Electronic Supplementary Material (ESI) for Nanoscale.
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# Supplementary material
# The effects of nanostructure geometry on cell labeling by multivalent DNA origami

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and Rebecca E. Taylor [abc*]

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# 1 CaDNAno design of the DNA origami nanotile and nanorod

## 1.1 CaDNAno design of the nanotile

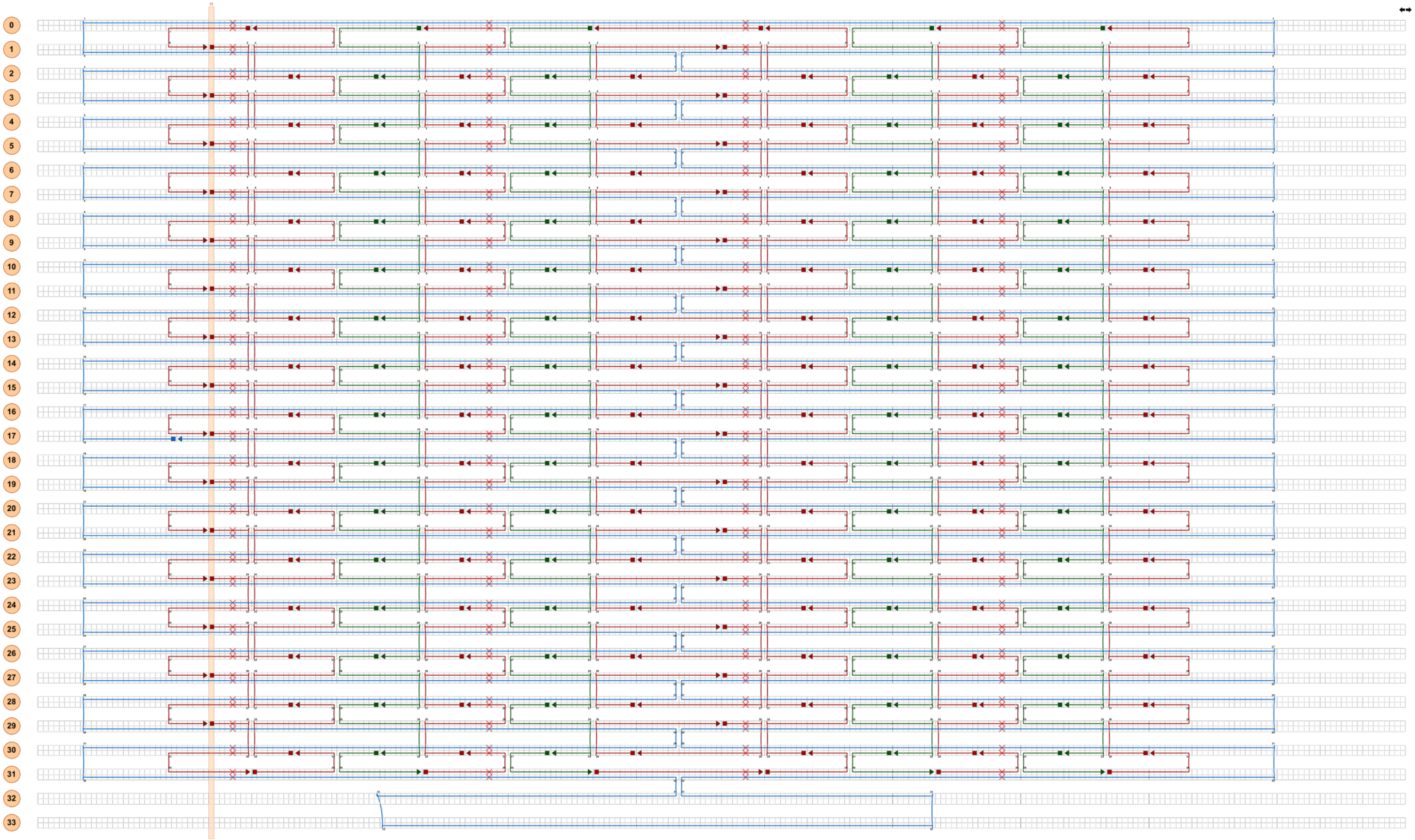


Figure 1: CaDNAno design of the DNA origami nanotile. Blue: M13 scaffold, red: staples with the break points pointing up from the plain, green: staples with the breaks point down from from the plain.

## 1.2 CaDNAno design of the nanorod

Figure 2: CaDNAno design of the DNA origami nanorod. Blue: M13 scaffold, green: plain staples, purple: edge sequences which are excluded except when we have overhangs on them, red: sequences with biotin tags, yellow: sequences with overhangs.

## 1.3 Design of the nanosphere

The DNA origami nanosphere was dierctly taken from Benson's work in 2015.[1] The screenshot of the vHelix design is as shown in Figure 3. The numbers next to each helix represents the name of that helix.

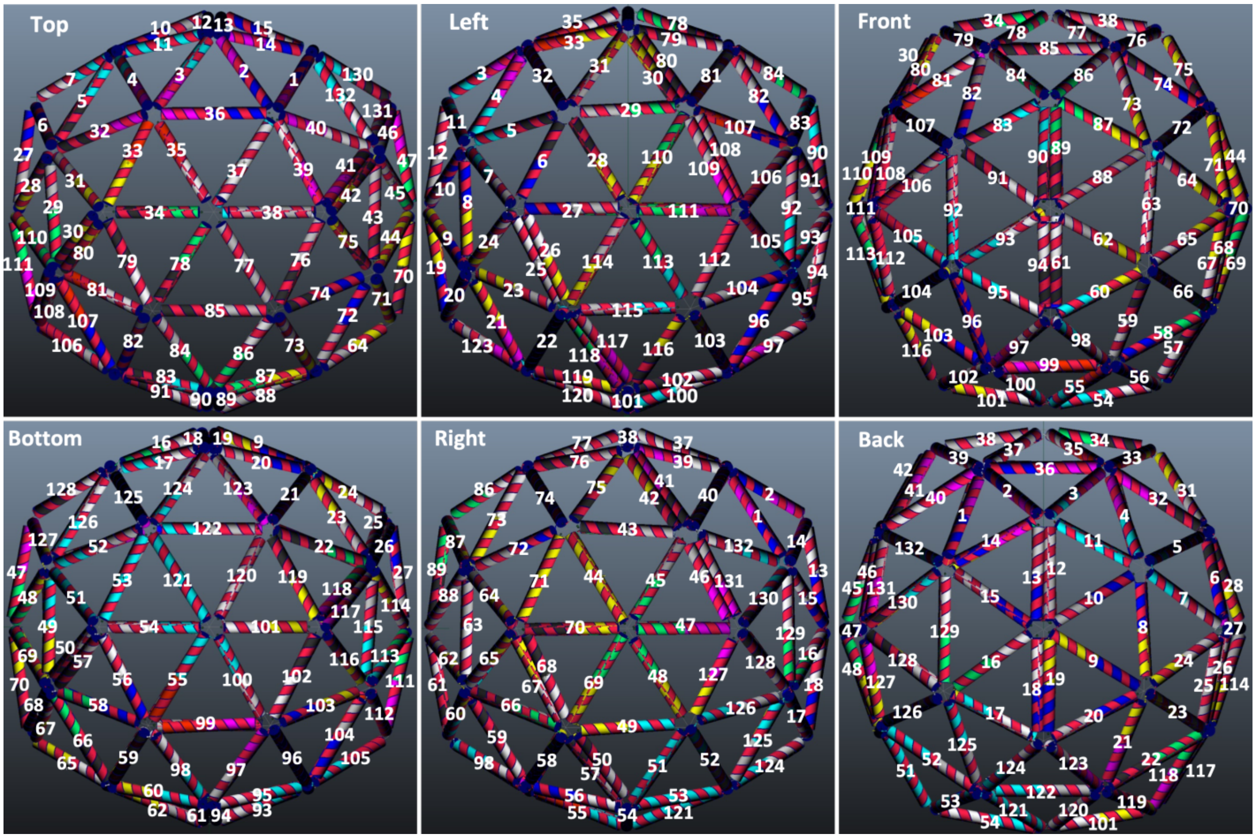


Figure 3: vHelix design of the DNA origami nanosphere. The numbers next to the helixes represent the name of that helix. Each staple would cross two helixes and was named as <starting helix> − <end helix>

