

## Supporting Information

### Purification of DNA nanoparticles using photocleavable biotin tethers

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**QUANTIFICATION ESTIMATE OF aPCR SCAFFOLD RECOVERY.** We performed 23 individual aPCR reactions of 50  $\mu$ L each by using the OneTaq enzyme to produce ssDNA scaffold at a length of 1,644 nucleotides from the M13mp18 phage template as previously described.<sup>1</sup> We purified 20 of these tubes by running them on a 75 mL, 1.2% low-melt agarose gel at 100 volts for 30 minutes and then recovered the ssDNA via the Zymoclean Gel DNA Recovery Kit (#D4008). From the remaining 3 unpurified tubes, a portion was run alongside known amounts of purified sample in a 40 mL, 1.2% high-melt agarose gel at 100 volts for up to 30 minutes. Finally, we measured the individual ssDNA band brightness with the ImageJ Rectangle & Measurements Tools to create a standard curve from the known purified samples and estimate the ssDNA concentration from the unpurified sample.

## DNA NANOSTRUCTURES DESIGN AND BIOTIN SITE SELECTION

**48hb Design.** The 48 helix bundle (48hb) was created using caDNAno2.<sup>2</sup> Structure file will be made available on nanobase.org and the cross-section helix layout (derived from caDNAno) is shown in **Figure S1**. The .JSON file was converted to a .PDB version using CanDo<sup>3</sup> and visualized in UCSF Chimera<sup>4</sup> to identify staple sites that would be PC-biotin modified. All sequences are available in **Table S2**.

**6hb and PB Design.** The other two structures were used using published works by Oktay et al.<sup>1</sup> Staples to be modified with PC-Biotin were identified in the same manner.

Choice of PC-Biotin staples were driven mainly by the accessibility of the staples in 3D atomic models. The staples chosen to tag with PC-Biotin were based on whether the 5' end of the staple strand was facing outward in the middle of a face or on the structure edge of 48hb. Five thymine residues were added to the beginning of the staple sequence to provide biotin/streptavidin binding flexibility.

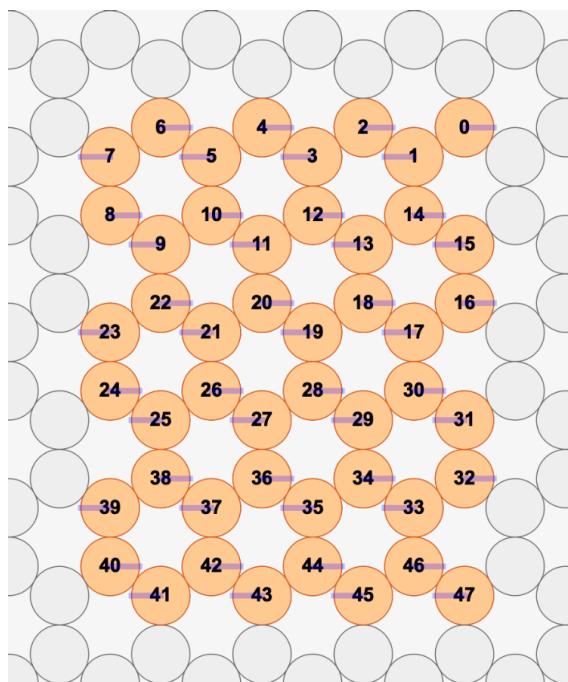
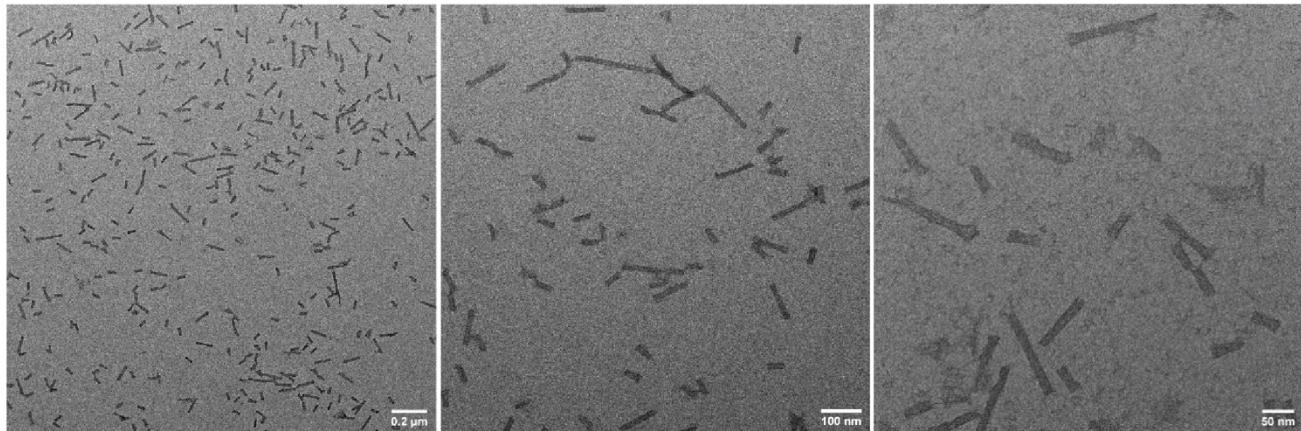


Figure S1: Cross sectional helix layout of the 48hb.



