Supporting Information

Control of the Stepwise Assembly-Disassembly of DNA Origami

Nanoclusters by pH Stimuli-Responsive DNA Triplexes

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MATERIALS

All chemicals including agarose, magnesium acetate, acetic acid, sodium hydroxyl, hydrogen chloride, were purchased from Sigma and used as received without further purification. All chemically synthesized DNA strands were purchased from Integrated DNA Technologies, Inc. (www.Idtdna.com). The unmodified staple DNA strands were ordered in a 96-well plate format, suspended in ultrapure water without purification. All modified strands were purified with PAGE. A circular single-stranded M13mp18 DNA genome was ordered from Bayou Biolabs. The DNA origami purification column (100kDa MWCO centrifuge filter) was purchased from Pall, Inc.

EXPERIMENTAL METHODS

The formation of cross-shaped DNA origami unit

The cross-shaped DNA origami was assembled by a slow cooling method. Specifically, M13mp18 viral DNA and all of the staple strands were mixed together at a ratio of 1:5, in a 1×TAE buffer solution containing 40 mM Tris-HCl, 20 mM of acetic acid, 2 mM of EDTA, and 11.5 mM of magnesium acetate. The mixture was slowly cooled from 90°C to 15°C over 12h in a thermocycler (BIO-RAD). The final concentration of M13mp18 DNA in the solution was 20 nM. The DNA origami was then purified to remove excess staple strands, using 100kDa MWCO centrifuge filters.

The assembly-disassembly of DNA origami dimer

The assembly/disassembly of DNA origami dimer (A1/A2) between pH = 5.0 and pH = 7.5: the prepared DNA origami monomers were mixed at a molar ratio of 1:1 in a 1×TAE buffer solution (pH = 5.0) containing 10 mM of magnesium acetate. Then, the mixture was adjusted to pH=7.5, and annealed from 38°C to 25°C at a rate of 2.1°C/h to form the corresponding DNA origami dimers. In order to disassembly of DNA origami dimer, the pH value of the dimer solution was adjusted from 7.5 to 5 by column exchange in a 1×TAE buffer with 10 mM Mg²⁺, then incubated at room temperature for 6h. The assembled/disassembled DNA dimer was directly used for AFM images, and gel electrophoretic characterization without further purification. The association/dissociation of the DNA origami dimer was performed by further buffer exchange following the same incubation step as the aforementioned

procedure. The same process was followed for assembly/disassembly of the dimer (A2/A3), except the pH values changed to between pH = 7.5 and pH = 9.0.

The assembly-disassembly of DNA origami trimer

A. Stepwise upstream assembly process of DNA origami trimer (pH: 5.0 - 7.5 - 9.0)

1. The prepared three DNA origami monomers (A1, A2, and A3) were mixed at a molar ratio of 1:1:1 in a 1×TAE buffer solution (pH = 5.0) containing 10 mM of magnesium acetate.

2. Then the mixture was adjusted to pH=7.5, and annealed from 35°C to 25°C, at a rate of 0.8/h to form DNA origami dimers by activating the sticky end interaction in DNA triplex set T1.

3. Next, the centrifuge column was used to exchange the buffer solution to pH = 9.0. Then the mixture was re-annealed from 30°C to 25°C at a rate of 0.8°C/h to form a DNA origami trimer through activating the sticky end interaction in DNA triplex set T2 (73%TAT). The assembled DNA origami trimers were then directly imaged by AFM without further purification.

B. Stepwise downstream disassembly process of DNA origami trimer (pH: 9.0 - 7.5 - 5.0)

1. The prepared DNA origami monomers were mixed at a molar ratio of 1:1:1 in a 1×TAE buffer solution (pH = 9) containing 10 mM of magnesium acetate.

2. Then the mixture was annealed from 35°C to 25°C at a rate of 0.8°C/h to form DNA origami trimer through activating the sticky end interaction in both DNA triplexes T1 (20%TAT) and T2 (73%TAT). The dissociation of the trimers was allowed to proceed for 6 h at room temperature after changing the pH value to 7.5 through deactivating the sticky end in DNA triplex set T2 (73%TAT) only.

3. With further adjustment of the pH value to 5 with another 6h incubation at room temperature, the trimers could be totally separated into monomers with the deactivation of sticky end interaction in both DNA triplex T1 (20%TAT), and T2 (73%TAT).

