# Addressing the Instability of DNA Nanostructures in Tissue Culture

**Authors**

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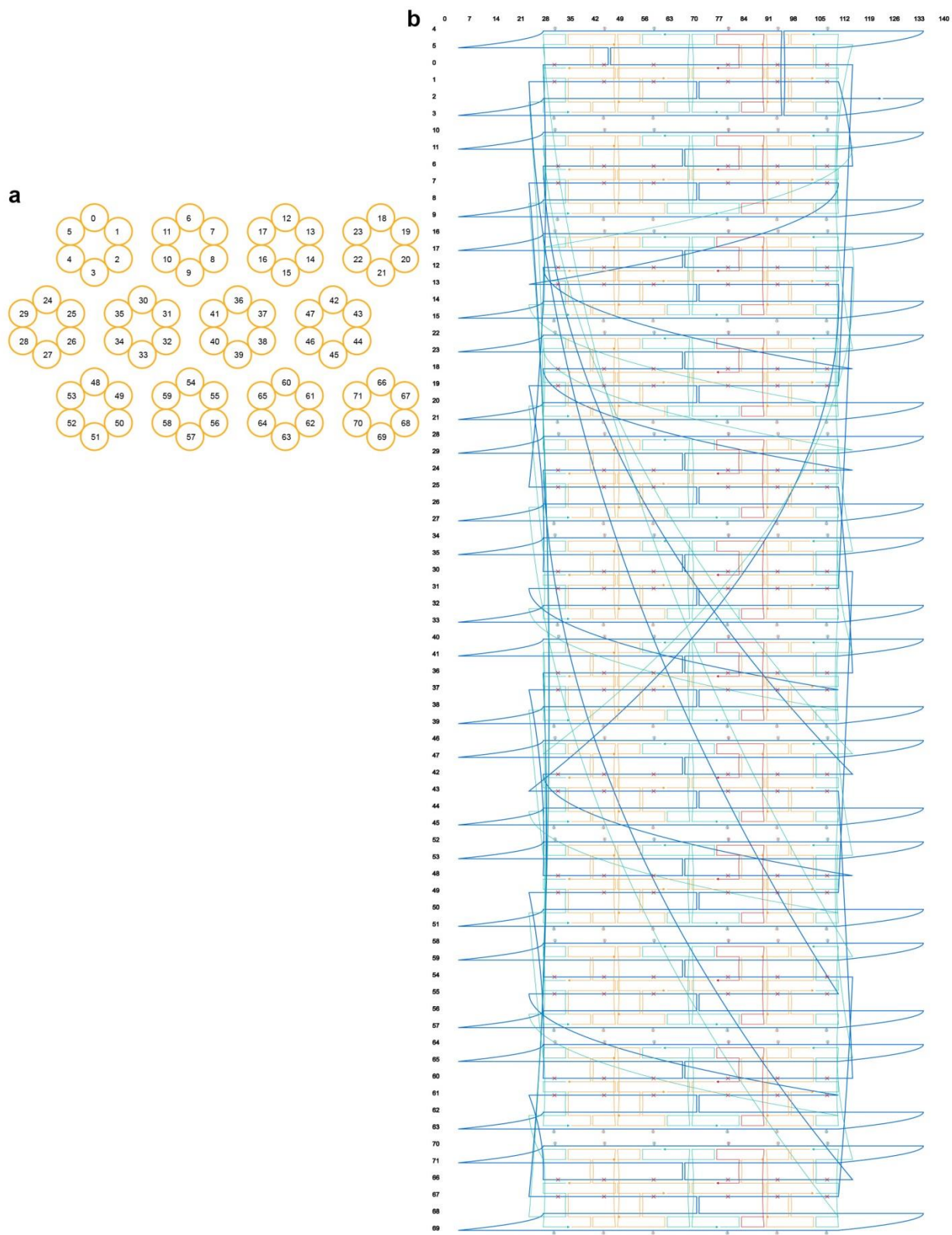
**Supporting Information Fig. 1. Schematic of the DNO design and scaffold routing. (a)** Organization of helices into six-helix bundles for the 12 struts. **(b)** Scaffold and staple strand organization.
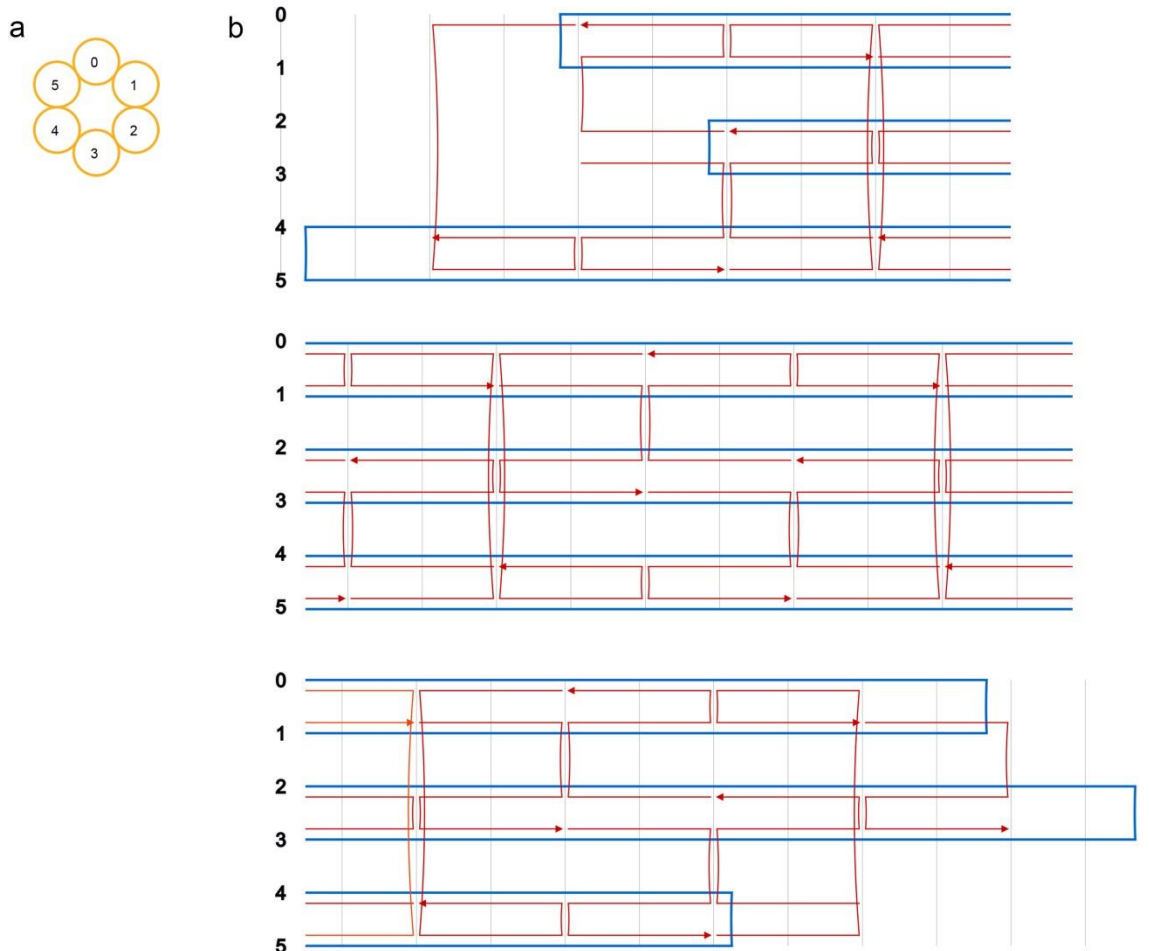
**Supporting Information Fig. 2. Schematic of the NT design and scaffold routing. (a)** Organization of helices into the six-helix bundle. **(b)** Representative scaffold and staple strand organization at the left (top), center (middle) and right (bottom) of the nanostructure. Note that the staple organization is repeated across the entire nanostructure length.
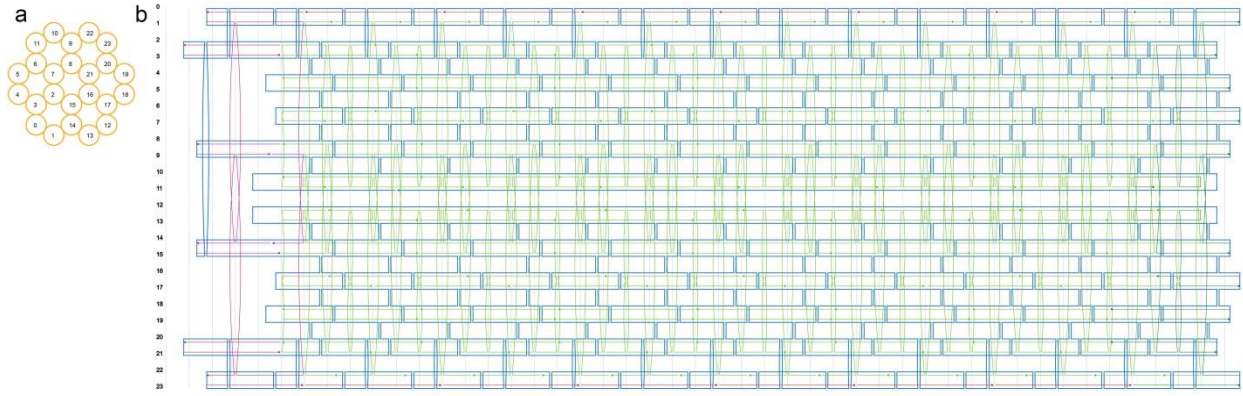
**Supporting Information Fig. 3. Schematic of the NR design and scaffold routing.** (a) Scaffold and staple strand organization. **(b)** Organization of helices into the 24-helix architecture.
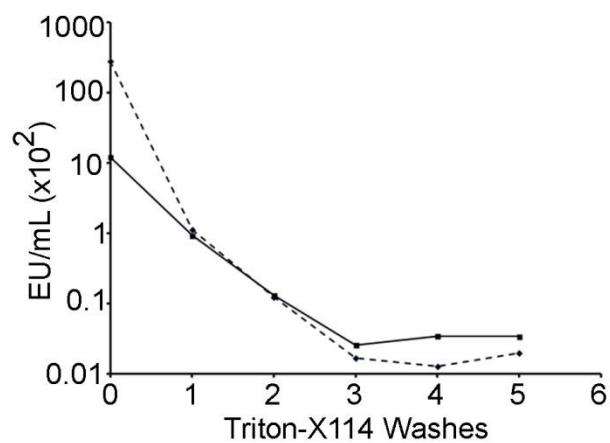
