAACTCAAGAA CAGCATTTTTTGCTTTGAGGACTAAAGAGCAACGGGGAGTT AGGTCATTTTTTTCAGAACCGCCACCCTCTCAGAGTATTAGC GTAGCGATTTTTAACCTGTTTAGCTATTTTCGCATTCATTC TGTTATCCTTTTAGCACCATTACCATTACAGCAAATGACGGA CCGCCTTTTTTAAAGGTGGCAACATAGTAGAAAATAATAA AATAGAAAATTTTTTTGCGTATTGGGCGCCCGCGGGGTGCGCTC AACAATGATTTTGTCCACTATTAAAGAACCAGTTTTGGTTCC GTGAATTTTTTTAAGTTTTAACGGGGTCGGAGTGTAGAATGG
c. Staple strands of cubic DNA origami frame
cub-staple-1
cub-staple-2
cub-staple-3
cub-staple-4
cub-staple-5
cub-staple-6
cub-staple-7
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GAGTAACAGTGCCATGAAAGTATTAACACGCATAAAGACAGC TAAATAAGGCGTTAGAAAAAGCCTGTACTACCTACGCGAGAA ATAGCTGTTTCCATAAAGTGTAAAGCTGTTGGGCCAGTCACG ATTAGACGGGAGGAGAGATAACCCACTTGATGGGGAACAAGA ACCAGTAGCACCCCGTAATCAGTAGCATTATACATGTTACTT ACGTAATGCCACCATCTTTGACCCCCCAGGAGGAGTCTCTGA AATCGTCATAAAAGTTCAGAAAACGAATAACGCATAGCGAGA TACGCAGTATGTAAAGACACCACGGAAGAATTATTTTGCGGG CGTTTTAGCGAATTGCACCCAGCTACATCCCATGAACAAGCA ATCGCACTCCAGCCATTCAGGCTGCGGCCATCAGCGGATTGA GGTTTATCAGCTATGACAACAACCATTCATAGTGGAGTGAGA TTTGCGGAACAATGGCAATTCATCAATTATCCTATCCCAATC CTCAGAGCCACCAGCCGCCGCCAGCAGAATCAAATCTTTTCA AGCTTAGATTAAAAATCATAGGTCTGACAAACAAATATATGT GAACTAACGGAATTCAACTAATGCAGATTGCTGCAGTTGATT
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GCTTTGATTTTGCGAGGCTTGCAGGGAGAACTATTTCGGAAC GATATTCAGAGCAAAAGCCCTTTTTAAGGAAGGAACTGAGTA TACGAGCCGGGCCTTTGGGTAACGCCAGGCCAGTGCGAATTC TTAAATCCTCACATTCGGGAAACCTGTCCGGGGAGGAAGATT TTAGGAAGCTCAACTGGAAGTTTCATTCAGTAGATAAATCTA TAGTTGCAAAGTTTACAACTTTCAACAGAAAGGAAAGGAGCC CGCTGGTGAGAGATCTGGAGCAAACAAGTGTCAATCCAGTGA AGAGGTCTCTTTACGCATCAAAAAGATTTTTTTAATACTCCAA TAGTGAATTAATTAAATGGAAACAGTACTTCTGTATCCTTGA GAGCGCTGCAAAATGGTTGAGTGTTGTTCGTGGACCATAAAA CTACAACATTAGGATATAAGTATAGCCCAGTACCGCATTTTC AGAACCATCAGACTGCCCCCTTATTAGCAACCAGACACCCTC CTATTATGTCGCTGGGATCGTCACCCTCCAACGGCTTAACGG ACAATAGCTTCTGAATTATTTGCACGTAGGTTTAAAAAGTAA TATAAAATAAAGCCAACATTATGACCCTACGCAAGCATGATT CAAAGCGCTGGCCTGATTCTCCGTGGGACACGTTGCAGTATC GATATTCAGAAAATGCGACATTCAACCGTTATTCAGATGAAC TTTCAATTCTTACCATTGAGAATCGCCAAGGCATTAAACAAT CAAATGCAGGCATACAGACGACGATAAAGTTTTGCATAGCGT TACACTAACGATTGTAAAGCCAGAATGGAGCGTCATCCATTA TGATTATCTAACGAAAATAAACAGCCATTTTTGTTGTTTGAG CATCGATAGTACAATCGAAATCCGCGACAGACGGTAATTAGA GGAATCATTAGGTTAATCCAATCGCAAGTTTTAGTTGAAATA GATTAGTATGTAGAACCAAGTACCGCACATCGTAGGTATTCT TTAACATTTGCCCTGCTTGAGATGGTTTTGCGATTTGTTTAG TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTCTCTTCTTACAATAGCTTC TGAATTATTTGCACGTAGGTTTAAAAAGTAA TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTСТСТТСТTTTAAATCCTCA CATTCGGGAAACCTGTCCGGGGAGGAAGATT

TСАСТТСАТАСТСТАССТТСТТСТТСТТСТТСТТСТТСТСТТСТТТTAGGAAGCTC AACTGGAAGTTTCATTCAGTAGATAAATCTA

ТСАСТТСАТАСТСТАССТТСТТСТТСТТСТТСТТСТТСТСТТСТТСТАТТАТGТСG CTGGGATCGTCACCCTCCAACGGCTTAACGG

TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTCTCTTCTTTTAACATTTGC CCTGCTTGAGATGGTTTTGCGATTTGTTTAG

ТСАСТТСАТАСТСТАССТТСТТСТТСТТСТТСТТСТТСТСТТСТТТТТСААТТСТТА CCATTGAGAATCGCCAAGGCATTAAACAAT

TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTCTCTTCTTTACACTAACGA TTGTAAAGCCAGAATGGAGCGTCATCCATTA

TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTCTCTTCTTCGCTGGTGAGA GATCTGGAGCAAACAAGTGTCAATCCAGTGA

Note: In order to position one gold nanoparticle in the body center of the cubic frame, 'TCACTTCATACTCTACCTTCTTCTTCTTCTTCTTCTTCTCTTCTT' sequence was added in the blue marked staple DNA strands.
d. Bridging strands of cubic DNA origami frame