The formation of 9-tile DNA origami

The prepared DNA origami monomers (A4, A5, and A6) were mixed at a molar ratio of 1:4:4 in a $1 \times TAE$ buffer solution (pH = 5.0) containing 10 mM of magnesium acetate. Then the mixture was adjusted to pH=7.5, annealed from 50°C to 25°C at a rate of 2°C/h by selectively bridging titles A4 and

A5 together to form 5-tile DNA origami through DNA triplex set T1, while keeping DNA title A6 as a monomer. Next, the centrifuge column was used again to exchange the buffer solution to pH = 9.0. The mixture was reannealed from 45°C to 25°C at a rate of 3.3°C/h to form a 9-tile DNA origami by bridging title A6 to preformed 5 title units through DNA triplex set T2.

The disassembly of 9-tile DNA origami

First, the prepared DNA origami monomers were mixed at a molar ratio of 1:4:4 in a 1×TAE buffer solution (pH = 9) containing 10 mM of magnesium acetate. Then the mixture was annealed from 45°C to 25°C at a rate of 1.2°C/h to form 9-tile DNA origami. Second, adjusting the pH value to 7.5, and incubating at room temperature for 6h, 9-tile DNA origami units could be dissociated to 5-tile DNA origami units, and monomer units through deactivating the sticky end cohesion in 73%TAT triplex (T2). By further adjusting the pH value to 5.0, and incubating another 6h at room temperature, the 5-tile DNA origami disassembled to monomers through deactivating the sticky end in 20%TAT DNA triplexes (T1).

AFM imaging

The AFM images of DNA origami were obtained through spotting each sample (3 μ l) onto freshly cleaved muscovite mica (Ted Pella, Inc.) for 15 s. After the fixation of the targeted structure of DNA origami on mica surface, doubly distilled H₂O (20-30 ul) was placed quickly on the mica to remove the buffer salts, the drop was wicked off, and the sample was dried with compressed air. Atomic force imaging was done by utilizing Nanoscope III (Digital Instruments) tapping in air; with ultra-sharp 14 series (NSC 14) tips that had been purchased from NANOANDMORE.

Agarose Gel Electrophoresis

For the agarose gel under pH =5.0 and 7.5; the samples were loaded into 0.8% agarose gel with adjusted pH values that contained 5 mM Mg (CH₃COO)₂ in a 1×TAE buffer solution under 55V at room temperature. For the agarose gel under pH =9, the concentration of Mg(CH₃COO)₂ was changed to 2 mM. The gel was stained with ethidium bromide for visualization.

Dynamic light scattering

The size distribution of DNA origami nanostructures was measured with a DLS analyzer (Zetasizer ZS90, Malvern, UK). The DNA origami was diluted to 10 nM by a $1 \times$ TAE buffer with 10 mM Mg²⁺, and injected into a 70 uL plastic cuvette to measure the size distributions. This procedure was repeated three times.



Figure S1: The representative AFM images of DNA origami monomer (A1) (left image) and dimer (A1/A2) (right image) without purification. The calculated yield of dimer is ~87% based on AFM results. Scale bar: 500 nm.

The equation below was used to calculate the yield of dimer.

%yield = $\frac{Numbers \ of \ dimers \ x2}{total \ numbers \ of \ DNA \ origami}$

pH values		Monomer (A1, A2)	Dimer (A1/A2)	Total origamis	
5.0	Origamis Counted	234	24	258	
	Yield (%)	91	9		
7.5	Origamis Counted	44	286	330	
	Yield (%)	13	87		

Table S1: The statistical analysis of AFM images of DNA origami monomer and dimer structuresgenerated at pH 5.0 and pH 7.5.



Figure S2. DNA triplexes (73% T-A·T) -driven assembly/disassembly of DNA origami dimer A2/A3. (A) Schematic drawing of the pH-stimulated cyclic assembly of DNA origami dimers through duplex-triplex transition of DNA triplexes between pH 7.5 and 9. (B) AFM images of DNA origami monomer at pH=7.5 and dimer at pH=9.0 (C). Scale bars: 500 nm.

pH values		Monomer (A2, A3)	Dimer (A2/A3)	Total origamis	
7.5	Origamis Counted	144	18	162	
	Yield (%)	89	11		
9.0	Origamis Counted	27	162	189	
	Yield (%)	14	86		

Table S2: The statistical analysis of AFM images of DNA origami monomer and dimer structures generated at pH 7.5 and pH 9.0.