**Supporting Information Fig. S4. Removal of endotoxin from M13 scaffold stock and DNO nanostructure.** Endotoxin was removed from a 500 nM M13 single-stranded DNA stock (—), and a 10 nM DNO sample (- - -) using 5x sequentially scrubs with Triton X-114. Endotoxin levels were reduced to a maximum of 5 EU/mL in scaffold stocks prior to synthesis and purification of nanostructures.
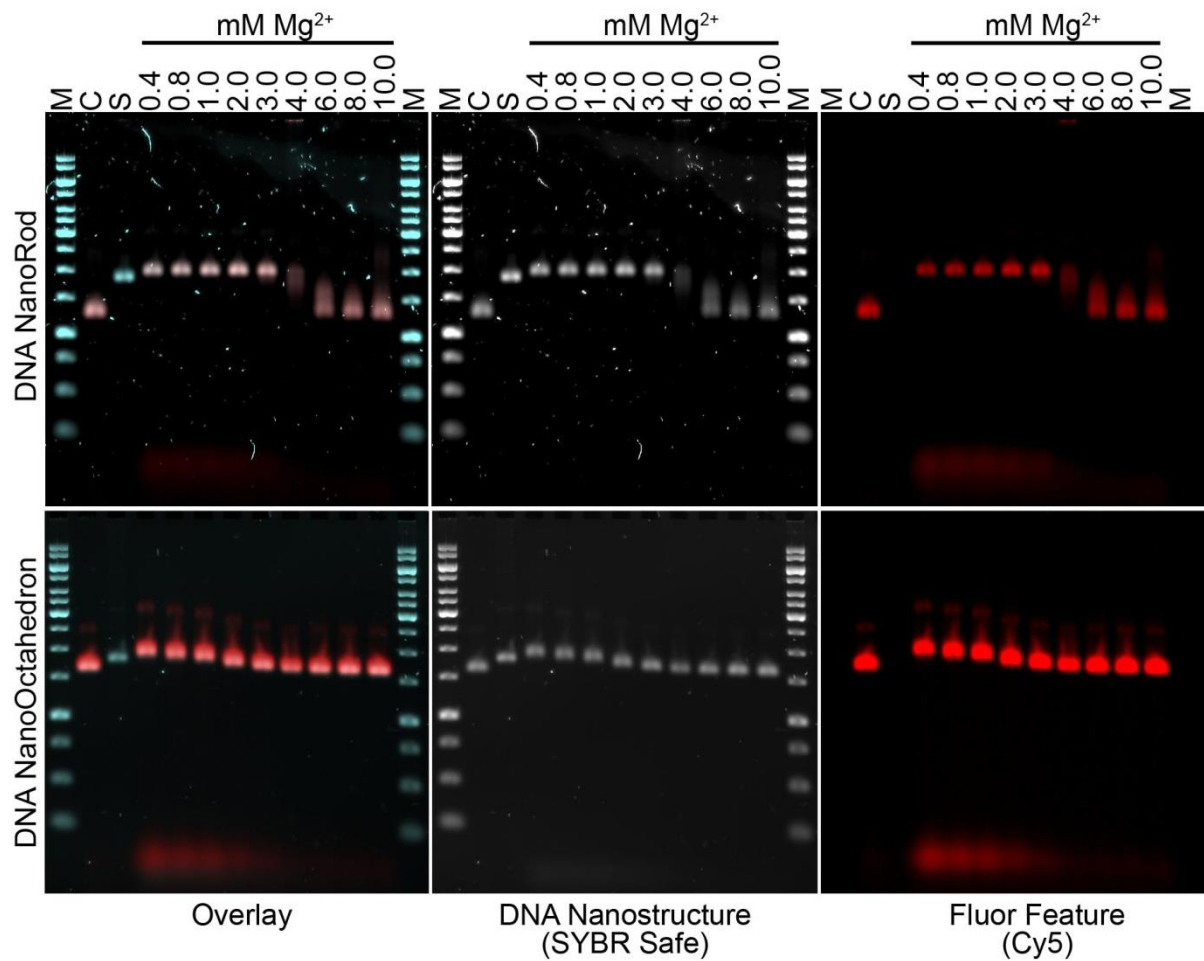
**Supporting Information Fig. 5**. **Nanostructure loss of molecular cargo during denautration in RPMI media.** A fluorescent Cy5-oligonucleotide feature (5'-GTGAGTTGTGGTAGATAATTT-3') was annealed to the DNO and NR and the products purified. These were then incubated in standard or $Mg^{2+}$-adjusted RPMI media at 37ºC for 24 hrs, and the products analyzed by AGE. Imaging of the gel in SYBR Safe and Cy5-fluoresence channels show a partial loss of the Cy5-labeled feature after incubation at $Mg^{2+}$ concentrations below ~6 mM.
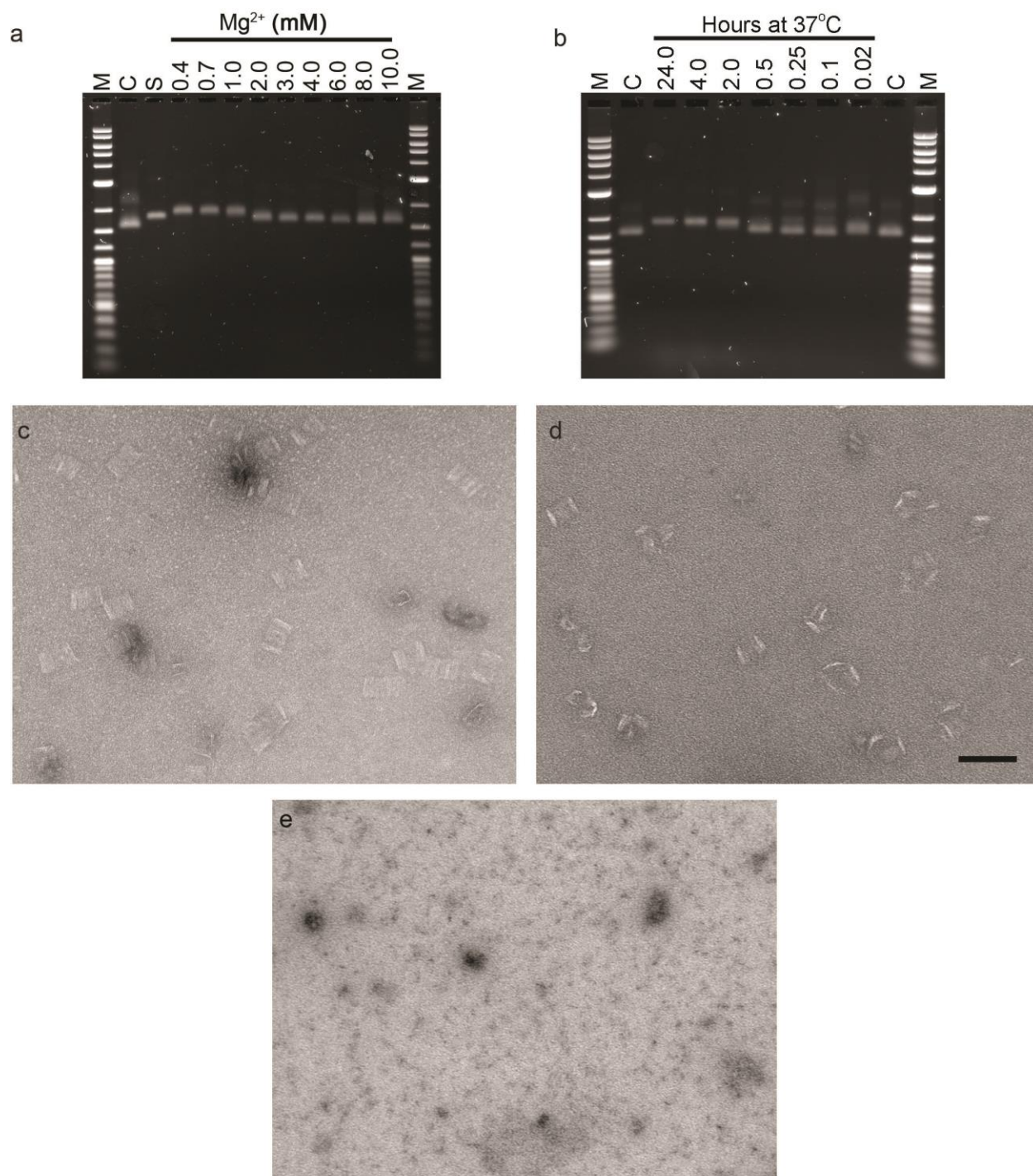
**Supporting Information Fig. 6. Sensitivity of the DNA nanorobot to denaturation in RPMI media.**