# 2 Sequence list that was used in this paper

## 2.1 Sequence list of the nanotile

| Name | Sequence | biotin sites | 28 face binding sites | | | | | | | 12 edge sites | | | | | | geometry study | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| seam01 | TCAGGAGGTTTAGTACCGCCACCCTCAGAAC | | | | | | | | | 12 | 8 | | | | | | g1 | | | | |
| seam02 | TTTGCTAAGTAAATGAATTTTCTGAGTGCCTT | | | | | | | | | | | | | | | | | | | | |
| seam03 | GAGTAACAGTTTTAACGGGGTCTATGGGAT | S1 | | | | | | | | | | | | | | | | | | | |
| seam04 | TAACCGATATGACAACAACCATCGCACCACCC | | | | | | | | | | | | | | | * | | | | | |
| seam05 | TCAGAGCCGCCACCCTCAGAGCCCCACGCA | | | | | | | | | | | | | | | * | | g2 | | | |
| seam06 | CACTAAAATAAAACGAAAGAGGCAACGTCACC | | | | | | | | | | | | | | | | | | | | |
| seam07 | AATGAAATTAGCAAGGCCGGAAAAAGAATA | S1 | | | | | | | | | | | | | | | | | | | |
| seam08 | TGACCTTCTACAGACCAGGCGCATACCACGGA | | | | | | | | | | | | | | | * | | | | | |
| seam09 | ATAAGTTAAGAAACGCAAAGACAGGCTGGC | | | | | | | | | | | | | | | * | | | g3 | | |
| seam10 | AAAATCTAATACCAGTCAGGACGTGCAAGAAA | | | | | | | | | | | | | | | | | | | | |
| seam11 | CAATGAAAGCCCAATAATAAGATGGGAAGA | S1 | | | | | | | | | | | | | | | | | | | |
| seam12 | GGGGTAATTTTGCAAAAGAAGTTTAAATAAAC | | | | | | | | | | | | | | | * | | | | | |
| seam13 | AGCCATAAATTTGCCAGTTACATGCCAGAG | | | | | | | | | | | | | | | * | | | | g4 | |
| seam14 | TTCGAGCTAAGACTTCAAATATCGATCGTAGG | | | | | | | | | | | | | | | | | | | | |
| seam15 | AATCATTGCCGTTTTTATTTTCCGTTTTAA | S1 | | | | | | | | | | | | | | | | | | | |
| seam16 | AGTAGATTAGTTGATTCCCAATTCTTCTGTCC | | | | | | | | | | | | | | | * | | | | | |
| seam17 | AGACGACCAAAAGGTAAAGTAATGCGAACG | | | | | | | | | | | | | | | * | | | | | g5 |
| seam18 | CCCTGTAATCGGTTGTACCAAAAATAAGGCGT | | | | | | | | | | | | | | | | | | | | |
| seam19 | TAAATAACGACCGTGTGATAAACATTATGA | S1 | | | | | | | | | | | | | | | | | | | |
| seam20 | AGGCTATCTAGCTATTTTTGAGAGAAGACGCT | | | | | | | | | | | | | | | | | | | | |
| seam21 | GAGAAGAGCGATAGCTTAGATTATCTACAA | | | | | | | | | | | | | | | | | | | | |
| seam22 | ACGCCATCCAGCTCATTTTTTAACAGGCGAAT | | | | | | | | | | | | | | | | | | | | |
| seam23 | TATTCATTACAAAATCGCGCAGCAATAGGA | S1 | | | | | | | | | | | | | | | | | | | |
| seam24 | AGCTTTCCCCTCAGGAAGATCGCACATCAATA | | | | | | | | | | | | | | | | | | | | |
| seam25 | TAATCCTCAGATGATGGCAATTCTCCAGCC | | | | | | | | | | | | | | | | | | | | |
| seam26 | GGTCGACTCAGTGCCAAGCTTGCAGGAGCACT | | | | | | | | | | | | | | | | | | | | |
| seam27 | AACAACTTCTAAAATATCTTTATGCCTGCA | S1 | | | | | | | | | | | | | | | | | | | |
| seam28 | TTAATGAAGGGAAACCTGTCGTGCATTAAAAA | | | | | | | | | | | | | | | | | | | | |
| seam29 | TACCGAACCCTAAAACATCGCCCAGCTGCA | | | | | | | | | | | | | | | | | | | | |
| seam30 | CCCGAGATATCCCTTATAAATCAAAAACGCTC | | | | | | | | | | | | | | | | | | | | |
| seam31 | ATGGAAACCATTGCAACAGGAAAAGAATAG | | | | | | | | | | | | | | | | | | | | |
| seam32 | GAGCTTGACGGGGAAAAAAGGGATTTTAGAC | | | | | | | | | 12 | 8 | | | | | | | | | | |
| X01Y01 | TAGGAACCCATGTACACAACGCC | | | | | | | | | | | | | | | * | | | | | |
| X01Y02 | TGTAGCATAATTTTTTCACGTTCCTTTAAT | | | | | | | | | | | | | | | * | | g2 | | | |
| X01Y03 | TGTATCGAGCGAAAGACAGCATTGAGGACT | | | | | | | | | | | | | | | * | | | | | |
| X01Y04 | AAAGACTCATCGCCTGATAAATTTAGCCGG | | | | | | | | | | | | | | | * | | | g3 | | |
| X01Y05 | AACGAGGATTCAGTGAATAAGGTAAATTGG | | | | | | | | | | | | | | | * | | | | | |
| X01Y06 | GCTTGAGTAGGAATACCACATTTTACGAGG | | | | | | | | | | | | | | | * | | | | g4 | |
| X01Y07 | CATAGTACCCCTCAAATGCTTTCAAAAATC | | | | | | | | | | | | | | | * | | | | | |
| X01Y08 | AGGTCTTTCCTTTTGATAAGAGCTGAATAT | | | | | | | | | | | | | | | * | | | | | g5 |
| X01Y09 | AATGCTGGGGCGCGAGCTGAAATTAACATC | | | | | | | | | | | | | | | * | | | | | |
| X01Y10 | CAATAAATTTAAATGCAATGCCGAGAAAGG | | | | | | | | | | | | | | | * | | | | | |
| X01Y11 | CCGGAGAATGTCAATCATATGTCAGGAAGA | | | | | | | | | | | | | | | * | | | | | |
| X01Y12 | TTGTATAACAACCCGTCGGATTTGGGATAG | | | | | | | | | | | | | | | * | | | | | |
| X01Y13 | GTCACGTTGGGAAGGGCGATCGGAAAGGGG | | | | | | | | | | | | | | | * | | | | | |
| X01Y14 | GATGTGCAATTGTTATCCGCTCAAAGTGTA | | | | | | | | | | | | | | | * | | | | | |
| X01Y15 | AAGCCTGAGTGAGACGGGCAACGAGTTGCA | | | | | | | | | | | | | | | * | | | | | |
| X01Y16 | GCAAGCGCAAAGGGCGAAAAACCATCACCCAAATCAA | | | | | | | | | 12 | 8 | 6 | 4 | | | * | | | | | |
| X02Y01 | GCGAATAATTCCACAGACAGCCCTGGGATAGCAAGCCCAA | | | | | | | | | 12 | 8 | 6 | 4 | 2 | 1 | | g1 | | | | |
| X02Y02 | CCCTCAGCGTTTATCAGCTTGCTTAAGGAATT | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y03 | ATTTGTATTTTTCATGAGGAAGTTGATCGTCA | | | | | | | | | | | | | | | | | | | | |
| X02Y04 | AGCTGCTCCGCAGACGGTCAATCACAACGGAG | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y05 | TTGAGATTATGGTTTAATTTCAACCGTAACAA | | | | | | | | | | | | | | | | | | | | |
| X02Y06 | ATTGAATCAGAGCAACACTATCATTTCATCAG | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y07 | TTAATTGCTACCCTGACTATTATAAAATATTC | | | | | | | | | | | | | | | | | | | | |
| X02Y08 | TTCATTTGTAGCTCAACATGTTTTGAGTACCT | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y09 | TCATATATTCATACAGGCAAGGCAGCTATATT | | | | | | | | | | | | | | | | | | | | |
| X02Y10 | AAACTAGCCAGTCAAATCACCATCTAGAACCC | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y11 | AGCGAGTAAGCAAATATTTAAATTTAATCGTA | | | | | | | | | | | | | | | | | | | | |
| X02Y12 | GCAACTGTTGGTGTAGATGGGCGCTAAATGTG | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y13 | CTGTGTGATGCAAGGCGATTAAGTCAGGCTGC | | | | | | | | | | | | | | | | | | | | |
| X02Y14 | TTTTCACCGGGTGCCTAATGAGTGGCTGTTTC | S1 | | | | | | | | | | | | | | | | | | | |
| X02Y15 | TCCAACGTGTCCACGCTGGTTTGCGGTTTTTC | | | | | | | | | | | | | | | | | | | | |
| X02Y16 | GTTTTTTGGGGTCGAGACGTGGAC | | | | | | | | | | | | | | | | | | | | |
| X03Y01 | ACCACCCTCATTTTCACATAGTTAGCGTAACGTAGAAAGG | | | | | | | | | | | | | | | | | | | | |
| X03Y02 | AACAACTATCGAGGTGAATTTCTTAAGGCCGC | | 28 | 16 | 10 | 6 | 4 | 2 | 1 | | | | | | | | | g2 | | | |
| X03Y03 | TTTTGCGGTCCATTAAACGGGTAAAGCGCGAA | | | | | | | | | | | | | | | | | | | | |
| X03Y04 | ACAAAGTATAAGGGAACCGAACTGTCATTACC | | 28 | | | | | | | | | | | | | | | | g3 | | |
| X03Y05 | CAAATCAATTTAATCATTGTGAATATTACAGG | | | | | | | | | | | | | | | | | | | | |
| X03Y06 | TAGAAAGAAACCCTCGTTTACCAGACTGCGGA | | 28 | 16 | | | | | | | | | | | | | | | | g4 | |
| X03Y07 | ATCGTCATGTCAGAAGCAAAGCGGACAGGTCA | | | | | | | | | | | | | | | | | | | | |
| X03Y08 | GGATTAGAAAATATGCAACTAAAGGTCAATAA | | 28 | | 10 | 6 | | | | | | | | | | | | | | | g5 |
| X03Y09 | CCTGTTTAAAGAATTAGCAAAATTCAAGGATA | | | | | | | | | | | | | | | | | | | | |
| X03Y10 | AAAATTTTAATATGATATTCAACCGAGAATCG | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X03Y11 | ATGAACGGGTAAACGTTAATATTTCAGCTTTC | | | | | | | | | | | | | | | | | | | | |
| X03Y12 | ATCAACATATCGTAACCGTGCATCAGCGCCAT | | 28 | | | | | | | | | | | | | | | | | | |
| X03Y13 | TCGCCATTTGGGTAACGCCAGGGTCGTAATCA | | | | | | | | | | | | | | | | | | | | |
| X03Y14 | TGGTCATAAGCTAACTCACATTAATATTGGGC | | 28 | 16 | 10 | 6 | 4 | | | | | | | | | | | | | | |
| X03Y15 | GCCAGGGTCCCAGCAGGCGAAAATAGTCCACT | | | | | | | | | | | | | | | | | | | | |
| X03Y16 | ATTAAAGAGTGCCGTAAAGCACTA | | | | | | | | | 12 | | | | | | | | | | | |
| X04Y01 | AGTGAGAAATCTAAAGTTTTGTCGCCACCCTCAGAGCC | | | | | | | | | 12 | | | | | | | g1 | | | | |
| X04Y02 | GGGAGTTAAAACAGCTTGATACCTCAGCGG | | | | | | | | | | | | | | | | | | | | |
| X04Y03 | TTATACCAAATACGTAATGCCACGCTTGCA | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y04 | CCGGATATACCAACTTTGAAAGACCAGCGA | | | | | | | | | | | | | | | | | | | | |
| X04Y05 | ACAACATTTACCTTATGCGATTTACAAGAA | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y06 | CGTCCAATACGACGATAAAAACCTAACGGA | | | | | | | | | | | | | | | | | | | | |
| X04Y07 | AAACTCCAATTGCATCAAAAAGATGGATAG | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y08 | CGCAAATGTACGGTGTCTGGAAGCGGAAGC | | | | | | | | | | | | | | | | | | | | |
| X04Y09 | TTTCAACGAAGCAATAAAGCCTCTACATTT | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y10 | GCAAACAAGTTCTAGCTGATAAAGCCTTTA | | | | | | | | | | | | | | | | | | | | |
| X04Y11 | CCTGTAGCTGTTAAAATTCGCATGTCTGGA | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y12 | CCAGGCAATGCCAGTTTGAGGGGTGGCCTT | | | | | | | | | | | | | | | | | | | | |
| X04Y13 | CTCGAATTTTTCCCAGTCACGACCCGGAAA | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y14 | GGTTTGCGTTGCGTTGCGCTCACTACCGAG | | | | | | | | | | | | | | | | | | | | |
| X04Y15 | GGAACAAGCCTGTTTGATGGTGGGAGAGGC | S1 | | | | | | | | | | | | | | | | | | | |