Figure S3: Gel electrophoresis used to compare the yield of dimer at pH 7.5 with and without thermal annealing process. Lane 1: DNA origami monomer control. Lane 2: Self-assembled dimer A1/A2 annealed from 38°C to 25°C over 6h. Lane 3: Assembled dimer A1/A2 incubated at room temperature. The dimer yield of lane 2 and lane 3 are 89%, and 75%, respectively.



Figure S4: A representative AFM image of DNA origami timer (A1/A2/A3) without purification. The calculated trimer yield was ~70% based on AFM results. Scale bar: 500nm.

pH values		Monomer (A1, A2, A3)	Dimer (A1/A2, A3)	Trimer (A1/A2/A3)	Total origami
ΕO	Origamis Counted	158	12	0	170
5.0	Yield (%)	93	7	0	
7 5	Origamis Counted	68	90	15	173
7.5	Yield (%)	39	52	9	
0.0	Origamis Counted	33	22	126	181
9.0	Yield (%)	18	12	70	

Table S3: The statistical analysis of AFM images of origami monomer, dimer and trimer structures generated at pH 5.0, pH 7.5 and pH 9.0.



Figure S5: Cross-section analysis of self-assembled DNA origami monomer, dimer, and trimer. The size of monomer is ~ 100 nm, dimer is ~200 nm, and trimer is ~300 nm, which is consistent with design.



Figure S6: Gel electrophoresis to show the reversible, multistep assembly of DNA origami nanostructures driven by DNA triplexes in response to pH. For each image, the left lane and right lane represent DNA origami monomer control and sample, respectively. For each of the two working cycles, the DNA trimer (pH=9) dissociates to dimer (pH=7.5) and further to monomer (pH=5), and the process reverses when the pH increases.



Figure S7: Hydrodynamic size distribution of the DNA origami nanostructures from DLS measurements. The three different colored (red, green, and blue) lines represent the three runs. The average size of monomer, dimer, and trimer is 49.43 ± 0.90 nm, 62.73 ± 3.81 nm, and 70.03 ± 1.39 nm, respectively.



Figure S8: DLS measurements to show the size variations of DNA origami nanostructures induced by pH titration. The size distribution shifted to the left when the pH changed from pH 9, pH 7.5, to pH 5, corresponding to the sizes of DNA origami trimers, dimers, and monomers, respectively, which is consistent with our design.



Figure S9: Time-dependent DLS study of the dynamic dissociation of DNA origami nanostructures driven by DNA triplexes. A) The DNA origami trimers dissociated to dimers when the pH was changed from 9 to 7.5. B) The DNA origami dimers dissociated to monomers when the pH was changed from 7.5 to 5.



Figure S10: AFM image of assembled 9-tile DNA origami. Rotation of the origami units exactly followed our theoretical design. Scale bar: 500nm.



Figure S11. Stepwise and reversible assembly of DNA origami 9-tile clusters demonstrated by agarose gel electrophoresis. Left lane of each image is DNA origami monomer, used as reference control, to show the bands mobility of targeted 5-titles and 9-titles. The yield of the 5-tile structure is 66.9%, while the yield of 9-tile is 72.8% based on gel electrophoresis.





Figure S12: AFM images of unpurified 5-tile and 9-tile DNA origami. A) A representative 5-tile DNA origami. B) A representative 9-tile DNA origami. Aggregation and partial formation of DNA origami coexist with targeted structures. Scale bar: 500nm

DNA Sequences used in this design:

