Supporting Online Information for

Self-Assembled DNA Crystals: The Impact on Resolution of 5'-Phosphates and the DNA Source

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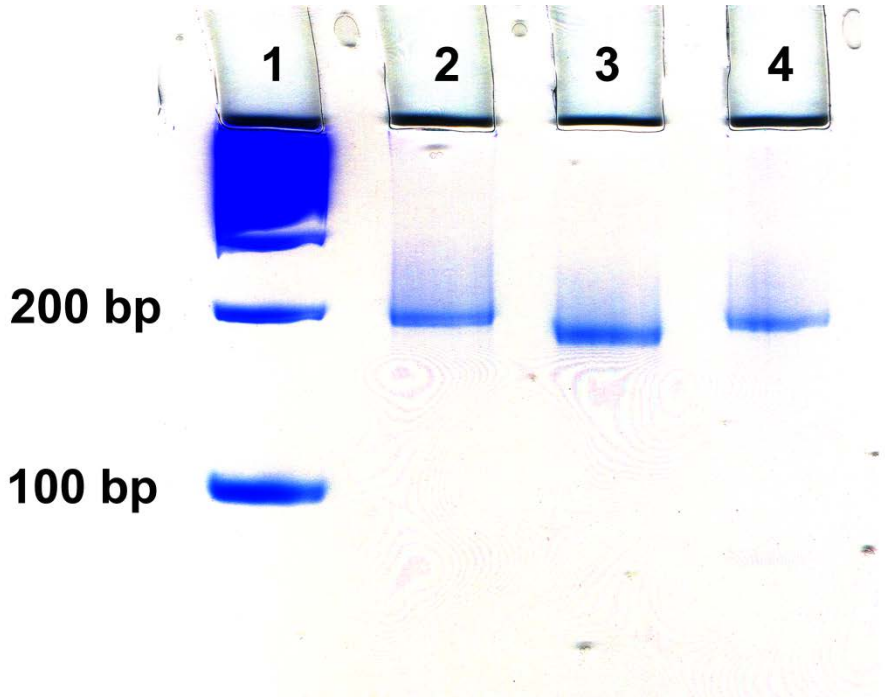

Figure S1. Gel containing the purified PCR products for strand 1, 2 and 3. This is an 8% nondenaturing gel run at 4 ^{o}C in TAE buffer with 10 mM Mg^{2+}. Lane 1 contains 100 bp DNA ladder. Lane 2 contains the PCR product (192 bp) for strand 1. Lane 3 contains the PCR product (172 bp) for strand 2. Lane 4 contains the PCR product (188 bp) for strand 3.

S2. Restriction enzymes used.

The cutting sites for the six selected restriction enzymes:

Pst I: CTGCA]G

G[ACGTC

Bgl II: A[GATCT

TCTAG]A

Hae II: AGCGC]T

T[CGCGA

Afl II: C[TTAAG

GAATT]C

Nla III: CATG]

[GTAC

Xba I: T[CTAGA

AGATC]T

The sequences for the desired DNA strands used to self-assemble the DNA triangle crystals:

Strand 1: (Pst I) GAGCAGCCTGTACGGACATCA (Bgl II)	NEBuffer 3 + BSA
Strand 2: (Hae II) TCTGATGTGGCTGC (Afl II)	NEBuffer 4 + BSA
Strand 3: (Nla III) ACACCGTACACCGTACACCGT (Xba I)	NEBuffer 4 + BSA

The remaining base after restriction matches the 5' or 3' end's sequence of the desired DNA strands and the buffer conditions for the double digestions also are indicated.

