Supplemental Information

Luyao Shen[1,2], Victor Pan[2], Haofei Li[1], Yunlong Zhang[3], Pengfei Wang[1*], Yonggang Ke[2,3*]

[1]Institute of Molecular Medicine, Shanghai Key Laboratory for Nucleic Acid Chemistry and Nanomedicine, Renji Hospital, School of Medicine, Shanghai Jiao Tong University, Shanghai 200127, China
pengfei.wang@sjtu.edu.cn

[2]Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology and Emory University, Atlanta, GA 30322, USA
yonggang.ke@emory.edu

[3]Department of Chemistry, Emory University, Atlanta, GA 30322, USA

Materials and Methods

Materials: DNA staple strands were purchased from IDT. M13 bacteriophage scaffold DNA (p7560) was produced following a published protocol.[1] 10 nm gold nanoparticles (AuNPs) were purchased from Ted Pella, Inc.

DNA origami hexagon tile design and assembly: DNA origami hexagon tile (DHT) was designed by using caDNAno. In a typical annealing protocol, staples were mixed with single stranded DNA scaffold (p7560, 10 nM) in 5-fold molar excess in aqueous buffer composing of 5 mM Tris base, 1 mM EDTA, and 10 mM $MgCl_2$, with a total volume of 100 µL. The mixed solution was slowly cooled down to room temperature (24 °C) in a PCR thermal cycler over 18 hrs under the following protocol: 65 °C for 5 mins, 60 to 24 °C, at 30 mins/°C.

Conjugating DNA onto AuNPs: 50 mL of colloidal citrated 10nm AuNP solution was added with 15 mg of Bis(p-sulfonatophenyl) phenylphosphine dihydrate dipotassium salt (BSPP) and shook overnight. Then NaCl was added until a color change of the solution from red to blue was observed. The AuNPs were centrifuged to the bottom at 1,000 rcf for 30 min and the clear supernatant was removed with a pipette. The particles were dissolved in BSPP solution (1 mL, 2.5 mM) followed by addition of 3 mL of methanol. The particles were centrifuged again and re-suspended in 1 mL of BSPP. The concentration of the AuNPs was determined from the optical absorption at a wavelength of 520 nm using a Nanodrop spectrophotometer. For reducing the disulfide bonds of the thiolated ssDNA strands to monothiol, the modified strands were incubated with 100-fold of TCEP (Tris(carboxyethyl) phosphine hydrochloride) for at least 30 mins. AuNPs and thiolated DNA were mixed in 0.5×TBE buffer at a designated ratio (1: 100). Within a period of 24 hrs, NaCl solution was added to the solution to achieve a final concentration of 300 mM. To remove the unbound DNA strands, the mixture was spun for 30 min at 18,000 rcf, and the supernatant was removed carefully without disturbing the pellet. 4 additional washing and spinning steps (30 min, 18,000 rcf) with 100 µL of 0.5 × TBE buffer containing 300 mm NaCl were conducted to fully removed unbound DNA.

Attaching AuNPs onto DNA origami templates: DNA origami structures were assembled first, as described above, which were then added with 5-fold (in terms of binding site, 1.5-fold for 2D lattice designs) of DNA-conjugated AuNPs, incubated for at least 2 hours at room temperature. Cluster structures were then subject to agarose gel electrophoresis and corresponding bands were extracted. Superlattice structures were directly characterized.

Gel electrophoresis: DNA origami with AuNPs forming clusters were run on 1% native agarose gel electrophoresis for 2 hours (gel prepared in 0.5 × TBE buffer supplemented with 10 mM $MgCl_2$ and 0.005% (v/v) EtBr) in an ice water bath. Then, the target gel bands were excised and placed into a

Freeze 'N Squeeze column (Bio-Rad Laboratories, Inc.). The gel pieces were crushed into fine pieces by a microtube pestle in the column, and the column was then centrifuged at 7000 rcf for 5 minutes. Samples that were extracted through the column were collected for subsequent experiments.

TEM imaging: 10 µL of samples were deposited onto glow-discharged, carbon-coated copper TEM grids for 5-30 minutes inside a moisture chamber. Residual solution was dried by filter paper. The grids were then stained for 1 minute using a 1% aqueous uranyl formate solution containing 25 mM NaOH. Imaging was performed using a Hitachi-7700 microscope operated at 80 kV.

Stability study: 9-AuNP clusters were prepared as illustrated in the above protocol. 10 µL of 10 nM nanoparticle clusters were incubated in 1×TE/Mg^{2+}(10 mM), 1×PBS, or RPMI-1640/10% FBS at 37 °C for 0.5, 1, 2, or 4 hours. Immediately after incubation, the samples were subject to 1% native agarose gel electrophoresis running in 0.5 × TBE buffer supplemented with 10 mM $MgCl_2$.

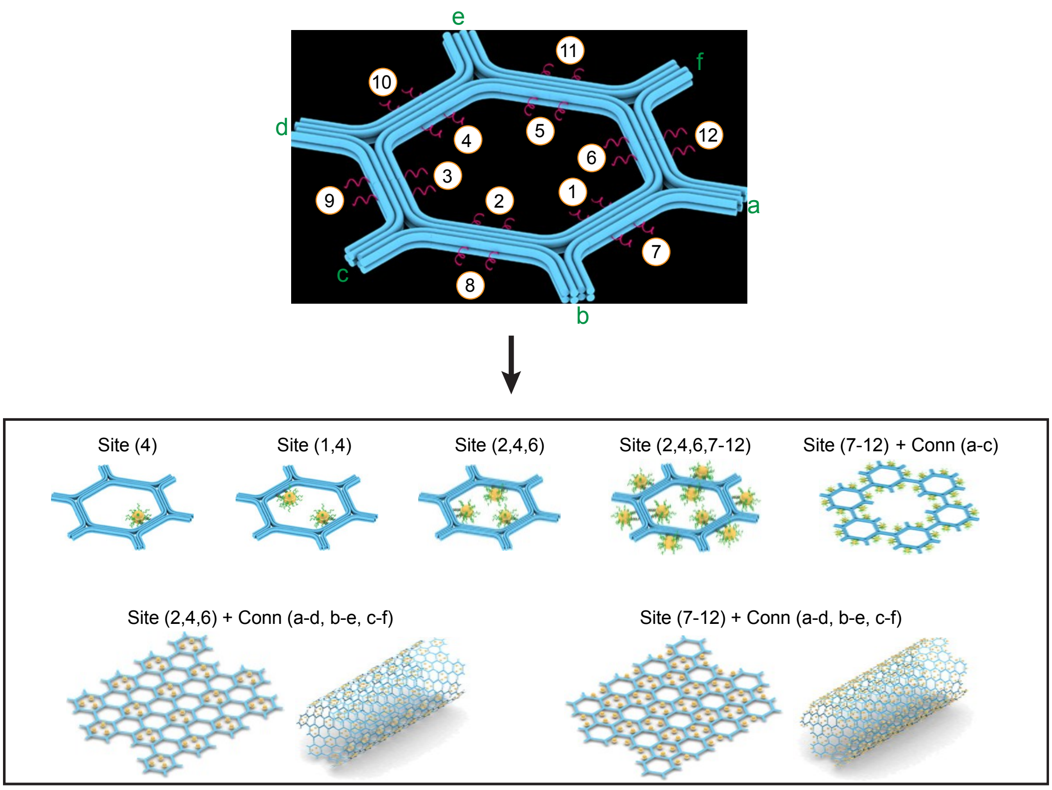

Figure S1. Summary figure. DHT-guided assembly of gold nanoparticle clusters and lattices. The use of docking handle strands and connector strands are indicated for each architecture.

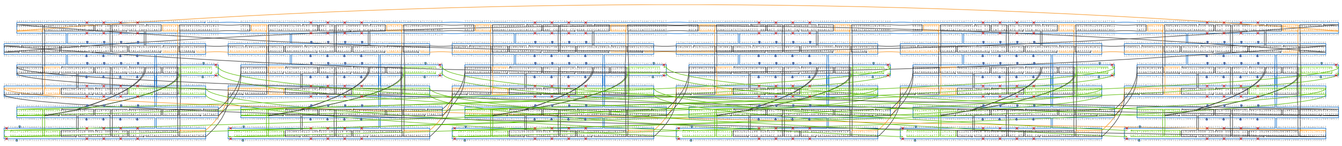

Figure S2. Strand diagram of DHT. Blue: scaffold DNA; black: core staples; orange: capture strands; green: connector strands. Zoom in to see details.