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RC-M1 AGCTAATGCAGAACGCGCCTGTTTTAATATCC
RC-M2 CATCCTAATTTGAAGCCTTAAATCTTTTATCC
RC-M3 TGAATCTTGAGAGAGATAACCCACAAAACAATGA
RC-M4 AATAGCAATAGATGGGCGCATCGTACCGTATC
RC-M5 GGCCTCAGCTTGCATGCCTGCAGGGAATTCGT
RC-M6 AATCATGGTGGTTTTTTCTTTTCACCCGCCTGG
RC-M7 CCCTGAGAGAGTTGCAGCAAGCGGGTATTGGG
RC-M8 CGCCAGGGTCATAGCTGTTTCCTGGACGGCCA
RC-M9 GTGCCAAGGAAGATCGACATCCAGATAGGTTA
RC-M10 CGTTGGTGTAGCTATCTTACCGAATTGAGCGC
RC-M11 TAATATCAACCTTCGCTAACGAGCCCGACTTG
RC-M12 CGGGAGGTTTTACGAGCATGTAGAACATGTTC
RC-M13 CTGTCCAGACGACGACAATAAACAAACCAATC
RC-M14 AATAATCGCGTTTTAGCGAACCTCGTCTTTCC
RC-M15 AGAGCCTACAAAGTCAGAGGGTAAGCCCTTTT
RC-M16 TAAGAAAAGATTGACCGTAATGGGCCAGCTTT
RC-M17 CCGGCACCCACGACGTTGTAAAACTGTGAAAT
RC-M18 TGTTATCCGGGAGAGGGGGGTTTGCTCCACGCT
RC-M19 GGTTTGCCCCAGCAGGCGAAAATCAATCGGCC
RC-M20 AACGCGCGGCTCACAATTCCACACCCAGGGTT
RC-M21 TTCCCAGTGCTTCTGGTGCCGGAAGTGGGAAC
RC-M22 AAACGGCGGTAAGCAGATAGCCGAAACTGAAC
RC-M23 ACCCTGAAATTTGCCAGTTACAAATTCTAAGA
RC-M24 ACGCGAGGGCTGTCTTTCCTTATCAAGTAATT
RC-M25 GTACCGACAAAAGGTAATTCCAAG
RC-M26 AACGGGTAGAAGGCTTATCCGGTAATAAACAG
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RC-M28 GTCGGATTCTCCACCAGGCA RC-M30 AGCCGGAAGCCAGCTGCATTAATGCTGTTTGATGGTGTCTTCCTGTAGCCAGCTTTAATCGATG RC-M31 GCAAAATTCGGGAAACCTGTCGTGCATAAAGTGTAAAGCGATGTGCT RC-M32 GCAAGGCGTTCGCCATTCAGGCTGCGCAACTG RC-M33 GGAAGCGCTTTATCCCAATCCAAAAAGCAAAT RC-M34 CAGATATATTAAACCATACGGAAATTACCCAAAAGAACTGGCATGATTA RC-M35 AGGCATTTTCGAGCCAGTACTCATCG RC-M36 AGAACAAGTACCGCGCCCAATAGCTAAGAAAC RC-M39 CCTAATGAACTGCCCGCTTTCCAGCCCTTATA RC-M40 AATCAAAAGAATAGCCCTTTAAATATGCATTCTACTA RC-M41 GAGATAGGGTTGTCAGGATTAGAGAGTACCTATTCATT RC-M42 TTGCGCTCGTGAGCTAACTCACATGATAGCCC RC-M43 TATTACGCGGCGATCGGTGCGGGCGAGGATTT RC-M44 CAGCCTTTGTTTAACGTCAAAAATTTTCAATT RC-M45 GGAATCATCAAGCCGTTTTTATTTGTTATATA RC-M46 TCGCCATATTTAACAACGTTGCGGGGTTTTAAGCCCAA RC-M47 CCAACAGTGTGTGCCCGTATAAACAGTTAACCAGAGC RC-M48 ACTATATGCTCCGGCTTAGGTTGGTCATCGTA RC-M51 TAAAACATCTTTAATGCGCGAACTTAATTGCG RC-M52 CTATTAGTCGCCATTAAAAATACCATAGATTA RC-M53 GAGCCGTCTAGACTTTACAAACAATTCGACAA RC-M54 AATCGCGCAAAAGAAGTTAGTTAGCTTAAACAGCTTGATACGCCCACGC RC-M55 TTTTTAACTAAATGCTGATGCAAAATTGAGAA RC-M56 CAAGACAAAAATCATAGGTCTGAGACAAACAT RC-M59 CACCAGCAGGCACAGATTTAATTTCTCAATCATAAGGGAAC RC-M60 TGCTGGTAATATCCAGAACAATATAAGCGTAA RC-M61 GAATACGTGAAGATAAAACAGAGGATCTAAAA RC-M62 TATCTTTAAAATCCTTTGCCCGAACCGCGACCTGC RC-M63 CGAAACAAAGTAATAACGGA RC-M64 TTCGCCTGCAAAATTAATTACATTAATAGTGA RC-M65 ATTTATCAAGAACGCGAGAAAACTAGTATAAAGCCAATAAAGAATACAC RC-M66 ATATGCGTTATACAAATTCTTACCTTTTCAAA RC-M67 TATATTTTGACGCTGAGAAGAGTCTAACAATT **RC-M69 ATTTGTATCATCGCTTCTGAATTACAGTAACA** RC-M71 TCAGTATTAACCCTTCTGACCTGATACCGCCA RC-M72 GCCATTGCAACAGGAAAAACGCTCTGGCCAAC RC-M73 AGAGATAGAACACCGCCTGCAACAAAATCAAC **RC-M74 AGTAGAAAAGTTTGAGTAACATTA** RC-M75 TTTGGATTATACCTGATAAATTGTGTCGAAATCGTTATTA **RC-M76 GTACCTTTATTACCTTTTTTAATGCGATAGCT RC-M77 TAGATTAAAGTTAATTCGATCTTCTTAGTATC RC-M78 TCATAATTACTAGAAAAAGCCTGTTGACCTAA RC-M79 ATTTAATGATCCTTGAAAACATAGGAAACAGT** RC-M80 ACATAAATACGTCAGATGAATATATGGAAGGA RC-M81 ATTGAACCAATATAATCCTGATTGTCATTTTG RC-M82 CGGAACAATATCTGGTCAGTTGGCGTGCCACG RC-M83 CTGAGAGCAATAAAAGGGACATTCATGGAAAT RC-M84 ACCTACATTTTGACGCTCAATCGTCAGTGCGC RC-M85 CGACCAGTCAGCAGCAAATGAAAATCAAACCC RC-M86 TCAATCAAAGAAACCACCAGAAGGATGATGGC **RC-M87 AATTCATCAACCATATCAAAATTATAGATTTT** RC-M88 CAGGTTTACAATATATGTGAGTGATTAATTTT RC-M89 CCCTTAGAGTTTGAAATACCGACCCACCGGAA RC-M90 AAAAGGGTAAGATTGTATAAGCAAAAATTCGC RC-M91 AATAACCTTTAGAACCCTCATATAAAAGATTC RC-M92 GAAAGACTCAATTCTGCGAACGAGAAATGGTC RC-M93 CATAGTAATGACTATTATAGTCAGGGAAGCCC RC-M94 TAACAAAGTTAGGAATACCACATTTTACGAGG RC-M95 GCTGGCTGACCTTCATCAAGAGTAAATCAACG RC-M96 GTTGAGATCTGCTCATTCAGTGAAGCGCATAG RC-M97 CTTTACCCGAGCAACACTATCATAATTCATCA **RC-M98 TTGATTCCTCAAATATCGCGTTTTAATCAGGT RC-M99 AAAAATTTGTTTAGCTATATTTTCTGTAACAG**