**Figure S2: Representative TEM images of crude 48hb.**

### Photocleavable biotin modified staples for the 48hb.

**Table S1: PC-Biotin staple sequences**

Structure	Name	Sequence (5' -> 3')
48hb	48hb_128_PCBio (corner)	/5PCBio/TTTTTTGCTCAGTACTGTATCAGCCAATCCTGTAGTAACAAACGAA
	48hb_106_PCBio (face)	/5PCBio/TTTTAATACCGATATACTTTCAAGGCCATTGAAA
6hb	6hb-1[2]-PCBio	/5PCBio/GTCAAAGGGCGAAAAACCGTCTA
	6hb-5[238]-PCBio	/5PCBio/TTTTGTCAAAGGGCGAAAAACCGTCTA
PB	PB-17-PCBio	/5PCBio/GATTTCAACCGCCTGCAACAGTGCCACGCT
	PB-24-PCBio	/5PCBio/AAAACAGAACATTGACGCTCAATCGTCTG
48hb-long linker	48hb_128_PCBioTE G (corner)	/5BiotinTEG/iSp18//iSpPC/TTTTTTGCTCAGTACTGTATCAGCCAATCC TGTAGTAAACAACGAA
	48hb_106_PCBio TEG (face)	/5BiotinTEG/iSp18//iSpPC/TTTTAATACCGATATACTTTCAAGGCCA TTCGAAA

**Table S2: 48hb staple sequences**

Name	Start	Sequence	Length
48hb_2	45[102]	CACCCGCCACAGAACCGTTGAGATCCTTATGCGAT	35
48hb_3	5[108]	GGGTCACAATTCAAGTCGACTCTAGCCAGGGTTGGAAAGTAGTTGTTG	50
48hb_4	15[46]	ATTACGTTATATTGAGCAGTTGAAAGCATAGAAGATTAGTCTTGGG	48
48hb_6	0[93]	GGACTCCAACGCAGGCAGAAATCCTATTAAAGTCATTGTTG	41
48hb_9	3[129]	TCACGGGAAACCTAACTCTGTGTGACCGGGTACCG	35
48hb_12	17[101]	GTAAGCTATTCCTGAGAGTCTGGAATTGTATTGTT	36
48hb_15	41[94]	GTTTATCAGCTCTCAAAAAAGAGGATTGTGTATCGTCAGGTAATAATAA	50
48hb_19	17[59]	AGTATGAATAAGATGGCAATTCCGTATTAAGACTTTCTGGTCTCAA	50
48hb_21	15[88]	CAGATTGAAACGTTCGAACGTGGTCAAAGGGCG	35
48hb_23	47[59]	CTGAAACATGACGTCATATCTCTGAAGAGGCCGCCACCAGCG	43

48hb_24	8[45]	ACATTCTGGCCTACCTACCTGCTGGTAATATGAGTAAAAGGT	43
48hb_28	2[80]	AGGAAGGGAAGAGCCGGCGACAACATAATATAATCCTGGGCTAT	43
48hb_32	45[60]	CAGCATGGCTAAATAGCCTAACGAGCTATTTGCA	35
48hb_36	2[59]	GAGCGGGCGCTGATTTAGTGCCGAATCAGATTGGAAGGGTTA	43
48hb_38	0[50]	GGCCCACACTAACGCCAGGGCGCACTATGGGGATTGTC	40
48hb_40	41[115]	GTGAATTCTTAATTTAAAACACATTGTAATCCCCAAAAGAACAAA	50
48hb_43	43[52]	ACCCTCAGAACCCACCAGCAATGAAGGGAGAAAGCCGTTCAATAGCAAC	49
48hb_44	0[113]	AGTCCACTATGGTGGTAGCGGTCTGGCGCGCATTAACTG	40
48hb_45	22[16]	GCAGGCACAGGTATTAATCAGTGAAATCCTGAGAAGT	37
48hb_47	31[46]	AAGTCAGATAATCGAGAATTACGAATGCAGCGAG	35
48hb_54	32[23]	AAAATAAGAAGGGTAATAGAATTGAAACGCATGATTAAAAATTCAAGA	48
48hb_57	40[24]	TAGCACCATTAAAAAGGGTATGGTTTCTTACCCGACAAACAT	43
48hb_59	0[72]	AAAAACCGTCCGGGAAAAAGCGAACGTATACTAACATTG	41
48hb_60	31[88]	TTGATACCACATTCAAGAAAGAACAAAATT	29
48hb_63	23[24]	CAAATATATTTATTACTAAAGCCAACAATAGAGAC	35
48hb_67	42[107]	AATTGCTTCCTTGCAGGGAGTTAAGCGAAAATGCCATATCGCGCGGA	49
48hb_69	5[45]	CATCTATCGGCATTGACGCTCAAAATAATGCAGGTTATATGTCA	50
48hb_71	32[44]	GAGAACGTCAAACACCCATAAGAGGTTACCAACAGT	35
48hb_74	46[44]	AGGAAGCCAGACCAGAGCAGAGCCTCGGTCAAGTAAATCAAAT	41
48hb_77	30[94]	AGGATGAATTAGGTTAATTCAACATGTAATCTTGACACCTCAGACCT	49
48hb_79	45[123]	CAACCGTACTAAATCAAAGAACGAGGCTCATTATACCAACATTATAGCA	49
48hb_80	23[45]	CATCTTCTGACAGAATAAGCTTAATATAAGTTTAGCAAGGCATTTGCC	49
48hb_81	40[45]	TAGAGCCAGCATTGAGGGTCACAATCGCTCAAGTAA	36
48hb_83	2[92]	CCCCAGCGATTGGAGAGGCAGGTTCGGATTAAATTCGTAATG	44
48hb_84	31[109]	TTTTCATCAGGAATTACAGAGGTAAATATAGCAAAGTTAATGCG	48
48hb_85	46[23]	TTTCAAACAAGACAGGACACCACCGCGTTGGAAACCACAG	41
48hb_89	40[87]	TTGCGGAATTATCACCGTCCTTAGCGCCTTAATTGTACTT	42
48hb_90	42[128]	TAAAAACAGCCGATATATTGGTCGAGGGTACATTAAATCAAAGCCTAT	49
48hb_92	41[60]	ATCTTCATCACGTAGAGATAGCCCTGTTAAATATCCAATTCAAATA	49
48hb_93	39[137]	AGAGCATAACTGATACCGATAGTAACAAACAGCGATTA	40
48hb_94	45[144]	TACTAGCCCGTCATTCACT	19
48hb_95	6[80]	AACATCACTGAATACTCATTAAATCAAACCTAAATCATACCTTTGAA	50
48hb_96	16[44]	GAAGATGAATAATCGCTAATTACTGCTCTGAGAACGAAACTATATT	48
48hb_98	15[25]	GGATGAGTAAAGAGCCGGTTATCCCAGCAGGCGG	35
48hb_99	8[87]	CGACGGCAGATTCAACCATAAAACATTAACCTATCATAGCAAC	43
48hb_100	6[59]	AGAACTCAAACACGCAAACACCAGCCACCTGATAACCTATT	43
48hb_101	0[30]	ACCCAAATCACTAAATCGTCACGCATGCGCCACGCCAGGGC	41
48hb_102	9[94]	TTCATTCGCAAATGGTACATGCTGTAGCTAACGTTAATCTT	42
48hb_103	24[129]	TGATAAGAGGTAAGTACGGTAGATTGGCGATCACTCCAGGAGTGAGCTG	49
48hb_106	23[74]	AATACCGATATACCTTTCAAGCGCCATTGAAA	34
48hb_112	2[38]	CAAGTGTAGCGGGAACCAAAGTTATTATCATATCAAATTA	43
48hb_121	4[122]	TCGTGCCAGCTCAGGGTATGTGAGTAAATCATTTAGAAAAGGGTAGAA	50
48hb_125	6[101]	CACAACATACGAGCCGGTAGTGCCAAGCTTGCGTTGTACCA	42