| X04Y16 | AATCGGAACCCTAAACCAGTTT | | | | | | | | | | | | | | | | | | | | |
| X05Y01 | CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT | | | | | | | | | | | | | | | | | | | | |
| X05Y02 | CAACAGTTGATAGTTGCGCCGACAATATTCGG | | | | | | | | | | | | | | | | | g2 | | | |
| X05Y03 | TCGCTGAGTACGAAGGCACCAACCCACTCATC | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X05Y04 | TTTGACCCGGACAGATGAACGGTGATCAAGAG | | | | | | | | | | | | | | | | | | g3 | | |
| X05Y05 | TAATCTTGTAAGAACTGGCTCATTCGTTAATA | | 28 | | | | | | | | | | | | | | | | | | |
| X05Y06 | AAACGAACAAAATAGCGAGAGGCTAGTAAAAT | | | | | | | | | | | | | | | | | | | g4 | |
| X05Y07 | GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG | | 28 | 16 | 10 | | | | | | | | | | | | | | | | |
| X05Y08 | AACCAGACTTTCATTCCATATAACTAGTTTGA | | | | | | | | | | | | | | | | | | | | g5 |
| X05Y09 | CCATTAGAAGAGCATAAAGCTAAATACTTTTG | | 28 | | | | | | | | | | | | | | | | | | |
| X05Y10 | CGGGAGAATTAATGCCGGAGAGGGAGGTCATT | | | | | | | | | | | | | | | | | | | | |
| X05Y11 | GCCTGAGATAAATTTTTGTTAAATAAAAATAA | | 28 | 16 | 10 | | | | | | | | | | | | | | | | |
| X05Y12 | TTCGCGTCACGACGACAGTATCGGGGCACCGC | | | | | | | | | | | | | | | | | | | | |
| X05Y13 | TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA | | 28 | | | | | | | | | | | | | | | | | | |
| X05Y14 | TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA | | | | | | | | | | | | | | | | | | | | |
| X05Y15 | CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X05Y16 | GTGTTGTTGGGAGCCCCCGATTTA | | | | | | | | | 12 | 8 | 6 | | | | | | | | | |
| X06Y01 | TGGTAATAAGTGCCCGTATAAACAAGGTGTATCACCGTAC | | | | | | | | | 12 | 8 | 6 | | | | | g1 | | | | |
| X06Y02 | CTCAGAACCGCCACCAGAACCACCGAGTGTAC | | | | | | | | | | | | | | | | | | | | |
| X06Y03 | CATTACCACCATCGATAGCAGCACCCGCCACC | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y04 | ACATATAATATTTTGTCACAATCAAGTAGCAC | | | | | | | | | | | | | | | | | | | | |
| X06Y05 | TTGAGTTAATAGCAATAGCTATCTAGGTGGCA | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y06 | CAGAGCCTTTATTTATCCCAATCCCACAAGAA | | | | | | | | | | | | | | | | | | | | |
| X06Y07 | ACAAGCAAACCGCGCCCAATAGCACGTCTTTC | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y08 | AGTACCGAGACAATAAACAACATGCATCGAGA | | | | | | | | | | | | | | | | | | | | |
| X06Y09 | TGAAATACGAATAAACACCGGAATGAATATAA | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y10 | AAAACATAGTCAATAGTGAATTTATAATGGTT | | | | | | | | | | | | | | | | | | | | |
| X06Y11 | TACCAAGTTTCAATTACCTGAGCAAATCCTTG | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y12 | CTGATTATGATTGTTTGGATTATAGCTTTGAA | | | | | | | | | | | | | | | | | | | | |
| X06Y13 | GAAGGTTAAATAGATTAGAGCCGTTCATATTC | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y14 | ACTGATAGCGAACCACCAGCAGAAGAATTGAG | | | | | | | | | | | | | | | | | | | | |
| X06Y15 | ACCGCCAGTACCTACATTTTGACGATGCGCGA | S1 | | | | | | | | | | | | | | | | | | | |
| X06Y16 | AGGAACGGTACGCCAGACAATATT | | | | | | | | | | | | | | | | | | | | |
| X07Y01 | AAGTATAGCCCGGAATGTTAATGCCCCCTGCCGCTTTTGA | | | | | | | | | | | | | | | | | | | | |
| X07Y02 | TGATACAGACCAGAGCCGCCGCCAACCGCCTC | | | | | | | | | | | | | | | | | g2 | | | |
| X07Y03 | CCTCAGAGCGTAATCAGTAGCGACAGCCAGCA | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X07Y04 | AAATCACCATAGAAAATTCATATGGAAAATAC | | | | | | | | | | | | | | | | | | g3 | | |
| X07Y05 | ATACATAATACCGAAGCCCTTTTTTATCAGAG | | 28 | | | | | | | | | | | | | | | | | | |
| X07Y06 | AGATAACCAAATAAGAAACGATTTTACCAACG | | | | | | | | | | | | | | | | | | | g4 | |
| X07Y07 | CTAACGAGAGCAAATCAGATATAGAACCAAGT | | 28 | 16 | 10 | | | | | | | | | | | | | | | | |
| X07Y08 | ACCGCACTTTCAGCTAATGCAGAACGAGCCAG | | | | | | | | | | | | | | | | | | | | g5 |
| X07Y09 | TAATAAGACATAATTACTAGAAAATCTTCTGA | | 28 | | | | | | | | | | | | | | | | | | |
| X07Y10 | CCTAAATTTCAAAATCATAGGTCTATTAATTT | | | | | | | | | | | | | | | | | | | | |
| X07Y11 | TCCCTTAGAAAGAAGATGATGAAAACGGATTC | | 28 | 16 | 10 | | | | | | | | | | | | | | | | |
| X07Y12 | GCCTGATTCTTCTGAATAATGGAAAGGAGCGG | | | | | | | | | | | | | | | | | | | | |
| X07Y13 | AATTATCACAATAGATAATACATTAATCAACA | | 28 | | | | | | | | | | | | | | | | | | |
| X07Y14 | GTTGAAAGGATAAAACAGAGGTGATGGCTATT | | | | | | | | | | | | | | | | | | | | |
| X07Y15 | AGTCTTTACTCAATCGTCTGAAATGCTGGTAA | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X07Y16 | TATCCAGAAATCCTGAGAAGTGTT | | | | | | | | | 12 | | | | | | | | | | | |
| X08Y01 | CATACATGTATTTCGGAACCTATCGAGAGGGTTGATAT | | | | | | | | | 12 | | | | | | | g1 | | | | |
| X08Y02 | CCACCGGAGCATTGACAGGAGGTTAAGCGT | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y03 | GGAATTAGAGAATCAAGTTTGCCAGAGCCA | | | | | | | | | | | | | | | | | | | | |
| X08Y04 | CAAACGTAGTTTACCAGCGCCAACCATTTG | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y05 | AGCGCTAAAAGAAAAGTAAGCAGATGTTAG | | | | | | | | | | | | | | | | | | | | |
| X08Y06 | CTGAATCTTTTGTTTAACGTCAAGTAATTG | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y07 | GGGTATTAAAGGCTTATCCGGTATTTTATC | | | | | | | | | | | | | | | | | | | | |
| X08Y08 | GGCATTTTCGCGCCTGTTTATCACAAGAAC | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y09 | TAATTTCAAGCCTGTTTAGTATCAGGCAGA | | | | | | | | | | | | | | | | | | | | |
| X08Y10 | CGCTATTAGAGAGACTACCTTTTTTTTAGT | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y11 | AAACAATACAAACATCAAGAAAAAAAATCGT | | | | | | | | | | | | | | | | | | | | |
| X08Y12 | CCACCAGAGGGTTAGAACCTACCTCGGGAG | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y13 | AGTTGGCATGAGGATTTAGAAGTAAAGAAA | | | | | | | | | | | | | | | | | | | | |
| X08Y14 | TTTTTGAAGGCGGTCAGTATTAATCTGGTC | S1 | | | | | | | | | | | | | | | | | | | |
| X08Y15 | TCGGCCTTGGATTATTTACATTGGACAATA | | | | | | | | | | | | | | | | | | | | |
| X08Y16 | TTTATAATCAGTGAGCAAACTA | | | | | | | | | | | | | | | | | | | | |
| X09Y01 | GGCGGATAAGTGCCGTTATTCTGAAACATGAAGAATTTAC | | | | | | | | | | | | | | | | | | | | |
| X09Y02 | CGTTCCAGTGAGGCAGGTCAGACGCAAAATCA | | 28 | 16 | 10 | 6 | 4 | | | | | | | | | | | g2 | | | |
| X09Y03 | CCGGAACCTTTAGCGTCAGACTGTCCGTCACC | | | | | | | | | | | | | | | | | | | | |
| X09Y04 | GACTTGAGAGACAAAAGGGCGACACTCCTTAT | | 28 | | | | | | | | | | | | | | | | g3 | | |
| X09Y05 | TACGCAGTATAGCCGAACAAAGTTTGAACAAA | | | | | | | | | | | | | | | | | | | | |
| X09Y06 | GTCAGAGGAAATGAAAATAGCAGCTTGCACCC | | 28 | 16 | | | | | | | | | | | | | | | | g4 | |
| X09Y07 | AGCTACAATTCTAAGAACGCGAGGTCTTTCCT | | | | | | | | | | | | | | | | | | | | |
| X09Y08 | TATCATTCACAATAGATAAGTCCTCGCCAACA | | 28 | | 10 | 6 | | | | | | | | | | | | | | | g5 |
| X09Y09 | TGTAATTTATATGCGTTATACAAAAACTTTTT | | | | | | | | | | | | | | | | | | | | |
| X09Y10 | CAAATATATAACCTCCGGCTTAGGATAACCTT | | 28 | 16 | | | | | | | | | | | | | | | | | |
| X09Y11 | GCTTCTGTCAAAATTAATTACATTAACAGTAC | | | | | | | | | | | | | | | | | | | | |
| X09Y12 | CTTTTACAATATCAAAATTATTTGTATCATTT | | 28 | | | | | | | | | | | | | | | | | | |
| X09Y13 | TGCGGAACATTAGACTTTACAAACAAACCCTC | | | | | | | | | | | | | | | | | | | | |
| X09Y14 | AATCAATACACCGCCTGCAACAGTAAGAATAC | | 28 | 16 | 10 | 6 | 4 | 2 | | | | | | | | | | | | | |
| X09Y15 | GTGGCACAGCAGATTCACCAGTCACCTGAGTA | | | | | | | | | | | | | | | | | | | | |
| X09Y16 | GAAGAACTGCCACCGAGTAAAAGA | | | | | | | | | 12 | 8 | 6 | 4 | 2 | | | | | | | |
| X10Y01 | CAGTCTCTAGTATTAAGAGGCTGAGTTTTGCTCAGTACCA | | | | | | | | | 12 | 8 | 6 | 4 | | | | g1 | | | | |
| X10Y02 | TTCATAATATTGGCCTTGATATTCGGAAAGCG | | | | | | | | | | | | | | | | | | | | |
| X10Y03 | AATTATCAAGCGCGTTTTCATCGGGCCATCTT | | | | | | | | | | | | | | | | | | | | |
| X10Y04 | GATTAAGATTCAACCGATTGAGGGTAAAGGTG | | | | | | | | | | | | | | | | | | | | |
| X10Y05 | GAACACCCACCAGAAGGAAACCGAACTGGCAT | | | | | | | | | | | | | | | | | | | | |
| X10Y06 | TTGCTATTCTTTACAGAGAGAATAAATTAACT | | | | | | | | | | | | | | | | | | | | |
| X10Y07 | ATCGGCTGCGTTTTAGCGAACCTCAAGATTAG | | | | | | | | | | | | | | | | | | | | |
| X10Y08 | TTTAACAAGAACAAGAAAAATAATAATCAATA | | | | | | | | | | | | | | | | | | | | |
| X10Y09 | CGCGAGAATTCTTACCAGTATAAATCGCCATA | | | | | | | | | | | | | | | | | | | | |
| X10Y10 | GTGAGTGATTGGGTTATATAACTAACAAAGAA | | | | | | | | | | | | | | | | | | | | |
| X10Y11 | TATACAGTTAACAATTTCATTTGACAATATAT | | | | | | | | | | | | | | | | | | | | |
| X10Y12 | AGTAACATCACGTAAAACAGAAATCAGATGAA | | | | | | | | | | | | | | | | | | | | |
| X10Y13 | CAAATATCAATTCGACAACTCGTAAAAGTTTG | | | | | | | | | | | | | | | | | | | | |
| X10Y14 | GAAAGCGTGCCACGCTGAGAGCCACTGAACCT | | | | | | | | | | | | | | | | | | | | |
| X10Y15 | ATCACTTGCACGACCAGTAATAAATCTGACCT | | | | | | | | | | | | | | | | | | | | |
| X10Y16 | GTCTGTCCATCACGCAGTAATAAC | | | | | | | | | | | | | | | | | | | | |