RC-M100 AAAACAGGGAGAGAAAGGCCGGAGACGCAAGGAT RC-M101 GTTAAATTTTTGTTAAATCAGCTCAAGCCCCA RC-M102 CACCATCACGGTTGATAATCAGAAATTTTTTA RC-M103 CGCGAGCTAAGCCTTTATTTCAACAGTCAAAT RC-M104 CTTCAAAGTGGAAGTTTCATTCCAATTTGGGG RC-M105 TTACCAGAATGACCATAAATCAAAAATTCGAG RC-M106 GCCCTGACTATTACAGGTAGAAAGACCCTCGT RC-M107 ACAGATGAACGGTGTACAGACCAGTAAGGCTT RC-M108 AACAACATGAGAACACCAGAACGAGAAAGAGG RC-M110 ACGGTGTCCGAACCAGACCGGAAGAGTTCAGA RC-M112 ATGTACCCATATGATATTCAACCGAATACTTT RC-M113 ACCAATAGGAACGCCATCAAAAATTCAATCAT RC-M114 GATAAATTTCGTAAAACTAGCATGAATTCGCGTCTGGCTGTTCCGAAATCG RC-M115 ATAGTAGTAACATTATGACCCTGTTTCTAGCT RC-M116 CAAACTCCAACAGTTGAGTGTTGTTCGTAGAAGAACTCAAACTTTGAATGG RC-M117 GAGGCTTTCTCAAATGCTTTAAAC RC-M118 TTGGGCTTTACGTTAATAAAACGAAATAGCGA RC-M119 CGAACTGACCAACTTTGTAGTAAA RC-M120 GAAAAATCGAGATGGTTCAATATTTATCGGCCT RC-M123 AACGGTAAAATGCCGGAGAGGGTAAATCGGTT RC-M124 TTAAATGTGAGCGAGTAACAACTTAAGGAAACCGAGGAAA RC-M125 CTGGAGCAAACAAGAGCATCAACA RC-M126 CTGAATCTAAATCATACAGGCAAGTCAGAGCATGAAAGGGGCTGGGGTG RC-M127 GGTAATAGGCGGAATCGTCATAAATTTAATTGCTCCTTTTCTTAATTG RC-M128 TCATTGTGTTATACCAGTCAGGACCCAGAGGG RC-M129 AACGAGGCGCAGACGGAACTTTAA RC-M130 CTGGCTCAAATTACCTTATGCGATAATGACAA RC-M132 GCTTAGAGGATAAGAGGTCATTTTTGAAACAT RC-M134 CTGAGAGTCTACAAAGGCTATCAGACTTGAGC RC-M135 CATTTGGGATTATCACCGTCACCGGTCATTGC RC-M136 CTCAGAGCACCGCCACCCTCAGAGATTAAGCA RC-M137 GAAAGTATTCGGAACCTATTATTCTGCGGATG RC-M138 CCACAGACACAAACTACAACGCCTGATAGCGT RC-M139 CAACCATCCGATAGTTGCGCCGACTTTAAGAA RC-M140 ATAACCGATCATCTTTGACCCCCAGCGATTATACCAAGTTCATGTTACTTAGCCGG RC-M142 TGCCTATTTAAGAGGCTGAGACTCGAGTTTCG RC-M144 AAAGGTGAAATTAGAGCCAGCAAAAGCCGCCA RC-M145 CGCAATAATAACGGAATATTCATT RC-M146 TAGCACCAAAATATTGTAGTACCGCAATAAGAGAATATAAA RC-M147 CGCCGCCAGAACCGCCTCCCTCAGATCACCAG RC-M148 CTAAAGTTCATGTACCGTAACACTCTCAAGAGAAGGATTAGGATTA RC-M149 TAAAACACTATATTCGGTCGCTGATTTCGAGGAGAATTTCGTAACGAT RC-M150 GGGAGTTAAACGAAAGAGGCGTCGCTCAACAGTAGGGCTTATCCAATCG RC-M153 AGACTCCTTTGAGGGAGGGAAGGTTTACCATTAGCAAGGCACCAGAGC RC-M154 AGTATGTTAGCAAACGTAGAAAATGCGCCAAA RC-M155 TCACCAATGGCGACATTCAACCGATATTACGC RC-M156 TCAGACGAAATCAAAATCACCGGACGGAAACG RC-M157 CCAGGCGGTTTTAACGGGGGTCAGTGAGGCAGG **RC-M158 AATGAATTCATTTTCAGGGATAGCGCTCAGTA** RC-M159 TTTTGCGGGAGCCTTTAATTGTATCGTTAGTA RC-M160 GCCACTACGAAGGCACCAACCTAAAAGGCCGC RC-M161 TCCAAAAGGATCGTCACCCTCAGCTACGTAAT RC-M162 ACCACCCTTTCTGTATGGGATTTTAAAAAGGC RC-M163 GTAATAAGATAAGTGCCGTCGAGATCAGAGCC RC-M164 CTTTTCATTTGGCCTTGATATTCAGTGTACTG RC-M165 GACAAAAGGAAACCATCGATAGCATTTGCCAT RC-M166 AAAGGTGGCAACATATAAAAGAAACACAATCA RC-M167 ATCAGTAGTTCATATGGTTTACCAACATACAT RC-M168 TGGATCTTAGCCCCCTTATTAGCGGCACCGTA RC-M169 ATAAGTATTTTTGATGATACAGGACAAACGAA RC-M170 ACTTTCAACTCAGAACCGCCACCCGGGTTGAT RC-M171 ACAGCATCGTTGAAAATCTCCAAAGCTAAACA RC-M172 GAAGTTTCCATTAAACGGGTAAAAAGCGAAAG RC-M173 TTTTTCACGGAACGAGGGTAGCAATTCATGAG