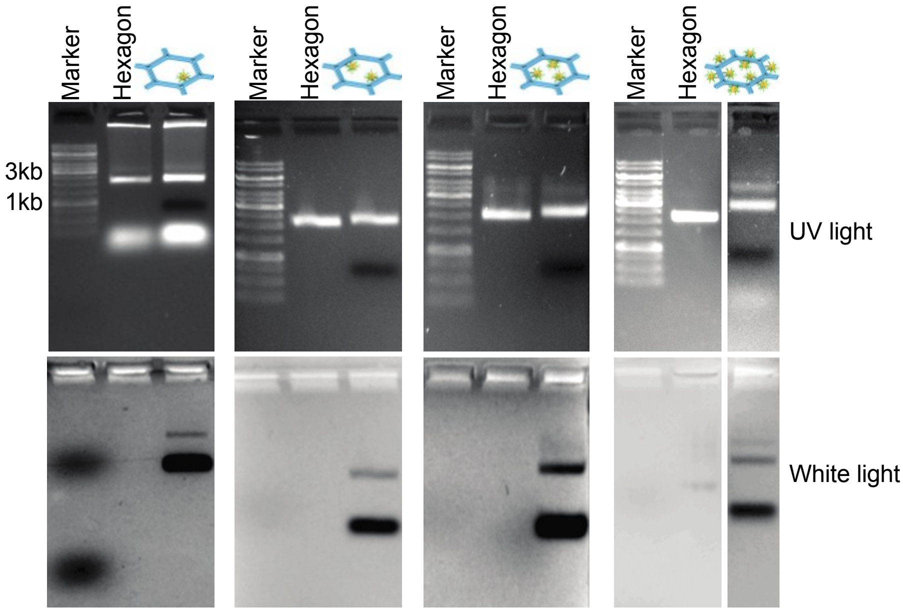

Figure S3. Agarose gel electrophoresis (1%) of nanoparticle clusters assembled on DHT. Top row: UV illumination; bottom row: white light.

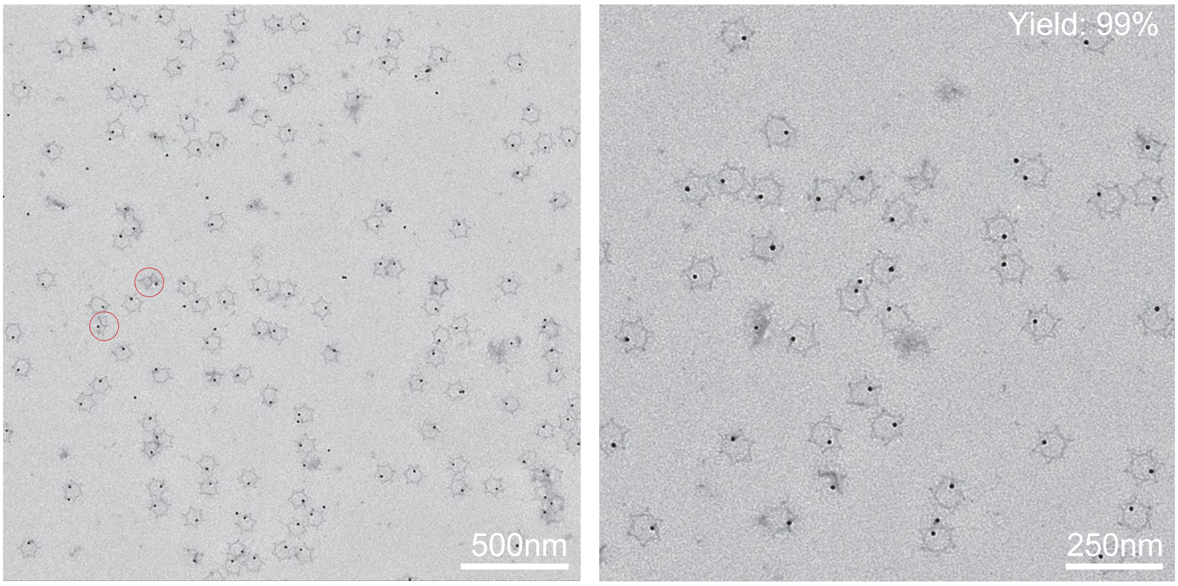

Figure S4. 1-AuNP cluster on DHT. Yield is calculated based on TEM images (N=116). Wrongly assembled clusters were marked by a red circle.

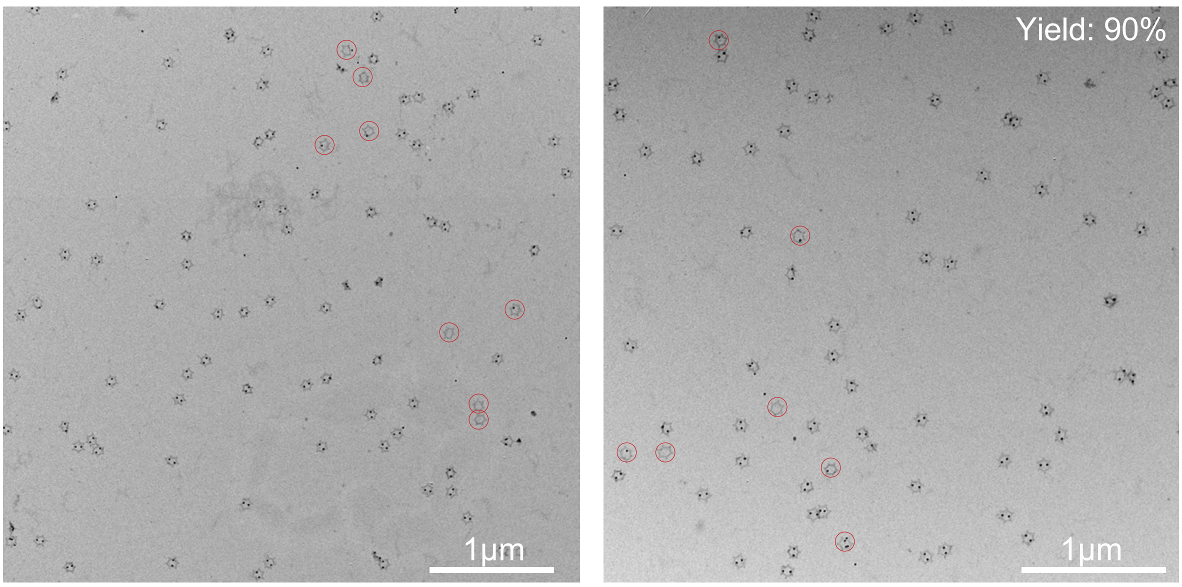

Figure S5. 2-AuNP cluster on DHT. Yield is calculated based on the images (N=205). Wrongly assembled clusters were marked by a red circle.

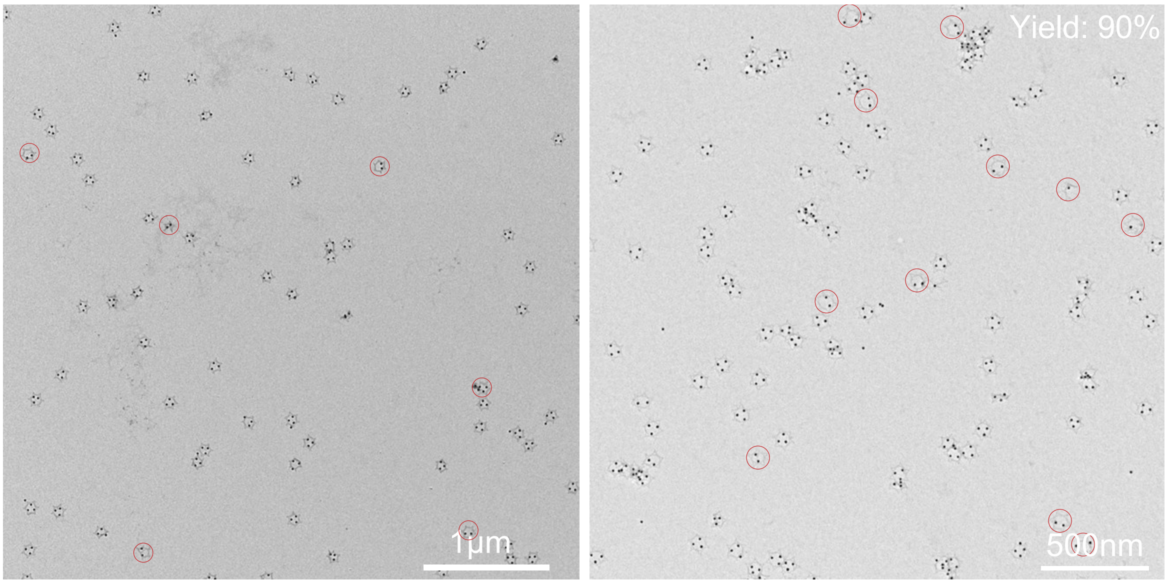

Figure S6. 3-AuNP cluster on DHT. Yield is calculated based on the images (N=155). Wrongly assembled clusters were marked by a red circle.