Figure 4: **The staple list of the nanotile.** The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin, binding overhangs without the bridge, and binding overhangs with the bridge.

## 2.2 Sequence list of the nanorod

| Name | Sequece | biotin sites | | 28 binding sites | | | | | | | Geometry layout | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0[2] | CTCAAATGCTTTCCCCTTATTAGCGTTTGCC | | * | 28 | 16 | 10 | 6 | 4 | 2 | 1 | | | | | | |
| 5[27] | CACCGGATCATAGCAAACAGT | | | | | | | | | | | | | | | |
| 2[28] | TTTCGGACCAGAGCGCCGAC | | | | | | | | | | | | | | | |
| 3[33] | TCAGAAATCGTCATGAGGCT | | | | | | | | | | | | | | | |
| 0[34] | TGCGGAAACGAGAAATCGGCAT | | | | | | | | | | | | | | | |
| 1[41] | TGCAGGGAATAGTTGCCACCAC | | | | | | | | | | | | | | | |
| 4[42] | GCCTCCCACAGCTTGATACCGGTTAAAGCCAATAC | | | 28 | | | | | | | | | | | | |
| 0[49] | AAATCAGGTCAGACTGTAGCG | | | | | | | | | | | | | | | |
| 3[55] | CGGAACCCGTTTTCTGACCATAAATCAAATAGCGTGCCGCTT | | | | | | | | | | | | | | | |
| 4[56] | GGTGAATATCGTCAAATGTTTAGACTGG | | | | | | | | | | | | | | | |
| 5[69] | TTGCGGGTTCTTAATCAGAGCCGCCACCCTTTAGCGTCTTTA | | | | | | | | | | | | | | | |
| 2[70] | GGGGGTATATTATAAGAATCAAGTTTGCCTCAGAACTTTCGA | | | | | | | | | | | | | | | |
| 1[83] | CCCTGACATAGTAACCCTCAGCAGCGAACAGCTTGCCGCCAC | S1 | | | | | | | | | | | | | | |
| 4[84] | GCCACCATTGTATCGGTTTATAGACAGCTGCCAGA | | | | | | | | | | | | | | | |
| 5[90] | CCTCAGATAGCGACGTCAGAA | | | 28 | 16 | | | | | | | | | | | |
| 0[91] | TGCAAAAGGATTGCAGCACCGTAATCAG | | | | | | | | | | | | | | | |
| 1[104] | GCAAAGCGAAGTTTATCGGAACGAGGGTCCTTTAACCCTCAG | | | | | | | | | | | | | | | |
| 4[105] | AAACCATACCAGAAGGCTCCAAAAGGAGAGCAACGAGGCTTT | | | | | | | | | | | | | | | |
| 5[111] | AGCCGCCCGATAGCATCAAAA | | | | | | | | | | | | | | | |
| 0[119] | ACCAAAAGAGGAAGACCAATG | | | | | | | | | | | | | | | |
| 1[125] | AGATTAATAGCGAGGCTACAGAGGCTTTAAAAAAACCACCAC | | | | | | | | | | | | | | | |
| 4[126] | GGCCGGGCCGCCAGTTGAAAATCTCCAGAGGACTGATAAAA | S1 | | | | | | | | | | | | | | |
| 0[139] | AATAATTGAGGAAGAACCCTCGTTTACCAATATCGATTAGCAA | | | | | | | | | | | | | | | |
| 3[139] | CAGAGCCAAACGTCCCCGAAAGACTTCAAGACGACAAAGACT | | | 28 | | 10 | | | | | | | | | | |
| 1[146] | TTTTCATTTTTCACGCATTGA | S1 | | | | | | | | | | | | | | |
| 2[154] | AGCAACACTTCAAAATCACCAGTAGCACTTGAGGCTGCGAAT | | | | | | | | | | | | | | | |
| 3[160] | CAGGAGGCATTACCCGTTTTAATTCGAGCTATCATTTTCCAT | | | | | | | | | | | | | | | |
| 4[168] | ACAACTAGTAAAATTAGTAAG | | | | | | | | | | | | | | | |
| 5[174] | TAAACGGAAGGAATAGGTCAGACGATTGCAGCAAAGCGAACC | | | | | | | | | | | | | | | |
| 2[175] | GGAATTAAAGCAAATTGGGAATTAGAGCGCCTTGAGAAAGGA | | | 28 | 16 | | | | | | | | | | | |
| 1[188] | AGACCGGCGAGGCAACGTAATGCCACTAGAGAATATATTCAC | | | | | | | | | | | | | | | |
| 4[189] | CGACTTTAAATCCAGTTTCAGCGGAGTCGAAGGCGCCAAAA | S1 | | | | | | | | | | | | | | |
| 5[195] | AAACAAAGAGCCATCTCCAAC | | | | | | | | | | | | | | | |
| 0[202] | TGCAGATGATTAGAACCGTCAC | | | | | | | | | | | | | | | |
| 1[209] | AGGTCAGACATAACACCAACCTAAAACGTTTCAACTCATTAA | S1 | | | | | | | | | | | | | | |
| 4[210] | AAAGGTGATGGAAATTTTGCTAAACAACAAAGAGGCAACTAA | | | | | | | | | | | | | | | |
| 3[223] | AGCCAGAAATTATCGAGTACCTTTAATTCCACATTCAAAAGA | | | 28 | | | 6 | | | | | | | | | |
| 0[224] | TTTCTGAAAACACGAGATTTAGGAATAGCTCCTTATTCATT | | | | | | | | | | | | | | | |
| 1[230] | ATACACTTATGGGAGCGCAGT | | | | | | | | | | | | | | | |
| 2[237] | AAGATTCTTTTTGCAGGTAAATATTGACTTTACCGAAATGAAT | | | | | | | | | | | | | | | |
| 3[244] | CTCTGAAGGAAATTTTGATAAGAGGTCAATCAGTTTCATCTT | | | | | | | | | | | | | | | |
| 1[251] | TGACCCCCGTTAGTTTCCAGT | | | | | | | | | | | | | | | |
| 4[252] | TTCCAGACAGCGATAGGTAGA | S1 | | | | | | | | | | | | | | |
| 2[259] | AACAACATTAATTGTTCAACCGATTGAGATACATGGTCGTCT | | | | | | | | | | | | | | | |
| 3[265] | AAGCGTCGGAGGGAGGATGGCTTAGAGCTTATTACTATACCA | | | | | | | | | | | | | | | |
| 1[272] | AGCGCGAAAGTTTTGCTTTTG | S1 | | | | | | | | | | | | | | |
| 4[273] | CGATCTAAACAAAGCTAACGG | | | 28 | 16 | 10 | | | | | | | | | | |
| 2[280] | GTTAATAGTAGCTCGCCAAAGACAAAAGAGGAGTGAGCGTAA | | | | | | | | | | | | | | | |
| 3[286] | ATGATACGGCGACACTGAATATAATGCTAAACGAATACAACG | | | | | | | | | | | | | | | |
| 4[294] | CAGCCCTGTATCATAATCTAC | | | | | | | | | | | | | | | |
| 5[300] | GAGATTTCATAGTTTACTGGTAATAAGTTACCAGCAACATGT | | | | | | | | | | | | | | | |
| 2[301] | ACGTTGGATGCAACAAATTCATATGGTTTTTAACGCCACAGA | | | | | | | | | | | | | | | |
| 1[314] | TTTAAATGAAGAAACGCCTGATAAATTGTAGCATTGGGTCAG | | | 28 | 16 | | | | | | | | | | | |
| 4[315] | TCACAATAGTAACAAACTACAACGCCTGTGTCGAAAGTCAGG | S1 | | | | | | | | | | | | | | |
| 3[328] | TGCCTTGCAATAGATAAAGTACGGTGTCTTATACCATCCGCG | | | | | | | | | | | | | | | |
| 0[329] | TCGTCACCCATGTTTAAGAACTGGCTCATGGAAGTTATTTTG | | | | | | | | | | | | | | | |
| 1[335] | ACCTGCTCAGTACAGTGCCCG | S1 | | | | | | | | | | | | | | |
| 2[343] | CCACGGAAGTTAATCTGAGTT | | | | | | | | | | | | | | | |
| 3[349] | TATAAACATAAGTTTTCATTCCATATAAGCGATTTACTTAGC | | | | | | | | | | | | | | | |
| 0[350] | CATGTACAGGCGCAGTGAATTACCTTATCAGTTGAAAAGACA | | | | | | | | | | | | | | | |
| 1[356] | CGGAACGCGTAACAGCCCCCT | | | 28 | | | | | | | | | | | | |
| 2[364] | CAACTTTAACGAGTGGCAACATATAAAATCGGAACAGGAACC | | | | | | | | | | | | | | | |
| 3[370] | GCCTATTGAAACGCTTCCCAATTCTGCGAATCATTGACGGTC | | | | | | | | | | | | | | | |
| 4[378] | ATAGCAAAGGGAACTTAATTT | S1 | | | | | | | | | | | | | | |
| 5[384] | AATCATAGCCCAATCTATTATTCTGAAATAAAGGTAGATTTA | | | | | | | | | | | | | | | |
| 2[385] | GGGCTTGCATTAGAAGAAAATACATACACATGAAATTCAGGG | | | | | | | | | | | | | | | |
| 1[398] | GTTTGACAGATGGTCGAACTGACCAACTCCTCATTGTATTAA | S1 | | | | | | | | | | | | | | |
| 4[399] | CCACCACTTGAAAGGTAAATT | | | | | | | | | | | | | | | |
| 5[405] | GAGGCTGCAAACGTTACATTT | | | | | | | | | | | | | | | |
| 2[406] | CACCAGAGGTCAATACGCAGTATGTTAGAGACTCCCTCAGAG | | | 28 | 16 | 10 | | 4 | | | | | | | | |
| 1[419] | CGCAAATACGAGTAAGGACAGATGAACGCGCCACCTCAAGAG | | | | | | | | | | | | | | | |
| 4[420] | TAAGACTAGGATTAGCCACCCTCAGAACGTGTACACGAGAAA | | | | | | | | | | | | | | | |
| 5[425] | AAGGATTCCTTATTAACCTG | | | | | | | | | | | | | | | |
| 0[434] | AAGGCTTTATTTTCGCATGAT | | | | | | | | | | | | | | | |
| 1[440] | TTTAGCTAGCCCTGAGACCAGGCGCATAGCAGAACCGCGGGGT | | | | | | | | | | | | | | | |
| 4[441] | ACCCAAAAGTACCAAGTACCGCCACCCTGCTGGCTAGTGAAT | S1 | | | | | | | | | | | | | | |
| 3[454] | TTTGCTCAGAACTGATTTGGGGCGCGAGCTCATTCGACCTTC | | | 28 | | | | | | | | | | | | |
| 0[455] | TACTCAGGTAATCTACGTAACAAAGCTGCTGAAAAACGGAAT | | | | | | | | | | | | | | | |
| 1[461] | ATCAAGAGAGGTTTGGCGGAT | S1 | | | | | | | | | | | | | | |
| 2[469] | GAAACGCGTCGAGAATCACCG | | | | | | | | | | | | | | | |
| 3[475] | AAGTGCCAATAATAGGTGGCATCAATTCCAAATCATGACAAG | | | | | | | | | | | | | | | |
| 0[476] | AGCATTCCCAGTTTGGAACATTCATTACCTACTAATAACCGAG | | | | | | | | | | | | | | | |
| 5[488] | AACCGGATAGGTGTGGGTTGATATAAGTAGAAGGAAGTAGT | | | | | | | | | | | | | | | |
| 3[490] | CCTAGCCCGGAATAAGAGTC | | | | | | | | | | | | | | | |
| 2[495] | CACTATTAAAGAAACGGATTCG | | | 28 | 16 | | 6 | | | | | | | | | |
| 1[496] | GTTGTTCAATAAATCGAACAAAGTTACCATGATTG | | | | | | | | | | | | | | | |
| 4[504] | AGTAAGCTTACAAACGGGAGAAACAATACGTGGACGTTGAGT | S1 | | | | | | | | | | | | | | |
| 5[510] | CTTTGAATACCAAGAGATAGCCATACAG | | | | | | | | | | | | | | | |
| 0[518] | AGTACCTGCGAAAAAAAAGAATAGCCCGAAAGAATTAAGAAA | | | | | | | | | | | | | | | |
| 1[524] | GCAAGGCAGATAGGTCCAACGTCAAAGGTTTACATATCGCGC | S1 | | | | | | | | | | | | | | |
| 2[532] | ACCGAAGAATTATTCAGTAAC | | | | | | | | | | | | | | | |
| 3[538] | AGAGGCGCCCTTTTTAGCAAAATTAAGCATAAATCACCGTCT | | | | | | | | | | | | | | | |
| 0[539] | GTCAGATCGATGGCCGGCAAAATCCCTTAATAAAGCTATCTT | | | | | | | | | | | | | | | |
| 1[545] | ATCAGGGGAATATACATTTCA | | | 28 | | 10 | | | | | | | | | | |
| 2[553] | GGTGGTTGCTAAATGAAACAATGAAATAGAGCAAAGTTTAAC | | | | | | | | | | | | | | | |
| 3[558] | ATTACCTGCAATAGCCTCAGAGCATAAACCGAAATCCACTA | | | | | | | | | | | | | | | |
| 4[567] | GCGTAGAATCACCCGTTTGAT | S1 | | | | | | | | | | | | | | |
| 5[573] | CGTGAACCTTTTCAGAGAAGATGATGAAAAGAGCAACGGTTGT | | | | | | | | | | | | | | | |
| 2[574] | CAGGCGAACATTATTAAGCCCAATAATACAAACATAGAAATT | | | | | | | | | | | | | | | |
| 1[587] | ACCAAAAAAATCCTAAATCAAGTTTTTTGAAATAACAAGAAA | S1 | | | | | | | | | | | | | | |
| 4[588] | CACAAGATAATTACTTGCACGTAAAACAGGGGTCGGCCCCAG | | | 28 | 16 | | | | | | | | | | | |
| 5[594] | ACAAAATATTGAGTGACCCTG | | | | | | | | | | | | | | | |