48hb_126	15[130]	GAAAAAAAGCCTTTAACATCAGCGCATCAGAT	35
48hb_127	6[114]	GCTGCCTAATCCAGCTTGGTGGCAAGGGTTGTACGTT	41
48hb_128	47[122]	TTGCTCAGTACTGTATCAGCCAATCCTGTAGTAAACAACGAA	43
48hb_132	31[67]	CCCCCGCGCTTATTGAAAAATTCAACAATAAT	35
48hb_135	16[107]	GTAAGATTCAACCCTCATAAATCGCAAAGAAATT	35
48hb_136	16[23]	TTTAGATTTTCATTCAAACATTAAATTAGATAGCTCAAATCCTT	48
48hb_138	45[82]	ACCGCCACCTCTAAAGTTGACCTTA	27
48hb_142	24[108]	GATGGCTTAGACATGTTGATACATGGCTGCCGCTCGTAAAGCTGA	49
48hb_150	5[66]	TAGCCCTGAGTAAATGGATTATTACATTGCCAAT	35
48hb_151	16[94]	AGAGATCTACAATCTGAGTAATGTGTT	28
48hb_156	5[24]	CACCCCAGAACAAACGCTCATGGAAAAACAGAGTTGAAGCTGATGTAGA	50
48hb_158	47[81]	GGCTGAGACTACCGCCACCCCTCTGAATAACTTATCCTGAA	41
48hb_161	33[17]	CCAATAAACAGCCGACTTGCGGGAGGGTATTCAATTAAACAATC	43
48hb_163	42[65]	CGTAAGTTGCACCGACTTGAGCCTTGACGCCACGGATGAGAATGGCA	49
48hb_164	4[101]	ATCGGCCAACGCGCGGAGTAGAAGCATAAAGTTGGTGCCGACC	43
48hb_166	42[86]	AAAAGGAGTCAGGTGGCCCTTTGTTAGCGTCCAATAAAGATT	44
48hb_168	45[31]	AATCCTCATTAAGTGTACTTGTTCCTAATTAGCCTTAAATC	43
48hb_170	32[73]	TCTTACCAACGAGCCTTATTAGACATAGCAAGTAAGCAAAAT	43
48hb_171	43[102]	TGAAGTTAGCTACTTAGTGGCTGAGCCAAAGTTGAGATAG	41
48hb_173	16[136]	TTCTAGCTGATGCCGGAGGCAAGGAATTATGACAATAATGAA	43
48hb_176	2[122]	GAGTTGCAGCATCCGAAACAGGAAGGCAAACATGCCGGAGAGG	43
48hb_1	35[39]	ATATGAACAACGCACTCTAGAAGGAACGTCACCTACCATCATATTCTG	49
48hb_5	10[128]	CGCGGTGCGGTAAGTTGGTAACGAGGATCCAATTGTTATCC	42
48hb_7	6[148]	GGTCATAGCTGTTCCACATTAACTCAGGAGTAA	34
48hb_8	8[155]	AGGGGGATGTGCTGCACGAATTCTG	25
48hb_10	26[44]	CCACAGTAGGACACCGGAATCATATAGTTAATGTAATTGGCTATAAAA	49
48hb_11	26[37]	TAAAGACGCTGTAATCAAAATCTAAGGAATGGCGCGTTGG	41
48hb_13	19[53]	AACCATCTAACAAAGCATTAACTGAAAATGATTGATGACCTATTATT	48
48hb_14	18[90]	AATGCAAGAAAGCCTCAGAGCGTAAACATACATAACCCTTCATC	43
48hb_16	27[95]	GGACGAAATCCGCGAGCAACAACCTAAACGAAAAAGGACGTTAGTAAA	49
48hb_17	35[81]	CCGAAACAGGAGACTAATGCAGATGTTAGACTGGACCTTTA	42
48hb_18	35[109]	AACCTGATAACAAAAGAAATACGTGACAGCATTGGAACGCTGAGGGAG	48
48hb_20	3[8]	CCCGCCTCTTAGACAACTACTGAGC	26
48hb_22	30[114]	AGAAAGAACTGTAGTAAATTGGCGATATTCCATAGGCCGG	42
48hb_25	10[58]	AACTTAACCGGGAGGCCGATTAATTGCTTAAATCAAGATT	42
48hb_26	19[8]	GAAGATTGTCTTTCCAAGTAATAT	26
48hb_27	35[8]	GAGATAGCAGGTGGCCTTGATATTCAAACGGGAAAT	37
48hb_29	18[58]	CCAAAGTATTAATCCTTAGCTTGTATATCAGGGCGAT	36
48hb_30	21[116]	GGGAGTCAGATCATTGATCATCGCGAGGCGCCAGACAGTCAGGGATAG	49
48hb_31	38[148]	AGACTTTGCAAACATAAAATCACAAATTCTAC	32
48hb_33	46[155]	ATATAAGTACGTAACACT	18
48hb_34	10[37]	CAGAGAGTCTTAGACAGGAACGGTGCTACAGTGAGGAATCAA	42
48hb_35	26[58]	GAGGTGAATTGAGTGACTGAACCAGTTGGCGACGAGCAAG	41