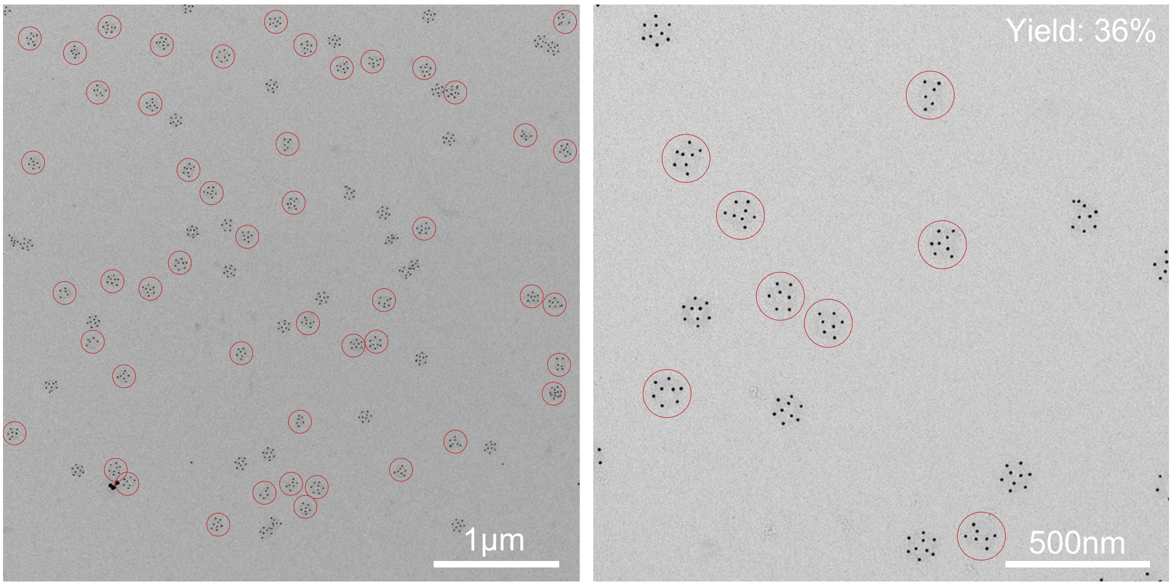

Figure S7. 9-AuNP cluster on DHT. Yield is calculated based on the images (N=87). Wrongly assembled clusters were marked by a red circle.

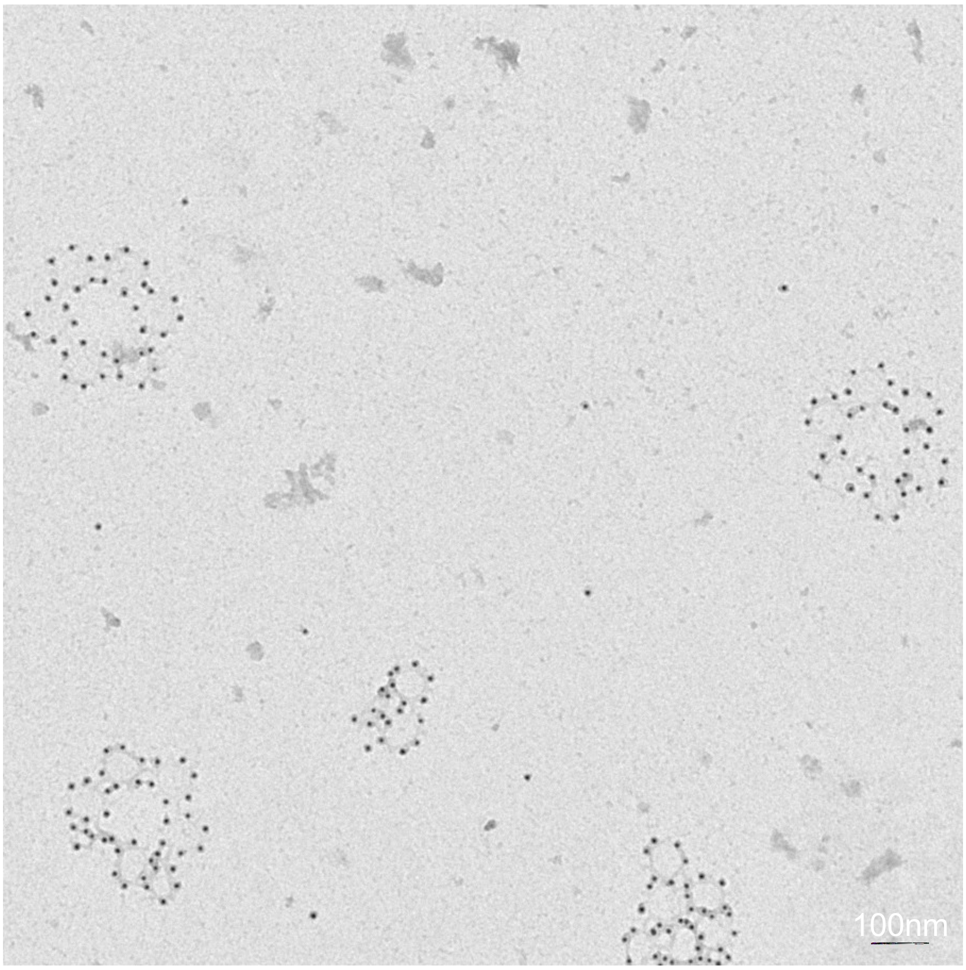

Figure S8. 36-AuNP cluster on DHT hexamer.

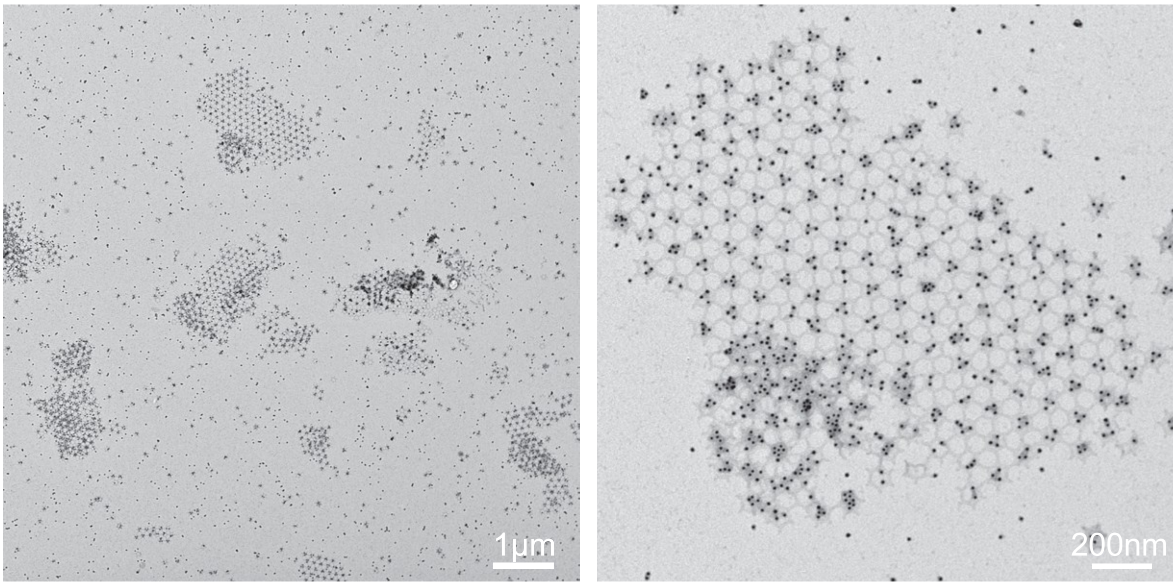

Figure S9. AuNP lattices on honeycomb array with type-1 configuration.

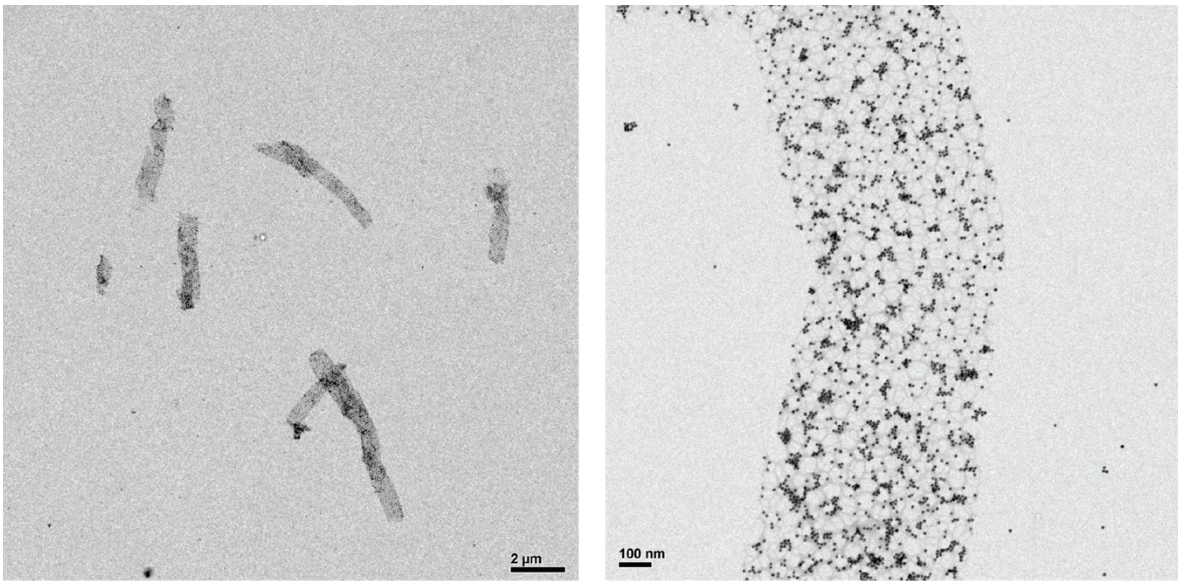

Figure S10. AuNP lattices on honeycomb tube with type-1 configuration.