| 3[601] | TAATACTCTGGTTTAGGTGCC | | | | | | | | | | | | | | | |
| 0[602] | GTCCACGTTTGCGGGATAACC | | | | | | | | | | | | | | | |
| 4[609] | GCTAATATTTGAATAACCTACCATATCAACTAAATGCAAGCG | | | | | | | | | | | | | | | |
| 5[615] | GTAAAGCAAATTATATTTAACAATTTCATCAGAGAGAGAAGC | | | | | | | | | | | | | | | |
| 0[623] | CTGAGAGTCAACGCATTGAGC | | | | | | | | | | | | | | | |
| 1[629] | CTTTATTAGTTGCACGGAACCCTAAAGGGGGTTAGTACCTTT | | | 28 | 16 | | | | | | | | | | | |
| 4[630] | AAAGTCAGAAACAGTCTGAATAATGGAAGAGCCCCCCTGGCC | S1 | | | | | | | | | | | | | | |
| 3[643] | TTTAATGGAGGGTAAAGGATAAAAATTTTTCACCGCGATTTA | | | | | | | | | | g6 | | | | | |
| 0[644] | GTTTGGAACGGGGAACAGCTGATTGCCCTTAGAACCCTGAAC | | | | | | | | | | | | | | | |
| 1[650] | GAGCTTGTTATACTTACATAA | S1 | | | | | | | | | | | | | | |
| 2[658] | CAGTGAGAATGCAAACGGGAGAATTAACTATGTGACCTGATT | | | | | | | | | | | | | | | |
| 3[664] | ATCAATATGAACACCCTCATATATTTTAACGGGCAAAGCCGG | | | | | | | | | | g6 | | | | | |
| 1[671] | CGAACGTATATAATGTGAATA | | | 28 | | 10 | | | | | | | | | | |
| 4[672] | TTCATCAGGCGAGATTTTCAC | | | | | | | | | | | | | | | |
| 2[679] | CAGGGTGGTAGGTAAAAAACAGGGAAGCTTCTGTAATGGCAA | | | | | | | | | | | | | | | |
| 3[685] | ACCTTGCGCATTAGTGCCTGAGTAATGTGTTTTTCAAGGAAG | | | | | | | | | | g6 | | | | | |
| 4[693] | AGAGAGAATTAATTCATATTCCTGATTAAGCGAAATGGGCGC | S1 | | | | | | | | | | | | | | |
| 5[699] | GGAAGAATCAGATGAATCGTCGCTATTAATAACATAAGATTC | | | | | | | | | | | | | | | |
| 0[707] | GGCGGTTTGAGAAACCTTTAC | | | | | | | | | | | | | | | |
| 1[713] | AAAAGGGTGCGTATGGAGCGGGCGCTAGTTATCATTTCCCTT | S1 | | | | | | | | | | | | | | |
| 4[714] | AATGAAATTGAAAACAGAAGGAGCGGAAGGCGCTGGGGGAGA | | | | | | | | | | | | | | | |
| 5[720] | AGAATCCATAGCAGGGCCGGA | | | 28 | 16 | | 6 | | | | | | | | | |
| 0[728] | AACAAAGCACGCTGTTAATGAATCGGCCAAATCACCGTCAAA | | | | | | | | | | | | | | | |
| 1[734] | GACAGTCAACGCGCGCAAGTGTAGCGGTAAACCACCATAGCG | | | | | | | | | | | | | | | |
| 2[742] | TCGTGCCTCAACCGAAGAAACGATTTTTAGATTAATTTGCGG | | | | | | | | | | | | | | | |
| 3[748] | ATAGCTTTGTTTAACATCAATATGATATAGCTGCACGCGTAA | | | | | | | | | | | | | | | |
| 1[755] | CCACCACTTATCATGACGCTG | | | | | | | | | | | | | | | |
| 4[756] | AGTAACAACCCGCCAAACCTG | S1 | | | | | | | | | | | | | | |
| 2[763] | GCTTTCCTTAATGCATTATTTATCCCAATCAATAGAAGTTTG | | | 28 | | | | | | | | | | | | |
| 3[769] | AGAAGAGTCCAAATTTCTAGCTGATAAAAGTCGGGGCGCTTA | | | | | | | | | | | g5 | | | | |
| 1[776] | ATGCGCCATTTTAATGAATTT | S1 | | | | | | | | | | | | | | |
| 4[777] | GTTATTAGCTACAGACTGCCC | | | | | | | | | | | | | | | |
| 2[784] | ATTGCGTATTTTTGAGTTACAAAATAAATCATAGGCCCGAAC | | | | | | | | | | | | | | | |
| 3[790] | ATCAAAACAGCCATCGGAGAGGGTAGCTTGCGCTCGGCGCGT | | | | | | | | | | | g5 | | | | |
| 4[798] | TATTAAATTGCTTTCACATTA | | | | | | | | | | | | | | | |
| 5[804] | ACTATGGTCCTTTGTCTGAGAGACTACCATTTGCCAGAGATC | | | | | | | | | | | | | | | |
| 2[805] | TGAGTGAGCTATCACTTTCCAGAGCCTATTTTTAACAACTCG | | | | | | | | | | | | | | | |
| 3[811] | TACAAAGGCTAACTGACGAGC | | | 28 | 16 | 10 | | 4 | | | | g5 | | | | |
| 4[819] | ACGCTAATGGGTTATAGACTTTACAAACACGTGCTTGCCTAA | S1 | | | | | | | | | | | | | | |
| 5[825] | ACGTATAAATTCGACCTCCGGCTTAGGTCGAGCGTGGTCATT | | | | | | | | | | | | | | | |
| 0[833] | GGATTTACAGAGCGCATAAAGTGTAAAGAGTCTGGCTTACCA | | | | | | | | | | | | | | | |
| 1[839] | GCCTGAGCCTGGGGTTCCTCGTTAGAATGAAGTATTATAACT | S1 | | | | | | | | | | | | | | |
| 5[846] | ATATGTACCTGAATAGCAAAC | | | | | | | | | | | | | | | |
| 2[847] | ATTTTATAATGCTGCATTTGA | | | | | | | | | | | | | | | |
| 0[854] | GTCAATAGGCCGATACACAACATACGAGTCGATGAAGCTACA | | | | | | | | | | | | | | | |
| 1[860] | AAGAGAACCGGAAGGGAGCTAAACAGGAGATAATAATGCAAA | | | 28 | | | | | | | | | | | | |
| 2[868] | CCGCTCAACTAGCAATTAGTTGCTATTTGCAAGACTAGAGCC | | | | | | | | | | | | | | | |
| 3[874] | TCCAATCTGCACCCACGGTAATCGTAAACAATTCCTAAAGGG | | | | | | | | | | | | g4 | | | |
| 1[881] | ATTTTAGAATAGATAAAGAAC | | | | | | | | | | | | | | | |
| 4[882] | AACAACTACAGGAATTGTTAT | S1 | | | | | | | | | | | | | | |
| 2[889] | TTTCCTGACCCCGGGTTTTGAAGCCTTAAACTTTTGAGCACT | | | | | | | | | | | | | | | |
| 3[895] | GCGAGAAAATCAAGTGTCAATCATATGTTGTGAAACGGTACG | | | | | | | | | | | | g4 | | | |
| 1[902] | CCAGAATTCTTTAGTCAAATA | S1 | | | | | | | | | | | | | | |
| 4[903] | TAAAATACCTGAGAATAGCTG | | | 28 | 16 | | | | | | | | | | | |
| 2[910] | TCGTAATAGCCCCAGAACCTCCCGACTTGTTAATTGGTTATC | | | | | | | | | | | | | | | |
| 3[916] | TATTTTAGCGGGAGTTGATAATCAGAAACATGGTCAGTGTTT | | | | | | | | | | | | g4 | | | |
| 4[924] | CGAGGCGAAATTTACAGTTGAAAGGAATCAGTGAGCTCGAAT | | | | | | | | | | | | | | | |
| 5[930] | TTATAATTGAGGAATCATCTTCTGACCTTTTTAGCAAAACAG | | | | | | | | | | | | | | | |
| 0[938] | CCCCGGGGTATAAGAAGAACG | | | | | | | | | | | | | | | |
| 1[944] | GAAGATTTACCGAGGCCACCGAGTAAAAAAATCAAATGGTTT | | | 28 | 16 | 10 | | | | | | | | | | |
| 4[945] | TTATCCGCGACCGTTCTGGTCAGTTGGCGAGTCTGAGAGGAT | S1 | | | | | | | | | | | | | | |
| 3[958] | GAAATACGTATTCTCAAATATTTAAATTCGACTCTTCCATCA | | | | | | | | | | | | | g3 | | |
| 0[959] | ACCCTCATAACCGTGCATGCCTGCAGGTGTAAACGAGAAGGC | | | | | | | | | | | | | | | |
| 1[965] | CGCAAATATCAATAGTGATAA | S1 | | | | | | | | | | | | | | |
| 2[973] | CCAGTGCAAATTCGAATAGCAAGCAAATGTTAAATATATCAA | | | | | | | | | | | | | | | |
| 3[979] | ATAAGGCCAGATATTTAATATTTTGTTACAAGCTTTGTAGCA | | | | | | | | | | | | | g3 | | |
| 1[986] | ATACTTCACCTCAAAAGAATA | | | | | | | | | | | | | | | |
| 4[987] | TTGCTGATTTGATTACGACGG | | | 28 | | | 6 | | | | | | | | | |
| 2[994] | CACGACGTAAATCAGTAGGAATCATTACGAATCATCATCACC | | | | | | | | | | | | | | | |
| 3[1000] | AACACCGCGCGCCCCATTAAATTTTTGTTTGTAAAAGTAATA | | | | | | | | | | | | | g3 | | |
| 4[1008] | TTTTTATGCCTGTTCAGCAAATGAAAAATTGCCTGTCCCAGT | S1 | | | | | | | | | | | | | | |
| 5[1014] | ACATCACTCTAAAGAATTACTAGAAAAATTTCATCGCTCATT | | | | | | | | | | | | | | | |
| 0[1022] | TAACGCCCAATAGGCAAGCCG | | | | | | | | | | | | | | | |
| 1[1028] | TTTTAACAGGGTTTAGTAGAAGAACTCAGAGCCAGTAGTATC | S1 | | | | | | | | | | | | | | |
| 4[1029] | TCATCGATTATACACAGTGCCACGCTGAAACTATCAGTTGGG | | | | | | | | | | | | | | | |
| 5[1035] | ATATGCGGAACAAGAACGCCA | | | 28 | 16 | | | | | | | | | | | |
| 0[1043] | CTGCAAGTAATTCGACCGCAC | | | | | | | | | | | | | | | |
| 1[1049] | TCAAAAAGCGATTAGGCCTTGCTGGTAACCTGCAAAATTCTT | | | | | | | | | | | | | | | |
| 4[1050] | GTATTAATAAAGCCCAGTATTAACACCGTATCCAGGGATGTG | | | | | | | | | | | | | | | |
| 3[1063] | ACCAGTAACCAAGTCGTCTGGCCTTCCTGAAAGGGAACAATA | | | | | | | | | | | | | | g2 | |
| 0[1064] | AGCTGGCGTAGCCAAGAACGG | | | | | | | | | | | | | | | |
| 1[1070] | TTACCGCAGGCGGTAACGCTC | | | | | | | | | | | | | | | |
| 4[1071] | AGAGGTGCAGCCATTTACGCC | S1 | | | | | | | | | | | | | | |
| 2[1078] | GGGCCTCTAAATGTCTGTCTTTCCTTATGGGCTTAATAAAAC | | | 28 | | 10 | | | | | | | | | | |
| 3[1084] | AACAGTACATTCCAGCTTTCATCAACATTTCGCTATGCAACA | | | | | | | | | | | | | | g2 | |
| 1[1091] | GGAAAAAGCAGAAGATTGAGA | S1 | | | | | | | | | | | | | | |
| 4[1092] | ACCACCACGCTCATTCGGTGC | | | | | | | | | | | | | | | |
| 2[1099] | GTTGGGACCGTCGGTAGAAACCAATCAATATTTAACGAACGA | | | | | | | | | | | | | | | |
| 3[1105] | ATCGCCATAATCGGGAGCGAGTAACAACAGGGCGAGGAAATA | | | | | | | | | | | | | | g2 | |
| 4[1113] | GCCATTATTTGACGCGCAACT | | | | | | | | | | | | | | | |
| 5[1119] | CCTACATAAAATACCAACGCCAACATGTGAGCATGATTCTCC | | | | | | | | | | | | | | | |
| 2[1120] | CGCCATTCAAACGGCCATCCTAATTTACAATTTAGAAACATC | | | 28 | 16 | | | | | | | | | | | |
| 1[1133] | GTGGGAACAGGCTGCTCAATCGTCTGAAAGCCCTAGCAGAGG | | | | | | | | | | | | | | | |
| 4[1134] | AGAAAAAGAGCCAGATGCGCGAACTGATATGGATTCGCCATT | S1 | | | | | | | | | | | | | | |
| 5[1140] | CATTTTCTAATATCCGGATTG | | | | | | | | | | | | | | | |
| 0[1148] | GCTATTAATTCACCGGTGCCGGAAACCATGGGATACTGAACA | | | | | | | | | | | | | | | |
| 1[1154] | ACCGTAAGGCAAAGATTTACATTGGCAGGTCTTTATAATAAG | S1 | | | | | | | | | | | | | | |
| 2[1162] | ACAATAGAAAGTACTTGAATG | | | | | | | | | | | | | | | |
| 3[1168] | AGAATATATAAGTCGGTCACGTTGGTGTCGCTTCTAGTCACA | | | | | | | | | | | | | | | g1 |
| 0[1169] | CACAGACTAATAAACAGCTTTCCGGCACAGATGGGTTTATCA | | | 28 | | | | | | | | | | | | |
| 1[1175] | CGACCAGAATATTTCGACAAA | | | | | | | | | | | | | | | |
| 2[1183] | GATCGCAGCATCTGAGCTAATGCAGAACGTAATTCTACGTGG | | | | | | | | | | | | | | | |
| 3[1189] | AGGTAAAGCGCCTGCGCATCGTAACCGTCTCCAGCAGGGACA | | | | | | | | | | | | | | | g1 |
| 3[1212] | ACAGTATCGGCCGATAGAACC | | * | | | | | | | | | | | | | g1 |
| 5[1215] | AACAACATGTTCCCAGTTTGAGGGGACGACG | | * | 28 | 16 | 10 | 6 | 4 | 2 | | | | | | | |