| cub-bridge-1 | TTCGCCTTTTAGAAGCCTTTATTTCAGTAATACGCAAAAT |
| :--- | :--- |
| cub-bridge-2 | TACAGACCTTTTCATGTAATTTAGGCAGTATTTAATGCGTTA |
| cub-bridge-3 | CGTGTGATTTTTAAATATTGACGGAAAATTGAGGTTGTCAC |
| cub-bridge-4 | TATATTTTCATTTTTAACTTTTTCAAATATAACAAAGATTTTAAC |
| cub-bridge-5 | ATAGCGATTTTTATTGTGAATTACCTTAAATTTCATCAGTGA |
| cub-bridge-6 | ACTCCTTATTTTTGAGTGAATAACCTTGCATAAATCTCAAGAA |
| cub-bridge-7 | TTAATAAAACTTTTAGCCGTTTTTATTTTCTCATCGACCTAATT |
| cub-bridge-8 | CATTATCATTTTTCCCAATTCTGCGAACGCATATAAAATATAA |
| cub-bridge-9 | TCAGGATTTTTTTAAATAAGAAACGATTATTATTTGAATCTT |
| cub-bridge-10 | TCCAGACTTTTGACTTCAAATATCGCGAAGAGGAAATCAAA |
| cub-bridge-11 | CTGCGGTTTTATTGCGTAGATTTTCAAAACAGATTGTTTG |
| cub-bridge-12 | GCGAGGTTTTGGCTTTTGCAAAAGAAAACCAAACAAAAGG |
| cub-bridge-13 | GTGCCTTTTTTGTCCACTATTAAAGAACCAGTTTTGGTTCC |
| cub-bridge-14 | TGTAGGTAATTTTATCGGAACGAGGGTAGAGCAGCGAACCGAT |
| cub-bridge-15 | TAATTGTATCTTTTCCGAACAAAGTTACCAAAAAGTATAAGCCC |
| cub-bridge-16 | GCAACAGTTTTATAGAAAGGAACAACTTTTCAGCTAGCGTA |
| cub-bridge-17 | ATAGCAAGTTTTAATCGTAAAACTAGCAAGAATCGGGGTAGC |
| cub-bridge-18 | AAGCGCTTTTCGTACTCAGGAGGTTTGGAATAGTCCTCAA |
| cub-bridge-19 | TAAGCAAATTTTTAGCCGGAACGAGGCGCCTGCTCCCAAGCGC |
| cub-bridge-20 | GCCACCTTTTTGAATCGGCCAACGCGGTGCCAGAATGAGT |
| cub-bridge-21 | CATGGTCTTTTTAATCAAAATCACCGGGTTTGCCGTTTGCC |
| cub-bridge-22 | GGGTAAAATTTTTACGTTGTAAAACGACGGGTTTTCAAGGGCG |
| cub-bridge-23 | TCAGGAAGTTTTATTTACCGTTCCAGTAAAAGCGCTTGAGGC |
| cub-bridge-24 | GCAAAATCTTTTCCGTAATGGGATAGGTACAAACGAAAATAA |