**(a)** AGE analysis of the nanorobot after incubation in RPMI media and a range of $Mg^{2+}$ concentrations for 24 hrs at 37°C. Relative to the controls, there is a shift in migration below ~2 mM $Mg^{2+}$. **(b)** This shift was apparent after 0.5 hrs of incubation at 37°C in RPMI media (0.4 mM $Mg^{2+}$). M = molecular weight

ladder, C = RPMI + 6 mM $Mg^{2+}$. **(c)** TEM imaging of the NanoRobot after incubation in 10 mM, and **(d)**

2 mM $Mg^{2+}$. In comparison to the 10 mM $Mg^{2+}$ sample, those incubated at 2 mM have a stressed

morphology, but were largely intact. **(e)** After incubation in standard RPMI with 0.4 mM $Mg^{2+}$, no intact

nanostructures were visible. Scale bar = 100 nm.
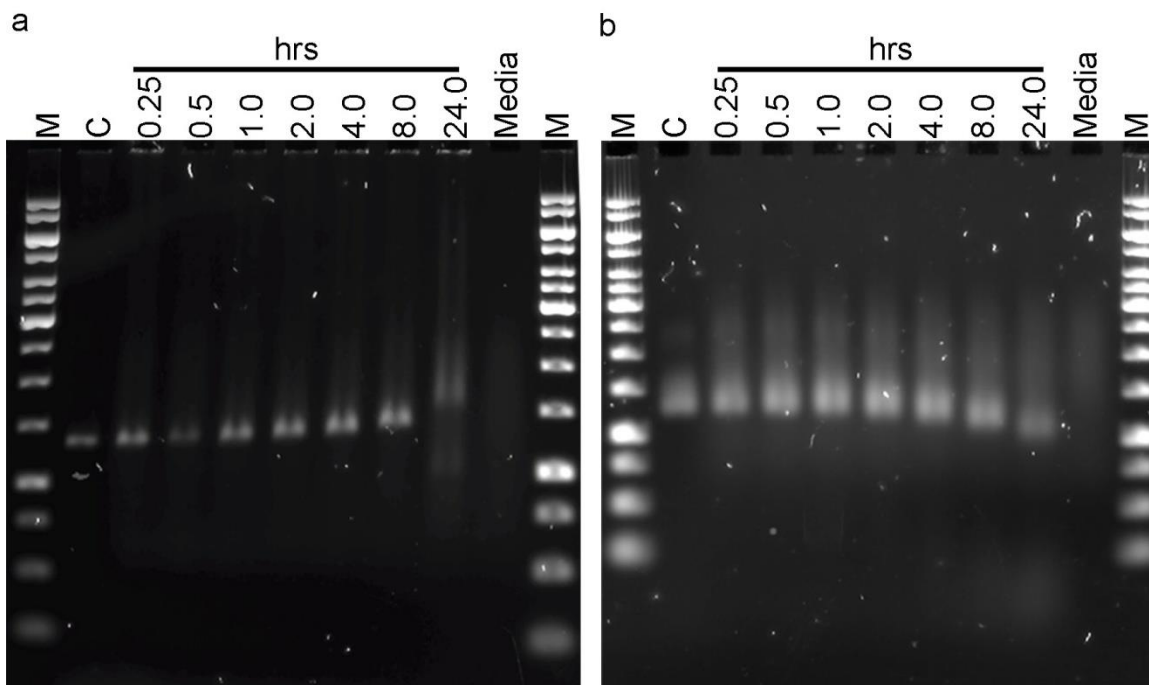
**Supporting Information Fig. 7. Time-dependent sensitivity of NT and NR nanostructures to digestion by nucleases in serum. (a)** NT and **(b)** NR were incubated at 37°C in RPMI + 6 mM $Mg^{2+}$ + 10% FBS for 0.25 – 24 hrs, and the products analyzed by AGE. Digestion of the nanostructures is indicated by increased smearing of the product bands. M = molecular weight ladder, C = TE + 10 mM $Mg^{2+}$.
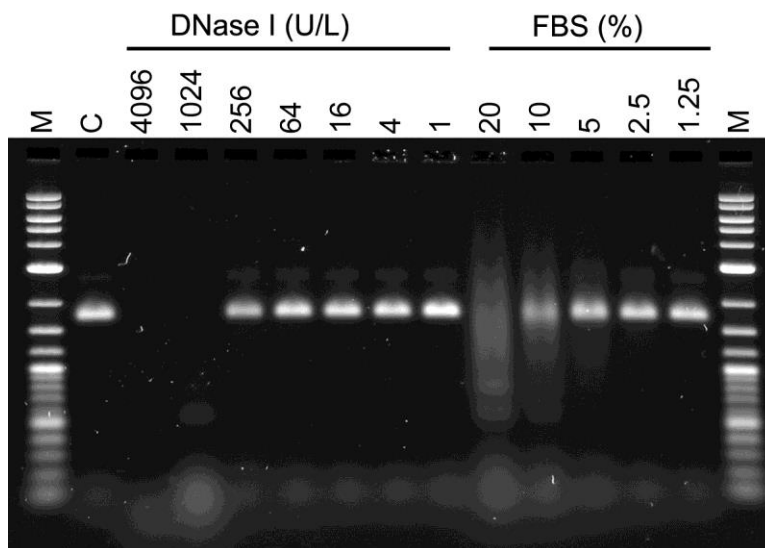
**Supporting Information Fig. 8. Digestion of the DNO nanostructure by DNase I *vs* RPMI + 6mM Mg$^{2+}$ + FBS.** 5 nM DNO was incubated at 37°C for 12 hrs in 6mM Mg$^{2+}$ RPMI with a range of added DNase I, or FBS, and the products were analyzed by AGE. In comparision to the control DNO lane, DNase I concentrations greater than 256 U/L resulted in complete loss of the product band, and FBS concentrations of 10 and 20% resulted in smearing, indicative of partially digested product. M = molecular weight marker, C = DNO in RPMI + 6 mM Mg$^{2+}$.
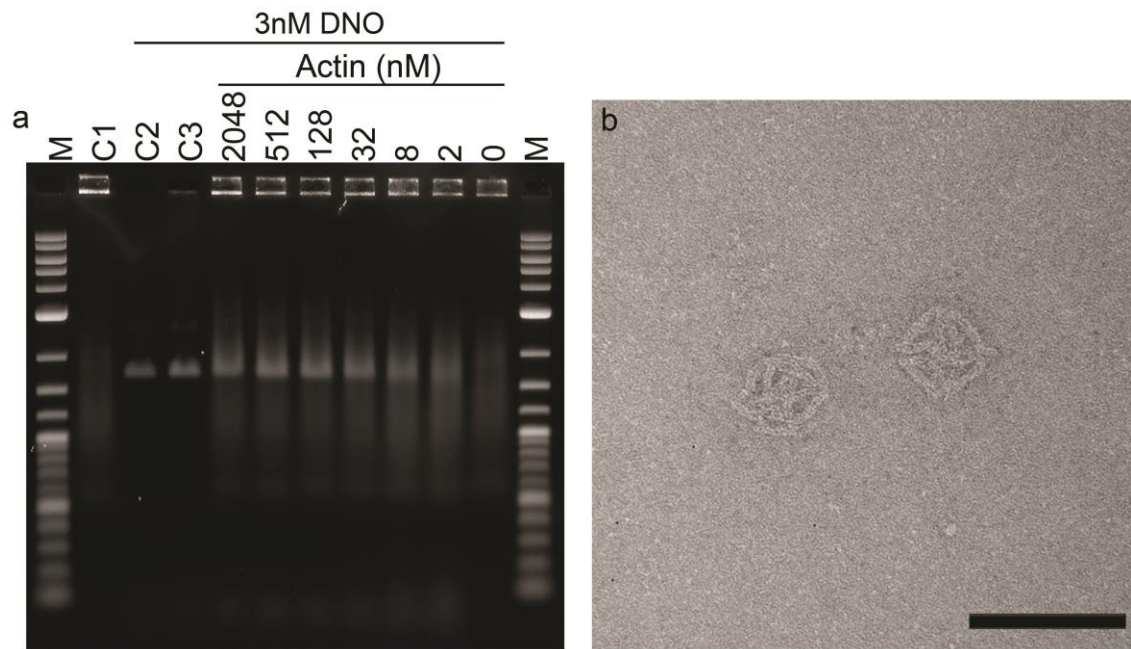
**Supporting Information Fig. 9. Concentration-dependent actin inhibition of DNO nuclease digestion. (a)** RPMI + 6 mM $Mg^{2+}$ + 10% FBS was prepared, and 0 – 2048 nM actin was added with 15 nM DNO. Following incubation for 24 hrs at 37°C, the products were analyzed by AGE to assess inhibition of DNO nuclease digestion. M = molecular weight marker, C1 = RPMI + 6mM $Mg^{2+}$ + 10% FBS + 1000 nM actin, C2 = RPMI + 6 mM $Mg^{2+}$ + DNO, C3 = RPMI + 6 mM $Mg^{2+}$ + DNO + 1000 nM actin. **(b)** TEM imaging showing intact DNO incubated in 250 nM actin. Scale bars = 100 nm.
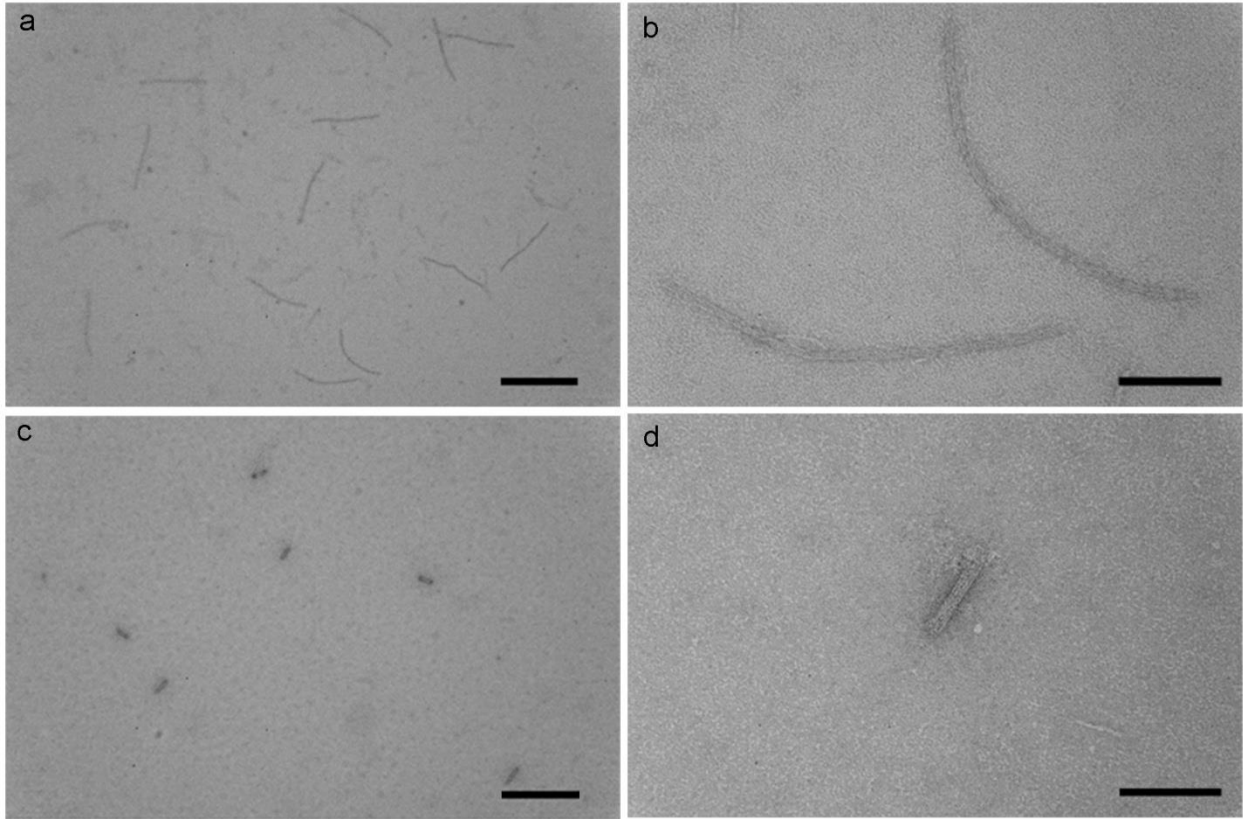
**Supporting Information Fig. 10.** TEM imaging of the **(a,b)** NT and **(c,d)** NR after incubation in RPMI + 6 mM Mg$^{2+}$ + 10% FBS + 200 mM actin at 37°C for 24 hrs. Scale bars = 500 nm (a,c) and 100 nm (b,d).
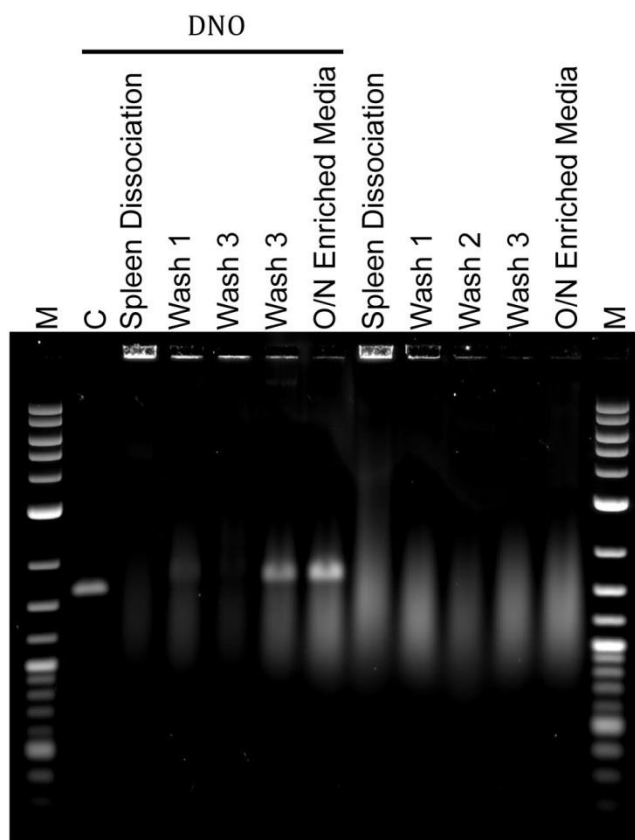
**Supporting Information Fig. 11. Analysis of nanostructure digestion by nucleases present in splenic tissue.** Immune cells were obtained from spleen dissociation. The cells were washed three times with large volumes of nuclease-free media to remove inherent nuclease activity by dilution. The cells were then incubated with media (RPMI + 10% heat-inactivated FBS) for 24 hrs. Aliquots of the dissociation supernatant, washes, and cell-enriched media were then incubated with 5 nM DNO for 24 hrs at 37°C, and the products were analyzed by AGE. The nanostructure remains intact after 3 washes, and nuclease activity is not regained by splenocyte enrichment. A slight shift in DNO migration is observed compared to the control, which may be due to an interaction with factors present in the media. The right side of the gel shows DNO-negative samples and smearing from heat-inactivation of the FBS. M = molecular weight marker, C = control DNO in TE + 10 mM $Mg^{2+}$.

