Supporting Information

Backbone-Branched DNA Building Blocks for Facile Angular Control in Nanostructures

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Table S1. DNA sequences used in this study.

Name	Sequence	Source
DNA1	5'- ctc gat cgg tct ccA(2'-*O*-propargyl) gcc tgg -3'	synthesized
DNA2	5'-N_3- cac tag gcg cct agt g-3'	synthesized
bbDNA3	5'- ctc gat cgg tct ccA(2'-cac tag gcg cct agt g) gcc tgg -3'	CuAAC
DNA4	5'-cca ggc tgg aga ccg atc gag-3'	IDT
DNA5	5'-acc gat cga gcc agg ctg gag-3'	IDT
DNA6	5'-cca ggc tgg aga ccg atc gag cca ggc tgg aga ccg atc gag -3'	IDT
DNA7	5'-cgc tagU(2'- *O*-propargyl)cat gca gU(2'- *O*-propargyl)ccacgc-3' [a]	synthesized
bbDNA8	5'-cgc tagU(2'- cac tag gcg cct agt g)cat gca gU(2'- cac tag gcg cct agt g)cca cgc-3' [a]	CuAAC
DNA9	5'-gcg tgg act gca tga cta gcg -3'	IDT
DNA10	5'-cat gac tag cgg cgt gga cag -3'	IDT
DNA11	5'-gcg tgg act gca tga cta gcg gcg tgg act gca tga cta gcg -3'	IDT

[a] The branching residue base is 'U' rather than 't' (i.e., 5-methyl-U) as the 2'-*O*-propargyl necessitates a ribosyl (RNA) phosphoramidite.

Table S2. Dihedrals between backbone extensions at the 2'-atom in B-form helix based on 10.5 residues per turn (360°) or helical pitch of 34.29° per residue**.** For angles greater than 180°, Θ is calculated in the other direction (i.e., the smaller angle corresponding to 360-Θ). Thus for N = 7, Θ = 274.32° ≡ (360-274.32) = 85.68°

Number of residues *between* branches (N)	Dihedral between branches (Θ; degrees)
0	34.29
1	68.57
2	102.86
3	137.14
4	171.43
5	154.29
6	120
7	85.68
8	51.39
9	17.10
10	17.10
11	51.39
12	85.68
13	120
14	154.29
15	171.43
16	137.14
17	102.86
18	68.57
19	34.29
20	0

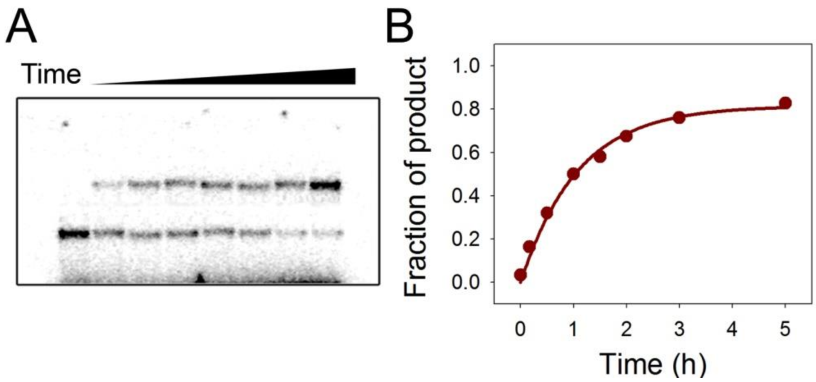

Figure S1. Optimizing timing for the click-branching reaction to obtain **bbDNA3**. **A.** A 20% polyacrylamide (8M urea) gel used to resolve click branching reaction mixtures over time. The **bbDNA3** (upper band) forms with disappearance of **DNA1** over time (t= 0 to 5hrs). **B.** Graph of **bbDNA3** formed over time as quantified from the gel, indicates maximal labeling is achieved in 3h with marginal improvement after 2 h.

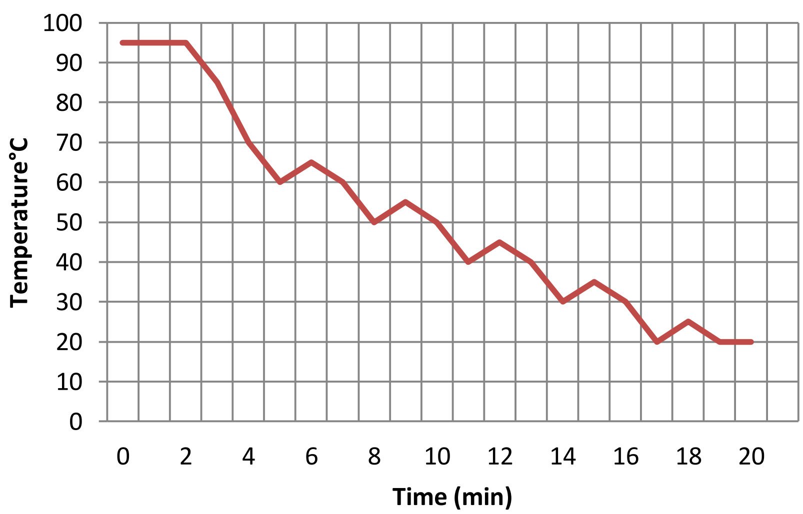

Figure S2. Time-temperature trace of the step-wise annealing for nanoassembly formation.