RC-M174 CCGCCACCCAGTTTCAGCGGAGTGATAATAAT
RC-M175 TACATGGCAGCCCGGAATAGGTGTCCTCAGAA
RC-M176 TCGGTCATCATTAAAGCCAGAATGAAGCGTCA
RC-M177 ATAGAAAACGACAGAATCAAGTTTCGGCATTT
RC-M27-AS CCATATTAATTAGACGGGAGAATTACAAAGTTACC
RC-M29-AS AAGCGCCAATTAAGTTGGGTAACGAACATACG
RC-M37-AS GATTTTTTACAGAGAGAATAACATAAAAAACAG
RC-M38-AS TTGGGAAGCAGCTGGCTTAAAGCTAGCTATTTTTGAGAGAGA
RC-M49-AS ACCTGAGCAGAGGCGAATTATTCAGAAAATAG
RC-M50-AS AGAAGTATAATAGATAATACATTTCTCTTCGC
RC-M57-AS CAAGAAAAATTGCTTTGAATACCAAGTTACAA
RC-M58-AS CTCGTATTGGTGCACTAACAACTAGAACGAAC
RC-M68-AS TGATTTGATACATCGGGAGAAACACAACGGAG
RC-M70-AS ATTTTAAAGGAATTGAGGAAGGTTTGAGGCGG
RC-M109-AS AAACGAGACGACGATAAAAACCAAACTAACGG
RC-M111-AS TGCGGGAGGAAAAGGTGGCATCAAACTAAAGT
RC-M121-AS GAATCCCCTGCAAAAGAAGTTTTGGTTGGGAA
RC-M131-AS CCAATACTTAAAATGTTTAGACTGGTAGCATT
RC-M133-AS ATAAAGCCGCAAAGAATTAGCAAACCACCACC
RC-M141-AS TCACCAGTAGCCCTCATATGATGAAAGACTACC
RC-M143-AS CCCTCAGACGCCACCAGAACCACCATGCCCCC
RC-M122-AS GTACCAAAAGCATTAACATCCAATGGTGCTGTAGCTCAACATGTTT
RC-M151-AS TAGGAACCTTGTCGTCTTTCCAGACGGTTTATCAGCTTGCGGCTTGCA
RC-M152-AS CACCACCGGCATTGACAGGAGGTTGCCTTGAGTAACATAATTTAGGCAG