**Supporting Table 1. Staple list for the DNO.**

| Number | Sequence | Length |
|---|---|---|
| 1 | CCAGCGAGTTACTTAGCCGACTAAAGACACTCATCAGCGCTAA | 43 |
| 2 | TTCTTAACAGGGAGTTAAATAGAAAGGAGCTTTCGATCATCAT | 43 |
| 3 | GAAAACACCTTGCTTCTGTCATCGGGAGTGAAACATTTTCCCA | 43 |
| 4 | CCTGCCTCGGCAAAATCCCTTATAAATCAAACAGTTGGTAATA | 43 |
| 5 | ACCGAACATATTGAATAACTTTTCTCAGAGCCGGAACCCGTAACAAA | 47 |
| 6 | CTCAGTGCCAGCAGAATGGTTTTAGCTACACTTAAATCCGCCACCCT | 47 |
| 7 | GTAGATATTTTGTTTTCACTTTTACAGACAACCAGTACATCAGATAT | 47 |
| 8 | GGAAACGCATCGGGTAAAATTTTAACCGATGCCGACAAATTATCATT | 47 |
| 9 | GGCTTTTTCATTGAATCCCTAGGAATACACCAAAATTTGACGA | 43 |
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| 11 | TTTAGTAAATCACCGAAAGTTTTGTATTGGAATCGGCCTCGAGCCAG | 47 |
| 12 | TATCAGATTTTTAAGAAAATTAACGTCAGTAATTGTTTGACCC | 43 |
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| 15 | ACCCATGATCTAAAGTTTTCGGAATAGGGCAAGCCTTTAGCGA | 43 |
| 16 | AGTACCTTTTTAAATATGCAGCAAAGCGAGGTCAGACGCGAGA | 43 |
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| 18 | TCCAGACATCCCATCCTAAAACAGTAGGGGTAAAGTCCAGTCG | 43 |
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| 21 | GCCCTGTATGCGACGCCAATTTTATCACCCGGGCGAAATAAAGAACG | 47 |
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| 42 | GCGAAACAATAGGAACGTTTTTTGCAAATCTATCAAACTAGCCAGCT | 47 |
| 43 | GAATGATTGACGTGTAGCGTTTTTACCGACTCATCTTCGAGCTTCAA | 47 |
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| 47 | TCTAAAGAAGGTTATCTAATAAAACATCGCAGCAACGGATTCT | 43 |

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**Supporting Table 2. Staple list for the 6-helix bundle NT.**

| Number | Sequence | Length |
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| 7 | ATCAGTGAGGCCACCTGATTGCCCTTCAGGAAGATCGCACTC | 42 |
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| 20 | CGGTGTACAGACCATTTAGACTGGATAGTGTAGGTAAAGATT | 42 |
| 21 | TAAGGGAACCGAACATTCATTGAATCCCTTTAGAACCCTCAT | 42 |
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| 23 | TTGTATCATCGCCTATTATAGTCAGAAGAGCTAAATCGGTTG | 42 |
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| 34 | CAGATAGCCGAACATGACCCTGTAATACAATCAAAAATCAGG | 42 |
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| 61 | CTTGAAAACATAGCCCACGCTGAGAGCCTCGGCCTTGCTGGT | 42 |
| 62 | CTTCTGTAAATCGTCCTTGCTGAACCTCTTAGTAATAACATC | 42 |
| 63 | GGAAACAGTACATATCAGTTGGCAAATCTGTCCATCACGCAA | 42 |
| 64 | TTAATTACATTTAATCTAAAATATCTTTGAAGTGTTTTTATA | 42 |
| 65 | TGAGCAAAGAAGACCGTCAATAGATAAATTAAAGGGATTTT | 42 |
| 66 | GTTACAAAATCGCGTTTACAAACAATTCCTTTCCTCGTTAGA | 42 |
| 67 | GGAGAAACAATAACACGTTATTAATTTTAGGGCGCGTACTAT | 42 |
| 68 | TTAACGTCAGATGAGGAACAAAGAAACCTGCGCGTAACCACC | 42 |
| 69 | GCACGTAAAACAGATCCTGATTATCAGAAAGGAGCGGGCGCT | 42 |
| 70 | TGAATAATGGAAGGTTGTTTGGATTATAGAAAGCCGGCGAAC | 42 |
| 71 | AGTAACAGTGCCCGGAAAGTATTAAGAGCGTTGGGAAGAAAA | 42 |
| 72 | AGGAGTGTACTGGTATTAGCGGGGTTTTCCTTATGCGATTTT | 42 |
| 73 | TTTACCGTTCCAGTGAGAGGGTTGATATGGCTTGAGATGGTT | 42 |
| 74 | TAAATCCTCATTAAGTACTCAGGAGGTTAGGCTTGCCCTGAC | 42 |
| 75 | TTGAGGCAGGTCAGCTCAGAACCGCCACATTACCCAAATCAA | 42 |
| 76 | ACCAGAACCACCACGATAGCAAGCCCAACTGACCTTCATCAA | 42 |
| 77 | CTCAGAACCGCCACTTCGTCACCAGTACAGAGGACAGATGAA | 42 |
| 78 | ACCAGAGCCACCACACAGCCCTCATAGTCAGACGGTCAATCA | 42 |
| 79 | CTTATTAGCGTTTGTTTCCAGACGTTAGAAATCCGCGACCTG | 42 |
| 80 | AGACTGTAGCGCGTTAAACAACTTTCAAAGTACAACGGAGAT | 42 |
| 81 | ACCGTAATCAGTAGAACAACTAAAGGAAACTCATCTTTGACC | 42 |
| 82 | AGCAAGGCCGGAAAAATCTCCAAAAAAAGCACCAACCTAAAA | 42 |
| 83 | GGAATTAGAGCCAGCGGTTTATCAGCTTAGTTTCCATTAAAC | 42 |

| | | |
|---|---|---|
| 84 | CATTAAAGGTGAATTGATACCGATAGTTCGGCTACAGAGGCT | 42 |
| 85 | TGAATATAATGCTGAACGAGGGTAGCAAGCGCCGACAATGAC | 42 |
| 86 | TGATAAGAGGTCATCTTTTTCATGAGGAGCTTTCGAGGTGAA | 42 |
| 87 | TCCAACAGGTCAGGATGCCACTACGAAGAGGCTCCAAAAGGA | 42 |
| 88 | GTTTTAATTCGAGCGAATACACTAAAACTTGCGAATAATAAT | 42 |
| 89 | TCAAAAGATTAAGCAAGCGCGAAACAACAGTTTCAGCGGAG | 42 |
| 90 | TCTTTACCCTGACTGATAAATTGTGTCGTAAATGAATTTTCT | 42 |
| 91 | AACAGTTCAGAAAAGCCGGAACGAGGCGTAGCGTAACGATCT | 42 |
| 92 | GAATCGTCATAAATTGACCAACTTTGAAAAACTACAACGCCT | 42 |
| 93 | GTAATAGTAAAATGGGCGCATAGGCTGGTAGGAACCCATGTA | 42 |
| 94 | AAATAGCGAGAGGCAGAACCGGATATTCCCTCAGAGCCACCA | 42 |
| 95 | ACACTATCATAACCTCATTCAGTGAATATAGTACCGCCACCC | 42 |
| 96 | GATACATAACGCCACGAGTAGTAAATTGAAGTATAGCCCGGA | 42 |
| 97 | TTCATCAGTTGAGAATCATTGTGAATTAGCTCAGTACCAGGC | 42 |
| 98 | ATAAAACGAACTAATATACCAGTCAGGAGCTGAGACTCCTCA | 42 |
| 99 | GGTGCCGTAAAGCATAGAGCTTGACGGGCTTTTCGGAACCTA | 42 |
| 100 | CACTACGTGAACCAAGGGAAGAAAGCGATGATGGCAATTCAT | 42 |
| 101 | CCAACGTCAAAGGGTGTAGCGGTCACGCACCAGAAGGAGCGG | 42 |
| 102 | TTCCAGTTTGGAACTAATGCGCCGCTACAAAGTTTGAGTAA | 42 |
| 103 | CTTATAAATCAAAAGCACGTATAACGTGGACAACTCGTATTA | 42 |
| 104 | CGAAAATCCTGTTTTAAACAGGAGGCCGTACATTTGAGGATT | 42 |
| 105 | GAGAGTTGCAGCAACGCCAGAATCCTGAAGGAGCACTAACAA | 42 |
| 106 | GAGACGGGCAACAGCGAGTAAAAGAGTCAACAGTTGAAAGGA | 42 |
| 107 | GTTTGCGTATTGGGCAATACTTCTTTGAAAATATCAAACCCT | 42 |
| 108 | GCCAGCTGCATTAAAAGAACTCAAACTAAGCAGCAAATGAAA | 42 |
| 109 | CGTTGCGCTCACTGTATTACCGCCAGCCGTCAGTATTAACAC | 42 |
| 110 | AAGCCTGGGGTGCCTACCTACATTTTGAACCGAACGAACCAC | 42 |
| 111 | TCACAATTCCACACCATTGGCAGATTCATAATGCGCGAACTG | 42 |
| 112 | AATCATGGTCATAGCATTCTGGCCAACAAATACGTGGCACAG | 42 |
| 113 | GCAAGTCCGCTAGCATCATAATTACTAGCAAAGAACGCGAGA | 42 |
| 114 | GCTTGCATGCCTGCATACAAATTCTTACATATAACTATATGT | 42 |
| 115 | GTTTTCCCAGTCACGCTTAATTGAGAATGTCTGAGAGACTAC | 42 |
| 116 | AGGGGGATGTGCTGTTTAGGCAGAGGCAAGACGCTGAGAAGA | 42 |
| 117 | GCGATCGGTGCGGGAGTACCGACAAAGTTTCCCTTAGAATC | 42 |
| 118 | AAAGCGCCATTCGCATAAACAACATGTTAGTGAATAACCTTG | 42 |
| 119 | CAGCCAGCTTTCCGAACAATAGATAAGTTTACCTTTTTTAAT | 42 |
| 120 | TGAGGGGACGACGATAATTTACGAGCATTCAAGAAAACAAAA | 42 |
| 121 | GTTGGTGTAGATGGTTCCTTATCATTCCTCATTTCAATTACC | 42 |
| 122 | CGTGGGAACAAACGCTCATCGAGAACAAGCTTTGAATACCAA | 42 |
| 123 | ATCAACATTAAATGATCATTACCGCGCCTACCTTTTACATCG | 42 |
| 124 | ATCAAAAATAATTCCTTATCCGGTATTCGTAGATTTTCAGGT | 42 |
| 125 | ATTTTTGTTAAATCCCCGACTTGCGGGATATCAAAATTATTT | 42 |
| 126 | TTTAAATTGTAAACTGCTATTTTGCACCGCCCCCTGCCTATC | 42 |