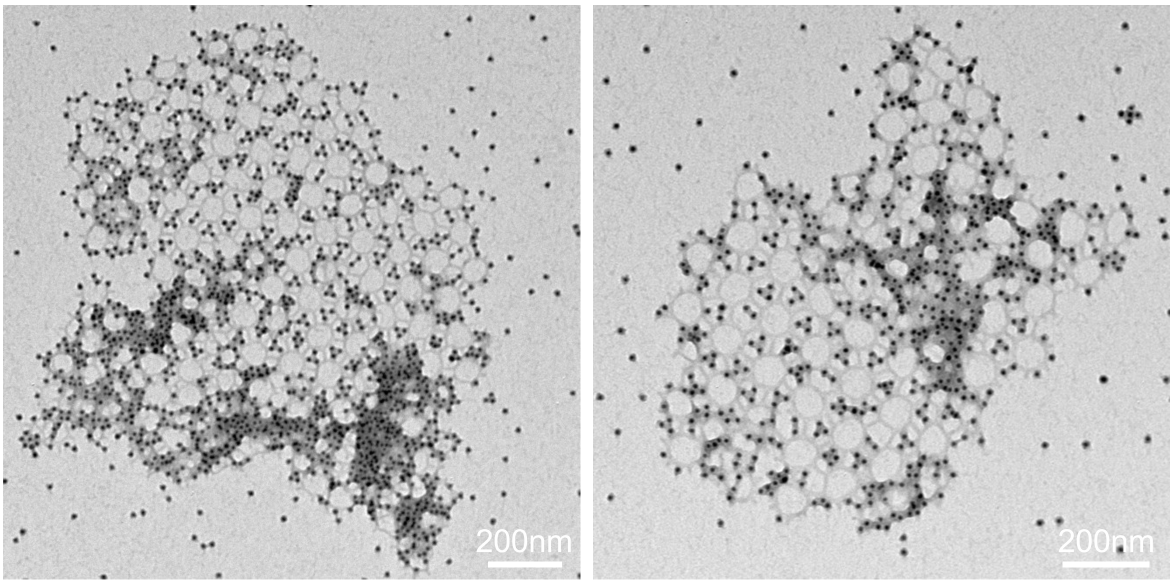

Figure S11. AuNP lattices on honeycomb array with type-2 configuration.

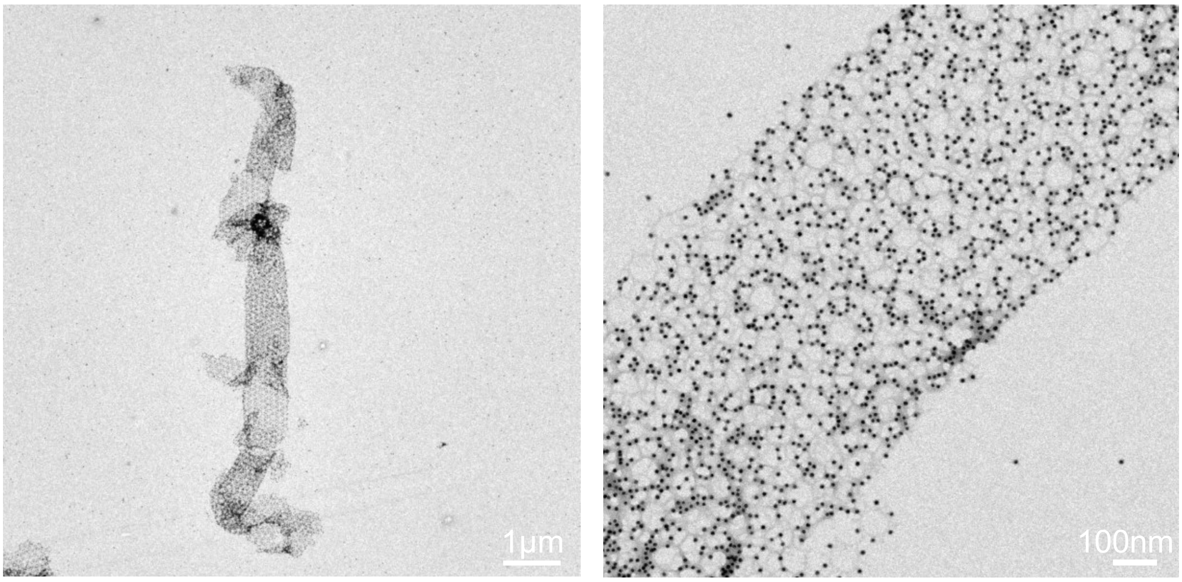

Figure S12. AuNP lattices on honeycomb tube with type-2 configuration.

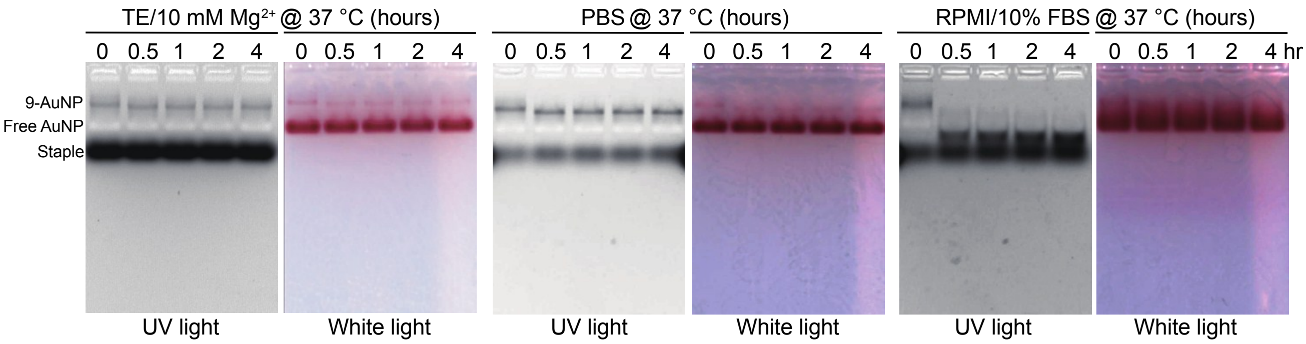

Figure S13. Stability of 9-AuNP clusters in various buffers and cell culture medium at 37 °C.

DNA strands sequences

p7560 scaffold DNA:

AGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA
AGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCTTTGCCTGGTTTCCGGCACCAGAAGCGGTGCCGGAAAGCTGGCTGGAGTGC
GATCTTCCTGAGGCCGATACTGTCGTCGTCCCCTCAAACTGGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTGACCTATCCCATTACGGTCAATCCGCCGTT
TGTTCCCACGGAGAATCCGACGGGTTGTTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTACAGGAAGGCCAGACGCGAATTATTTTTGATGGCGTTCCTATTGGTT
AAAAAATGAGCTGATTTAACAAAAATTTAATGCGAATTTTAACAAAATATTAACGTTTACAATTTAAATATTTGCTTATACAATCTTCCTGTTTTTGGGGCTTTTCTGATT
ATCAACCGGGGTACATATGATTGACATGCTAGTTTTACGATTACCGTTCATCGATTCTCTTGTTTGCTCCAGACTCTCAGGCAATGACCTGATAGCCTTTGTAGATCTCTC
AAAAATAGCTACCCTCTCCGGCATTAATTTATCAGCTAGAACGGTTGAATATCATATTGATGGTGATTTGACTGTCTCCGGCCTTTCTCACCCTTTTGAATCTTTACCTAC
ACATTACTCAGGCATTGCATTTAAAATATATGAGGGTTCTAAAAATTTTTATCCTTGCGTTGAAATAAAGGCTTCTCCCGCAAAAGTATTACAGGGTCATAATGTTTTTGG
TACAACCGATTTAGCTTTATGCTCTGAGGCTTTATTGCTTAATTTTGCTAATTCTTTGCCTTGCCTGTATGATTTATTGGATGTTAATGCTACTACTATTAGTAGAATTGAT
GCCACCTTTTCAGCTCGCGCCCCAAATGAAAATATAGCTAAACAGGTTATTGACCATTTGCGAAATGTATCTAATGGTCAAACTAAATCTACTCGTTCGCAGAATTGGGA
ATCAACTGTTATATGGAATGAAACTTCCAGACACCGTACTTTAGTTGCATATTTAAAACATGTTGAGCTACAGCATTATATTCAGCAATTAAGCTCTAAGCCATCCGCAA
AAATGACCTCTTATCAAAAGGAGCAATTAAAGGTACTCTCTAATCCTGACCTGTTGGAGTTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTAAAACGCGATATTTG
AAGTCTTTCGGGCTTCCTCTTAATCTTTTTGATGCAATCCGCTTTGCTTCTGACTATAATAGTCAGGGTAAAGACCTGATTTTTGATTTATGGTCATTCTCGTTTTCTGAAC
TGTTTAAAGCATTTGAGGGGGATTCAATGAATATTTATGACGATTCCGCAGTATTGGACGCTATCCAGTCTAAACATTTTACTATTACCCCCTCTGGCAAAACTTCTTTTG
CAAAAGCCTCTCGCTATTTTGGTTTTTATCGTCGTCTGGTAAACGAGGGTTATGATAGTGTTGCTCTTACTATGCCTCGTAATTCCTTTTGGCGTTATGTATCTGCATTAGT
TGAATGTGGTATTCCTAAATCTCAACTGATGAATCTTTCTACCTGTAATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTTTCTTCCCAACGTCCTGACTGGTAT
AATGAGCCAGTTCTTAAAATCGCATAAGGTAATTCACAATGATTAAAGTTGAAATTAAACCATCTCAAGCCCAATTTACTACTCGTTCTGGTGTTTCTCGTCAGGGCAAG
CCTTATTCACTGAATGAGCAGCTTTGTTACGTTGATTTGGGTAATGAATATCCGGTTCTTGTCAAGATTACTCTTGATGAAGGTCAGCCAGCCTATGCGCCTGGTCTGTAC
ACCGTTCATCTGTCCTCTTTCAAAGTTGGTCAGTTCGGTTCCCTTATGATTGACCGTCTGCGCCTCGTTCCGGCTAAGTAACATGGAGCAGGTCGCGGATTTCGACACAAT
TTATCAGGCGATGATACAAATCTCCGTTGTACTTTGTTTCGCGCTTGGTATAATCGCTGGGGGTCAAAGATGAGTGTTTTAGTGTATTCTTTTGCCTCTTTCGTTTTAGGTT
GGTGCCTTCGTAGTGGCATTACGTATTTTACCCGTTTAATGGAAACTTCCTCATGAAAAAGTCTTTAGTCCTCAAAGCCTCTGTAGCCGTTGCTACCCTCGTTCCGATGCT
GTCTTTCGCTGCTGAGGGTGACGATCCCGCAAAAGCGGCCTTTAACTCCCTGCAAGCCTCAGCGACCGAATATATCGGTTATGCGTGGGCGATGGTTGTTGTCATTGTCG
GCGCAACTATCGGTATCAAGCTGTTTAAGAAATTCACCTCGAAAGCAAGCTGATAAACCGATACAATTAAAGGCTCCTTTTGGAGCCTTTTTTTTGGAGATTTTCAACGT
GAAAAAATTATTATTCGCAATTCCTTTAGTTGTTCCTTTCTATTCTCACTCCGCTGAAACTGTTGAAAGTTGTTTAGCAAAATCCCATACAGAAAATTCATTTACTAACGT
CTGGAAAGACGACAAAACTTTAGATCGTTACGCTAACTATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAACTCAGTGTTACGGTACAT
GGGTTCCTATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGG
TGATACACCTATTCCGGGCTATACTTATATCAACCCTCTCGACGGCACTTATCCGCCTGGTACTGAGCAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGTCTCAGCC
TCTTAATACTTTCATGTTTCAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCACTGTTACTCAAGGCACTGACCCCGTTAAAACTTATTACC
AGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTGGCTTTAATGAGGATTTATTTGTTTGTGAATATC
AAGGCCAATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTGGCGGCGGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAG
GGTGGCGGCTCTGAGGGAGGCGGTTCCGGTGGTGGCTCTGGTTCCGGTGATTTTGATTATGAAAAGATGGCAAACGCTAATAAGGGGGCTATGACCGAAAATGCCGATG
AAAACGCGCTACAGTCTGACGCTAAAGGCAAACTTGATTCTGTCGCTACTGATTACGGTGCTGCTATCGATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAAT
GGTGCTACTGGTGATTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCTCCCTCAA
TCGGTTGAATGTCGCCCTTTTGTCTTTGGCGCTGGTAAACCATATGAATTTTCTATTGATTGTGACAAAATAAACTTATTCCGTGGTGTCTTTGCGTTTCTTTTATATGTTG
CCACCTTTATGTATGTATTTTCTACGTTTGCTAACATACTGCGTAATAAGGAGTCTTAATCATGCCAGTTCTTTTGGGTATTCCGTTATTATTGCGTTTCCTCGGTTTCCTTC
TGGTAACTTTGTTCGGCTATCTGCTTACTTTTCTTAAAAAGGGCTTCGGTAAGATAGCTATTGCTATTTCATTGTTTCTTGCTCTTATTATTGGGCTTAACTCAATTCTTGTG
GGTTATCTCTCTGATATTAGCGCTCAATTACCCTCTGACTTTGTTCAGGGTGTTCAGTTAATTCTCCCGTCTAATGCGCTTCCCTGTTTTTATGTTATTCTCTCTGTAAAGGC
TGCTATTTTCATTTTTGACGTTAAACAAAAAATCGTTTCTTATTTGGATTGGGATAAATAATATGGCTGTTTATTTTGTAACTGGCAAATTAGGCTCTGGAAAGACGCTCG
TTAGCGTTGGTAAGATTCAGGATAAAATTGTAGCTGGGTGCAAAATAGCAACTAATCTTGATTTAAGGCTTCAAAACCTCCCGCAAGTCGGGAGGTTCGCTAAAACGCC
TCGCGTTCTTAGAATACCGGATAAGCCTTCTATATCTGATTTGCTTGCTATTGGGCGCGGTAATGATTCCTACGATGAAAATAAAAACGGCTTGCTTGTTCTCGATGAGTG
CGGTACTTGGTTTAATACCCGTTCTTGGAATGATAAGGAAAGACAGCCGATTATTGATTGGTTTCTACATGCTCGTAAATTAGGATGGGATATTATTTTTCTTGTTCAGGA
CTTATCTATTGTTGATAAACAGGCGCGTTCTGCATTAGCTGAACATGTTGTTTATTGTCGTCGTCTGGACAGAATTACTTTACCTTTTGTCGGTACTTTATATTCTCTTATT
ACTGGCTCGAAAATGCCTCTGCCTAAATTACATGTTGGCGTTGTTAAATATGGCGATTCTCAATTAAGCCCTACTGTTGAGCGTTGGCTTTATACTGGTAAGAATTTGTAT
AACGCATATGATACTAAACAGGCTTTTTCTAGTAATTATGATTCCGGTGTTTATTCTTATTTAACGCCTTATTTATCACACGGTCGGTATTTCAAACCATTAAATTTAGGTC
AGAAGATGAAATTAACTAAAATATATTTGAAAAAGTTTTCTCGCGTTCTTTGTCTTGCGATTGGATTTGCATCAGCATTTACATATAGTTATATAACCCAACCTAAGCCGG
AGGTTAAAAAGGTAGTCTCTCAGACCTATGATTTTGATAAATTCACTATTGACTCTTCTCAGCGTCTTAATCTAAGCTATCGCTATGTTTTCAAGGATTCTAAGGGAAAAT
TAATTAATAGCGACGATTTACAGAAGCAAGGTTATTCACTCACATATATTGATTTATGTACTGTTTCCATTAAAAAAGGTAATTCAAATGAAATTGTTAAATGTAATTAA
TTTTGTTTTCTTGATGTTTGTTTCATCATCTTCTTTTGCTCAGGTAATTGAAATGAATAATTCGCCTCTGCGCGATTTTGTAACTTGGTATTCAAAGCAATCAGGCGAATCC
GTTATTGTTTCTCCCGATGTAAAAGGTACTGTTACTGTATATTCATCTGACGTTAAACCTGAAAATCTACGCAATTTCTTTATTTCTGTTTTACGTGCAAATAATTTTGATA
TGGTAGGTTCTAACCCTTCCATTATTCAGAAGTATAATCCAAACAATCAGGATTATATTGATGAATTGCCATCATCTGATAATCAGGAATATGATGATAATTCCGCTCCTT
CTGGTGGTTTCTTTGTTCCGCAAAATGATAATGTTACTCAAACTTTTAAAATTAATAACGTTCGGGCAAAGGATTTAATACGAGTTGTCGAATTGTTTGTAAAGTCTAATA
CTTCTAAATCCTCAAATGTATTATCTATTGACGGCTCTAATCTATTAGTTGTTAGTGCTCCTAAAGATATTTTAGATAACCTTCCTCAATTCCTTTCAACTGTTGATTTGCC
AACTGACCAGATATTGATTGAGGGTTTGATATTTGAGGTTCAGCAAGGTGATGCTTTAGATTTTTCATTTGCTGCTGGCTCTCAGCGTGGCACTGTTGCAGGCGGTGTTAA
TACTGACCGCCTCACCTCTGTTTTATCTTCTGCTGGTGGTTCGTTCGGTATTTTTAATGGCGATGTTTTAGGGCTATCAGTTCGCGCATTAAAGACTAATAGCCATTCAAA
AATATTGTCTGTGCCACGTATTCTTACGCTTTCAGGTCAGAAGGGTTCTATCTCTGTTGGCCAGAATGTCCCTTTTATTACTGGTCGTGTGACTGGTGAATCTGCCAATGT
AAATAATCCATTTCAGACGATTGAGCGTCAAAATGTAGGTATTTCCATGAGCGTTTTTCCTGTTGCAATGGCTGGCGGTAATATTGTTCTGGATATTACCAGCAAGGCCG
ATAGTTTGAGTTCTTCTACTCAGGCAAGTGATGTTATTACTAATCAAAGAAGTATTGCTACAACGGTTAATTTGCGTGATGGACAGACTCTTTTACTCGGTGGCCTCACTG
ATTATAAAAACACTTCTCAGGATTCTGGCGTACCGTTCCTGTCTAAAATCCCTTTAATCGGCCTCCTGTTTAGCTCCCGCTCTGATTCTAACGAGGAAAGCACGTTATACG
TGCTCGTCAAAGCAACCATAGTACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCG
CTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGA
CCCCAAAAAACTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTT
CCAAACTGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAAC
CAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATACGCAA
ACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACT
CATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGAATT
CGAGCTCGGTACCCGGGGATCCTCCGTCTTTATCGAGGTAACAAGCACCACGTAGCTTAAGCCCTGTTTACTCATTACACCAACCAGGAGGTCAGAGTTCGGAGAAATG
ATTTATGTGAAATGCGTCAGCCGATTCAAGGCCCCTATATTCGTGCCCACCGACGAGTTGCTTACAGATGGCAGGGCCGCACTGTCGGTATCATAGAGTCACTCCAGGGC
GAGCGTAAATAGATTAGAAGCGGGGTTATTTGGCGGGACATTGTCATAAGGTTGACAATTCAGCACTAAGGACACTTAAGTCGTGCGCATGAATTCACAACCACTTAG
AAGAACATCCACCCTGGCTTCTCCTGAGAA