Modified DNA Sequences used for the formation of DNA origami trimer:

20%TAT Triplex Triplex-A1R1 GTGTGATAAATAAGGCTTTTT Triplex-A1R2ATAACCTTGCTTCTGTTTTTT Triplex-A1R4 AGCGGAATTATCATCATTTTT Triplex-A1R5 ATCTAAAGCATCACCTTTTTT Triplex-A1R1G GTTAAATAAGAATAAA Triplex-A1R2G AAATCGTCGCTATTAA Triplex-A1R4G TATTCCTGATTATCAG Triplex-A1R5G TGCTGAACCTCAAATA Blunt RE3 TTTTAAATAAAGAAATTGCGTTAGCACGTAAAACAGTTTT Blunt RE6 TTTTACATTGGCAGATTCACCTGAAATGGATTATTTTTT Triplex-A2L1 GGGAGGCATGAGTTTTTTTTTCCTGAACAAGAAAAAATCAACAATAGATAAGTTTTT Triplex-A2L2 GGGAGGCATGAGTTTTTTTTTGCACCCAGCTACAAAAGATTAGTTGCTATTTTTT Triplex-A2L4 GGGAGGCATGAGTTTTTTTTTTTTGTTTGAGGGGGACGACGAACCGTGCATCTGCCATTTTT Triplex-A2L5 GGGAGGCATGAGTTTTTTTTCCCGGGTACCGAGGTCTCGACTCTAGAGGATCTTTTT TTTTAATAATAAGAGCAAGAGAATTGAGTTAAGCCCTTTT Blunt LE3 Blunt LE6 TTTTAGCTGATTGCCCTTCACAGTGAGACGGGCAACTTTT 73%TAT Triplex Triplex-A1R1 GTGTGATAAATAAGGCTTTTT Triplex-A1R2ATAACCTTGCTTCTGTTTTT Triplex-A1R4 AGCGGAATTATCATCATTTTT Triplex-A1R5 ATCTAAAGCATCACCTTTTTT Triplex-A2R1 TCGTATTTCTTCTTCTTGTTTCTTCTTCTTCTTCTTCTTATTTAAGAAGAAGAAGAAGAATTTTTTTGT TAAATAAGAATAAA

Triplex-A2R2

Blunt RE3 TTTTAAATAAAGAAATTGCGTTAGCACGTAAAACAGTTTT

Blunt RE6 TTTTACATTGGCAGATTCACCTGAAATGGATTATTTTTT

Triplex-A3L1 GAAGAAATACGATTTTTTTTCCTGAACAAGAAAAAATCAACAATAGATAAGTTTT Triplex-A3L2 GAAGAAATACGATTTTTTTTTGCACCCAGCTACAAAAGATTAGTTGCTATTTTTT Triplex-A3L4 GAAGAAATACGATTTTTTTTGTTTGAGGGGACGACGAACCGTGCATCTGCCATTTT Triplex-A3L5 GAAGAAATACGATTTTTTTTCCCGGGTACCGAGGTCTCGACTCTAGAGGATCTTTTT Blunt LE3 TTTTAATAATAAGAGCAAGAGAATTGAGTTAAGCCCTTTT Blunt LE6 TTTTAGCTGATTGCCCTTCACAGTGAGACGGGCAACTTTT