| 127 | ATCAGAAAAGCCCCAACGCTAACGAGCGGGGTCAGTGCCTTG | 42 |
| 128 | ATCGTAAAACTAGCAAAATAAACAGCCAGCTTTTGATGATAC | 42 |
| 129 | TGCCTGAGAGTCTGCGATTTTTTGTTTAGCGCAGTCTCTGAA | 42 |
| 130 | GGGTAGCTATTTTTCAGAGAGAATAACATATTCACAAACAAA | 42 |
| 131 | TATGATATTCAACCGAATTAACTGAACAGCATTGACAGGAGG | 42 |
| 132 | CAAAAGGGTGAGAACGCTAATATCAGAGCCCTCAGAGCCGCC | 42 |
| 133 | ATATTTTAAATGCACAATAATAAGAGCATCAGAGCCGCCACC | 42 |
| 134 | CCTTTATTTCAACGTACCGAAGCCCTTTTCAAAATCACCGGA | 42 |
| 135 | TACCAAAAACATTAAAGTTACCAGAAGGTCGGTCATAGCCCC | 42 |
| 136 | AATTAAGCAATAAATACCCAAAAGAACTTTGCCTTTAGCGTC | 42 |
| 137 | TAACATCCAATAAATATGTTAGCAAACGCCATCGATAGCAGC | 42 |
| 138 | GAGCTGAAAAGGTGATATAAAGAAACGGCACCATTACCATT | 42 |
| 139 | AATGGTCAATAACCGTCACAATCAATAGACTTGAGCCATTTG | 42 |
| 140 | GCGAACGAGTAGATGACAAAAGGGCGACTGACGGAAATTATT | 42 |
| 141 | AACAACCATCGCCCGGGAAGGTAAATATATTCAACCGATTGA | 42 |
| 142 | TTTCTTAAACAGCTTATCACCGTCACCGAAAATTCATATGGT | 42 |
| 143 | GCCTTTAATTGTATCAAAATCACCAGTACAAAGACACCACGG | 42 |
| 144 | TTTTTCACGTTGAACGTCACCAATGAAATAGAAAATACATAC | 42 |
| 145 | TGAGAATAGAAAGGCGACAGAATCAAGTGGCATGATTAAGAC | 42 |
| 146 | GTATGGGATTTTGCTTTCATCGGCATTTAAACCGAGGAAACG | 42 |
| 147 | AAAGTTTTGTCGTCCCATCTTTTCATAATTAAGAAAGTAAG | 42 |
| 148 | GTAGCATTCCACAGCGGAACCGCCTCCCAGAAACAATGAAAT | 42 |
| 149 | CCGTAACACTGAGTCCTCAGAGCCACCAAGATAACCCACAAG | 42 |
| 150 | CCCTCATTTTCAGGCAGAGCCGCCGCCACCCTGAACAAAGTC | 42 |
| 151 | TCAGAACCGCCACCACGATTGGCCTTGATAAAAACAGGGAAG | 42 |
| 152 | ATAGGTGTATCACCAGCCAGAATGGAAAACGTCAAAAATGAA | 42 |
| 153 | GGATAAGTGCCGTCAAGCGTCATACATGTATTATTTATCCCA | 42 |
| 154 | AGAGAAGGATTAGGAATAAGTTTTAACGTCTTTCCAGAGCCT | 42 |
| 155 | TTATTCTGAAACATTATAAACAGTTAATCAGCTACAATTTTA | 42 |
| 156 | CAATATAATCCTGAGTTAGAACCTACCAGGTTTTGAAGCCTT | 42 |
| 157 | AATTATCATCATATAATAAAGAAATTGCTAAGAACGCGAGGC | 42 |
| 158 | CATTATCATTTTGCATATACAGTAACAGCAATAGCAAGCAAA | 42 |
| 159 | AATCCTTTGCCCGAGGATTCGCCTGATTGCAAGCCGTTTTTA | 42 |
| 160 | TAGAAGTATTAGACCAGAGGCGAATTATAAGAACGGGTATTA | 42 |
| 161 | CTAATAGATTAGAGTGATGAAACAAACAGTAGAAACCAATCA | 42 |
| 162 | ATTGAGGAAGGTTACAATTTCATTTGAACCTGAACAAGAAAA | 42 |
| 163 | CAATCAATATCTGGAATCAATATATGTGCAGCTAATGCAGAA | 42 |
| 164 | AATCTAAAGCATCACGCTATTAATTAATGTAAAGTAATTCTG | 42 |
| 165 | CGCCTGCAACAGTGGATAGCTTAGATTATTTTCGAGCCAGTA | 42 |
| 166 | CAGCAGAAGATAAATATCAAAATCATAGCGCCATATTTAACA | 42 |
| 167 | ATAGCCCTAAAACAGCTTAGGTTGGGTTCAGTATAAAGCCAA | 42 |
| 168 | ACAATATTTTTGAAATCCAATCGCAAGAAAAAAGCCTGTTTA | 42 |
| 169 | GGATGTAAATGCTGTTCCATATAACAGTTTAAATATGCAACT | 42 |

170 TTATATAACTATGAACGCATAACCGATACACCCTCAGCAGCG    42
171 AAAGTACGGTGTACTTTTGCGGGATCGTTATTCGGTCGCTGA    42
172 AGGATCCCCGGGTACCGGCTAGTACCCGTATA    32
173 ATATTTAGTTAATTTCATCTTCTGACCTAAATTTAATGG    40
174 TTTGAAATACCGACCGTGTGATAAATAAGGCGTTAAATAA    40

**Supporting Table 3. Staple list for the 24-helix bundle NR.**

| Number | Sequence | Length |
|---|---|---|
| 1 | CGCCTGTAGCATAACAGCTCGGTTTATCAGCTTCACTACGGG | 42 |
| 2 | TAAAGAACTTTTGGGAATTAGAGGAATTATCGCCTGGCCCTG | 42 |
| 3 | AACATTATGACCAACAAGAAAGGCTATCAGGTCTCATCAAAA | 42 |
| 4 | AAGCCCGAAAGATTGACCAGTTGATTCCCAATTAGCCTTTAA | 42 |
| 5 | ACCTTATGCGATTTTGCCAAAACCAAAATAGCGTCGAGCTGG | 42 |
| 6 | AAGTTTCCATTAGAACGGTGGAACCGAACTGACCCAGTCATT | 42 |
| 7 | TAAGAAAACATGTAAATGCTGATTCCGGCTCAGTAGGGCTTA | 42 |
| 8 | ATTTCTTACGTAGAAACCAATCAATAATATGATTAGTTGCTA | 42 |
| 9 | AACCACCACCAGTGCCGTCATTAGCGGGGTTTTTAGCGTAAA | 42 |
| 10 | TTTGCGGGACCCTGAACAAAGTCCGCATTATACGCAGTATGT | 42 |
| 11 | ATAAATACCGTCAGTATTAACACCAGCAGAATTAGACTTTAC | 42 |
| 12 | AATAGATAAATTTGCACGTAAAAAAGGGTTTTTCATTTGAAT | 42 |
| 13 | CATTAATGAATCGGTGGTTTTTCTTTTCAC | 30 |
| 14 | CAGAATGTTGATATTCACAAAGAGGTTGAG | 30 |
| 15 | AGCCCGAGATAGCATTAAAGC | 21 |
| 16 | GTTCCAGTTTCATTGACAGCAAATAAATCCTGGTTGAGTGTT | 42 |
| 17 | GCGGGGAGAGGGAAACCTGTC | 21 |
| 18 | TGAATTTACCGTTCCAGTAAGCGTCATACA | 30 |
| 19 | CAAAATCCCTTATAAATCAAAAGAAT | 26 |
| 20 | GGTCAGACGATTGGCCGAAAGCGCAGTCTC | 30 |
| 21 | CGTTTGCCATCTTTTCATAATCACCAGCTG | 30 |
| 22 | GTGAAATCACCGGAACCAGAGCCACC | 26 |
| 23 | GCTTTCCAGTCGGCGGTTTGCGTCAACAGCTGCTCACTGCCC | 42 |
| 24 | AGAGACGGGATTGGGCGCCAGGGCCAACGC | 30 |
| 25 | AAATATTCCAATGAAACCAGGGCGACCACGCAATACACCACC | 42 |
| 26 | AGTAGATAAAACCGGAGACAGTCATAGGTAAAGGGATTTAGA | 42 |
| 27 | TCAACAACCGCACTCATCGACATGTTTTTAGTATCCAGGCTT | 42 |
| 28 | GCGTACATTTTGATATTTAAATTGGCCCCAAGCAGAGGTGAG | 42 |
| 29 | CATCGCCCATCACCTTGCTTAGTCTTCTTGCAACAAATAAAC | 42 |
| 30 | TCATAGGTTAGTTAATTTCCGCTGAGCTAGAAGATCAATGAC | 42 |
| 31 | CGTTTTAGACAGATCGTAACCGTGGGGATAGAAACGCTCAAT | 42 |
| 32 | TATGACGGGAGATAGAAAGGAACACAACTTTCAAAGACTCCT | 42 |
| 33 | TACAGAGAAGCCCAATAATTTGTTTATCGCGTTTTGCACCCT | 42 |
| 34 | CACCACCGTCACTAAACAGTTAATGGGTCAGCGATTGCCCTT | 42 |
| 35 | ACAAATGAGTAGCTACCTTTTTAACCGCAATATTGAAACAAA | 42 |
| 36 | CATCACCTTAATCTTCTGAATAATGGCAGAATAATTAGAGCC | 42 |
| 37 | CCAGGCATGATTCCCTCAGAGCCACCCTCAGTACGACTTGAG | 42 |
| 38 | GATTGTTCAGTAACAGTACTATCAGAAAAACTAATAAATAAA | 42 |
| 39 | GTCAAACAATTTACCGAACGAACCACCGCCCCCAAAAACGCT | 42 |
| 40 | CAATTGAAAATAGGTAATTGAGCGCTTACCAGAACGTAGAAA | 42 |