48hb_37	21[18]	AGCATTTCCTGAGAGTAAAATAGCGCTATGCGCGTAACCAC	44
48hb_39	18[37]	AGGATAATACTAATTTAAAGGGCGTAACCATC	35
48hb_41	13[109]	TGTGAGTAAAGGTCACTCCGGCACAAC	28
48hb_42	34[30]	AGAACGATTGGTAATATGCCCTGCCTATTGGAATAC	42
48hb_46	29[130]	ACACTTTGCTCAAATGACCGTGAGAACAGTTT	34
48hb_48	13[32]	TAGCGAATTACAGGTTCTTATCCGTTTGATGCCAGTTACA	42
48hb_49	21[130]	AAGCGAACGAGTGTCTGGAAGTTTGCTCCACCGAACATGAGGTGAC	49
48hb_50	26[121]	TATCGCGAGCTCATACATAGATGGACATTAAGTTTCAGA	41
48hb_51	37[46]	ATGTATTTGAGGGAAAGTAAATAATTGGGGTAGCGACAGA	42
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48hb_53	11[67]	ATAAAATACCGATAGCCCCTCACACGACCAGTCGTCTGAGA	41
48hb_55	13[53]	TAGAGTTACAATACAGTAAGCAAAATTAGTTGCGTCTTCCA	42
48hb_56	24[155]	TAGAGAGTACCTTAACATTCCATA	25
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48hb_61	21[53]	ATAGCATTAAACGCGGAACAAACAAGAAAACCACCAATGGAAAGCG	49
48hb_62	40[155]	AAACAACCATGCCAACGGCTTGAG	25
48hb_64	18[135]	AACACAGTCACGGAACAGTCAGGATGACGAGAACACCCGTAACAGAAC	49
48hb_65	34[148]	TTGAAAGAGAACCCCTCGAACTAAAATCACCAT	32
48hb_66	23[7]	ACGCGAGAGTATCAATACAATACCAG	27
48hb_68	42[155]	GAAAGGAACTGCGCCGAC	18
48hb_70	33[8]	TATCCCTCAGTGCCAGTGCCGTATAAACAGTTAAAGT	38
48hb_72	4[148]	TGCCCCGCTTCCAGTCCAGTGAGGCCAGCTCAATAGGTTTC	41
48hb_73	18[16]	TACATAGATTCAATTCTAAAGCAAGTTTTGGGT	37
48hb_75	11[95]	GTAAATTAAAGCAATAAAAGCAATAACCTGTTCATCAAACGTG	42
48hb_76	26[100]	TTGTAGCTATTAGCAAATGGATCAACCGTGCATCACGCTGGTTG	50
48hb_78	37[67]	ACAAAAGACAAAATTATTCAATTAAAGGTGGATATAAAAACAAGCC	45
48hb_82	26[65]	TTACGCCATATAAGCGTTAAACTAAATTAGGTTGGCGAACTGAACG	49
48hb_86	10[30]	GAGCAAATGAGTCGCTACAAGAAAAGAAACCAAGTACAGTC	42
48hb_87	9[109]	TGTTTCCCAGTCACGAATGCCGCCA	27
48hb_88	27[137]	AAAAAAAGTACAAGGGAATACAACGAGGAACCCATG	35
48hb_91	5[8]	TTATAACACCGCCTGCCACGCTTAGA	26
48hb_97	34[122]	CAGATAGTAAGTACAGGTGAGAAAGAAATTAAAGAGAATCGAT	43
48hb_104	0[148]	AGATAGGTTGAGTGTGTTCAAATCCCTGGCCCTGTT	40
48hb_105	22[148]	TTGATTCCCCGCTATTATCGGCTTGCCTG	32
48hb_107	47[94]	CAAGAGAAGGATTAGGATTTAGTACCTCATTCCCTCATATTCTTGAA	50
48hb_108	34[128]	GGTCAATCATAACGGAGTCATCTAACGACTCGACGGCTAC	42
48hb_109	25[94]	CAAACCTACGAAGGCACCATCGTCACCCCTCAGCAAGGCCGTCG	42
48hb_110	21[109]	TCAACCATTATAAAATGCAACTACATTTCGAGCTCGGGTAAATA	48
48hb_111	34[89]	AAGAAAAACCTGCTCCATGTGTAACGACTCAGAGCCAC	38
48hb_113	28[115]	TTGCCGAGGCACCAGCGATTACCCAGGAGGTAGCGGGTT	42
48hb_114	36[16]	TAAACGACGAAATCGCGATGAAACAAT	28
48hb_115	37[74]	TAAAGACTGTCTCAGAGCCTCGTCTTCCAGCTCC	35
48hb_116	21[8]	TTGAAAAAGGTAATGTCCAGCGGAAT	26

