### **Electronic Supplementary Information**

# Fabrication of Zigzag and Folded DNA nanostructures

# by an Angle Control Scheme

Junwye Lee<sup>1</sup>, Rashid Amin<sup>1</sup>, Byeonghoon Kim<sup>1</sup>, Soyeon Kim<sup>1</sup>, Chang-Won Lee<sup>2</sup>, Jong Min Kim<sup>2</sup>, Thomas H. LaBean<sup>3</sup> and Sung Ha Park<sup>\*1</sup>

<sup>1</sup> Sungkyunkwan Advanced Institute of Nanotechnology (SAINT) and Department of Physics, Sungkyunkwan University, Suwon 440-746, Korea.
 <sup>2</sup> Frontier Research Laboratory, Samsung Advanced Institute of Technology (SAIT), Yongin 446-712, Korea.
 <sup>3</sup> Departments of Computer Science, Chemistry, and Biomedical Engineering, Duke University, Durham, NC 27708, USA.

**Table ESI1.** All possible helical angles by angle control scheme (ACS). When a number of nucleotides are added or removed, adjacent DNA tile is rotated with an angle of  $34.3^{\circ} \times N$  in clockwise or counter-clockwise directions.

Number of manipulated nucleotides	Angle	Number of manipulated nucleotides	Angle
1	34.3°	11	17.3°
2	68.6°	12	51.6°
3	102.9°	13	85.9°
4	137.2°	14	120.2°
5	171.5°	15	154.5°
6	205.8°	16	188.8°
7	240.1°	17	223.1°
8	274.4°	18	257.4°
9	308.7°	19	291.7°
10	343°	20	326°

# Fig. ESI1. DNA base sequence maps of plane lattice (PL).

		d' GATG TGCTA CTAC	GCGT CCGT TTAC AGTC GAGG CGCA GGCA AATG TCAG CTCC	ACGG ATCG b' TGCC TAGC CATAC
PL-A2 a GCGG TTGT AGTGA CGCC AACA	CCAA CTTA GGTC TAGG GGTT GAAT CCAG ATCC	ACAT CTCG C TGATC GTAA TGTA GAGC ACTAG C CATT	GACC TGCG GTAT AGCA CTGG ACGC CATA TCTA TCGT	GGCT ACTG TCACT CCGA TGAC a' PL-B3
PL-A1 GTATG GGCA ATCC <sup>b</sup> CCGT TAGG	PL-A TGTA ACGT GCCG AACA ACAT TGCA CGGC TTGT	GGCA AGCG ACGAT		

#### Table ESI2. Strand reference table for PL.

PL	PL-A	PL-B
strand1	PL-A1	PL-B1
strand2	PL-A2	PL-B2
strand3	PL-A3	PL-B3
strand4	PL-A4	PL-B4

# Table ESI3. Strand details; number of bases and base sequences from 5' to 3' for PL.

Strands	Number of Bases	Base sequences (5' to 3')
PL-A1	26	GTATG GGCAATCCACAACCGC AGTGA
PL-A2	48	GCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTACA GGATTGCC
PL-A3	48	GCTCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGT CCGTTCGC
PL-A4	26	TAGCA GCGAACGGTGTAGAGC ACTAG
PL-B1	26	TGCTA CTACCGCACCAGAATG CTAGT
PL-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
PL-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
PL-B4	26	CATAC CGATCCGTGGCTACTG TCACT

## Table ESI4. Sticky-end table for PL.

	5' to 3'	3' to 5'	
а	AGTGA	TCACT	a'
b	GTATG	CATAC	b'
С	ACTAG	TGATC	с'
d	TAGCA	ATCGT	d'

## Fig. ESI2. DNA base sequence maps of zigzag lattice 1 (ZL1).



## Table ESI5. Strand reference table for ZL1.

ZL1	Z1-A	Z1-B
strand1	Z1-A1	Z1-B1
strand2	Z1-A2	Z1-B2
strand3	Z1-A3	Z1-B3
strand4	Z1-A4	Z1-B4

## Table ESI6. Strand details; number of bases and base sequences from 5' to 3' for ZL1.

Strands	Number of Bases	Base sequences (5' to 3')
Z1-A1	28	GAGTGA GGCAATCCACAACCGC ACTAGT
Z1-A2	48	GCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTACA GGATTGCC
Z1-A3	48	GCTCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGT CCGTTCGC
Z1-A4	24	TATG GCGAACGGTGTAGAGC TAGC
Z1-B1	24	CATA CTACCGCACCAGAATG GCTA
Z1-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
Z1-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
Z1-B4	28	TCACTC CGATCCGTGGCTACTG ACTAGT

#### Table ESI7. Sticky-end table for ZL1.

	5' to 3'	3' to 5'	
a	ACTAGT	TGATCA	a'
b	GAGTGA	CTCACT	b'
с	TAGC	ATCG	c'
d	TATG	ATAC	d'

## Fig. ESI3. DNA base sequence maps of ZL2.



## Table ESI8. Strand reference table for ZL2.

ZL2	Z2-A	Z2-B
strand1	Z2-A1	Z2-B1
strand2	Z2-A2	Z2-B2
strand3	Z2-A3	Z2-B3
strand4	Z2-A4	Z2-B4

#### Table ESI9. Strand details; number of bases and base sequences from 5' to 3' for ZL2.

Strands	Number of Bases	Base sequences (5' to 3')
Z2-A1	30	GAGTGA GGGCAATCCACAACCGCC ACTAGT
Z2-A2	50	GGCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTACA GGAT TGCCC
Z2-A3	46	CTCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGTCCGT TCG
Z2-A4	22	TATG CGAACGGTGTAGAG TAGC
Z2-B1	24	CATA CTACCGCACCAGAATG GCTA
Z2-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
Z2-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
Z2-B4	28	TCACTC CGATCCGTGGCTACTG ACTAGT