Thiolated DNA strands:

5’-ThioMC6-D/TTTTTTTTTTTTTTTTTTTT-3’ for AuNP functionization.

DNA strands of hexagon tile

Name	Sequence	Note
0[47]	ACAATATTTTGAATGAGGTGAGGTCGCCATTAGCCAGCA	core
0[79]	CCTGAAAGCGTAAGGTTTGGATTAGAGACTACCTTTTTAACCTCCGGCT	core
0[153]	GACTCCAACGTCAAAGAAGGCGTTTTCTGACCCCTGTTTA	core
0[185]	GAACAAGAGTCCACAAGCAAGCCCAATGAAATAGCAATAGCTATCTTAC	core
0[259]	TCGGCAAAATCCCTTAATACATAAATTAAGACTAAGTTTA	core
0[291]	AAAATCCTGTTTGAGAGCCACCATAGGTGTATCACCGTACTCAGGAGGT	core
0[365]	CCTTCACCGCCTGGCCTTCCACAGGTAACACTTCTTTCCA	core
0[397]	ACCAGTGAGACGGGGAGGCTTTGAATTTCAACTTTAATCATTGTGAATT	core
0[471]	TGAATCGGCCAACGCGTGCAGATATAGAAAGAACTATCAT	core
0[503]	GGGAAACCTGTCGTTCCTTTTGAGTAAAGATTCAAAAGGGTGAGAAAGG	core
0[577]	GGGGTGCCTAATGAGTGGTAATCGCAGGTCATCAGAAAAG	core
0[609]	CGAGCCGGAAGCATCCAGGCAAACAGGGCTTAAGCTACGTGGTGCTTGT	core
0[636]	TATCCGCTCACACATAAATCATTTCCAGCAGA	core
1[32]	ATAGCCCTAAAGGGTTATATAACGGCACAG	core
1[72]	GATGCAAATAGGTCTGATACTTCTGAATAACGA	core
1[96]	AAGAACGCGAGAAAACTTTTTCAAACCGTCTATCATCTGGCCAACAGAATTAAGAC	core
1[138]	TAGTTAATTTCCCTTTTTAAGAAGAACGTG	core
1[178]	CCGAACAAGCAAGAAAGTTTTTATTTTCATGCG	core
1[202]	ACCGAGGAAACGCAATAATAACGGAAGAATAGCCCGAGATAGGGTTGAAGAGAGAT	core
1[244]	AAAGAACTGGCCCGCCACCCTCATCCGAAA	core
1[284]	AGAACCGAGCCCGGAACCGGAACCGCCTCCGTT	core
1[308]	CACCCTCATTTTCAGGGATAGCAAGTTGCAGCAAGCGGTCCACGCTGGTACCAGGC	core
1[350]	GGAACCCATGTTGCGATTTTAAGTGATTGC	core
1[390]	ACCAGTCAGATGGTTTAGGACTAAAGACTTGAA	core
1[414]	AAATCTACGTTAATAAAACGAACTGGCGGTTTGCGTATTGGGCGCCAGGCCCTGAC	core
1[456]	AACATTATTACACAGTCAAATCAGCATTAA	core
1[496]	TTCAACCAATGTGTAGTAAGAGGTCATTTTGCA	core
1[520]	TAATGCCGGAGAGGGTAGCTATTTTCACATTAATTGCGTTGCGCTCACAATTTTTA	core
1[562]	TCTACAAAGGCGATAAAGACGGAAAAGCCT	core
1[602]	CGAGCTCATGAGTAAAGCGCCATTCGCCATTGA	core
2[20]	ACGAACCACTCCGAACTCTGATCTGTAAGCAA	core
2[48]	TAGGTTACACGGAATTCATCAATATA	core
2[87]	TCAAAATCATCCAATCCCTTCTGA	core
2[126]	GTTTGAAAGAAGAGTCAATAGTAAATCGTCGC	core
2[154]	CGAAGCATCAAACAAGTACCGCACTC	core
2[193]	ATAATAAGAAGTTACCCCAGTTTG	core
2[232]	CAGTATGTACAAGAATTGAGTAGACGGGAGAA	core
2[260]	TTAGTAATGAGGCATAATCAAAATCA	core
2[299]	ATAAGTATCCACCCTCAGCAGGCG	core
2[338]	CCAGTACAAGTGCCGTCGAGAAAGTATTAAGA	core
2[366]	ACCTTAACCACAGAACGAGGGTAGCA	core
2[405]	TGGGCTTGAGGACGTTTTCTTTTC	core
2[444]	AGATTTAGACACCAGAACGAGAACCGGATATT	core
2[472]	CCGGAGAGGCATGATTAGAGAGTACC	core

2[511]	GCCTGAGTGTTCTAGCTTCCAGTC	core
2[550]	CTGGAGCACTCATATATTTTAAAACATTATGA	core
2[578]	TACCTCTATTAAGGCACCGCTTCTGG	core
2[617]	TTGGTGTAGAATTCGTACAACATA	core
3[21]	AGATAAAACAGGCTATTAGTCTTTGAAATTGT	core
3[56]	ATCCTGATTAATACGTTATATGTAAATGCT	core
3[162]	ATCGAGAACTATTAAAAAGTAAGCAGATAG	core
3[268]	CCGGAACCATGGTGGTGAACCGCCACCCTC	core
3[374]	ACGGCTACACAACAGCAACTGGCTCATTAT	core
3[480]	TTTAATTGCGCCAGCTCCATCAATATGATA	core
3[586]	TGCCGGAAAAAAGTGTGGATCCCCGGGTAC	core
4[71]	TATCATCATCATTTGATCTGGTCAGTTGGC	core
4[177]	TTTCCTTATTGTCCAGATTGAGAATCGCCA	core
4[283]	CATAGCCCCATCACCATTCAACCGATTGAG	core
4[389]	ATCGTCACCTTATCAGGAGTGAGAATAGAA	core
4[495]	AACCAGACCAGAAAACTTTGCCAGAGGGGG	core
4[601]	CCTCAGGAATAAATGTAAATTCGCATTAAA	core
5[40]	GCAAATGACAGTTGAATTAGAGCCGTCAATA	core
5[72]	CTCAAATATCAAACAACACCAGAAGAAAACAGA	core
5[146]	GTATCATACAACGCCACCGACAAAAGGTAAA	core
5[178]	AAGCCAACGCTCAATAAATCAATAAATAGAAGG	core
5[252]	TTTTGTCAAGGTAAATTTTGGGAATTAGAGC	core
5[284]	CCAGCGCCAAAGACCCGTCATCGGCCACCCTCA	core
5[358]	GACGTTAGACTAAAGGAGGAGCCTTTAATTG	core
5[390]	CTAAACAACTTTCAACAAAGGCCGCGCCACTAC	core
5[464]	AACCCTCGAAAATGTTCCTCAAATGCTTTAA	core
5[496]	TAGCGAGAGGCTTTCGGATTCGAGCGCTCAACA	core
5[570]	CCCCAAAATAAATCAGTGTAGCCAGCTTTCA	core
5[602]	AAATTGTAAACGTTATAGACGACGATCTTCGCT	core
6[55]	AAATCAAAAAATCTAATATCAGATGATGGCTCA	core
6[161]	TATTTAATGCGTTATAAACGGGTATTAAACTAA	core
6[267]	GGAGGGACAATCAATAGTTTGCCATCTTTTTGG	core
6[373]	AGGAACATAAATGAATGAAAGACAGCATCGGCC	core
6[479]	TAATAGTTTTACCAGACTCCAACAGGTCAGAAC	core
6[585]	TTTTTGTACAGGAAGACCAGCCAGCTTTCCAAC	core
7[21]	AGCACTAACAAACCGCCTGCAACATGGGCACG	core
7[56]	GATAATAATTCCTGATAGCATCACCTTGCTGAAC	core
7[84]	TATTAGACTTTAAAGAAACCGTTATTAATCAGATGA	core
7[127]	AATAAGAGAATACCGGAATCATAAAATTTTCC	core
7[162]	GTAATTCCATTCCAAGCAAATTCTTACCAGTATA	core
7[190]	AAACAACATGTTAGAAACCAGTCCTGAAGCGAACCT	core
7[233]	CCGTCACCGACAAAAGAAACGCAAACACCCTG	core
7[268]	CAGCAAACTTATTAGCGAAAATTCATATGGTTTA	core
7[296]	ACCATTAGCAAGGCGCGTTTTAATCAGTCAGCATTG	core
7[339]	CCAAAAAAAAGTAGCGTAACGATCCTCCTCAA	core