48hb_117	25[84]	CGAAAGATGCTGAATACCGTGTGATAAATTAAACAGAACGCTACA	46
48hb_118	7[8]	TTGCAAACCTGAAAATACGTAGACAAA	27
48hb_119	16[148]	GATATTCAACGTAAAATAGCATGT	25
48hb_120	37[31]	TCCTCTTATTAGGAACCGCCTCCCTCCGCCGCCCA	36
48hb_122	19[102]	AGCTATATTCACTAAAAAGCAAATGTTGATTAAAGAACGT	42
48hb_123	30[155]	TAATAAAACGTTTACCAAG	18
48hb_124	37[115]	CACTTCACGTGTATGGGATTTGCCATTCCAAGACGGTGTA	42
48hb_129	16[78]	GTTGGATTATACTCCCTTTATGCT	27
48hb_130	26[84]	AAGAGGGCGTCTGAGCAGTACACTAAACGGCGATTGGAAAC	42
48hb_131	26[72]	ATGTAGATAAAAGAAAATAGCTATCACCTCATTTACCGTAGA	43
48hb_133	28[155]	ATAAAAACCGAAAACGAG	18
48hb_134	10[84]	CAGGCAGCCTTGATAATCAGAGCGGGAGACGTGCTATCAATAACAA	47
48hb_137	10[23]	TCAACAATATATAGAACCCCTCTGCAGGAAAATATTACCGCCA	44
48hb_139	14[155]	TATGTACCCCTCAAAAATA	18
48hb_140	12[155]	GTCTGGCCTGCCAGTTG	18
48hb_141	39[8]	AAAGACCCATTAGGAAACGTACCAATCCATCTTACTGGCAATAA	45
48hb_143	19[123]	AACTAAAATGCTATTCAAAAATCGGCAAGTTGGAACAAG	43
48hb_144	34[16]	CGCAACGGGTTAAGAACATTGCGTGCACGTACCAGAAGGAGC	42
48hb_145	26[155]	CATAAAATCACCAACAGGT	18
48hb_146	37[137]	CCCGGAATTGCTTCAACAGTTCTACAAACCCGAACGTGA	40
48hb_147	18[148]	AAGCCTTAAACGCCACGGTGACAAAAGAAT	32
48hb_148	28[23]	AATCAATAAATAAAGTACAGTATAGAAAAAGCCTGTTAAAACCTAATC	49
48hb_149	39[24]	CATTCAACCGAAAATCACTCGATAGCAGCACCTAGCCCCTATT	43
48hb_152	2[148]	TTGCCCTTCACCGCCTTATAAAATTAAATCAGCGGTAATCCG	40
48hb_153	10[155]	CGACGACAGACGCCAGCT	18
48hb_154	17[8]	AAAGAAGCGAGGCGAACCTCCATAT	26
48hb_155	20[148]	TAGTAGCATTGCATCTCCTGTAACGGGCAAC	32
48hb_157	36[148]	GCGCGAAACCAGTTCAAAAATAGATACTTTG	32
48hb_159	1[8]	GTGCCGATTTGCGAACCAAAACAG	26
48hb_160	7[136]	AGCTAGGCATGCCCTTAATTCTGGTGGCATGGCTTTCTTT	43
48hb_162	18[65]	TTGTTGAATATATATGTATCAAACCGGCTTAATGGTTGA	42
48hb_165	37[39]	ACGGAAGGAATTCACTAGCATGTACAAAATGCAG	35
48hb_167	44[155]	CGTCACCAGAGCGGAGTG	18
48hb_169	21[32]	TTAGAGAATACACATGACCGAGGAGTTAAGCAGCATTATA	41
48hb_172	34[135]	GATAAGCTCGAATAGGCAGGCCGATAAGTGCCGTCGAGA	40
48hb_174	11[137]	CCGTAACATCCCCGTACGAGAGGCTATCATGACA	35
48hb_175	19[81]	ATGCGGATTCTATAATATTTGTTACTCCGTGGGAACCATTCCCTCGGAA	48
48hb_177	37[8]	AAAAGATTCTAAACCGGAACCAGAGCGGTTGAGACCCACATGAG	45
48hb_178	28[72]	CAATCATCGTGAAGCGCACAGAGACAGTAAGAAGTATTAAGA	42