e. Staple strands of hexagonal bipyramid DNA origami frame
hb-staple-1 GTGGCATCAGATGACGAAAAACCGTCAAAACATTATGAAAAG
hb-staple-2 AGTCAGAAGCAAATCAAAAAGATTAAATCCCCCTGACCATAA
hb-staple-3 TCATCAGTTGAGATGATGGTTTAATTCTTAAATCATTTATTT
hb-staple-4 CAATCGCAAGACTTAGTTAATTTCATGCGAAAGACGACGTTG
hb-staple-5 TAATTTAATTAATTACCTGAGCAAAAACAATAAACTAGGGCT
hb-staple-6 GCCTTTAAGCAAGAGAATTGAGTTAAGCAGGTAATAGAGGAG
hb-staple-7 CAGATGAGATCGAGCTTCAAAGCGAACCAGAGAGTGCTCCTT
hb-staple-8 TTTTTAACCAATTCAAAAATAATTCGAATTATTGAGCCATTT
hb-staple-9 GAAACCTCGAATGTGAGCGAGTAACAACTTGACCGGGTCACG
hb-staple-10 CGGTAATCGTAAATAATCAGAAAAGCATGATATGATCTACAA
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hb-staple-49 AGCCGTTAGATTAGCGGGAGGTTTTGAAAAAAGAAATTCTGA GCCCGTATAAACTATTCTGAAACATGGCCAGAATTGATGATA AATAATGAATAAGGATAAGGGAACCGAATAATAAGCAGAGAG AAAAAAAGGCTCGCTTGCTTTCGAGGTTGTCGTTTCAACAGT TAAGTGCTGTTTCCCTGAGAAGAGTCCTTTTTCAAAGGCGAT TGAATCTAATGCGTTCATAATACCGACCCACCGGATAAACAG TACATAAATCCGCGAAATACGTAATGACCGATTGAAAATACA GACGTTATTTATCACAAAAGGAGCCTTTTAATTTTGAACAAC AGCATCGGAACGTAAAGACTTTTTCATTTCTTACATAACCGA TAAAGGAGCTCTGTATGGGATTTTGCTATAGAAAGTTCACGT GGCTTGATTAGGAAGGTAGAAAGATTCAACGTTAAGTCAGGA AGCGCCAAAGACAAGGTAAATATTGACAGTATGCAAAGACAC TTACCTTGTATCGGGTAAATGAATTTCTATTTCGGTCTGAAT TAGCGACTCAGAGCAGAGCCACCACCGGCGGTTTGTTAGCCT TCAAATATAATGCTTGGCTTAGAGCTTAACTAATTACCTTGT ATGTACCAGCTCAGAACCGCCACCCTCACCCAATAAGTTTTG TAGATACATTTCAATAACCTGTTTAGTATTAAGTAGCGGGGT AAGGGTGAGAAAAGTCAAATCACCATCACCCTCCACCACCAG ACGGGTAACCTGCTCTGATAAATTGTGTAGCGCGATCTTTGA TTCATCACCAACTGACCAACTTTGAAAGTAGGCTGACCGGAT CTTTTTTCGGAAGATGATGAAACAAACATTCATTTATCAATA CCAGCTTCGACGACCCGTGCATCTGCCATCGGATATAATGGG ACGAGCCCCAGGGTGGAGAGGCGGTTTGGTCGTGCTGCCCGC TTGTATCATCGCCCATGTTACTTAGCGAAGTTTGAAAGAGGC AACATTATTACATACCACATTCAACTCGAGTAGTATGCGATT TAAGACGTGTGTGACGTAATCATGGTCAGTCGACTGGTTGGG GAGCGGAATTATTCATCAATATAATCGTGGACTTATTAAATC CCACCCTGAGAGACGGCCGTAAAAATTTTGAGTAAGGTTGAG CCACCACAGCCCTCAATTACGAGGCACCAATACTGAGAACCG CCGAAATGTGCCGGAGAGGGTAGCTATTGCCTGAGAAACAAG TTTCCAGGTTGTAAAGCCTGGGGTGCCTCGCTCACCAGCTGC TTATATAAAAATAGTGAATTTATCAAAACGGCTTACTAGAGG TAACCTTGCTTCAGAATCCTTGAAAAGGCGAATAACAAAATT TCAACAGAACATGTTTCTGTCCAGACGAAATAAGAAGTAATG CTTTAAAAAATTGCAGCGGGTCCTGAACCATGTAGATAATCG CATTTTTGCGGAGTAGCTCAACATGTAAGCCCGAAGCAAACT GGCGCATCGTAAAGTATCGGCCTCAGTGGCCTTATTCTCCGT CGAGCTCGAATTAATTGTTATCCGCTGCGATAGTCTGAGAGA GTCAATCCTTGCCCAAAGCTGCTCATTCGACAAGAGCTGACC
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AAAATCTTCGTAGGAATCATTACCGCGCATCCGGTCGCGAGG CGGGAGAAACAAGTTACAAAATCGCGTTGTTTGTGCACGTAA AGTTTCAGAGGCTTGATAGTTGCGCCCCGCCTCCCAGAATCA TTTGCGGTAGCCTTTAGCGTCAGACTGTCCCCTTACCATCTT TGCTGCAATATATTAAAGAACGCGAGAAACTATATTTGCATG TCCCAATCCAAATTTTTTGTTTAACGTGACCTAAAATAAGGC AATCAACGTAACTGACGAGAAACACCACGAGGCATGAACGGT TATACCACGAAAGGTGGCAACATATAAATTTGTCAAAAATTC TTCAATTTTCCCTTTGTAAATCGTCGCTTACATAAGAATTAC CATTATATTGGGCGGGAAGCATAAAGTTGAGGGGATCATCAA GATAACCCACAAAACAATGAAATAGCAAATGAAGGGAGAATT CGCAGTCAACCTATAGTTAATGCCCCCTATGGGGTTTAACTG AAGGTAAAGTAATCAGCTAATGCAGATATAAAGACATGTAAT GAAACAGATGAGAATCGCCATATTTAACTCGAGCCGAATATA CGAATAAAAGTTCCAGTAAGCGTCATACATAAGTTCAGTGCC TAAAGGCAAGACAATGACAACAACCATCGGCTTGCACCCTCA GCCAACGCGCGGGGTTTTTCTTTTCAATTCCACGAGCTAACT ATACCCAAAAGATTAAGACTCCTTATATCGCACCGGAAACCA ATCACCGGAACCCGCCACCCTCAGAAAGCACCGTTTCATCGG ATAGTAAAATGTGTCATAAATATTCAAGGTTTACACCCTCAT TAGCAAGGCCGGAATGAAACCATCGAAAAACAGACGTTAATA GCTGATTGAACAAGTAGGGTTGAGTGTTCGGCAAATCCTGTT TTAATTCCAGTTTGGCCCTTCACCGCATATGTACCTGATAAA TAATCTTAGCATAAAAACAGGGAAGCGCCAAAGTCTGAGCGC TGATGGTTCCTGGCCCTGAGAGAGTTGCGCGAAAAATCCCTT TATCATTCCAAGAAACCAAGTACCGCGCCTGTTATAATATCC GCCCTTTCGCCTCTGCGGGGCACCGCTTCCATTCAGAAACGC CACCCTCCGGAATCTTAGACTGGATAGCCAAAAGAGGAACCC AAACTACAACGCGCGTAACGATCTAACAGATACTCGTTTACC CTTCTGAATACCAATAACGGATTCGCCTATATACAGATTTTC GCCTGTTTAGTATATACAAATTCTTACTACAATTCTTTCCAG CAAAAGGATAGTTACTGTAGCATTCCACGTAACACGCGAGAG TTGAGTACATATCATACAAACAATTCGATTAATTTACAAAGA CCCCCAGCACCACTACGAAGGCACCAACACACTCAAACAAAG TGATACCTGAGGACAGGGTAGCAACGGCGATCGTCAGGGAGT CGTTGGGGCTCAACTTTAATCATTGTGATATACCATAAAACG TTAATTTGCTTTGAATAATGGAAGGGTGCTGAATATCGCGTT CAAAGGGTGGCAATCATCATATTCCTGATTGCGGATAAAAGT CCTCCCGACTTGTTGCTATTTTGCACATCGAGACAAGCAAAT AGAGCATAAAGCGTAATACTTTTGCGATTTTCATAACATCCA
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ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTACGCAAGCACAAACAT TCAGAGCCGCCAGACAGGATGTGTAG

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTGTATAAGTATCACCAA ACGTCACCGTCAAAAATCATTTTGTT

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTAGCTTTCTTCATGAACT GGAAGAAAAGTAACCGAGGGCTGCG ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTTGGTTTGTAAACGATAA GACCAACGCTATACAAAAATCATAA

ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTAATAGATCAGTATTAA CGGGTTCAGAAATTAATCAAAACCAC

Note: In order to position one gold nanoparticle in the body center of the hexagonal bipyramid frame, 'ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTT' sequence was added in the blue marked staple DNA strands.
f. Bridging strands of hexagonal bipyramid DNA origami frame
hb-bridge-1 GGGTTGATTTTGGGAATTAGAGCCAGCCCGACTTCATTAAA
hb-bridge-2 AGCTCATTTTTTTGATTCCCAATTCTGTCATTCCAACTAAA
hb-bridge-3 ATAAGAGGTTTTTGGGAACAAACGGCGGACCGTCGGCCTGTAG
hb-bridge-4 TGTAGATGTTTTCCAACAGGTCAGGATTAGACCGGAAAGACT
hb-bridge-5 TGACTATTATTTTTGGCAAAGCGCCATTCGCTGGTGCTCCAGCC
hb-bridge-6 ATAACGGATTTTATCAAAAATCAGGTCTACGAGAATCAAATG
hb-bridge-7 GGGGGTATTTTCACGGAATAAGTTTATAGAAACGTTAGCAA
hb-bridge-8 GGTTTACCTTTTTTTCAGGGATAGCAAGGAGCCACGTACCGC
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hb-bridge-32 AAGATTCAATTTTCATCCTAATTTACGAGAAGAAAATATCAAC TCTTTCCTTTTTAGCCGCCGCCAGCATTCCAGAACAGAGCCA TCGATGAATTTTTTAGGCAGAGGCATTTAACGCCACCAACGC CCGACAATTTTAGGCTATCAGGTCATTTTTGAGATCAACCG CATTACCATTTTTAGCCTAATTTGCCAGTACGAGCGTTTATCC CTAGAAAAATTTTTTTTGTTAAAATTCGCATTGTAAGAAGATT CATAATCAAATTTTCAGATATAGAAGGCTTCCAATAGACAAGCA TAGCGAATTTTCATTTTCGGTCATAGCAGCGCGTTAATCAG TTGACCATTTTTGTTAAATAAGAATAAAGTGTGATAATTTAA CATATTATTTATTTTTTTGCTCAGTACCAGGTTAGGATAGGCTGA AAGCCTCTTTTTAAAACGACGGCCAGTCCCAGTCGGGGATG TGCAAATCTTTTATAAATCATACAGGCAGTAGCATTTTGGGG TCAGACGTTTTAAAGTTACCAGAAGGAAAGCAGATACCGAA GTTGGGATTTTTTTTAAATGCAATGCCTTAGAACTATTTCA GTAACAGTTTTTAACTGAACACCCTGAAATTAGACAATAGCA TATCAGAGATTTTCAGGAGTGTACTGGTAATGGCTTTGGAAAG CTTTTACATTTTTAGACGACGATAAAAACATAACCCATAACGC ACCAGTACTTTTAACAGAAATAAAGAAAAATTATTGATTATA ACCAGAAGTTTTTTCAGCGGAGTGAGAAAACAACTCTTTCCA AATCTCCATTTTCTTTGCCCGAACGTTACAACTCGCCAACGT ATGAATCGTTTTAAAAGAATACACTAAACTAAAACCCATTAA CGGAGATTTTTCACATTAATTGCGTTGAATGAGTACAACAT CGGGTACTTTTGTACAGACCAGGCGCAAGGACAGGCAGACG ATTACCCATTTTCTACCTTTTTAACCTCTCATAGGCTTAGAT
g. Staple strands of elongated octahedral DNA origami frame
loct-staple-1
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AAAGTACAACGGGTTACTTAGCCGGACTCAGCAATACGTAAT TACTGCGGAATCTCAGGTCTTTACCCTATTCTGGGGTTGATA ATAGTTGCGCCGTTTTGCGGGATCGTGTTAGCGAGGAATTGC ATTAAGCAATAAAATACTTTTGCGGGAGTTTCATATTTTCAT TTTAATGCGCGAAAGATAAAACAGAGCCAGCCAACCAGTAAT TGGGATAGGTCAAGATCGCACTCCAGCGGTTGAAATAGGAAC GTGAATTACCTTAACGGAACAACATTGGCGCAGGATATTCAT TAATAAGTTTTAGCCTATTTCGGAACTTGATGGGGAACAAGA TAAGAATAAACAAATTCTTACCAGTACCTTATTGGAATAAGT AACCAATCAATAGTTTTTATTTTCATGCCAACGTAATTCTGT CGTGGCGAGAAAGTCACGCTGCGCGTCCACCACTCCTCATTA CGGATGGCTTAGTAAAGTACGGTGTCCTTTCCGTCGGTGCGG GAAATTGCGTAGGGAGAAACAATAACGTTATTAGCAATTCAT ACCACCGGAACCTCAGAGCCGCCACCAAAATCACTTTAGCGT
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CGACGTTGTAAACGGGTACCGAGCTCTATTATAGAGCTTCAA AGGTCATTGCCTTGTCAATCATATGTGCCTTTAGCCGGAGAC TAACCGTTGTAGTCCAGAACAATATTTCGCCTGAACAAAATT CAATAGATAATATAAATCCTTTGCCCGGCGGTCTCAATCAAT TCACCAGTGAGAAGCAGGCGAAAATCTCGTAATTTAATTGCG AAGGTAAATATTTTGGGAATTAGAGCTTTTTAAGAAAACTTT CCTTTTTAAGAAACTGGCATGATTAAATATTATAACACCCTG TCTTACCAACGCGTTACAAAATAAACGGAATCAGAACCTCCC TTAATTTTCCCTTAGGTCTGAGAGACACCACACTAAACAGGA TTTTCAGGGATACCACAGACAGCCCTCAGGTAGATCATAACC ACAGCATGCTCCATAGATTTGTATCATCCCCAGCGAAACGAA GAAATCGGCCCCCTACGGGGTCAGTGCCCTTTTGATCCAACG AACGGGTCCTGAACAAGAAAAATAATATCTTATCATTCCAAG AAAAGCCCTCAGGACGTTGGTGTAGATGGGGAACAGGCCTTC ATTAAATCAGCTTTCATCAACATTAAATTTGTTAAAATTCGC TACATTTAATAGTACATCCAATAAATCAAAGCTAACCAAAAA GCCCAATTTTGCCATAACGAGCGTCTTTGCACCCATTAAATC ATAGCGAAATTACGTAGGAATACCACATCAGTACAGTACCGT GTTGGGATGAAAGAGGACAGATGAACGGAGTAGATCATTAGA СTTTTTCAAAGAATACTCATCTTTGACCGCCTGATGAAATCC AAGCCTGCGTGCCAGCTGCATTAATGAAAAGCATAAAGTGTA TCAGTGATCATCAAGAACTGACCAACTTAGAAAAATCTACGT TAACAGTACCCTGTAGCCTCAGAGCATATACAGGCGCATCAA CTAATGCGAATATAAGAATCGCCATATTTACCGCACTCATCG ATAGCTGTTGCCCCCGGGCAACAGCTGAATTGGGCGTCGGGA GCCGCCATGTAGCGGGAAGGGAAGAAAGAGAGCTTTCTGAAT GGAATTAAATGGAACTACCATATCAAAACGTCAGAGTAACAG TCTGAATTCATCATTTATCATTTTGCGGTAATACATGAATGG AGAGGCAATGAGGAAGGGTAGCAACGGCAGGTGTCAAATTCC CGTTCTATAGGTAATTTTAGAACCCTCAAGGATGAACGGTAA TTCTACTCGCAAATCAATTCTGCGAACGTGTTGTAATCGGTA AGGAAAACCAGCAGACTGATAGCCCTAAACAATATAGATAGA GAGCCGGTCGTAAGAAAGCGGCCAACGCTGATCGTGCTCAAG AAACAGGAGATAACCCACAAGAATTGAGAGAGAATAACATAA GTGCATCACAACCCGTCGGATTCTCCGTGGCGCATCGTAACC CTAAAGTAGGCCGCACAATGACAACAACTGAATTTAAATCTC AATCCAACAAAAGAAAGTAAGCAGATAGAATAGCACGCTAAT TAACGTGAGAATCCGTGAGTGAATAACCACATAGCGATAGCT GGATTATTGACCTGAATACGTGGCACAGAACATCGTACCGAA GTACGCCCTTTCCTTACAGGGCGCGTACAGAGTCAATAGTGA