Figure 5: The staple list of the nanorod. The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin and the binding overhangs to target to cells. The stars represent the sequences at the end. And we generally exclude those sequences to prevent DNA origami stacking except when we need to add the binding overhangs to that location.

## 2.3 Sequence list of the nanosphere

| name(5'-3') | sequence | biotin sites | 28 binding sites | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| helix1-helix14 | CCACCCTCAGAGCCACCACCCTCATAGCTATCTTACCGAAGCCCT | S1 | | | | | | | |
| helix2-helix36 | AGCCACCACCGGAACCGCCTCCCACTATATGTAAATGCTGATGCAAATCC | | 28 | | | | | | |
| helix3-helix11 | TTATTAGCGTTTGCCATCTTTTCATGTTAGCAAACGTAGAAAAT | | | | | | | | |
| helix4-helix32 | CGTCAGACTGTAGCGCGTTTTCAATCATATGCGTTATACAAATTCTTACC | S1 | | | | | | | |
| helix5-helix7 | GATAGCAGCACCGTAATCAGTAGAAAGGTGAATTATCACCGTCACCG | | | | | | | | |
| helix6-helix28 | ACCATTACCATTAGCAAGGCCATGTTCAGCTAATGCAGAACGCGC | | 28 | 16 | | | | | |
| helix7-helix24 | ACTTGAGCCATTTGGGAATTAGATTTCATCGTAGGAATCATTAC | | 28 | 16 | 10 | 6 | 4 | 2 | 1 |
| helix8-helix10 | AATATTGACGGAAATTATTCATTTATAAAAGAAACGCAAAGACACCA | | 28 | | | | | | |
| helix9-helix20 | AGCGCCAAAGACAAAAGGGCGACATTCGAGCGTCTTTCCAGAGCCTAATT | S1 | | | | | | | |
| helix10-helix12 | CGGAATAAGTTTATTTTGTCACAGGAATACCCAAAAGAACTGGCATG | | | | | | | | |
| helix11-helix4 | ACATACATAAAGGTGGCAACACGACAGAATCAAGTTTGCCTTTAG | | 28 | 16 | 10 | | | | |
| helix12-helix13 | ATTAAGACTCCTTATTACGCAGTAGCCGAACAAAGTTACCAGAAGGA | | | | | | | | |
| helix13-helix15 | AACCGAGGAAACGCAATAATAACAATTGAGTTAAGCCCAATAATAAG | | 28 | 16 | | | | | |
| helix14-helix2 | TTTTAAGAAAAGTAAGCAGATATAATCAAAATCACCGGAACCAG | | | | | | | | |
| helix15-helix129 | AGCAAGAAACAATGAAATAGCAATACCGTTCCAGTAAGCGTCATACATGG | | 28 | 16 | 10 | | | | |
| helix16-helix18 | ATATCAGAGAGATAACCCACAAGCAAAAATGAAAATAGCAGCCTTTA | | | | | | | | |
| helix17-helix125 | ATTAACTGAACACCCTGAACAGATTAGCGGGGTTTTGCTCAGTAC | S1 | | | | | | | |
| helix18-helix19 | CAGAGAGAATAACATAAAAACAGATATTATTTATCCCAATCCAAATA | | | | | | | | |
| helix19-helix9 | AGAAACGATTTTTTGTTTAACGTATCAATAGAAAATTCATATGGTTTACC | | | | | | | | |
| helix20-helix123 | TGCCAGTTACAAAATAAACAGCCAGGTTTAGTACCGCCACCCTC | | 28 | | | | | | |
| helix21-helix23 | ATCCTGAATCTTACCAACGCTAACAGATATAGAAGGCTTATCCGGTA | | | | | | | | |
| helix22-helix119 | TGAAGCCTTAAATCAAGATTAGTTGCAGTTTTGTCGTCTTTCCAGACGTT | | 28 | | | | | | |
| helix23-helix25 | TTCTAAGAACGCGAGGCGTTTTAATTAAACCAAGTACCGCACTCATC | | | | | | | | |
| helix24-helix8 | CGCGCCCAATAGCAAGCAAATCAACCGATTGAGGGAGGGAAGGTA | S1 | | | | | | | |
| helix25-helix26 | GAGAACAAGCAAGCCGTTTTTATAACCAATCAATAATCGGCTGTCTT | S1 | | | | | | | |
| helix26-helix114 | TCCTTATCATTCCAAGAACGGGTATAGTTGCGCCGACAATGACAACAACC | | | | | | | | |
| helix27-helix6 | ATCCTAATTTACGAGCATGTAGAGCCAGCAAAATCACCAGTAGC | S1 | | | | | | | |
| helix28-helix110 | CTGTTTATCAACAATAGATAAGTCCATTAAACGGGTAAAATACGTAATGC | | | | | | | | |
| helix29-helix31 | TCCAGACGACGACAATAAACAACGGCTTAATTGAGAATCGCCATATT | | | | | | | | |
| helix30-helix80 | GTAATAAGAGAATATAAAGTAACCTGTCGTGCCAGCTGCATT | | | | | | | | |
| helix31-helix33 | TAACAACGCCAACATGTAATTTATAAGAATAAACACCGGAATCATAA | | | | | | | | |
| helix32-helix5 | AGTATAAAGCCAACGCTCAACAGTAGGGAAACGTCACCAATGAAACCATC | | | | | | | | |
| helix33-helix35 | TTACTAGAAAAAGCCTGTTTAGTACTTTTTCAAATATATTTTAGTTA | S1 | | | | | | | |
| helix34-helix79 | TGTGATAAATAAGGCGTTAAAGGAGAGGCGGTTTGCGTATTGGGC | | 28 | | | | | | |
| helix35-helix37 | ATTTCATCTTCTGACCTAAATTTGTCTGAGAGACTACCTTTTTAACC | | | | | | | | |
| helix36-helix3 | AATCGCAAGACAAAGAACGCGAGAAATCGGCATTTTCGGTCATAGCCCCC | S1 | | | | | | | |
| helix37-helix39 | TCCGGCTTAGGTTGGGTTATATATTAATTTTCCCTTAGAATCCTTGA | | | | | | | | |
| helix38-helix77 | GTGAATTTATCAAAATCATAGAGAGTTGCAGCAAGCGGTCCACGC | | | | | | | | |
| helix39-helix41 | AAACATAGCGATAGCTTAGATTACATTTAACAATTTCATTTGAATTA | | | | | | | | |
| helix40-helix1 | TTGCTTCTGTAAATCGTCGCTATTAATCAGAGCCGCCACCCTCAGAACCG | | | | | | | | |
| helix41-helix42 | CCTTTTTTAATGGAAACAGTACAAGCAAAAGAAGATGATGAAACAAA | | 28 | | | | | | |
| helix42-helix75 | CATCAAGAAAACAAAATTAATTAAAAGAATAGCCCGAGATAGGG | S1 | | | | | | | |
| helix43-helix45 | GAATTATTCATTTCAATTACCTGATTGCGTAGATTTTCAGGTTTAAC | | | | | | | | |
| helix44-helix71 | CGGATTCGCCTGATTGCTTTGAATACGGGAGCCCCCGATTTAGAGCTTGA | | | | | | | | |
| helix45-helix47 | GTCAGATGAATATACAGTAACAGTCCTGATTGTTTGGATTATACTTC | S1 | | | | | | | |
| helix46-helix131 | ACGTAAAACAGAAATAAAGAAAGGTTGAGGCAGGTCAGACGA | | | | | | | | |
| helix47-helix127 | TGAATAATGGAAGGGTTAGAACCAACAGTTAATGCCCCCTGCCT | | | | | | | | |
| helix48-helix69 | ATGATGGCAATTCATCAATATAACAAGTGTAGCGGTCACGCTGCGCGTAA | S1 | | | | | | | |
| helix49-helix51 | GAAACCACCAGAAGGAGCGGAATGAGGATTTAGAAGTATTAGACTTT | | 28 | 16 | 10 | 6 | 4 | | |
| helix50-helix57 | ATTAATTTTAAAAGTTTGAGTTGATAGCCCTAAAACATCGCC | | | | | | | | |
| helix51-helix53 | ACAAACAATTCGACAACTCGTATTGGCAAATCAACAGTTGAAAGGAA | S1 | | | | | | | |
| helix52-helix126 | TAGAGCCGTCAATAGATAATACATTTAAACATGAAAGTATTAAGAGGCTG | | | | | | | | |
| helix53-helix121 | TTGAGGAAGGTTATCTAAAATATTAGGAACCCATGTACCGTAACACTGAG | | | | | | | | |
| helix54-helix56 | CCCTCAATCAATATCTGGTCAGTACCAGCAGAAGATAAAACAGAGGT | S1 | | | | | | | |
| helix55-helix100 | CAGCAAATGAAAAATCTAAAGCATCATGGCTCATTATACCAGTCAGGACG | | 28 | 16 | | | | | |
| helix56-helix58 | GAGGCGGTCAGTATTAACACCGCGGCACAGACAATATTTTTGAATGG | | | | | | | | |
| helix57-helix50 | ATTAAAAATACCGAACGAACCTAAATCCTTTGCCCGAACGTT | | | | | | | | |
| helix58-helix66 | CTATTAGTCTTTAATGCGCGAACAAAGGGATTTTAGACAGGAACGGTACG | | | | | | | | |
| helix59-helix98 | GACCTGAAAGCGTAAGAATACGTAGTTGAGATTTAGGAATACCA | | | | | | | | |
| helix60-helix62 | ACCAGTAATAAAAGGGACATTCTACAATATTACCGCCAGCCATTGCA | S1 | | | | | | | |
| helix61-helix94 | CGTCTGAAATGGATTATTTACGCGTCCAATACTGCGGAATCG | | | | | | | | |
| helix62-helix88 | ACAGGAAAAACGCTCATGGAAATTTGCGGATGGCTTAGAGCTTAATTGCT | | | | | | | | |
| helix63-helix65 | CGGCCTTGCTGGTAATATCCAGAATCAGTGAGGCCACCGAGTAAAAG | S1 | | | | | | | |
| helix64-helix72 | GATTAGTAATAACATCACTTGGTTTTTTGGGGTCGAGGTGCCGTA | S1 | | | | | | | |
| helix65-helix67 | AGTCTGTCCATCACGCAAATTAATGCTTTCCTCGTTAGAATCAGAGC | | | | | | | | |
| helix66-helix59 | CCAGAATCCTGAGAAGTGTTTTTATAGGCCAACAGAGATAGAACCCTTCT | S1 | | | | | | | |
| helix67-helix68 | GGGAGCTAAACAGGAGGCCGATTCCGCTACAGGGCGCGTACTATGGT | | 28 | | | | | | |
| helix68-helix70 | TGCTTTGACGAGCACGTATAACGGAGAAAGGAAGGGAAGAAAGCGAA | | | | | | | | |
| helix69-helix49 | CCACCACACCCGCCGCGCTTAATGCGAACATTATCATTTTGCGGAACAAA | | | | | | | | |
| helix70-helix44 | AGGAGCGGGCGCTAGGGCGCTGGTACCTTTTACATCGGGAGAAACAATAA | S1 | | | | | | | |
| helix71-helix64 | CGGGGAAAGCCGGCGAACGTGGCCCGTTGTAGCAATACTTCTTT | | 28 | 16 | 10 | 6 | 4 | 2 | |
| helix72-helix74 | AAGCACTAAATCGGAACCCTAAAAACAAGAGTCCACTATTAAAGAAC | | 28 | 16 | | | | | |
| helix73-helix87 | ACTACGTGAACCATCACCCAAATCAATTTAAATATGCAACTAAAGTACGG | S1 | | | | | | | |
| helix74-helix76 | GTGGACTCCAACGTCAAAGGGCGTCCTGTTTGATGGTGGTTCCGAAA | | | | | | | | |
| helix75-helix43 | TTGAGTGTTGTTCCAGTTTGGCAAGTTACAAAATCGCGCAGAGGC | | | | | | | | |
| helix76-helix38 | TCGGCAAAATCCCTTATAAATCAAGACGCTGAGAAGAGTCAATA | S1 | | | | | | | |
| helix77-helix85 | TGGTTTGCCCCAGCAGGCGAAAATAGATACATTTCGCAAATGGTCAATAA | | | | | | | | |
| helix78-helix34 | GCCCTTCACCGCCTGGCCCTGAGAATGGTTTGAAATACCGACCG | | | | | | | | |
| helix79-helix81 | GCCAGGGTGGTTTTTCTTTTCACACTCACATTAATTGCGTTGCGCTC | S1 | | | | | | | |
| helix80-helix30 | AATGAATCGGCCAACGCGCGGGGCAGAGGCATTTTCGAGCCA | | 28 | 16 | 10 | 6 | 4 | | |
| helix81-helix107 | ACTGCCCGCTTTCCAGTCGGGAACTGATAAATTGTGTCGAAATCCGCGAC | | 28 | | | | | | |
| helix82-helix84 | TGGGGTGCCTAATGAGTGAGCTAGCGCGAGCTGAAAAGGTGGCATCA | S1 | | | | | | | |
| helix83-helix91 | ACAATTCCACACAACATACGACAAAAAGATTAAGAGGAAGCCCGA | | 28 | 16 | 10 | | | | |
| helix84-helix86 | ATTCTACTAATAGTAGTAGCATTAACAGTTGATTCCCAATTCTGCGA | | 28 | | | | | | |
| helix85-helix78 | CCTGTTTAGCTATATTTTCATTTGGGCAGTGAGACGGGCAACAGCTGATT | S1 | | | | | | | |
| helix86-helix73 | ACGAGTAGATTTAGTTTGACCATAAAAACCGTCTATCAGGGCGATGGCCC | | | | | | | | |
| helix87-helix89 | TGTCTGGAAGTTTCATTCCATATAGGATTAGAGAGTACCTTTAATTG | | | | | | | | |
| helix88-helix63 | GAATATAATGCTGTAGCTCAACATGTCCTGAGTAGAAGAACTCAAACTAT | | | | | | | | |
| helix89-helix90 | CTCCTTTTGATAAGAGGTCATTTATTCGAGCTTCAAAGCGAACCAGA | | | | | | | | |
| helix90-helix83 | CCGGAAGCAAACTCCAACAGGTCGTGTGAAATTGTTATCCGCTC | | | | | | | | |
| helix91-helix93 | AAGACTTCAAATATCGCGTTTTACCCTCAAATGCTTTAAACAGTTCA | S1 | | | | | | | |
| helix92-helix106 | ATAGTCAGAAGCAAAGCGGATTGCATAGGCGCAGACGGTCAATCATAAGG | | | | | | | | |
| helix93-helix95 | GAAAACGAGAATGACCATAAATCAAGAAGTTTTGCCAGAGGGGGTAA | | | | | | | | |
| helix94-helix61 | TCATAAATATTCATTGAATCCACCTACATTTTGACGCTCAAT | | | | | | | | |
| helix95-helix97 | TAGTAAAATGTTTAGACTGGATATAACGCCAAAAGGAATTACGAGGC | | | | | | | | |
| helix96-helix104 | ACCAAAATAGCGAGAGGCTTTTGCAACTTCATCAAGAGTAATCTTGACAA | | 28 | 16 | 10 | 6 | | | |
| helix97-helix99 | ATAGTAAGAGCAACACTATCATATAAAACGAACTAACGGAACAACAT | S1 | | | | | | | |
| helix98-helix60 | CATTCAACTAATGCAGATACAATTGGCAGATTCACCAGTCACACG | | 28 | 16 | | | | | |
| helix99-helix55 | TATTACAGGTAGAAAGATTCATCCTGCAACAGTGCCACGCTGAGAGCCAG | | | | | | | | |
| helix100-helix102 | TTGGGAAGAAAAATCTACGTTAAAGAAACACCAGAACGAGTAGTAAA | | | | | | | | |
| helix101-helix120 | ACCTTATGCGATTTTAAGAACCCTGTAGCATTCCACAGACAGCCC | | | | | | | | |
| helix102-helix116 | TTGGGCTTGAGATGGTTTAATTTCTCCAAAAAAAAAGGCTCCAAA | | | | | | | | |
| helix103-helix96 | AGTGAATAAGGCTTGCCCTGACGACCCTCGTTTACCAGACGACGATAAAA | | 28 | | | | | | |
| helix104-helix112 | GAACCGGATATTCATTACCCAAACACCCTCAGCAGCGAAAGACA | S1 | | | | | | | |
| helix105-helix92 | ACCAGGCGCATAGGCTGGCTGACAAAAATCAGGTCTTTACCCTGACTATT | | | | | | | | |
| helix106-helix108 | GAACCGAACTGACCAACTTTGAAATTATACCAAGCGCGAAACAAAGT | | | | | | | | |
| helix107-helix82 | CTGCTCCATGTTACTTAGCCGGAACGGCCGGAAGCATAAAGTGTAAAGCC | | | | | | | | |
| helix108-helix109 | ACAACGGAGATTTGTATCATCGCAAAGAGGCAAAAGAATACACTAAA | S1 | | | | | | | |
| helix109-helix111 | ACACTCATCTTTGACCCCCAGCGCGGCTACAGAGGCTTTGAGGACTA | | | | | | | | |
| helix110-helix29 | CACTACGAAGGCACCAACCTAAAACGCCGACAAAAGGTAAAGTAATTCTG | S1 | | | | | | | |
| helix111-helix113 | AAGACTTTTTCATGAGGAAGTTTGGTCGCTGAGGCTTGCAGGGAGTT | | 28 | 16 | | | | | |
| helix112-helix105 | GCATCGGAACGAGGGTAGCAAAGAGGACAGATGAACGGTGTACAG | | | | | | | | |
| helix113-helix115 | AAAGGCCGCTTTTGCGGGATCGTTTTATCAGCTTGCTTTCGAGGTGA | S1 | | | | | | | |
| helix114-helix27 | ATCGCCCACGCATAACCGATATATTCCCTGAACAAGAAAAATAATATCCC | | | | | | | | |
| helix115-helix117 | ATTTCTTAAACAGCTTGATACCGGGAACAACTAAAGGAATTGCGAAT | | | | | | | | |
| helix116-helix103 | AGGAGCCTTTAATTGTATCGGTCAACGTAACAAAGCTGCTCATTC | S1 | | | | | | | |
| helix117-helix118 | AATAATTTTTTCACGTTGAAAATATTTTGCTAAACAACTTTCAACAG | | | | | | | | |
| helix118-helix22 | TTTCAGCGGAGTGAGAATAGAAAGCGAACCTCCCGACTTGCGGGAGGTTT | S1 | | | | | | | |
| helix119-helix101 | AGTAAATGAATTTTCTGTATGGGCAACTTTAATCATTGTGAATT | S1 | | | | | | | |
| helix120-helix122 | TCATAGTTAGCGTAACGATCTAAGCCACCCTCAGAGCCACCACCCTC | S1 | | | | | | | |
| helix121-helix54 | TTTCGTCACCAGTACAAACTACAACGCCTTGCTGAACCTCAAATATCAAA | | 28 | | | | | | |
| helix122-helix124 | ATTTTCAGGGATAGCAAGCCCAAGGGTTGATATAAGTATAGCCCGGA | | | | | | | | |
| helix123-helix21 | AGAACCGCCACCCTCAGAACCTATTTTGCACCCAGCTACAATTTT | | 28 | | | | | | |
| helix124-helix17 | ATAGGTGTATCACCGTACTCAGGGGAAGCGCATTAGACGGGAGA | | | | | | | | |
| helix125-helix52 | CAGGCGGATAAGTGCCGTCGAGACTTTAGGAGCACTAACAACTAATAGAT | | | | | | | | |
| helix126-helix128 | AGACTCCTCAAGAGAAGGATTAGTAATAAGTTTTAACGGGGTCAGTG | S1 | | | | | | | |
| helix127-helix48 | ATTTCGGAACCTATTATTCTGTATCATCATATTCCTGATTATCAG | | 28 | 16 | 10 | | | | |
| helix128-helix130 | CCTTGAGTAACAGTGCCCGTATAAAATAAATCCTCATTAAAGCCAGA | | | | | | | | |
| helix129-helix16 | CTTTTGATGATACAGGAGTGTACTGGAAGTCAGAGGGTAATTGAGCGCTA | | | | | | | | |
| helix130-helix132 | ATGGAAAGCGCAGTCTCTGAATTGAGCCGCCACCAGAACCACCACCA | | | | | | | | |
| helix131-helix46 | TTGGCCTTGATATTCACAAACTACCATATCAAAATTATTTGC | | | | | | | | |
| helix132-helix40 | GAGCCGCCGCCAGCATTGACAGGTAAATCAATATATGTGAGTGAATAACC | | 28 | 16 | 10 | 6 | | | |

