Supplemental Material

Combinatorial self-assembly of DNA nanostructures

Kyle Lund, Yan Liu and Hao Yan*

The sequences of the strands used:
TILE 1:
CST1-1 (28) 5'-ACGGTAGTGAATGTGGGTAGCTCCATAC-3'
CST1-2 (28) 5'-GATTGACGAGGCGTGGTGCTCGACACTC-3'
CST1-3 (28) 5'-GAACAGCGGTTCGTGGGCATCATCGTGC-3'
CST1-4 (28) 5'-GTGAAGCGGCTTGTGGCACTTGCAGTCT-3'
CST1-5 (35) 5'-GCTACCCTGTAGACCCGTTTCTCACGGGACGCCTC-3'
CST1-6 (35) 5'-GAGCACCTGATCTAAGTCGTTCCGACGGACGAACC-3'
CST1-7 (35) 5'-GATGCCCTGACCGAGTCCCCATAGATGGACAAGCC-3'
CST1-8 (35) 5'-AAGTGCCTGGTCGAAATGCACACGTAGGACATTCA-3'
CST1-9 (100)
5'-G A T C A C C C G T G A G A A T T T T A C G G G T C T A C A C C T A C G T G T G T T T T C A T T T C G A C C A C C A T C T A T G G T T T T G G A C T C G G T C A C C G T C G G A A C T T T T G A C T T A-3'

TILE 2:
CST2-1 (28) 5'-GTTGGTCTGAATGTGGGTAGCCATTCGC-3'
CST2-2 (28) 5'-GACGCAAGAGGCGTGGTGCTCTCTGAGC-3'
CST2-3 (28) 5'-TTAGCCTGGTTCGTGGGCATCACCTTGA-3'
CST2-4 (28) 5'-TGCCGACGGCTTGTGGCACTTAGCGGAA-3'

TILE 3:
CST3-1 (28) 5'-TGCTGGATGAATGTGGGTAGCAACCTCT-3'
CST3-2 (28) 5'-AAGTGGCGAGGCGTGGTGCTCCAATAGT-3'
CST3-3 (28) 5'-ACCTAGAGGTTCGTGGGCATCTTGTGAC-3'
CST3-4 (28) 5'-GTCTGTAGGCTTGTGGCACTTTAGGATC-3'

TILE 4:
CST4-1 (28) 5'-TATCGGATGAATGTGGGTAGCGATCGCC-3'
CST4-2 (28) 5'-TAAGGACGAGGCGTGGTGCTCTCTTTCT-3'
CST4-3 (28) 5'-GCCTAATGGTTCGTGGGCATCTACGGAG-3'
CST4-4 (28) 5'-CACATAAGGCTTGTGGCACTTAGGGATT-3'

LINKER 1
CSL1-1 (14) 5'-GGCTTGTGGCACTT-3'
CSL1-2 (14) 5'-TCGACCACCATCGG-3'
CSL1-3 (28) 5'-GCTGTTCAAGTGCCTGGTCGAGCGAATG-3'
CSL1-4 (28) 5'-GACCAACCCGATGGACAAGCCGCACGAT-3'

LINKER 2

CSL2-3 (28) 5'-TCTAGGTAAGTGCCTGGTCGAGGCGATC-3'
CSL2-4 (28) 5'-TCCGATACCGATGGACAAGCCGTCACAA-3'

LINKER 3
CSL3-3 (28) 5'-GCTTCACAAGTGCCTGGTCGAACTATTG-3'
CSL3-4 (28) 5'-GCCACTTCCGATGGACAAGCCAGACTGC-3'
LINKER 4
CSL4-3 (28) 5'-GTCGGCAAAGTGCCTGGTCGAAGAAAGA-3'
CSL4-4 (28) 5'-GTCCTTACCGATGGACAAGCCTTCCGCT-3'

LINKER 5
CSL5-3 (28) 5'-AGGCTAAAAGTGCCTGGTCGAAGAGGTT-3'
CSL5-4 (28) 5'-TCCAGCACCGATGGACAAGCCTCAAGGT-3'

LINKER 6
CSL6-3 (28) 5'-TTATGTGAAGTGCCTGGTCGAGCTCAGA-3'
CSL6-4 (28) 5'-TTGCGTCCCGATGGACAAGCCAATCCCT-3'

Methods and Materials

a. DNA purification

The DNA oligos were designed using the SEQUIN program[10] and the sequences are listed in the supplemental material. Each DNA oligo was synthesized by Integrated DNA Technology, Inc. (www.idtdna.com) and were purified by denaturing polyacrylamide gel electrophoresis (PAGE). The DNA concentration was determined by absorption at 260 nm.

b. Formation of the DNA tiles and designed structures

The cross-shaped tiles and the linker tiles were formed separately by combining a stoichiometric quantity (1 μM) of the DNA oligos for each cross-shaped tiles and linker tiles in 1xTAE/Mg^{2+} buffer (40 mM Tris-base, 20 mM acetic acid, 2 mM EDTA and 12.5 mM magnesium acetate, pH 8.0) and then the mixtures were heated to 94^{o}C and cooled down at a rate of 0.8 ^{o}C per minutes to 30^{o}C using a PCR machine (Eppendorf). The three designs were formed by bringing the four 4x4 tiles (T1, T2, T3 and T4) together with linker tiles (L1, L2, L3 and L4) for the square, or L2, L3, and L5 for the chair and L1, L2 and L6 for the line. The right amount of cross-shaped tiles and the linkers were combined and heated to 33^{o}C and cooled down at 0.1^{o}C per minutes to 25^{o}C.

c. AFM imaging

For AFM imaging, the freshly cleaved mica was pretreated with 3 μL 1 mM $NiCl_2$, 3 μL of a 15x diluted sample was spotted onto the mica for 5 min. and 400 μL of 1xTAE/Mg^{2+} buffer was placed onto the mica. AFM images were obtained using a Molecular Imaging PicoSPM II controller (www.molec.com) by tapping mode with NP-S tips (Veeco Inc.).