7[374]	TATCGGTCTCAGCAGCTTTCTGTATGGGATTTTG	core
7[402]	GGTGAATTTCTTGGGAGTTAACCATCGCATACACTA	core
7[445]	TAAATATTCATGAATTACGAGGCAAAATCAAC	core
7[480]	ACAGTTCGGAAGCAAACGACGATAAAAACCAAAA	core
7[508]	TAAATCAAAAATGCGTTTTAATTGCATCAAGTTTCA	core
7[551]	AATTCGCGTCTCAATCATATGTACTACTTTTG	core
7[586]	TCAACATGATCGCACTTTGTATAAGCAAATATTT	core
7[614]	AACCCGTCGGATTTTGAGGGGGTCACGTAGGCGATT	core
8[71]	CCTACCATAAACAATTGAATACCAAGTTAC	core
8[106]	CTTAGAATCCTGGAAACAGTACATGAGCCAGT	core
8[177]	CCGCGCCCAAACGATTACAATTTTATCCTG	core
8[212]	AACAAAGTCAGAATAGCAGCCTTTAATTATCA	core
8[283]	CCTCAGAACCAGTGCCTAAAGCCAGAATGG	core
8[318]	GAGAAGGATTACAGTTAATGCCCCGAAAATCT	core
8[389]	TTCCATTAATTTGAAATGTATCATCGCCTG	core
8[424]	GTAACAAAGCTACCAGGCGCATAGAATCGTCA	core
8[495]	AGCTTAATTAATCATACATTTCGCAAATGG	core
8[530]	CGGGAGAAGCCAATTAAGCAATAATCAAAAAT	core
8[601]	TGTTGGGAACGCCAAACTTTCTCAGGAGAA	core
8[636]	AATATAGGGGCACGCTCGCCCTGGTCTTTAGG	core
9[40]	ATATACAGCGCAGAGGGAAAACAA	core
9[64]	CGGGAGAAACAATAACGGATTCGCCTTAGTGGAAGGGTTAGAA	core
9[107]	TATTAATTTTACTAGAAAAAGTAAATTTAATG	core
9[146]	CCCGACTTCCAACGCTATTTATCC	core
9[170]	TTAAATCAAGATTAGTTGCTATTGGATGACGTAGGAATCATTA	core
9[213]	TTAACTGAAGACACCACGGAATCCTTATTACG	core
9[252]	ACAGGAGGAGTCTCTGTGGTAATA	core
9[276]	TTGGCCTTGATATTCACAAACAACTGGGGCTCAGAGCCGCCAC	core
9[319]	GGCTGAGATAAAGTTTTGTCGGAGTTTCGTCA	core
9[358]	AAACACTCGTGTCGAATAAGGGAA	core
9[382]	TTATACCAAGCGCGAAACAAAGTATCAGTTTTCATGAGGAAGT	core
9[425]	CATTACCCTAGTAAGAGCAACTTCATCAGTTG	core
9[464]	TTCCATATCCTGTTTAGTAGTAGC	core
9[488]	CTGCGAACGAGTAGATTTAGTTTGGTAACTGCGGATGGCTTAG	core
9[531]	CCCTGTAACCCGGTTGATAATTGCCTGAGAGT	core
9[570]	AAGTTGGGTGGATGTTTGTCAACC	core
9[594]	AGTCACGACGTTGTAAAACGACGCGGGGCTCAGGCTGCGCAAC	core
9[637]	CTCGTCGGGTGCCACGCTGAGAAAAATACCGA	core
10[55]	AAAATCGTAACAGTACTTTGCACGTGAGCGGAAT	core
10[95]	TGAGTGAATAACCTGATTGCTTTTCATTTG	core
10[161]	AATCTTAGCGGGAGGTAAATCAGATTCGGCTGTC	core
10[201]	CATAAAAACAGTTGCACCCAGCTTTTTGTT	core
10[267]	AAAGCGCTTGAGGCAGCAGAGCCACATTTTCGGT	core
10[307]	AACCTATTATTATAAATCCTCATTTGAGTA	core
10[373]	ATAAATTATCTTTGACATACGTAATTTTTGCGGG	core

10[413]	CATCAAGAGTAACAACGGAGATTGAGGACA	core
10[479]	TCAATAAAACAGTTGAAATGCTGTATTCAAAGCG	core
10[519]	AAAGCTAAATCGACCATTAGATACAGGCAA	core
10[585]	GCCAGGGTAACGCCAGGTGCGGGCCCAGTATCGG	core
10[625]	TACCGACAGTGGCCAGTGCCAAGATAACCC	core
11[48]	AATTAATTACATTTTCAAAATTACTTTTACAT	core
11[80]	AATTACCTTTTTTAATTGAAAACATGCTTCTGTGAATTTA	core
11[154]	CAATCCAAATAAGAATAGCAAGCTTTGAAGCC	core
11[186]	TAACGTCAAAAATGAAAGGGTAATAGCGCATTTAAGCCCA	core
11[260]	AGTTTTAACGGGGTCGCCACCCTGTCAGACGA	core
11[292]	ACAGTGCCCGTATAAAGGATTAGCAAACATGAGGGTTGAT	core
11[366]	CCGAACTGACCAACACGGGTAAACCCCAGCGA	core
11[398]	GATGAACGGTGTACAGGCTCATTCTTGACAAGTAGTAAAT	core
11[472]	ATTAACATCCAATAGCTGAATATTTCCCAATT	core
11[504]	GGCAAAGAATTAGCAATTTATTTCTGTACCAAAATGCAAT	core
11[578]	TTATGACAATGTCCGGGCGATCGGGTTTTCCC	core
11[610]	CGCTTCTAATCTATTTCTTGAATCCCCTGCCACCTCCTGG	core

3[88]	TAGCTTAGGATAGAACGCAAGACA AAAAAAAAAAAAAAAAAAAA	Site1 handle
3[104]	GCTGATACCGACCGTGTGATAAATGGCGAAAAATATATTT AAAAAAAAAAAAAAAAAAAA	Site1 handle
3[194]	CTAATATCGTGTTGTTAGAAGGAA AAAAAAAAAAAAAAAAAAAA	Site2 handle
3[210]	AACCCTAGCAAACGTAGAAAATACTAAATCAAAATACCCA AAAAAAAAAAAAAAAAAAAA	Site2 handle
3[300]	TTGCTCAGTTTGCCCCAGAGCCAC AAAAAAAAAAAAAAAAAAAA	Site3 handle
3[316]	GGATAAACTACAACGCCTGTAGCACTGAGAGAGCCCAATA AAAAAAAAAAAAAAAAAAAA	Site3 handle
3[406]	TAAGGCTTGGTGGTTTGGGAAGAA AAAAAAAAAAAAAAAAAAAA	Site4 handle
3[422]	GAGAAGAATACCACATTCAACTAACGGGGAGAAACGGAAC AAAAAAAAAAAAAAAAAAAA	Site4 handle
3[512]	AGGATAAATGCCCGCTTGATAAAT AAAAAAAAAAAAAAAAAAAA	Site5 handle
3[528]	GAACCAACAAGAGAATCGATGAACGAGCTAACTTGAGAGA AAAAAAAAAAAAAAAAAAAA	Site5 handle
1[626]	TCATAGCTGTTTCCTGTGTAATGCGCGAACTG AAAAAAAAAAAAAAAAAAAA	Site6 handle
3[618]	CGCATTTCAATTCCACAATCATGG AAAAAAAAAAAAAAAAAAAA	Site6 handle
4[145]	GAATAAACATAAAGTAACATGTAA AAAAAAAAAAAAAAAAAAAA	Site7 handle
6[137]	TTTAGGCAGAGGCATTTTCAAATCAATATATG AAAAAAAAAAAAAAAAAAAA	Site7 handle
4[251]	CAACATATTTGAGCCAATTGACGG AAAAAAAAAAAAAAAAAAAA	Site8 handle
6[243]	AAATTATTCATTAAAGGTGACAGAGAGAATAA AAAAAAAAAAAAAAAAAAAA	Site8 handle
4[357]	CTCATAGTGCTCCAAAAATTGCGA AAAAAAAAAAAAAAAAAAAA	Site9 handle
6[349]	ATAATAATTTTTTCACGTTCTGCCTATTTCGG AAAAAAAAAAAAAAAAAAAA	Site9 handle
4[463]	GCCAAAAGTGAATCCCTAGACTGG AAAAAAAAAAAAAAAAAAAA	Site10 handle
6[455]	ATAGCGTCCAATACTGCGGGCTGGCTGACCTT AAAAAAAAAAAAAAAAAAAA	Site10 handle
4[569]	TAGCATGTGGCCTTCCCTCATTTT AAAAAAAAAAAAAAAAAAAA	Site11 handle
6[561]	TTAACCAATAGGAACGCCAAGCCTCAGAGCAT AAAAAAAAAAAAAAAAAAAA	Site11 handle
4[39]	GTATTAACCTAATAGAAGGAATTG AAAAAAAAAAAAAAAAAAAA	Site12 handle
6[31]	AGGAAGGTTATCTAAAATAAGTGACTCTATGA AAAAAAAAAAAAAAAAAAAA	Site12 handle