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ATCATTTCGAAAGGAGCGGGAATAGCCCGCGAAAAAGCGTCA TTAATTGATATAATGCTGTGGAAGCCCGATTAGAGAAGGCGA ATCATAAACGAACTATGCGATTTTAAGAATGGTTTTGCTCAT AAGCATCGAGGAAGATATCTTTAGGAGCGAAGTATAAACAAT AAAGTATTCAAAAAGTCATAAATATTCAAAATGTTATCACCG GCAAGGAACTAGCAGAGAGTCTGGAGCATTTTTGAATTCAAC ATCAGAGGAAGCGCACGATTTTTTGTTTACGCAATAATAACG CACCATTACCACCCGCCTCCCTCAGAGCTAATCAAGCATTTT TTTGCTAAAAGCGTTTATTTTGTATCGGATACCATATGAAAT TAATGTGGCTGATAAATTATGCTATTTTCCGCAATGCCTGAG TAGATTAAATATATTGAGAAGTGTTTTTTGGACGAGCACGTA CGAGGAAAACGTCAAAAATGAAAATAGCTACAGAGCTAAAGA ATGTTAGTTATACACCGGAATCATAATTGACCGTGAATTCAT CAAAAGGGAGGCTTGCCACCCTCAGAACAACCCATAACTACA AAGATTAGTATTCTAAATCAGATATAGATATATTTTAAATAG AACCGATTTTATCAGCTTGCTTTCGAGGCATCGCCCACGCAT CAAAAAACGGAGTGTCTTTCCAGACGTTCTGAGGCTTGCAGG TCGGTCGAGTAAATGAATTTTCTGTATGGTCACCACGATAGC CAGACCAAAATTAAGTAGCCACCAGAACGGTTGACTTAGTAC CAGAGGCAAAGAACGGGTTTAGATAAGTATACCAGAAACCTA GTTTCAGAAGGCTCCAAAAGGAGCCTTTAACAACTTTCAACA AACCTGTGGGTGCCTGTGAAATTGTTATCAGCAAGCGGTCCA CAGAAGGAATAAGAGCAAGAAACAATGACCGAACAAAGTTAC TTTACAGTTAAAACACACTAAGCCCAATAAGAGGAGCTTTAC GTAGGGCGCAAGCCATCGGCTGTCTTTCCCCATCCTGTTCAG AAGTTTGTACATCGATTTTCAGGTTTAATTATTTGTTATACT ACTTGCCATAATCAACAGTACATAAATCAGATTTCTATTCAC TAATATTGTCTAAAGTTATGAGCGAGTATGATGAAAGCAACC ATGGTTTACATATAAGAAAATACATACAAACTGTTTAGTATC CGGTCATTAATCAGGCAAGGCCGGAAACGGAACCGCTCAGAT ACCCTTCTTACATTTGGAAATACCTACAATAAAAACCATTAC CAGTTCAGAGAAGGATTAGTTTCGTCACTCAACTAATAACGC GGTCAGGAAAGACTATCAAAAAGATTAACACCTGCAGGTCGA TGAGCAAAATGGAAGTGAGGCCACCGAGTTAGTAACTATCGG AGAGTTGCCGCTCACAATTCCACACAACTTTTGACCTGAAAT AGCACCGAGCCCCCTTGCCATCTTTTCACGCCACCCCACCCT CTTTTTTAAGAAGACAAAATCGCGCAGAACTCAAATAACATC AGGAATTACCTTGCAGTGCCACGCTGAGACTTTACTAGACGT CCAGTCAGAGTAGTAAATTGGGCTTGAGACTGGCTCATTATA GCAAAGCGGATCCCACGACGGCCAGTGCGGGTAACTCCAACA
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AACACTGCAGAACCTTGCAAAAGAAGTTTAGATACATGCAAA CCACCCTAGGATTAGCGGGGTTTTGCTCGAGGTTTAGGGGGT GCTGAGATATGGTTGCTTTAGTAGAAGAGGCGAATAATTACC AGTTTGAAAGCAAATATTTAAATTGTAAAGCCAGCAAATCTA GCTTAATAAAATCATAGAATCCTTGAAATTGCTTCAGGAACG TCAAAGGGAGATAGCCCTTATAAATCAAAGGCCCGTATAAAC TTCTGGTATGCAACAGCTTAATTGCTGACTCCTTTGGCGAAA AATAAGAAGAACGCGCCTGTTTATCAACATTTTCGAGCCAGT CTTAGGTGAGCCATGACGGAAATTATTCGCGACATCATCTTC AAATACCACTAGAAAAAGCTGCTGATGCAATTTAACCAAAGA TGAATACGGTAATACAATACTTCTTTGATAAAAGAGAATTAC TGACCTAAAATCCATATAACTATATGTATATTATCACCGTCA CTGTAGCTTTTGTTCAGGAAGATTGTATGGGGACGACGACAG GGGGGATCAGGCTGACCAGGCAAAGCGCGAAGCTCAACATGT ACACCGCCTCGTATCATTTGAGGATTTAACTAACAAGTTGAA CTGGCCCGCGGGGAGAGGCGGTTTGCGTTTGCCCTTCACCGC TACTCAGAGTACCACTGAGACTCCTCAAGAAAACGAGAATGA AATAGTATTGAATCCCCCTCAAATGCTTTTGCCAGAGTACCG CAAAAGGATTAAAGGTGAAAAGGTGGCAACCAGCGTGGTTTG TTACCGTTTGGCCTCAGGAGGTTGAGGCAAGCGCTAGGGCGC TACATGGTTGAGTAACAGTGTCAGACGATCCAGTAACCGTCT TTAAGTTCAAGCTTGCATGTTCGCCATTGTGCTGCAGTACCT TTATCCGGTATGCCGGAGAGGGTAGCTAAACAAGAGAATCGC CTGACCTATAAGGCTTGCCCTGACGAGAGGCGCATAGGCTGG AACCAAGTAACAACGCCAACATGTAATTAACAAAGAAGGAGC CATCAGTTAGCATTGCAAGCCCAATAGGCGCCACCAACCAAA AGTTAATGCAAAATGGTTGAGTGTTGTTCGTGGACTGATACA GAATACCATAAGAAATTAGACGGGAGAAAATTGAGATAGCTA GCGACCTCGGAACGAGTTTCCATTAAACCAACCTAATTATAC TATCGGCCCAAAAAAAATCAGCTCATTTCGCGTCTAACGGCG TCGTAAATAAAAATAGATTCAAAAGGGTATATGATGAGATCT CATTATGTGATTCCGGTCAATAACCTGTAAAGGTGAAGGCAA AGAACAATTAATTGAAGTACCGACAAAAAACAACATAATTTA ATATGCGCAAACGTAAAGAAACGCAAAGAATAGAATGATAAA CCGACTTTGGGTTAATCGCAAGACAAAGTTAATTTTCAACCG ACGCCTGTGAGATTAGGCATAGTAAGAGCGATAAACTCAGAG CGCTGGTTTTCCTGTAATGAGTGAGCTACTTTCCAGCCAGGG CGAACCAACGCTCAGGCAGATTCACCAGCCAACAGTTTTGAA TAATAAAGGGAACCGAGTAATCTTGACAACAAAGCAATTTCA CCTTGCTCAAGTTATGATGAAACAAACATTCATTTGTCTGTC