Figure 6: The staple list of the nanosphere. The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin and the binding overhangs to target to cells.

## 2.4 Sequence list of the binding overhangs and decorations

| name | sequence | Note |
|---|---|---|
| S1 | staples - TT GAGAGCAGACCTGGAACTCG | stalks on the origami |
| S1' | biotin - CGAGTTCCAGGTCTGCTCTC | sequence with biotin |
| S2 | staples - TT CAGTCAGTCAGTCAGTCAGT | binding sites to target to cells |
| S2' | Chol-TEG - ACTGACTGACTGACTGACTG | cholesterol-ssDNA initiator |
| S3 | staples - TT GTCTCGTCGTCTACCGCAAT | stalks to attach the bridge sequences |
| bridge 1 | CAGTGATATTCGTTCACCTCAGGCAGGTTGTACTAGCACCAGTTCGGAGACACATTCCTGCAGTCAGTCAGTCAGTCAGT | dsDNA bridge part1 |
| bridge 2 | CAGGAATGTGTCTCCGAACTGGTGCTAGTACAACCTGCCTGAGGTGAACGAATATCACTGATTGCGGTAGACGACGAGAC | dsDNA bridge part2 |

Figure 7: The sequences of the binding overhangs and decorations used in this paper.

# 3 Agarose gel results for the DNA origami

All the gels shown below was 2% agarose gel with 1x TBE and 12.5 mM $MgCl_2$ pre-stained with 1x SYBR Safe dye. We loaded 15 $\mu$l of 15 nM purified DNA origami to each well and run under 100 V voltage for 1.5 - 2 hours in a cold room. The gel was imaged under the SYBR Safe channel with a Bio-rad ChemiDoc Imaging System.

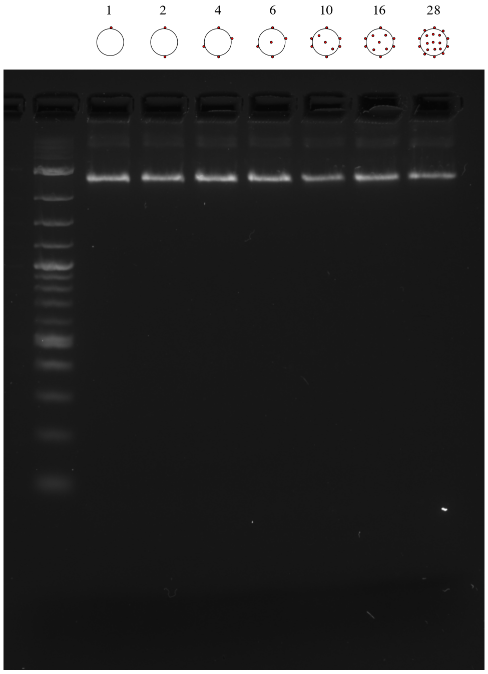


Figure 8: The agarose gel result of the nanosphere shape with different number of binding overhangs. From left to right: Ladder, nanosphere with 1, 2, 4, 6, 10, 16, 28 binding overhangs.

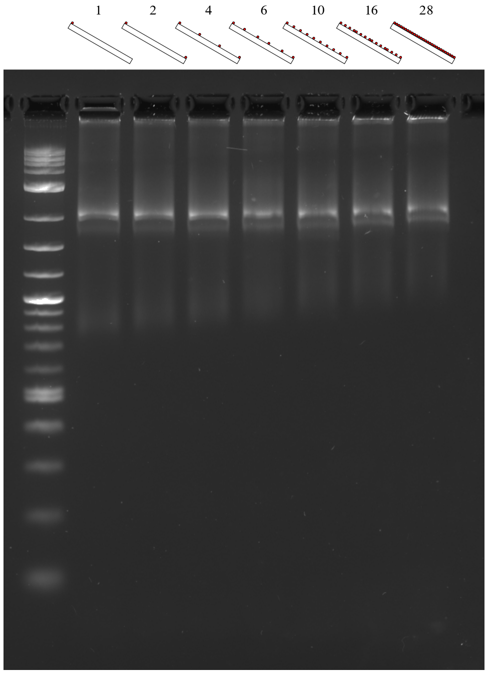


Figure 9: The agarose gel result of the nanorod shape with different number of binding overhangs. The gel image implies that there are some impurities and aggregations other than the brightest band. But further AFM images (Figure SI 15) show that the nanorods are intact. From left to right: Ladder, nanorod with 1, 2, 4, 6, 10, 16, 28 binding overhangs.

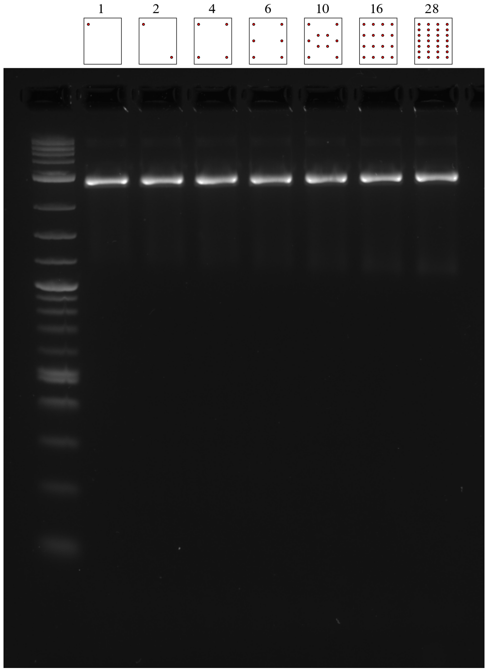


Figure 10: The agarose gel result of the nanotile shape with different number of binding overhangs on the face. From left to right: Ladder, nanotile with 1, 2, 4, 6, 10, 16, 28 binding overhangs on the face.

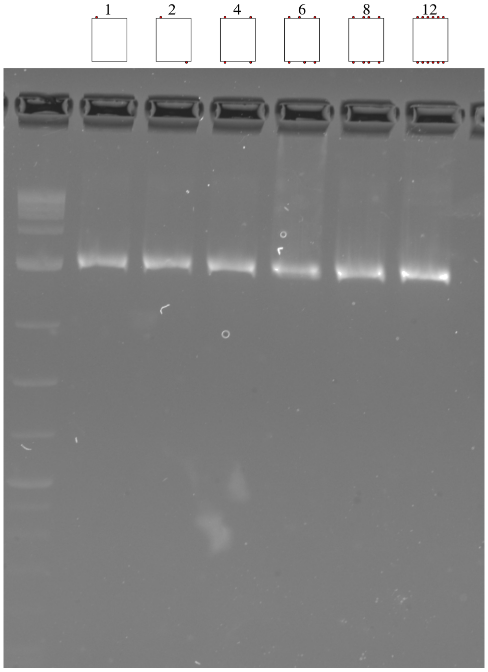


Figure 11: The agarose gel result of the nanotile shape with different number of binding overhangs on the edge. From left to right: Ladder, nanotile with 1, 2, 4, 6, 8, 12 binding overhangs on the edge.

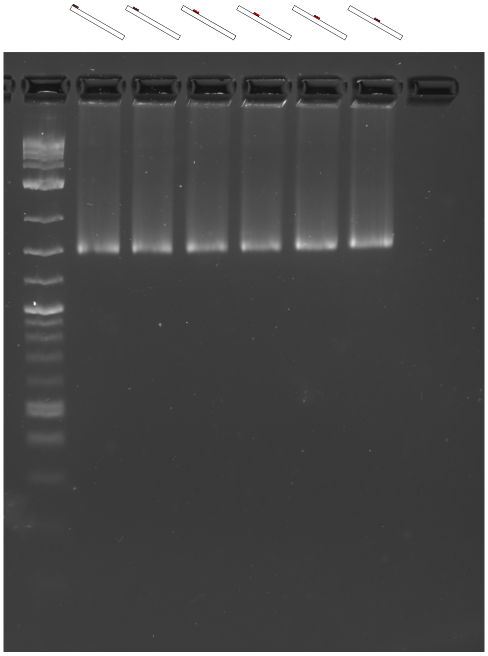


Figure 12: The agarose gel result of the nanorod shape with 3 binding overhangs at different location of the nanorod. From left to right: Ladder, nanorod with binding overhangs at position 1, 2, 3, 4, 5, 6.

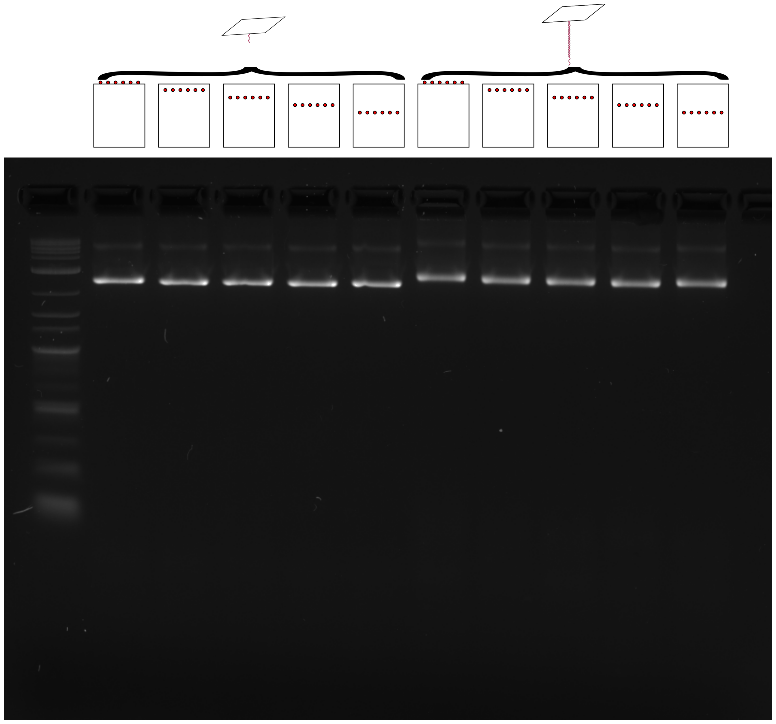


Figure 13: The agarose gel result of the nanotile shape with 6 binding overhangs at different location of the nanotile and with/without the dsDNA bridge sequences. From left to right: Ladder, nanotile with 6 binding overhangs without bridge at position 1, 2, 3, 4, 5, nanotile with 6 binding overhangs with bridge at position 1, 2, 3, 4, 5.