#### Table ESI10. Sticky-end table for ZL2.

	5' to 3'	3' to 5'	
a	ACTAGT	TGATCA	a'
b	GAGTGA	CTCACT	b'
с	TAGC	ATCG	c'
d	TATG	ATAC	d'



# Fig. ESI4. DNA base sequence maps of folded lattice 1 (FL1) and fabricating process.

## Table ESI11. Strand reference table for FL1.

FL2	F1-A	F1-B	F1-C
strand1	F1-A1	F1-B1	F1-C1
strand2	F1-A2	F1-B2	F1-C2
strand3	F1-A3	F1-B3	F1-C3
strand4	F1-A4	F1-B4	F1-C4

#### Table ESI12. Strand details; number of bases and base sequences from 5' to 3' for FL1.

Strands	Number of Bases	Base sequences (5' to 3')
F1-A1	26	CAAGA GCAATCCACAACCGCT ATGCA
F1-A2	48	AGCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTACA GGAT TGC
F1-A3	48	CTCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGTCCGT TCGCT
F1-A4	26	GTATG AGCGAACGGTGTAGAGAAGTC
F1-B1	26	CTAGA CTACCGCACCAGAATGGACTT
F1-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
F1-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
F1-B4	26	TCTAG CGATCCGTGGCTACTG TGCAT
F1-C1	26	CATAC CTACCGCACCAGAATG GTTGA
F1-C2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
F1-C3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
F1-C4	26	TCTTG CGATCCGTGGCTACTG TCAAC

#### Table ESI13. Sticky-end table for FL1.

	5' to 3'	3' to 5'	
а	ATGCA	TACGT	a'
b	CAAGA	GTTCT	b'
С	AAGTC	TTCAG	c'
d	GTATG	CATAC	d'
e	CTAGA	GATCT	е'
f	GTTGA	CAACT	f'

# Fig. ESI5. DNA base sequence maps of FL2.



#### Table ESI14. Strand reference table for FL2.

FL2	F2-A	F2-B	F2-C
strand1	F2-A1	F2-B1	F2-C1
strand2	F2-A2	F2-B2	F2-C2
strand3	F2-A3	F2-B3	F2-C3
strand4	F2-A4	F2-B3	F2-C4

#### Table ESI15. Strand details; number of bases and base sequences from 5' to 3' for FL2.

Strands	Number of Bases	Base sequences (5' to 3')
F2-A1	26	CAAGA CTATCCACAACCGCTAATGCA
F2-A2	48	TAGCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTA CAGGATAG
F2-A3	48	TCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGTCC GTTCGCTC
F2-A4	26	GTATG GAGCGAACGGTGTAGA AAGTC
F2-B1	26	CTAGA CTACCGCACCAGAATG GACTT
F2-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
F2-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
F2-B3	26	TCTAG CGATCCGTGGCTACTGTGCAT
F2-C1	26	CATAC CTACCGCACCAGAATG GTTGA
F2-C2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
F2-C3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
F2-C4	26	TCTTG CGATCCGTGGCTACTG TCAAC

#### Table ESI16. Sticky-end table for FL2.

	5' to 3'	3' to 5'	
а	ATGCA	TACGT	a'
b	CAAGA	GTTCT	b'
с	AAGTC	TTCAG	c'
d	GTATG	CATAC	d'
е	CTAGA	GATCT	е'
f	GTTGA	CAACT	f'

## Fig. ESI6. DNA base sequence maps of open tube (OT).



#### Table ESI17. Strand reference table for OT.

ОТ	OT-A	ОТ-В
strand1	OT-A1	OT-B1
strand2	OT-A2	OT-B2
strand3	OT-A3	OT-B3
strand4	OT-A4	OT-B4

## Table ESI18. Strand details; number of bases and base sequences from 5' to 3' for OT.

Strands	Number of Bases	Base sequence (5' to 3')
OT-A1	26	CAAGA GCAATCCACAACCGCT ATGCA
OT-A2	48	AGCGGTTGTCCAACTTACCAGATCCACAAGCCGACGTTAC AGGATTGC
OT-A3	48	CTCTACAGGATCTGGTAAGTTGGTGTAACGTCGGCTTGTC CGTTCGCT
OT-A4	26	GTATG AGCGAACGGTGTAGAG TGGAA
OT-B1	26	CATAC CTACCGCACCAGAATG TTCCA
OT-B2	48	CATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCC TGCGGTAG
OT-B3	48	CAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGG ACGGATCG
OT-B4	26	TCTTG CGATCCGTGGCTACTG TGCAT

#### Table ESI19. Sticky-end table for OT.

	5' to 3'	3' to 5'	
a	CAAGA	GTTCT	a'
b	ATGCA	TACGT	b'
с	GTATG	CATAC	c'
d	TGGAA	ACCTT	d'

**Fig. ESI7.** AFM image analyses by Fourier transformation. a) AFM image of PL. b) Magnified AFM image of (a). c) Power spectrum of (b) and its calculated results by fast Fourier transform (FFT). d) Noise-filtered reconstructed image of (b). e-t) AFM images analyses of ZL1 (e-h), ZL2 (i-l), FL1 (m-p), FL2 (q-t). AFM images in the same column as the FFT processes (a-d) corresponding to those steps. The scale bars in all the AFM images are 50nm.