| loct-staple-135 | GAGTTAATTTGTCGAGAATAGAAAGGAAACGTTGACTTAAAC |
| :--- | :--- |
| loct-staple-136 | TGGCAAGGCATTGATGATATTCACAAACCGCAGTCGACGGGG |
| loct-staple-137 | TCGACAACTGCAACTGAACCTCAAATATAATCAACACTAATA |
| loct-staple-138 | AGCCTAAAGCAAGCAAGAACGCGAGGCGTGAAGCCGCTACAA |
| loct-staple-139 | CAGAGCCACCATTATAGCGACAGAATCATTCATCGAATCACC |
| loct-staple-140 | TACCTTTAGTAACAATTCCTGATTATCAGTTTGGACACGTAA |
| loct-staple-141 | CTCTAGAGGATTGCTCAAATATCGCGTTAGCAAACGCCAGGG |
| loct-staple-142 | TTTAAATGCCGGAACGCAACTGTTGGGAGCCAGCTTGATAAG |
| loct-staple-143 | ATTTATCGCGCCGCCGTTAGAATCAGAGTTTAGACTGTAAAT |
| loct-staple-144 | CCATAAATAAGAGGGGCGGATAAGTGCCTAGGTGTTAGACTG |
| loct-capture-1 | ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTAGCCTAAAGCAA <br> GCAAGAACGCGAGGCGTGAAGCCGCTACAA |
| loct-capture-2 | ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTTCGTAAATAAAA <br> ATAGATTCAAAAGGGTATATGATGAGATCT |
| loct-capture-3 | ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTATATGCGCAAAC <br> GTAAAGAAACGCAAAGAATAGAATGATAAA |
| loct-capture-4 | ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTTCCGACTTTGGGTT |
| AATCGCAAGACAAAGTTAATTTTCAACCG |  |

Note: In order to position one gold nanoparticle in the body center of the elongated octahedral frame, 'ATCCATCACTTCATACTCTACGTTGTTGTTGTTGTTGTT' sequence was added in the blue marked staple DNA strands.

## f. Bridging strands of the binary system

| bs-bridge-1 | CGTCCAATTTTTCAGAACCGCCACCCTCTCAGAGTATTAGC |
| :--- | :--- |
| bs-bridge-2 | CCAGTCATTTTAGCACCATTACCATTACAGCAAATGACGGA |
| bs-bridge-3 | GTTTTTCTTTTTTTTAAAGGTGGCAACATAGTAGAAAATAATAA |
| bs-bridge-4 | TGTACTGGTTTTAAGTTTTAACGGGGTCGGAGTGTAGAATGG |
| bs-bridge-5 | CCGAAGCTTTTGCTTTGAGGACTAAAGAGCAACGGGGAGTT |
| bs-bridge-6 | TATCCTGAATTTTTAACCTGTTTAGCTATTTTCGCATTCATTC |
| bs-bridge-7 | GCATGTAGATTTTTTGCGTATTGGGCGCCCGCGGGGTGCGCTC |
| bs-bridge-8 | GCGTTAAATTTTGTCCACTATTAAAGAACCAGTTTTGGTTCC |
| bs-bridge-9 | GGGAGGGTTTTGTTAAAATTCGCATTATAAACGTAAACTAG |
| bs-bridge-10 | CGCTATTAATTTTCTCCAGCCAGCTTTCCCCTCAGGACGTTGG |
| bs-bridge-11 | GGCGAATTTTCAGGTCGACTCTAGAGCAAGCTTCAAGGCG |
| bs-bridge-12 | CAGAGCCTTTTGTAAAGATTCAAAAGGCCTGAGTTGACCCT |