We then mixed the 15 $\mu$l DNA origami with 6FAM conjugated initiator ssDNA that was complementary to the overhangs. The final concentration of the 6FAM-ssDNA was 1.25 $\mu$M. The mixture was incubated at room temperature for one hour to allow hybridization. The samples was run through a non-stained agarose gel at 100 V for 1.5 - 2 hours and observed the bands under the Cy2 channel. And the total intensities of each band was analyzed by ImageJ. The result in Fig. S14 shows that the linear relationship of the 6FAM band intensity versus the number of binding overhangs in each shape, which indicates that the number of binding overhangs corresponds to the design.

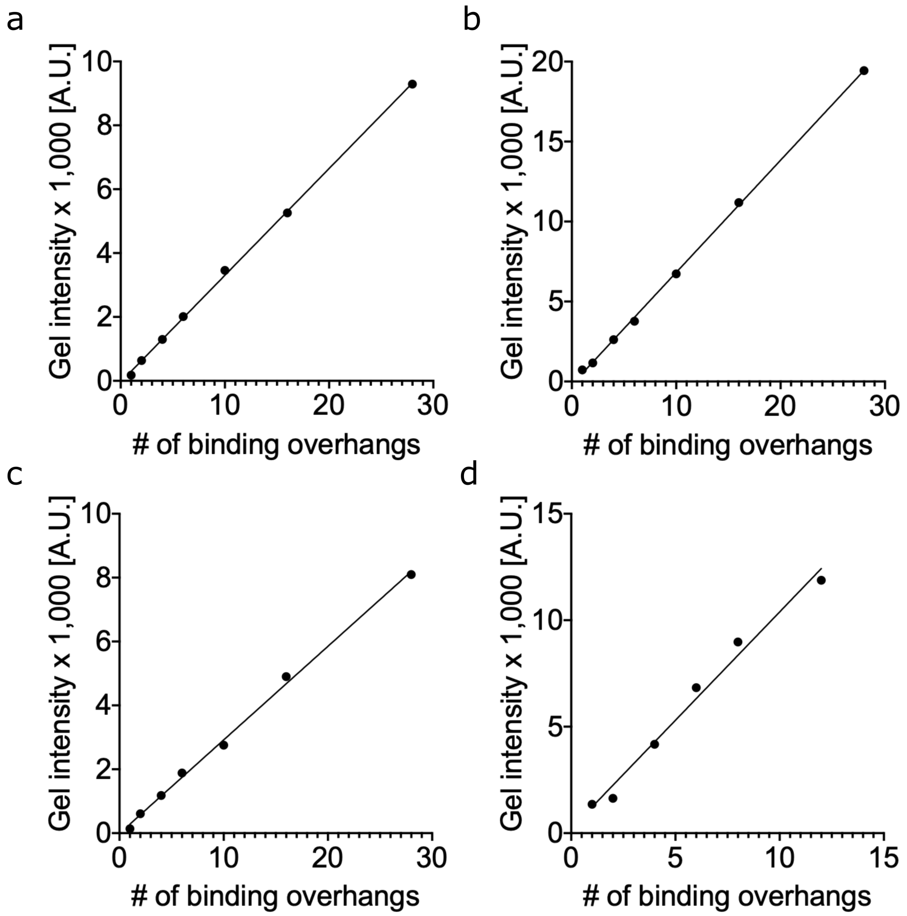


Figure 14: The 6FAM labeled DNA origami running through agarose gels. The linear relationship of the 6FAM band intensity versus the number of binding overhangs in each shape indicates that the binding overhangs are successfully assembled. (a) The DNA origami nanosphere with different number of binding overhangs. (b) The DNA origami nanorod. (c) The DNA origami nanotile with the binding overhangs located on the face. (d) The DNA origami nanotile with the binding overhangs on the edge.

# 4 AFMs for the selected samples

To further prove that the DNA origami was intact after purification, we selectively imaged some conditions used in the cell experiment.

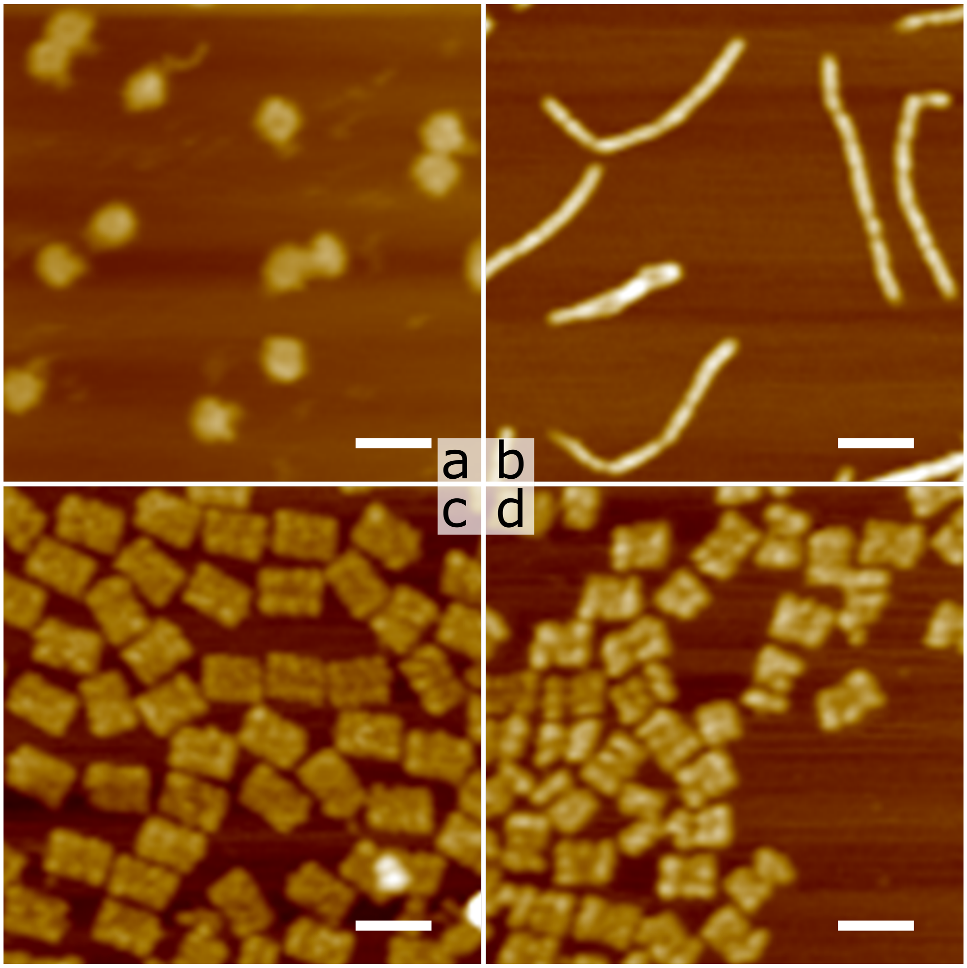


Figure 15: The AFM of the purified samples. (a) The nanosphere with 6 binding overhangs. (b) The nanorod with 28 binding overhangs. (c) The nanotile with 28 binding overhangs on the face. (d) The nanotile with 12 binding overhangs at the edge. Scale bars: 100 nm.

The dimension of DNA origami was determined by the measuring the profile of AFM images in 1 with FIJI ImageJ, as shown in 16. The measured dimension suggested that the distance of neighboring double-stranded helices is around 2.8 nm, instead of 2 nm, the diameter of a single dsDNA helix. This agrees with previous literature report.[2]

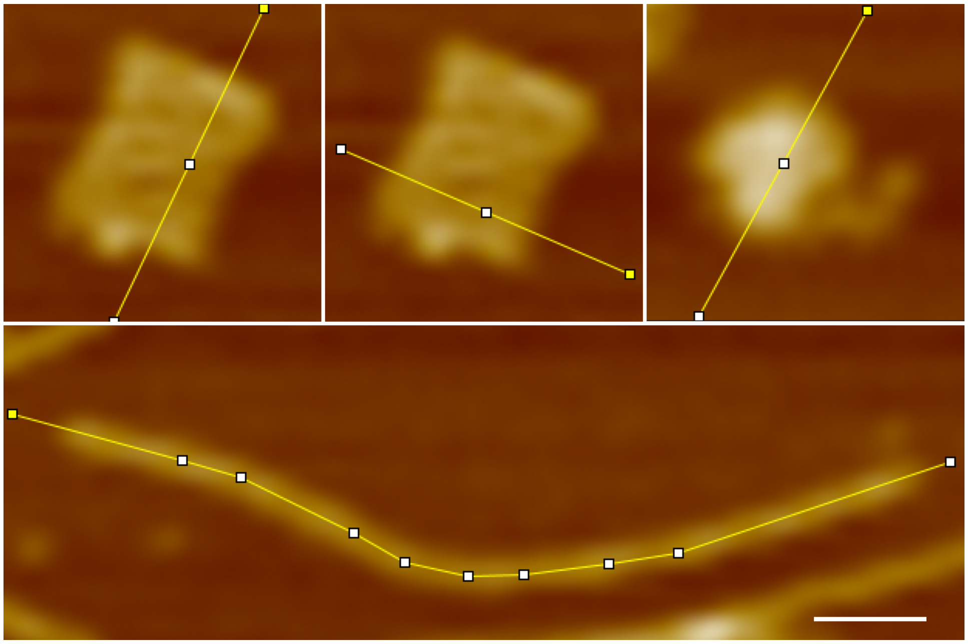
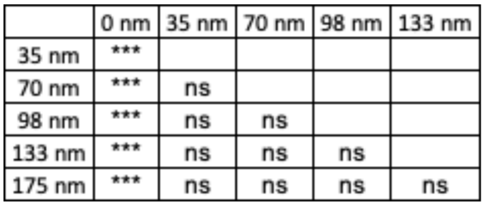


Figure 16: Using ImageJ to measure the dimension of the three DNA origami nanostructures. The AFM image showed the approximate dimension of a nanotile is around 66 by 88 nm. The lenth of a nanorod is around 398 nm. And the diameter of a nanosphere is around 68 nm. Scale bar: 50 nm.

# 5 Statistical analysis of the fluorescence data

We ran an one-way ANOVA analysis with post hoc Tukey's test between the targeted and non-targeted condition to show the significance of the labeling. The results are shown below.

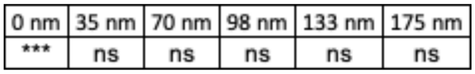
a



| | 0 nm | 35 nm | 70 nm | 98 nm | 133 nm |
|---|---|---|---|---|---|
| 35 nm | *** | | | | |
| 70 nm | *** | ns | | | |
| 98 nm | *** | ns | ns | | |
| 133 nm | *** | ns | ns | ns | |
| 175 nm | *** | ns | ns | ns | ns |

Proximity of nanorod: P values among different test conditions

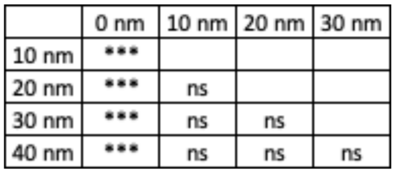
b



| 0 nm | 35 nm | 70 nm | 98 nm | 133 nm | 175 nm |
|---|---|---|---|---|---|
| *** | ns | ns | ns | ns | ns |

Proximity of nanorod: P values between with and without initiator conditions

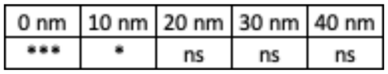
c



| | 0 nm | 10 nm | 20 nm | 30 nm |
|---|---|---|---|---|
| 10 nm | *** | | | |
| 20 nm | *** | ns | | |
| 30 nm | *** | ns | ns | |
| 40 nm | *** | ns | ns | ns |

Proximity of nanotile without spacers: P values among different test conditions

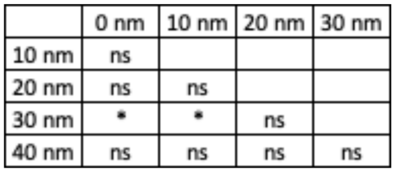
d



| 0 nm | 10 nm | 20 nm | 30 nm | 40 nm |
|---|---|---|---|---|
| *** | * | ns | ns | ns |

Proximity of nanotile without spacers: P values between with and without initiator conditions

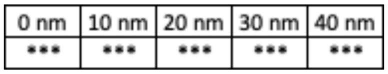
e



| | 0 nm | 10 nm | 20 nm | 30 nm |
|---|---|---|---|---|
| 10 nm | ns | | | |
| 20 nm | ns | ns | | |
| 30 nm | * | * | ns | |
| 40 nm | ns | ns | ns | ns |

Proximity of nanotile with spacers: P values among different test conditions

f



| 0 nm | 10 nm | 20 nm | 30 nm | 40 nm |
|---|---|---|---|---|
| *** | *** | *** | *** | *** |

Proximity of nanotile with spacers: P values between with and without initiator conditions

Figure 17: The P value of each conditions in the proximity dependent experiment. One-way ANOVA test was done with the proximity dependent experiment data including the proximity study with the nanorod ((a), (b)), and nanotiles with ((c), (d)) and without ((e), (f)) the bridge tethers. *ns P>0.05, * P≤0.05, ** P≤0.01, *** P≤0.001*

E. Benson, A. Mohammed, J. Gardell, S. Masich, E. Czeizler, P. Orponen and B. Högberg, *Nature*, 2015, **523**, 441–444.

D. Schiffels, T. Liedl and D. K. Fygenson, *ACS nano*, 2013, **7**, 6700–6710.