## UV PHOTOCLEAVAGE SETUP USING STRING OF LIGHTS

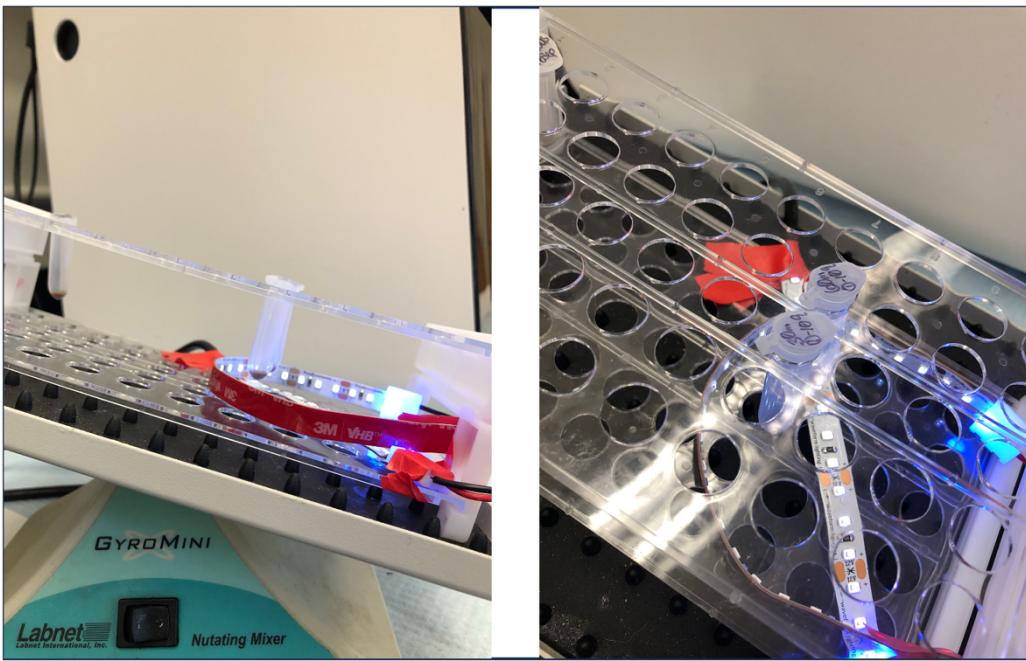
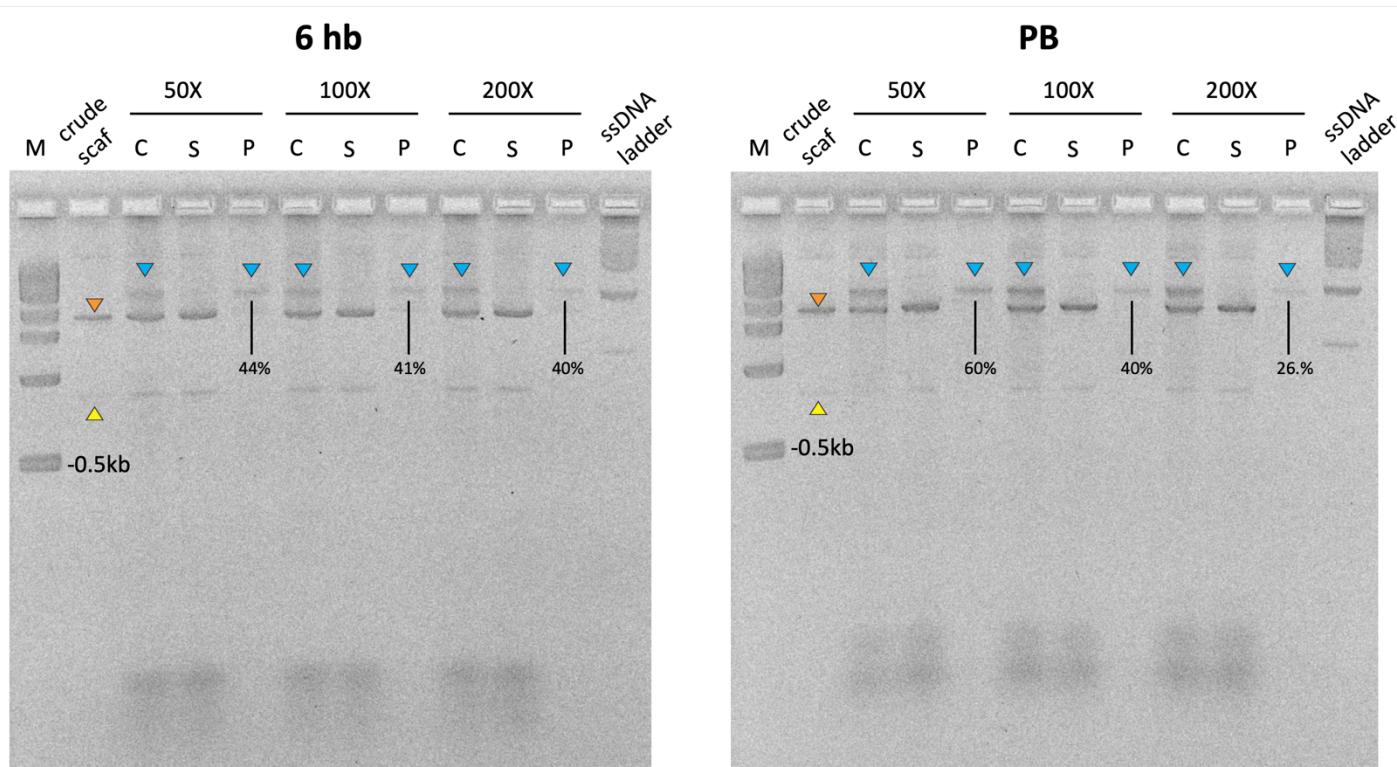
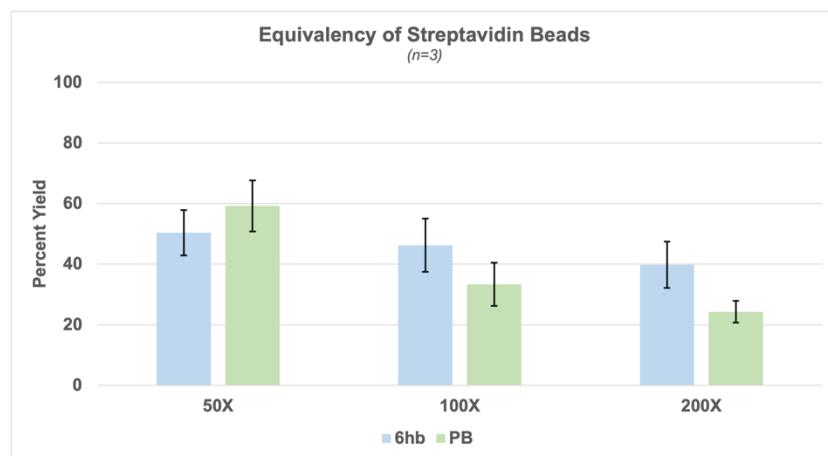