| bs-bridge-13 | AGGCTATCTTTTGTCAGAGGGTAATTGAGAACACCAAAATAG |
| :---: | :---: |
| bs-bridge-14 | GACCGTAATTTTATTGCGTAGATTTTCAAAACAGATTGTTTG |
| bs-bridge-15 | TCATTTTTGTTTTTTCACGTTGAAAATCTTGCGAATGGGATTT |
| bs-bridge-16 | ATTAGCAAATTTTCAGAGCCACCACCCTCTCAGAACTCGAGAG |
| bs-bridge-17 | CAGAAATAAATTTTATTTTAAGAACTGGCTTGAATTATCAGTGA |
| bs-bridge-18 | AGCCGTTTTTGGTAATAGTAAAATGTAAGTTTTACACTAT |
| bs-bridge-19 | GCTATTAGTCTTTTTCAAAGCGAACCAGACCGTTTTATATAGTC |
| bs-bridge-20 | CGCAAATTTTTAAGGGAACCGAACTGAGCAGACGGTATCAT |
| bs-bridge-21 | GCGAAACTTTTGATAAGTCCTGAACAACTGTTTAAAGAGAA |
| bs-bridge-22 | CTTTAATCATTTTTTAGGCGTTAAATAAGAAGACCGTGTCGCAAG |
| bs-bridge-23 | ACCCTCATTTTGTAAATCGTCGCTATTGAATAACTCAAGAA |
| bs-bridge-24 | TGATACCGTTTTAAGCCTTAAATCAAGACTTGCGGAGCAAAT |
| bs-bridge-25 | AGGTCATTTTTTAACAAAGTCAGAGGGTTTAACTGTTATCCC |
| bs-bridge-26 | TTGTTATCCTTTTGACTTGCGGGAGGTTTTTTTAGCTTACCGC |
| bs-bridge-27 | CCGCCTTTTTCCAGACGACGACAATAGGTAAAGCTCAACA |
| bs-bridge-28 | GGTGAATTTTTTTTTATTTTGTCACAATCACACCACACGCAGT |
| bs-bridge-29 | CCAGCATTTTTTTAAGTATAGCCCGGAAGTCGAGAAAACATG |
| bs-bridge-30 | GTAGCGATTTTAGCGAACCAGACCGGATTAATTCGTCAGAA |
| bs-bridge-31 | AATAGAAAATTTTTTTGCGCTCACTGCCCGACTCACACATGGTC |
| bs-bridge-32 | AAACAATGATTTTGTCCACTATTAAAGAACCAGTTTTGGTTCC |
| bs-bridge-33 | CTATTATTCTTTTTAGTCAAATCACCATCAGAGAAAGTTTCAAC |
| bs-bridge-34 | GTCTTTCCTTTTGCCATCAAAAATAATTTTTAACCTAATCAG |
| bs-bridge-35 | ACATTATCATTTTTGCCTCTTCGCTATTACAGGGCGAGCACCGC |
| bs-bridge-36 | CAACGCCTTTTTTGGGGCGCGAGCTGATTAGCTATTCCATA |
| bs-bridge-37 | CTGTAGCCTTTTTTCAAATATATTTTAGAACGCGACCTCCGG |
| bs-bridge-38 | TGCGCATTTTGGCCGATTAAAGGGATCGGGAGCCCGCCGC |
| bs-bridge-39 | AACATCCATTTTAAGCCAGAATGGAAAGAAATAAACAGAGCC |
| bs-bridge-40 | CGGAGAGTTTTCAGACTGTAGCGCGTTAGTTTGCCCAGTAG |
| bs-bridge-41 | CATTCCAAGTTTTGCCACTACGAAGGCACGGGTAAAGCGAAAG |
| bs-bridge-42 | GTATAAAGCTTTTTACCCAAATCAACGTAAGAACCGACGGTCA |
| bs-bridge-43 | AGTGAATTTTTTTCTCGTTTACCAGACGACAACACTAAAGATT |
| bs-bridge-44 | ATTCGCCTTTTGAATAATAATTTTTTCCAACTAATAACGAT |
| bs-bridge-45 | ACAGGTAGTTTTCAATATAATCCTGATTGATGATGATTTTAA |
| bs-bridge-46 | TCCCCCTTTTTATCTGGTCAGTTGGCACAAACCCAGTATTA |
| bs-bridge-47 | CCAACCTATTTTAAAAGGGACATTCTGGTCACACGTTGCAAC |
| bs-bridge-48 | GGCTGACTTTTAATTACATTTAACAATTCAAGAAATTGCTT |

vex-capture-1 ATATTCA

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vex-capture-2
vex-capture-3
vex-capture-4
vex-capture-5
vex-capture-6
vex-capture-7
vex-capture-8
fc-staple-1
fc-staple-2
fc-staple-3
fc-staple-4
fc-staple-5
fc-staple-6
fc-capture-1
fc-capture-2
fc-capture-3
fc-capture-4
fc-capture-5
fc-capture-6
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vex-capture-2
fc-staple-1
fc-staple-2
fc-staple-3
fc-staple-4
fc-staple-5 fc-staple-6
fc-capture-1
fc-capture-2
fc-capture-3
fc-capture-4
fc-capture-5
fc-capture-6

ATCCATCACTTCATACTCGATTATAAGCGGAGACTTCAAATATCGCGGAAG CCTACGAA

ATCCATCACTTCATACTACATAACTTGCCCTAACTTTAATCATTGCATTATA ACAACAT

ATCCATCACTTCATACTGATATTCTAAATTGAGCCGGAACGAGGCCCAACT TGGCGCAT

ATCCATCACTTCATACCATAACCTAAATCAACAGTTCAGAAAACGTCATAA GGATAGC
ATCCATCACTTCATACAGAAGCAACCAAGCCAAAAGAATACACTAATGCC AAAACTCC

ATCCATCACTTCATACATAAGGCGCCAAAAGTTGAGATTTAGGATAACGGA CCAGTCA

ATCCATCACTTCATACCGCCTGAATTACCCTAATCTTGACAAGACAGACCA TGAAAGA

CGCCTGAATTACCCTAATCTT
CAGCCTTGGTTTTGTATTAAG
GTTTGCCTATTCACAGGCAGG
AGCCGAAAGTCTCTCTTTTGA
ACATAACTTGCCCTAACTTTA
TGTCGTCATAAGTACAGAACC
ATCCATCACTTCATACTTCAGACGCCACCACACCACCC
ATCCATCACTTCATACTATCATTGCATTATAACAACAT ATCCATCACTTCATACTGACAAGACAGACCATGAAAGA ATCCATCACTTCATACTGCCACCCATTTTCACAGTACA ATCCATCACTTCATACTTGATACAAGTGCCTTAAGAGC ATCCATCACTTCATACTAGGCTGACTGCCTATATCAGA

Note: In order to position one gold nanoparticle near a vertex of the octahedral frame, 'ATCCATCACTTCATACT' sequence or 'ATCCATCACTTCATAC' sequence was added in the red marked staple DNA strands. In order to position one gold nanoparticle in the center of a triangular face of the octahedral frame, 'ATCCATCACTTCATACT' sequence was added in the green marked staple DNA strands.
h. Modified DNA sequence attached on gold nanoparticles

ThioM-1 GAAGTGATGGATGAT-SH
ThioM-2 GTAGAGTATGAAGTGATGGATGATGATGATGAT-SH

## Figures S1-S35



Figure S1. Schematics of the bridge pattern for a six-helix rod-shape model. Hybridization regions are designed inside the two ends of rods. Bridging strands hybridize with two adjacent rods to form a DNA bridge and further expand into a one-dimensional linear structure.