Modified DNA Sequences used for the formation of 9-tile origami:

pH-A4-Left-linearSE1 GGGAGGCATGAGTTTTTTTTTCCTGAACAAGAAAAAATCAACAATAGATAAGTTTTT pH-A4-Left-linearSE2 GGGAGGTCTCAATTTTTTTTTGCACCCAGCTACAAAAGATTAGTTGCTATTTTTT pH- A4-Left-linearSE4 GGGAGGATACATTTTTTTTTTGTTTGAGGGGACGACGAACCGTGCATCTGCCATTTTT pH- A4-Left-linearSE5 GGGAGGTAGTCATTTTTTTCCCGGGTACCGAGGTCTCGACTCTAGAGGATCTTTTT pH-A4-Right-linearSE6 GGGAGGCATGAGTTTTTTTACATTGGCAGATTCACCTGAAATGGATTATTTTTTT pH-A4-Right-linearSE5 GGGAGGTCTCAATTTTTTTTTGCTGAACCTCAAATAATCTAAAGCATCACCTTTTTT pH-A4-Right-linearSE3 GGGAGGATACATTTTTTTTTAAATAAAGAAATTGCGTTAGCACGTAAAACAGTTTTT pH-A4-Right-linearSE2 GGGAGGTAGTCATTTTTTTTAAATCGTCGCTATTAAATAACCTTGCTTCTGTTTTTT pH-A4-Down-linearSE1 **GGGAGGCATGAGTTTTTTTCGTTAATATTTTGTTAATATTTAAATTGTAAATTTTTTT** pH-A4-Down-linearSE2 GGGAGGTCTCAATTTTTTTTGAGTAATGTGTAGGTTTTTAAATGCAATGCCTTTTT pH-A4-Down-linearSE4 GGGAGGATACATTTTTTTTTTTTATCAAAAAGATTAAGAAAGCAAAGCGGATTGCTTTTT pH-A4-Down-linearSE5 GGGAGGTAGTCATTTTTTTTTATAACGCCAAAAGGAACAACTAATGCAGATACTTTTT pH-A4-Top-linearSE6 pH-A4-Top-linearSE5 GGGAGGTCTCAATTTTTTTTACTAAAGGAATTGCGAAGAATAGAAAGGAACATTTTT pH-A4-Top-linearSE3 GGGAGGATACATTTTTTTTTAATTTACCGTTCCAGTGAAAGCGCAGTCTCTGTTTTT pH-A4-Top-linearSE2 GGGAGGTAGTCATTTTTTTTTGTAGCGCGTTTTCATGCCTTTAGCGTCAGACTTTTT pH-A5-Right-Triplex SE1 GTTAAATAAGAATAAA pH-A5-Right-Triplex SE2 ATCGTCGCTATTAAATAACCTT

pH-A5-TOP-linearSE2 GAAGAAACGATTTTTTTTTTTGTAGCGCGTTTTCATGCCTTTAGCGTCAGACTTTTT pH-A5-TOP-linearSE4 GAAGAACTACCGTTTTTTTGGTTTAGTACCGCCACATCACCGTACTCAGGATTTTT

pH-A5-Down-linearSE2 GAAGAAGATGACTTTTTTTGAGTAATGTGTAGGTTTTTAAATGCAATGCCTTTTT pH-A5-Down-linearSE4 GAAGAACCTCGATTTTTTTTTTTATCAAAAAGATTAAGAAAGCAAAGCGGATTGCTTTTT

pH-A6-Right-TriplexS3 CGGTAGTTCTTCTTCTTGTTTCTTCTTCTTCTTCTTCTTATTTAAGAAGAAGAAGAAGAATTTTTTAAA TAAAGAAATTGCGTTAGCACG pH-A6-Right-TriplexS5 AATCGTTTCTTCTTCTTGTTTCTTCTTCTTCTTCTTCTTATTTAAGAAGAAGAAGAAGAATTTTTTTGC TGAACCTCAAATAATCTAAAG