Figure S3: String of Lights for UV-photocleavage of the DNA NPs from the beads.

## EFFECT OF DIFFERENT BEAD AMOUNTS ON 6HB AND PB PURIFICATION

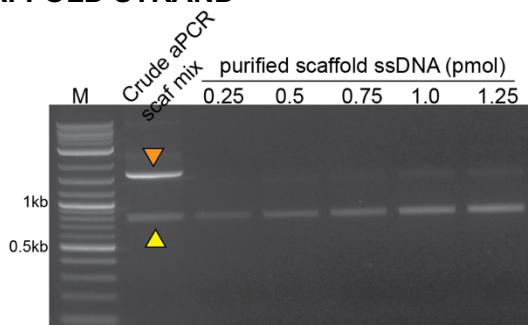


**Figure S4:** Agarose gel electropherogram testing different bead dosage on 6hb and PB purification. Color triangles represent: dsDNA byproduct (orange), ssDNA scaffold (yellow), and the formed PB NP (blue).



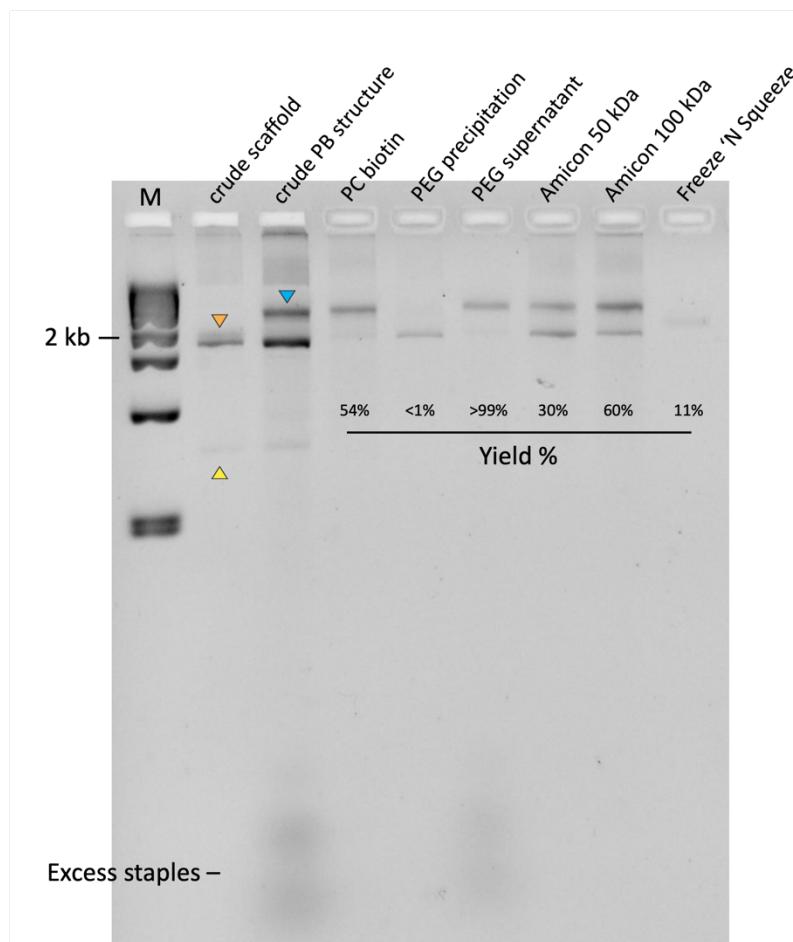
**Figure S5:** Yield of purification for 6hb and PB assembled using crude scaffold. Error bars represent standard deviation from the mean ( $n = 3$ ).