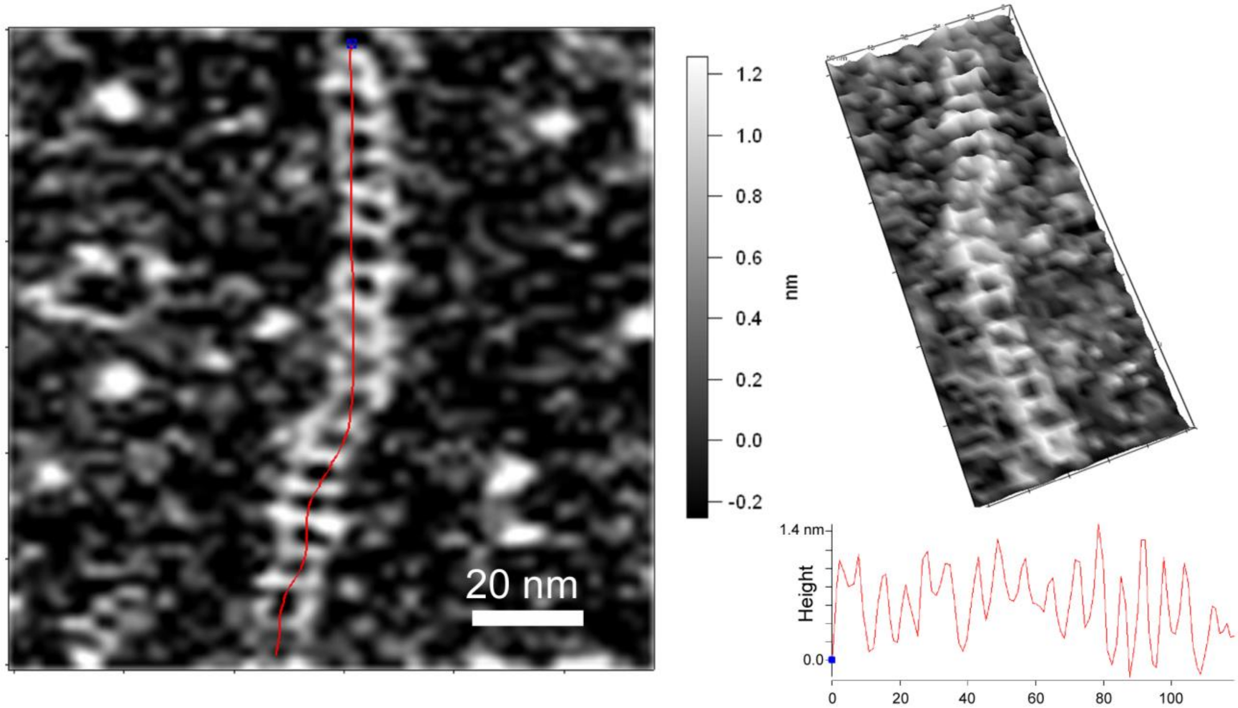

Figure S3. AFM scans of DNA nanoassembly based on co-planar branches and associated line profile

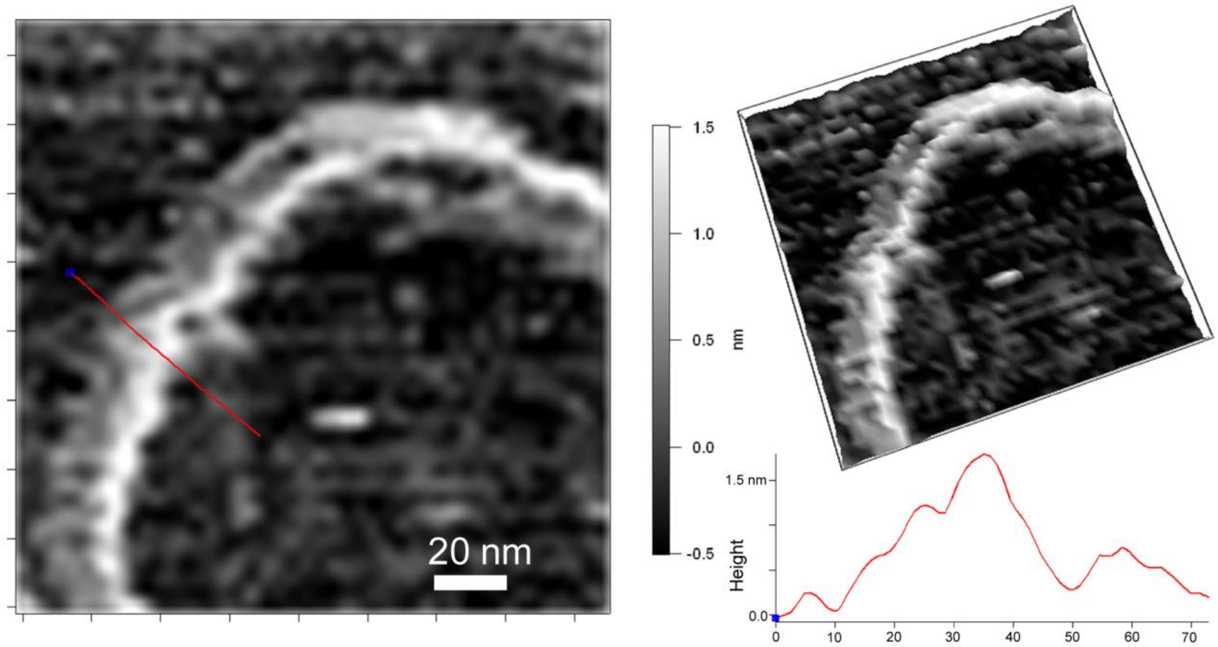

Figure S4. AFM scans of DNA nanoassembly based on dual perpendicular branches and associated line profile.