41  ATTTAGAACGCGTCGGCTGTCTTTCCTCCGGTAACCCAGCTA          42
42  AAACAGTGAATTATCCAATCGCAAGATAATTACAATCGCCAT          42
43  TCGTACATCAATAATAAAGAAATTGCTCATTTCTTTTAATGG          42
44  TTCACCTGATAGTGCAACAGTGCCACAAATATCTTCGACAAC          42
45  CAGTGAGAGTAGTATTCATTAAAGGTCCAGGGGAACGGAATA          42
46  CTGGTTTGCCCCATTTGCACCATTACCATTAGCCGATTACAT          42
47  AAAGGTGGCAACAAGTAATATCAGAGAGATAACAAATTTATC          42
48  CTGAATCTTACCCTTATTATCATTCCAAGAACGTGCAACAAC          42
49  GCCAACATGTAAATCACAAAGAACGCGAGAAAAATAGTACA           42
50  TAAATCAATATATTATGTAGATTTTCAGGTTTAAATTTTAAA          42
51  TCCTTTGCCCGATCTAGCTGAGAGCCAGCAGCACGAACAGTC          42
52  ATACATGAGGGACAAAATCACCAGTATCGGTCATTGCAGCAA          42
53  CGGAAACAAAACCGTCAAGTTTGCCTTTAGCGTAAACGTCAA          42
54  AGAATTGCCCAAATCTTACCGAAGCCCTTTTTAATTACGTGA          42
55  TAAACCAAATCGGAGAATCATTACCGCGCCCAATAGCCGTAA          42
56  CGACTTTGCTTCCCTGAACAAGAAAAATAACCTATGCGTTAT          42
57  AGATGAAAAAGGAGCTGATTGCTTTGAATACCACCAAGGGAA          42
58  AAAATCTCTGCGCGGGTCAGTTGGCAAATCAACAGGTGTAGC          42
59  CCCAAGCAAAGGTAAAAACAGGGAAGAGAGGCACGAACCTCC          42
60  GTTTTCAGACGGAACGGCCCCCTGCCTATTTCGGCATAAGGT          42
61  GATAGTTAGAATAAAAACTAAAGGAATTGCGAATCAGGCCTT          42
62  AGATATATAGATAAGATCGCCTGATAAATTGTGTTATGTTTA          42
63  ATAAATTTCTGAGAAACAGATACATAACGCCAATTGACAAAA          42
64  CGCAGTATGGATTACTGCTGAATATAATGCTGTGAAGATCCT          42
65  TGAGGAGATTAAAATGAATCACCATCAATATGAAAGGTAAAA          42
66  GGGGTGCTGTGCCTTGAGTAACAGTGCCAAAGTGTAACATGA          42
67  TCTCCACCGATAAGCCTGTGTGAAATTGAGTGCAGGGAGTTA          42
68  TTGTCAATCGTCTTAATAGTACCGAACCTATTATTCCGGAAT          42
69  ACAAATTACGAAGCGTATTCGGTAATAATTTTTTATGACAA           42
70  AAAGTAAAATCTACAGCCGGATATCGAAATCCGCGGCTGACC          42
71  ATTAAAACGGAAGCCCATAAATAAAGGAATTACGAAGACTGG          42
72  GCGGATGAAAAATTGCGCGAGCTAGCTCAACATGTAATAACC          42
73  GACCTCTGTAACAATTTAATCAGTATTCAACCGTTAACTAGC          42
74  AACTATTGGGGCAACTGCAGGTCGACTCGGATCAATTCTACT          42
75  ATTAACGGTTGAAATCACGACGTTGTAAAGAAACAGGAAGAT          42
76  CGTTAAAATTCGCACCCGTCGGATTCGGGGTAGAACCCTTCT          42
77  GTTTACCAGCGCAATCTATCAGGGCGATCGATTCAACAAGGC          42
78  CAATCCAAATAAATCAAGTTTTTTGGGGCGACGTCAACCACA          42
79  TGTCCAGACGACAGACCCTAAAGGGAGCCACAGCTAAGGTAT          42
80  CATAGCGATAGCACCGGCGAACGTGGCGACAAGAGTCCTTTT          42
81  TCAAATAGGAAAGCCGACCGTGTGATAAATAAGAATTAGAGC          42
82  AGACAATATTTTCTTAACCACCACACCCTTTAATGCGAATGA          42
83  AGGGCGAGTCATCGGCAGCAGGCGAAAAGACTCCACAAGAGT          42

| 84 | ACCATCAAGCCGAACAATATAAAAGAAAGGCCCACTCATATG | 42 |
| 85 | AGCACTAAGTAGAAGGAACGCTAACGAGTCGAGGTTTTATCC | 42 |
| 86 | TTGACGGTACACCGGATTTAGGCAGAGGCCCCGATGTAATTC | 42 |
| 87 | GAAAGCGTAAGGCGAATGTGAGTGAATAAGAAAGGTTGAAAA | 42 |
| 88 | TATAAAATTAATCAGAAAACGAGATTGAATCACTTATATAAC | 42 |
| 89 | CAAAGAACCTACTAGAGCTTAATTTTTGATATTTACATTTAA | 42 |
| 90 | CAACCCATCCTAAGATTTGTATCATTATACCTTGCCTTAAAT | 42 |
| 91 | TTCCACAGCCAACAGTTTCAGCGGAGTGTTATCCGTTGAAAA | 42 |
| 92 | GGTCATACTAAGCGCGAAACAAAGTACAGAATTCGGCTCCAT | 42 |
| 93 | CGTATAACTCAGTTGAGATTTAGGAATAGCATGGCTAGTAAG | 42 |
| 94 | CGAGGCAAGAGAGGTCATTTTTGCGGATTAGACCTAATATGC | 42 |
| 95 | CCAAGCTGTAGATTCAAAAGGGTGAGAAAACGACGCTGATAA | 42 |
| 96 | GAGGACATAAAAAAAAAGGCTCCAAATTCTCCGTAACACTGA | 42 |
| 97 | ATTGCGTCTAATGACCCTCAGAACCGTGGTAATGAAAAGCCT | 42 |
| 98 | CAGAACCCAACATAGGAACCCATGTAGTATGGGCGCTCACAA | 42 |
| 99 | AAGGCCGGCTGTTTGGTAGCAACGGCATCTTTGCTTAATCAT | 42 |
| 100 | AAAGCTGGGATCCCGTAAATTGGGCTCATTATTCATAGTACC | 42 |
| 101 | TTTAAACAGTCCGCGACTATTATAGTGTACCTTTATTGATAG | 42 |
| 102 | AATAGTATGCATGCAATTAAGCAATACAATGCCAGGCCAGTG | 42 |
| 103 | TGTATAATTCCCAGATTTTTGTTAAACGGCGGATCGTAACGC | 42 |
| 104 | TTAACACCCTGCCGGAGAGGGTAGCTAATGAAGCCTCAGAGC | 42 |
| 105 | ATAAATCATAAGTACGGTGTCTGGAAGAGACAGAAGCAAAGC | 42 |
| 106 | GGGTAAAATATTAGCAAGTTTATTTTCATCAGGACAGATAAC | 42 |
| 107 | ACCGGAACCGCCAAATCCCCCTTATTAGGTTTGATGGTGGGC | 42 |
| 108 | CTCATTTTCAGGTACAAAACCGAGGAAAAAGACACCACGGCA | 42 |
| 109 | CAGCAGCGAAAGGCGTTAAGAACGCGAGTTTCCAGAGCCTTC | 42 |
| 110 | GCCCTGACGAGAGAGAAAAAAGCCTGTTTTCGAGCCAGTAGA | 42 |
| 111 | CATAAATCAAAATCTATACCTGAGCAAATGCTTCTGTAAACG | 42 |
| 112 | TCATACAGGCAATGATAGGAGCACTAACAAGTTTGAGTAAAT | 42 |
| 113 | GTTAATATTTTGTAAAACCGCCAGCCATGGCCAACAGAGACC | 42 |
| 114 | TTTCCCTCAGAGCCTGGCTTTTGATGAAGCTTCCGAAATCGG | 42 |
| 115 | GCGATAGCAAGCCCTCCAGACGTTAGGCAGAATAAGTTTATT | 42 |
| 116 | CAACAGCATCGGAAAGGCAAAAGAATCAAAAATTTGCCAGTT | 42 |
| 117 | TAAACACCAGAACGGTTAATAAAACGAAAAATAAGAGAATAT | 42 |
| 118 | GCATCAGGTCTTTAAAACTCCAACAGCAATTCGTCGCTATTA | 42 |
| 119 | AAGGCAAAGAATTATTTAGAACCCTCTAGACATTATCATTTT | 42 |
| 120 | CAAATATCGATAGTTACAACAATAACGGATAGATTTAGTCTT | 42 |
| 121 | CCTTCCTGTATCAAACTATTAGTAATAACATCGCCATTCTGG | 42 |
| 122 | AAGTAGGAGGTTTACGAGCCGGAAGCATCGAACCGCCACCCT | 42 |
| 123 | TAATACTTTCCAGTTGAACCCTCAATCAATTCTGGAGCACTG | 42 |
| 124 | GTTACACAAGAATACGGGTACCGAGCTCACAATCAACGTAAC | 42 |
| 125 | AGCAAAATCGTCCTTAGCGACCGTATACCCCCCCTCAAATGC | 42 |
| 126 | CTTTGAAAGGTGACAATAACCGACAAAAGGCTCATTATACAA | 42 |