## YIELD OF aPCR-PURIFIED SCAFFOLD STRAND



**Figure S6: Estimation of scaffold concentration in crude aPCR mix using standardized pure scaffold series.** Yellow triangle indicates scaffold and orange triangle indicates dsDNA by-product of the aPCR.

## COMPARISON OF PC-BIOTIN PURIFICATION METHOD WITH EXISTING TECHNIQUES



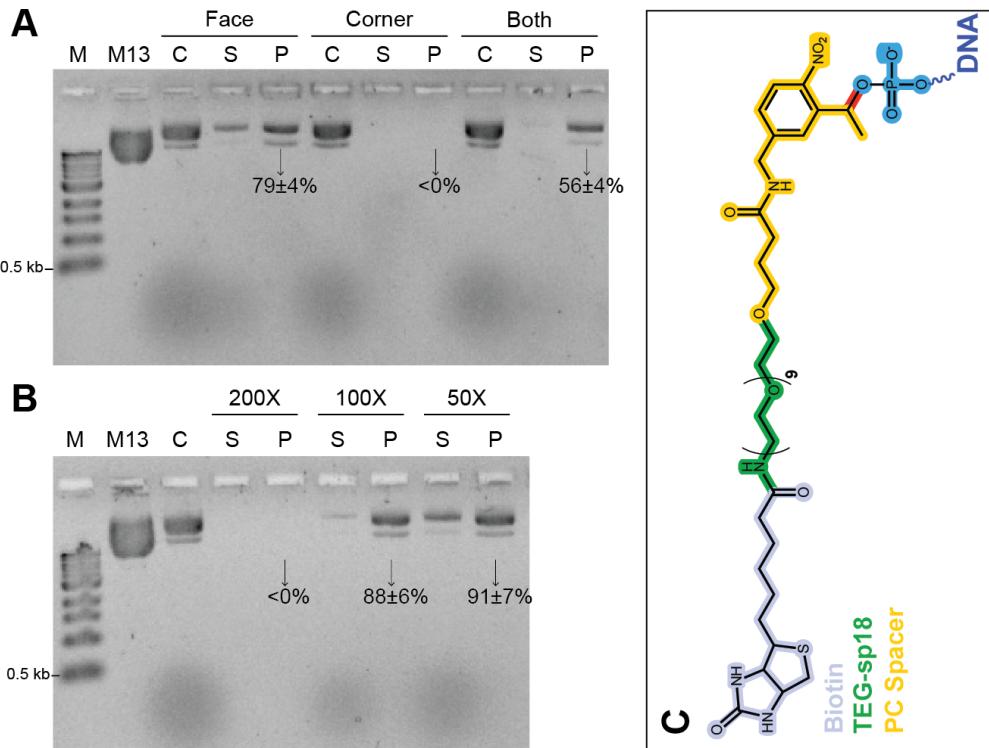
**Figure S7: Yield and quality of PB purification via commonly used techniques.** 2% agarose gel electropherogram showing PB purification using current method (PC biotin tag), PEG precipitation, two filter types of ultrafiltration, and gel extraction Freeze 'N Squeeze column. Color triangles represent: dsDNA byproduct (orange), ssDNA scaffold (yellow), and the formed PB NP (blue).

**Table S3: Broad differences between the PC-biotin based purification technique and other leading techniques.**

	Time	Quality	Requires concentration	Yield	Refs
<b>PC-Biotin</b>	4 hours	1 step custom scaffolded DNA NP purification	No	<90%*	<b>This work</b>
<b>Precipitation</b>	overnight	Cannot remove dsDNA aPCR byproduct; May be challenging to purify wireframe DNA NPs	No	>90%**	<b>5-6</b>
<b>Ultrafiltration</b>	2 hours	Cannot remove dsDNA aPCR byproduct	No	20-80%	<b>1, 7-9</b>
<b>Gel-extraction</b>	2-3 hours	Residual agarose particulates, variable yield	Yes	< 20%	<b>Figure S7</b>
<b>Biotin-strand displacement</b>	overnight	Theoretically 1 step, requires DSD staple extensions	Yes	> 90%	<b>9-10</b>

\*Longer PC-biotin linker with 50-fold beads. \*\*PEG precipitation on wireframe PB was 0% efficient but sufficient literature points to >90% efficacy of the technique to purify helix bundle DNA NPs. DSD = DNA strand displacement.

## 48HB PURIFICATION USING A LONGER PC-BIOTIN LINKER



**Figure S8: Purification of 48hb using BiotinTEG-sp18-PCspacer linker.** 1% agarose gel electropherograms representing the yield of 48hb purification using a longer PC-biotin (referred to as PC-biotin-L) tether staples. (A) Gel separation and purification yield of 48hb when using either face or corner or both PC-biotin-L staples simultaneously and 200X BBC. Surprisingly, the face PC-biotin-L tether (staple 106 in **Table S1**) resulted in highest yield ~80%, even higher than when using both staples together. (B) Gel separation and purification of 48 hb (corner PC-biotin-L only) with 200-, 100-, 50-fold excess magnetic beads per PC-biotin-L staple. In this case, fewer beads lead to the highest yield of 91%. Sample abbreviations M13: scaffold only, C: Crude 48hb, S: supernatant, P: Photocleaved/purified 48hb. (C) Chemical formula of the PC-biotin-L tether. IDT formula: 5'-BiotinTEG//sp18//PCspacer/. Standard deviation about the average yields were calculated from n = 3 samples.

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