S3. Constructs of PCR templates and the restricted fragments:

BGST-1:

5'-
AGTGGGGACTGGAGAAAAAAGACCGTTCTGCA[GAGCAGCCTGTACGGACA

TCA]GATCTTTGCCACTGCA[GAGCAGCCTGTACGGACATCA]GATCTACTGA
CTGCA[GAGCAGCCTGTACGGACATCA]GATCTTCAGTCTGCA[GAGCAGCCT
GTACGGACATCA]GATCTTGTCTGTCATATACCTCGCAACCCT-3’

BGST-2:

5’-
AGTGGGGACTGGAGAAAAAAGACCGTTAGCGC[TCTGATGTGGCTGC]TTAA
GTTGCCAACAGCGC[TCTGATGTGGCTGC]TTAAGGACACTGAAGCGC[TCTG
ATGTGGCTGC]TTAAGTCAGTTGCAGCGC[TCTGATGTGGCTGC]TTAAGTGT
CTGTCATATACCTCGCAACCCT -3’

BGST-3:

5’-
AGTGGGGACTGGAGAAAAAAGACCGTTCATG[ACACCGTACACCGTACACC
GT]CTAGATTGCCACATG[ACACCGTACACCGTACACCGT]CTAGAACTGACA
TG[ACACCGTACACCGTACACCGT]CTAGATCAGTCATG[ACACCGTACACCG
TACACCGT]CTAGATGTCTGTCATATACCTCGCAACCCT -3’

The colors of the sequences match the schematic drawing in Figure 1b. Red sections are primer regions, blue sections are strands to be PCR-generated, the left bracket [and the right bracket] indicate the cutting positions for the restriction enzymes. After the PCR product for strand 1 was digested by the restriction enzymes, the lengths of the fragments in the Watson strand are 32-mer, 30-mer, 21-mer, 16-mer and 15-mer and the lengths of the fragments in its complement, the Crick strand, are 29-mer, 28-mer, 26-mer, 8-mer and 7-mer. Our desired 21-mer strand 1 is unique from other unwanted fragments and could be purified by the denaturing gels easily. The length of the fragments in both the Watson and the Crick strands of the PCR product for strand 2 are 32-mer, 30-mer, 18-mer, 14-mer, 28-mer, 26-mer, 22-mer, and 10-mer. Our desired 14-mer strand 2 is unique. The length of the fragments in both the Watson and the Crick strands of the PCR product for strand 3 are 31-mer, 30-mer, 21-mer, 15-mer, 14-mer, 29-mer, 27-mer, 26-mer, 7-mer and 6-mer. Our desired 21-mer strand 3 is also unique.

S4. The sequences of PCR templates and primers.

In order to make sure that all of our desired strands for the DNA crystal self-assembling are generated by PCR, we synthesized the complementary

sequences of the desired sequences as the templates for PCR. The sequences of the PCR templates and primers are the following:

BGST-RC-1 (192-mer):

AGGGTTGCGAGGTATATGACAGACAAGATCTGATGTCCGTACAGGCTGCTC
TGCAGACTGAAGATCTGATGTCCGTACAGGCTGCTCTGCAGTCAGTAGATC
TGATGTCCGTACAGGCTGCTCTGCAGTGGCAAAGATCTGATGTCCGTACAG
GCTGCTCTGCAGAACGGTCTTTTTTCTCCAGTCCCCACT

BGST-RC-2 (172-mer):

AGGGTTGCGAGGTATATGACAGACACTTAAGCAGCCACATCAGAGCGCTGC
AACTGACTTAAGCAGCCACATCAGAGCGCTTCAGTGTCCTTAAGCAGCCAC
ATCAGAGCGCTGTTGGCAACTTAAGCAGCCACATCAGAGCGCTAACGGTCT
TTTTTCTCCAGTCCCCACT

BGST-RC-3 (188-mer):

AGGGTTGCGAGGTATATGACAGACATCTAGACGGTGTACGGTGTACGGTGT
CATGACTGATCTAGACGGTGTACGGTGTACGGTGTCATGTCAGTTCTAGAC
GGTGTACGGTGTACGGTGTCATGTGGCAATCTAGACGGTGTACGGTGTACG
GTGTCATGAACGGTCTTTTTTCTCCAGTCCCCACT

Sequences of PCR primers:

BGST-Forward: AGGGTTGCGAGGTATATGAC

BGST-Backward: AGTGGGGACTGGAGAAAAAA