| 127 | GGCTTTTGCATTTAGATTTTTTCCCTTAGACGTTTTAATAGA | 42 |
| 128 | GTTTCCTCATTAAGAGGCTGAGACTCGTACCCACCCTCAGAG | 42 |
| 129 | ACCAACCTAATCGTATTGATACCGATAGTTTAACTACACGAT | 42 |
| 130 | ATTTCCTTGTTAGCCGGAACGAGGCGACTCTACAGAGGCTTT | 42 |
| 131 | GGATTGCGGCACTATCATAACCCTCGACAATGAGATGGTTTA | 42 |
| 132 | TTCGAGGTGCTGAAACGAATAAACAGCCATACGTAATGCGCT | 42 |
| 133 | GCGAACCAGGTCATAAGAGGGGGTAATAGTAACTGAAGGACG | 42 |
| 134 | GCCTGAGAGATTGAATGGGAAAGCGTAAGAAGCCAGCTTATT | 42 |
| 135 | CAGAGCCGCCAGGAGTCTCAAGAGAAGGATCACCGTAGTCAC | 42 |
| 136 | CAGTACAAAATGAATTAGGAGCCTTTAATTGCCCACGCTAAA | 42 |
| 137 | GACTTTTTCCTAAAACCAGACGGTCAATCAGAGTAATAACTT | 42 |
| 138 | TAATCATTGTAACGGATTTACCAGACGACGCAATACTGCATC | 42 |
| 139 | AAAAAGATTAGGATTAGTTTCATTCCATATTATATTTGCTAA | 42 |
| 140 | ATCGGTTGTTATTTTAATTTTTGAGAGATCCATATGTCAATA | 42 |
| 141 | CGAACGAGTTCATATTCCACAAAGAAACCATGCGGGAGACTG | 42 |
| 142 | ACAGACAGCAAAGAAAGAAATAGCAATAGAATTTCTTATCC | 42 |
| 143 | CTAAAGTTTTATTAGGGAGAGGGTTGATATATACACCAGGCA | 42 |
| 144 | AGGTGTGAATCGATAGCAGCACCGTATAGTATAGCCTAAGTT | 42 |
| 145 | TTGGGAAGACAATAAGGTACAGACCAGGCGACAATGAAAGGC | 42 |
| 146 | CAACCAATTAAGAGCAAGAAACAATGTAGCCGACACAATTTT | 42 |
| 147 | AACGCAAGGAGCAACATTAGATACATTTCGGTCAAGATCAAA | 42 |
| 148 | AATGTGAGCAATTACAGAATCGATGAACGGATAACCAATTTC | 42 |
| 149 | CAGTACCAGAGCAAAGACACAATCAATAGACCTCATAGTGCT | 42 |
| 150 | ATAGCACGAATCTTCTGACCTAAATTATAATGTTTGGACAGG | 42 |
| 151 | TTCATAACAAGAACAAGCAAGCCGTTCATAGGCTGACACCCC | 42 |
| 152 | CGCCGCCAGGGCAGACTGATCAGTAGCGACGCGGATAAGAGC | 42 |
| 153 | ATGTCGAATGAACCTCAAATATCAAAGATCGTAACTTGAGT | 42 |
| 154 | TGTTTATATCTTTTACATCGGGAGAAAAAATGGTCTTTAATT | 42 |
| 155 | CATCAGTATAAATTCAGTGAATAATTACCCAGGATTTACGAG | 42 |
| 156 | ATTTACATTTGACATTAACATCCAAGGTGGCCTCATATCAAA | 42 |
| 157 | ACAGGTTTTGAATGCGGGATCGTCTGAGGCTAAATTAACTGA | 42 |
| 158 | CAATAGGTTGGGATTCAACTAATGGATTCATCAGCCAACGCT | 42 |
| 159 | GGTCACGAAAAGGTTAACGTTATTAATTCTGGCAAAAGGAGC | 42 |
| 160 | GCCGCTACGGGTAATAATAAAAGGGACAGCCGCGCGTGGCAC | 42 |
| 161 | GGAATTATCATCGCCGGGCGCTAGGGCGTTTGATGGCACGTC | 42 |
| 162 | AAGAACTGGTAGCGTTAATAATGGTTTGAAAAAGAAGTTTT | 42 |
| 163 | TGCTGCAGCGAACGGTACGCC | 21 |
| 164 | TTTCCTCTTTATAATCAGTGAGAACAATATTGGCAGA | 37 |
| 165 | GTATAACGTCTGTCCATCACAGGGCGTTGCCTGAGTAGAAGAACTACTTA ATGC | 54 |
| 166 | CATGGTTACATTCAGGAGGCCGATTATGTTGTT | 33 |
| 167 | TTGCTCAGGAGCTAATCATCTGCCAGTTTGAGGGATG | 37 |
| 168 | CAGGGTTGCGTCACGTTGGTGTAGATGGAAGTTGGGGCCTCAGGAAGGCT | 54 |

GGCG

169 ACACGACCAGTATCCAGGCCACCGAGTAAAAGAGTGC                37
170 TTGATAGCAATACTTCTTTGATCGCGATCGTATTGAC                37
171 AGAATCAGAGCGAATTAACCGTTGCGAGCAC                      31
172 AGAATCCTGAGAAGAAGGGATCTGAAATGGATT                    33
173 AAAGGGGGGACGACGACAGGTGCGGGCCTCT                      31
174 GCCAATCGCACTCCAGCCAGCCAAATCAGCTCATTTT                37
175 GGAACGCCAGTGGGAATTTCCGGCACCGCTCTATTAC                37
176 TCGTCTGGCAACTGTTGGGAATCCTCAACATTA                    33
177 GCAAAGCGCCATTCGGTTGCT                                21
178 ATAATTCGCGTCAGGCTGCGTGCCGGAAACCAG                    33

**Supporting Table 4. Staple list for the Nanorobot.**

| Number | Sequence | Length |
|---|---|---|
| 1 | TTTAGTTAATTTCAATTAATTTTCCCTTTGAGTGA | 35 |
| 2 | AGAAAACTTTTTCATTGAAAACATAGCG | 29 |
| 3 | AATCGCAAGACAAAAGATTAAGACGCTG | 28 |
| 4 | GTTATATTCATAGGTCTGAGACATCAAGAAAACAAATTTCAA | 43 |
| 5 | TGAATTTTACATTTAACAATTTCGCGCA | 29 |
| 6 | ATAACCTCCTTTTACATCGGGTTTCAGGTTTAACGAAAAGTT | 42 |
| 7 | ACAATATATGAGAATCCAATATAT | 24 |
| 8 | ATTCGCCAAATAAAGAAATTGATTTTGC | 28 |
| 9 | TGCATGGAAAATAGCTTGAACGCG | 24 |
| 10 | AAATCATTTGAGAAGAGCAAATCC | 25 |
| 11 | GAGGCGAGGTTAGAACCTACCATCATAT | 28 |
| 12 | TTACCTGTATACTTCTGAATATGATGGC | 28 |
| 13 | TGAGTAAACTCGTATTAAATCCAGAGATACATCGCCATTA | 40 |
| 14 | GGAACAAGACTTTACAAACAACTGAAAGGCGCGAAAGATAAA | 42 |
| 15 | GGAGCGGTTTGAGGATTTAGAGCACAGACAATAATCTCAATC | 42 |
| 16 | TCCTGATGAGCCGTCAATAGACAGTTGGATCAAACAACAGTG | 42 |
| 17 | AATTCATGCACTAACAACTAAAAAGGAATCACCTTAGCAGCA | 42 |
| 18 | TAAAGCATTGAGGATGCAACAGGAAAAATTGC | 32 |
| 19 | AAAATACCGAACGAACCACCAGTGAGAATTAACCGTTGTAATTC | 44 |
| 20 | AGACTGATAGCCCTAAAAGAACCCAGTCACA | 31 |
| 21 | ACAGAGGCCTGAGATTCTTTGATTAGTAATGG | 32 |
| 22 | GCGTATTAGTCTTTAATCGTAAGAATTTACA | 31 |
| 23 | TTAACACACAGGAACACTTGCCTGAGTATTTG | 32 |
| 24 | CCACGCTGGCCGATTCAAACTATCGGCCCGCT | 32 |
| 25 | GCCGCTGAACCTCAAATCAAATCAGGAAATA | 31 |
| 26 | AATGAAACAGAGCGTAATATC | 22 |
| 27 | CGACCAGTCACGCAGCCACCGCTGGCAAAGCGAAAGAAC | 39 |
| 28 | ACCTTCTGACTTCGACACATTATCCGTAGATAGAA | 35 |
| 29 | TTGGCAGGCAATACAGTGTTTCTGCGCGGGCG | 32 |
| 30 | ATTATACGTGAGTATTAAGAAACCAAAACAGTGAT | 35 |
| 31 | GTCTGAAATAACATCGGTACGGCCGCGCACGG | 32 |
| 32 | ACGATCTGGTTAATACAAATTATCATATCAATACA | 35 |
| 33 | CCTACATGAAGAACTAAAGGGCAGGGCGGAGCCCCGGGC | 39 |
| 34 | CATACAGTTGTAGATTATATCAGAATGGAAGATTA | 35 |
| 35 | TGGGGAGCTATTTGACGACTAAATACCATCAGTTT | 35 |
| 36 | GGAAGAAGTGTAGCGGTCACGTTATAATCAGC | 32 |
| 37 | AGAGAACGTGAATCAAATGCGTATTTCCAGTCCCC | 35 |
| 38 | CGAACGTTAACCACCACACCCCCAGAATTGAG | 32 |
| 39 | GGAAGGGCGAAAATCGGGTTTTTCGCGTTGCTCGT | 35 |
| 40 | GAGCTTGTTAATGCGCCGCTAATTTTAGCGCCTGCCCTCAAT | 42 |