Octahedron


Cube



Hexagonal pyramid


Elongated octahedron

Figure S2. Geometric models for the four polyhedral DNA origami frames are octahedron, cube, hexagonal bipyramid, and elongated octahedron. $d_{1}, d_{2}, L_{1}, L_{2}, L_{3}$ and $L_{4}$ represent the width and length of the edges and their values are as follows: $d_{l}=5.5 \mathrm{~nm} ; d_{2}=6.0 \mathrm{~nm} ; L_{l}=$ $29.9 \mathrm{~nm} ; L_{2}=22.8 \mathrm{~nm} ; L_{3}=15.7 \mathrm{~nm} ; L_{4}=37.1 \mathrm{~nm}$.


Figure S3. a) Representative negative-stained TEM images of octahedral DNA origami frames.
b) Representative negative-stained TEM images of AuNP-octahedron monomers.

Corresponding schematics are shown on the left.


Figure S4. a) Representative negative-stained TEM images of cubic DNA origami frames. b) Representative negative-stained TEM images of AuNP-cube monomers. Corresponding schematics are shown on the left.


Figure S5. a) Representative negative-stained TEM images of hexagonal bipyramid (HB) DNA origami frames. b) Representative negative-stained TEM images of AuNP-HB monomers. Corresponding schematics are shown on the left.


Figure S6. The magnified schematics of the bridge pattern for octahedral frames at vertex junctions. $S_{\text {unit }}$ represents the distance between the body centers of adjacent frames in equivalent crystallographic axis directions.


Figure S7. The magnified schematics of the bridge pattern for hexagonal bipyramid frames at vertex junctions. $S_{\text {unit }, 1}$ and $S_{\text {unit }, 2}$ respectively represents the distance between the body centers of adjacent frames in non-identical crystallographic axis directions.


Figure S8. The magnified schematics of the bridge pattern for cubic frames at vertex junctions. $S_{\text {unit }}$ represents the distance between the body centers of adjacent frames in equivalent crystallographic axis directions.


Figure S9. 2D pattern of the AuNP lattice formed by octahedral frames measured by SAXS.


Figure S10. 2D pattern of the AuNP lattice formed by cubic frames measured by SAXS.


Figure S11. 2D pattern of the AuNP lattice formed by hexagonal bipyramid frames measured by SAXS.


Figure S12. Enlargement of structure factor result for the simple cubic lattice shown in Figure 2d: black curve for the experimental data and red curve for the model.


Figure S13. Enlargement of structure factor result for the body-centered cubic lattice shown in
Figure 2e: black curve for the experimental data and red curve for the model.


Figure S14. Enlargement of structure factor result for the simple hexagonal lattice shown in Figure 2f: black curve for the experimental data and red curve for the model.


Figure S15. The close-packed models of simple cubic lattice formed by octahedral frames in different angles.


Figure S16. The close-packed models of body-centered cubic lattice formed by cubic frames in different angles.


Figure S17. The close-packed models of simple hexagonal lattice formed by hexagonal bipyramid frames in different angles.


Figure S18. Representative TEM images of siliconized 3D lattices for octahedral frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S19. Representative TEM images of siliconized 3D lattices for cubic frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S20. Representative TEM images of siliconized 3D lattices for hexagonal bipyramid frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S21. Representative SEM images of siliconized 3D lattices for octahedral frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S22. Representative SEM images of siliconized 3D lattices for cubic frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S23. Representative SEM images of siliconized 3D lattices for hexagonal bipyramid
frames. The schematic of the corresponding lattice model is shown on the upper left.


Figure S24. Representative negative-stained TEM images of 2D planar structures formed by
AuNP-octahedron monomers. The corresponding schematic is shown on the upper left.


Figure S25. Representative negative-stained TEM images of 2D planar structures formed by AuNP-cube monomers. The corresponding schematic is shown on the upper left.


Figure S26. Representative negative-stained TEM images of 2D planar structures formed by AuNP-hexagonal bipyramid monomers. The corresponding schematic is shown on the upper left.


Figure S27. Representative SEM images of siliconized 2D planar structures formed by AuNP-
hexagonal bipyramid monomers. The corresponding schematic is shown on the upper left.


Figure S28. Representative negative-stained TEM images of 2D planar structures for the conjugated monomer with AuNPs near the vertex. The corresponding schematic is shown on the upper left.


Figure S29. Representative negative-stained TEM images of 2D planar structures for the conjugated monomer with AuNPs in the face center. The corresponding schematic is shown on the upper left.


Figure S30. a) Representative negative-stained TEM images of elongated octahedral DNA origami frames. b) Representative negative-stained TEM images of AuNP-elongated octahedron monomers. Corresponding schematics are shown on the left.


Figure S31. The magnified schematics of the bridge pattern for the binary system at vertex junctions. $S_{\text {unit }, 1}$ and $S_{u n i t, 2}$ respectively represents the distance between the body centers of adjacent frames in non-identical crystallographic axis directions.


Figure S32. 2D pattern of the AuNP lattice in the binary system measured by SAXS.


Figure S33. Enlargement of structure factor result for the tetragonal lattice shown in Figure 5b:
black curve for the experimental data and red curve for the model.


Figure S34. The close-packed models of tetragonal lattice of the binary system in different angles.


Figure S35. Representative negative-stained TEM images of 2D planar structures of the binary system. The corresponding schematic is shown on the upper left.

| Assembly method | Bridge pattern | Sticky-end hybridization <br> (Nat. Mater., 2020) |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Frame shape | Octahedron | Cube | Octahedron | Cube |
| Lattice type | SC | BCC | SC | BCC |
| Identifiable peaks in <br> SAXS | $\sim 15$ | $\sim 18$ | $\sim 25$ | $\sim 15$ |
| Average size of <br> ordered grains |  | $\sim 1 \mu \mathrm{~m}$ |  | $\sim 3-5 \mu \mathrm{~m}$ |
| Anisotropy control |  | Yes |  | No |

Table S1. Comparison of bridging method and sticky-end hybridization method (Nat. Mater., 2020, 19, 789-796.).

## References

1. X. Liu, F. Zhang, X. Jing, M. Pan, P. Liu, W. Li, B. Zhu, J. Li, H. Chen, L. Wang, J. Lin, Y. Liu, D. Zhao, H. Yan and C. Fan, Nature, 2018, 559, 593-598.
2. Y. Tian, J. R. Lhermitte, L. Bai, T. Vo, H. L. Xin, H. Li, R. Li, M. Fukuto, K. G. Yager, J. S. Kahn, Y. Xiong, B. Minevich, S. K. Kumar and O. Gang, Nat. Mater., 2020, 19, 789-796.