4[109]	CATTTTGCGGAACACAAACAATTCGACATGGC	Hexamer connector
4[321]	AGCGTCAGACTGTAGCCGGAAACGTCAAAAAG	Hexamer connector

5[110]	GTAACCCAGAGCCGCCGCAGCGACAGAATCAA	Hexamer connector
5[322]	GTTTGTTCAGGTTTAACGTTTTAAAAGTTTGA	Hexamer connector
8[39]	AATAAAGAAACATCAACGAATTATTCATTTCAATTACC	Hexamer connector
8[251]	GAGCCGCCGAGTGTACAATTTACCGTTCCAGTAAGCGT	Hexamer connector
10[17]	TGAGCCCAATGAAACCATCGATAGCAGCAAAAAGGGCGACAGTAGCACCATT	Hexamer connector
10[229]	CATACAACTCGTATTAAATCCTTTGCCCGCCTCAATCAATAGGATTTAGAAG	Hexamer connector
11[18]	AAGATGATGAAACAAATTGCGTAGATTCCTTT	Hexamer connector
11[230]	TTTTGATGATACAGACCAGAACCACCAATTAT	Hexamer connector
4[111]	TATCATTTTGCGGAACACAAACAATTCGACC	2D connector
4[217]	CTAATTTACGAGCATGTCAGCTAATGCAGAG	2D connector
4[323]	TTTAGCGTCAGACTGTAGCCGGAAACGTCAA	2D connector
4[429]	GGTCGCTGAGGCTTGCAAAACAGCTTGATAA	2D connector
4[535]	GAAAGACTTCAAATATCCAGGTCTTTACCCG	2D connector
4[641]	AACCGTGCATCTGCCAGTCTCCGTGGGAACA	2D connector
5[113]	CAAGAGGCAAAAGACCACGCATAACCGATAT	2D connector
5[219]	AGTACGGTGTCTGGAAAAAGATTAAGAGGAA	2D connector
5[325]	GGGGATGTGCTGCATGGTGTAGATGGGCGCA	2D connector
5[431]	TTTCAGGTTTAACGTTTTAAAAGTTTGAGTA	2D connector
5[537]	CGCGAGGCGTTTTACAAGAAAAATAATATCC	2D connector
5[643]	CCCAGAGCCGCCGCAGCGACAGAATCAAGTT	2D connector
8[39]	AATAAAGAAACATCAACGAATTATTCATTTCAATTACCTGA	2D connector
8[145]	CTTATCCGGCCATATTAACGAGCGTCTTTCCAGAGCCTAAT	2D connector
8[251]	GAGCCGCCGAGTGTACAATTTACCGTTCCAGTAAGCGTCAT	2D connector
8[357]	GAAGGCACGTCAATCAATCCGCGACCTGCTCCATGTTACTT	2D connector
8[463]	TGTTTTAATACTAATAGCTATATTTTCATTTGGGGCGCGAG	2D connector
8[569]	ATTACGCCTGCTGAATCTTCTAAGTGGTTGTGAATTCATGC	2D connector
10[14]	CCCGATAGTTGCGCCGACAATGACAACAGTTTCAGCGCTTGCTTTCGA	2D connector
10[120]	TTGACTATTATAGTCAGAAGCAAAGTGCAAAAGAAGTGAGAATGACCA	2D connector
10[226]	CAAACGGCGGATTGACCGTAATGGGAATATTTTGTTAGAGCGAGTAAC	2D connector
10[332]	GAACTCGTATTAAATCCTTTGCCCGCCTCAATCAATAGGATTTAGAAG	2D connector
10[438]	TACGCGCCTGTTTATCAACAATAGACAGTAGGGCTTAACGACGACAAT	2D connector
10[544]	CCCAATGAAACCATCGATAGCAGCAAAAAGGGCGACAGTAGCACCATT	2D connector
11[16]	AAGAAGATGATGAAACAAATTGCGTAGATTT	2D connector
11[122]	CAGTTACAAAATAAACAGTATTCTAAGAACC	2D connector
11[228]	GGCTTTTGATGATACAGACCAGAACCACCAG	2D connector
11[334]	GGAACGAGGCGCAGACGCAACCTAAAACGAA	2D connector
11[440]	AAAGGTGGCATCAATTCATATGCAACTAAAT	2D connector
11[546]	GACTTAAGTGTCCTTAGAGCTGGCGAAAGGC	2D connector
4[112]	TTATCATTTTGCGGAACACAAACAATTCGACC	Tube connector
4[218]	CCTAATTTACGAGCATGTCAGCTAATGCAGAG	Tube connector
4[324]	CTTTAGCGTCAGACTGTAGCCGGAAACGTCAA	Tube connector
4[430]	CGGTCGCTGAGGCTTGCAAAACAGCTTGATAA	Tube connector
4[536]	CGAAAGACTTCAAATATCCAGGTCTTTACCCG	Tube connector

4[642]	TAACCGTGCATCTGCCAGTCTCCGTGGGAACA	Tube connector
5[113]	CAAGAGGCAAAAGACCACGCATAACCGATATA	Tube connector
5[219]	AGTACGGTGTCTGGAAAAAGATTAAGAGGAAG	Tube connector
5[325]	GGGGATGTGCTGCATGGTGTAGATGGGCGCAT	Tube connector
5[431]	TTTCAGGTTTAACGTTTTAAAAGTTTGAGTAA	Tube connector
5[537]	CGCGAGGCGTTTTACAAGAAAAATAATATCCC	Tube connector
5[643]	CCCAGAGCCGCCGCAGCGACAGAATCAAGTTT	Tube connector
8[39]	AATAAAGAAACATCAACGAATTATTCATTTCAATTACCTGAG	Tube connector
8[145]	CTTATCCGGCCATATTAACGAGCGTCTTTCCAGAGCCTAATT	Tube connector
8[251]	GAGCCGCCGAGTGTACAATTTACCGTTCCAGTAAGCGTCATA	Tube connector
8[357]	GAAGGCACGTCAATCAATCCGCGACCTGCTCCATGTTACTTA	Tube connector
8[463]	TGTTTTAATACTAATAGCTATATTTTCATTTGGGGCGCGAGC	Tube connector
8[569]	ATTACGCCTGCTGAATCTTCTAAGTGGTTGTGAATTCATGCG	Tube connector
10[14]	CCCGATAGTTGCGCCGACAATGACAACAGTTTCAGCGCTTGCTTTCGA	Tube connector
10[120]	TTGACTATTATAGTCAGAAGCAAAGTGCAAAAGAAGTGAGAATGACCA	Tube connector
10[226]	CAAACGGCGGATTGACCGTAATGGGAATATTTTGTTAGAGCGAGTAAC	Tube connector
10[332]	GAACTCGTATTAAATCCTTTGCCCGCCTCAATCAATAGGATTTAGAAG	Tube connector
10[438]	TACGCGCCTGTTTATCAACAATAGACAGTAGGGCTTAACGACGACAAT	Tube connector
10[544]	CCCAATGAAACCATCGATAGCAGCAAAAAGGGCGACAGTAGCACCATT	Tube connector
11[15]	AAAGAAGATGATGAAACAAATTGCGTAGATTT	Tube connector
11[121]	CCAGTTACAAAATAAACAGTATTCTAAGAACC	Tube connector
11[227]	TGGCTTTTGATGATACAGACCAGAACCACCAG	Tube connector
11[333]	CGGAACGAGGCGCAGACGCAACCTAAAACGAA	Tube connector
11[439]	AAAAGGTGGCATCAATTCATATGCAACTAAAT	Tube connector
11[545]	CGACTTAAGTGTCCTTAGAGCTGGCGAAAGGC	Tube connector

References

1. Douglas, S. M.; Chou, J. J.; Shih, W. M., DNA-nanotube-induced alignment of membrane proteins for NMR structure determination. *Proceedings of the National Academy of Sciences of the United States of America* **2007,** *104* (16), 6644-6648.