| 41 | CTAAAGGCGTACTATGGTTGCAACAGGAGAGA | 32 |
| 42 | 42 core GCCGTAAAGCAGCACGTATAA | 29 |
| 43 | AAGTAGGGTTAACGCGCTGCCAGCGGCTAGTAGTCCGC | 39 |
| 44 | GATTCCTGTTACGGGCAGTGAGCTTTTCCTGAACGACG | 38 |
| 45 | GCCTTCACCGAAAGCCTCCGCTCATTCCCAG | 31 |
| 46 | GTCCACGCTGCCCAAATCAAG | 21 |
| 47 | GGCGGTTAGAATAGCCCGAGAAGTCCACTATTAAAAAGGAAG | 42 |
| 48 | CAGGGTGCAAAATCCCTTATAGACTCCAACGTCAAAAGCCGG | 42 |
| 49 | CAGTGAGTGATGGTGGTTCCGAAAACCGTCTATCACGATTTA | 42 |
| 50 | ATTGCCCCCAGCAGGCGAAAAGGCCCACTACGTGACGGAACC | 42 |
| 51 | AAATGCCAGTTTGAGGGGGATTGAGTGAGCGAATAGGA | 38 |
| 52 | GGGTAGACCTTTGATAGATTAAATCCGTAAT | 31 |
| 53 | CTCGAATGCTCACTACAGTAT | 21 |
| 54 | AATTGCATGCCTGCAGGACCCGTCGGATTTCAAATCAG | 38 |
| 55 | GCTCATGGTCATAGCTGAACTCACTCGCACT | 31 |
| 56 | TAATGTGAAATTGTTATGGGGTGCGGCACCG | 31 |
| 57 | TCACGACTGTGCTGGCGCAAC | 22 |
| 58 | AACGCCAGGGTTCAATTCCACACAACATACG | 31 |
| 59 | GGGATAGGTGCATCCCTGTCGGGGGAGA | 28 |
| 60 | AAACGGCGACGACGGCCCGCTTGGGCGC | 28 |
| 61 | CGGGCCTAGGAAGAATTAATTTTTTCAC | 28 |
| 62 | TGTTGGGGCTTTCCCTAATGAACAGCTG | 28 |
| 63 | TCGCCATTGCCGGAAAAGTGTCCTGGCC | 28 |
| 64 | CGTAACCGTCACGTCAGCTTTAATTCGC | 28 |
| 65 | CCAGCCAAAGGGCGTGGCGAAAATTCGC | 28 |
| 66 | CTTCTGGTCAGGCTCAAGGCGTAAACGT | 28 |
| 67 | AATCATCAACCGAGGCAACCCGTATAAGGATCGGG | 35 |
| 68 | ACGCCATGAACGGTAATCGTAGAGATCTACAAAGGTAAAAAT | 42 |
| 69 | CTCATTTCATGTCAATCATATGGAGAGGGTAGCTATATATTT | 42 |
| 70 | ATTAAATGGTTGATAATCAGATCTAGCTGATAAATGAGTAAT | 42 |
| 71 | TAATATTCAAAAACAGGAAGAATCAATATGATATTTCAAAAG | 42 |
| 72 | ATATTTAAATTGATTAAGTTGGGT | 25 |
| 73 | ACAAGAGGTCATTGCCTGAGAGCCTTTATTTCAACAATACTT | 43 |
| 74 | TGAAAACTAGTTTAACCAGTAACATCGACTCTACCGAG | 38 |
| 75 | GCCGTACCCCTTTTGTTGCTATTACCAA | 28 |
| 76 | TTTTAGACCAAAAACATTATGCAATAAC | 28 |
| 77 | TAAATGCCATAAAGCTAAATCTTTCATTTGGGGCG | 35 |
| 78 | GGTGAGACAAGGCAAAGAATT | 21 |
| 79 | AGCAAAATAAAGATCAACCGTAAAGCCCTTGTTAAAGGGGGAGTTG | 46 |
| 80 | ATTTCGCAAATGGTACCCTGTGCAAGGACTATCAGAATCGATCAAA | 46 |
| 81 | 81 core CTGTTTAGCTATATGGTTGTAACCCTCATTTT | 40 |
| 82 | CGAGCTGCTCAGAGAATGCCTTAAT | 25 |
| 83 | TAGATTTAGTTTGAAACCAGAGCGTTTTAGGG | 32 |

| | | |
|---|---|---|
| 84 | CCATATATACCTTTCATCAAACTGCGGACCCT | 32 |
| 85 | TTTTAAATGGCTTAGGTCTTTCTTTAAACAAA | 32 |
| 86 | AGGGCCCGAATAGACTGTAAAAACAAATCTATCAT | 35 |
| 87 | TAGAGAGACAGTTGATTCCCAATTCTGCCAAC | 33 |
| 88 | CCTTTTGCTGGAAGTTTCATT | 21 |
| 89 | TCAAAAATCAGAGCTTAATTG | 21 |
| 90 | GGTGCTTTTGCAGTCAGGATTTTAACAG | 28 |
| 91 | AAATGTTAGACTTCAAATATCCCGGAAGCAAACTCGAACGAG | 42 |
| 92 | TGAGTAAGAGCAGGTAGGAGTAGTCAAGAACAATC | 35 |
| 93 | ACGACGAGATAGCGTCCAATAAAGATTAAGAGGAATCAGGAT | 42 |
| 94 | CGTACTAACGATGGTTTCTTCATCTACTTAGGAGG | 36 |
| 95 | ATCATAAATCGTCATAAATATAGCAAAGCGGATTGAATTGCT | 42 |
| 96 | AGGCATAATCCCCCTCAAATGACCCTGACTATTATGTCATTT | 42 |
| 97 | AGGTGAGATTCCTGACGCCAAATCTCGCCTGCGAT | 35 |
| 98 | TACATAACGCCAGTTCAGAAA | 21 |
| 99 | CTTATGCGACGTTGGGAAGAACAAAATAGCGAGAGAATAGTA | 42 |
| 100 | TGTCAGGCGCAGACGGTAGGCACCTGAGGAC | 31 |
| 101 | ACTTTAACGTTAATAAAACGATTACCAG | 28 |
| 102 | GCTTGAGGAACAACATTATTACAACACT | 28 |
| 103 | CCAGAACAAAGATTCATCAGTAATTACG | 28 |
| 104 | GGCTTGCTAGGAATACCA | 18 |
| 105 | ATGCCGAACTAAATACGTGAGGAA | 24 |
| 106 | CGCACACTCAAAGACAGCATCGGAATATGACAACAACC | 38 |
| 107 | AACGAAACCGGAACTTTTTCACGTTGAAGGGA | 32 |
| 108 | CAATAGCAACGGCTACATTTCCAGTGCTAAA | 31 |
| 109 | CACTAAAGACCTGCAAAAAAAGGCTCCGTTGCGCC | 37 |
| 110 | CCCCCAGATAAATTGCCTTTAATTGTATTTAA | 32 |
| 111 | TATGATCGTCACCCTCAACGCATAGCTTGATACCGATAAAAA | 42 |
| 112 | TCATAATGCCACTACGACAATCATAAAGGAATTGCGAACAAC | 42 |
| 113 | TAAAGACACGATCTTTCAGCGGAGTGAG | 28 |
| 114 | GGCCGCTTCGCTGATCGAGGTGAATTTCCGGTTTATGTATCAAACGTAA | 49 |
| 115 | AGTAAAGTTTTCACCAGTACAAACGGATAAG | 31 |
| 116 | CAACTTTTAATAATGAGGCGC | 21 |
| 117 | GACATTTCTGTATAATCTCCTCCATGT | 27 |
| 118 | ACAACCGATACCACCCTCATTTTCGGAGGTT | 31 |
| 119 | AAAGGAACAACTAAGGGAAAACGGTGTACAGACGAATTAC | 40 |
| 120 | GGAGTGTCGACGGATATTCATTACAGAAACA | 32 |
| 121 | CATTAAATGAACGAGGGAAGAATA | 24 |
| 122 | GAACCGCCACCCTCTCAGAAC | 22 |
| 123 | TGCCGTCAGAGGCTGAGACTCCCAGAATGGAAAGCGGTTGAG | 42 |
| 124 | GGGAGTTTCGTGTCGTCGAGGCTTAACCTAA | 31 |
| 125 | AAGTATATTCTGAAACATGAACTGAATTTACCGTTCCGCCGCCAG | 45 |
| 126 | TATCACCTGCCTATTTCGGAAGCGTCATACATGGCCCACCAG | 42 |

| 127 | TCAAGGGATAATCGCCCGCAGCGATCTTTGA | 32 |
| 128 | TAGTACCGTATAAACAGTTAAGATACAGGAGTGTAGAGCCAC | 43 |
| 129 | CCCAGAGCCATATTCGGTTTGCGGACCAAGC | 31 |
| 130 | AAGCTCAAGAACCAGGCTACAACGTAGCGTATTTT | 35 |
| 131 | GCAGGTCAACCGATTTGGGAAACCATTA | 28 |
| 132 | AACCACCCAATAATCAAAATCTATAAAA | 28 |
| 133 | CACCCTCCCAGAGCCCCTTATGACAGAA | 28 |
| 134 | AACCGCCCTCCCTTCGGCATAGCGTCA | 28 |
| 135 | ATTACCAGAGCCAGTAACCTATTAGCCCGGAAACC | 35 |
| 136 | GCAAGGCGAAACAATAGCCGAACAAAGTTATT | 32 |
| 137 | AACCCGACTTGAGCCATTGAGGGATCACAAT | 31 |
| 138 | ATGAAACTAAGCCCAGGAAACCGAGGAAAAAGACAAATT | 39 |
| 139 | GATAAAGGTGAATTATCTGACGGACCACGGA | 31 |
| 140 | CCGTAATGATAACCAATAACGGAATACCGGCA | 32 |
| 141 | TCAAGTTATTGAGCACTGGCATGATTAAAGAA | 33 |
| 142 | TTTTTTCGGTCATAGCCCACCACCACATACATAAAGGTCAAAAGAGCTA | 49 |
| 143 | CAATAGAAAGCAGATGAAATAAAACGATAGTT | 33 |
| 144 | TTGGGGAAGGGACAGGAGCAGTCTAGTATTAGAGA | 36 |
| 145 | ATAAGTTTACCAGAAATAATACAAAAATCTTT | 32 |
| 146 | GAAACGCACGCAATCACAAGATTACAGACTTACCATTCTAAGCATT | 46 |
| 147 | ACAACCGGAAAGAGCCGTTTTGATTGCCCCCGTAC | 36 |
| 148 | AATGGAACCGACCCTCACTGGTAAAGTGCCCGCCA | 35 |
| 149 | CAAACGTGACTCCTAAAGTCAGGAGAATATTA | 32 |
| 150 | GAAAAGTAAATTCAGACATTCAGACGATATTA | 32 |
| 151 | ATAAACAGGGAGCTACATAGCGAATAATCGGATAGATA | 38 |
| 152 | AAATAAGGCAATAGCACCATTTTAGAGCCAGCAAAAAAGGGCTATGGTT | 49 |
| 153 | ACAGCCCAATGAACAAGCTGTCCACCAGTAACCGACCG | 38 |
| 154 | ATTTGCCTTTTTGTTTAACGTAGAGCAACGGA | 32 |
| 155 | CCAATATAGAACCAAGTACAACATTTAGGCACGTTAAA | 38 |
| 156 | CGAGCGTGAAAATAGCAGCCTATTGAGTCATC | 32 |
| 157 | CCTGAATGAGAATAACATAAATCAGAGACAGTAGCTAGCGTT | 42 |
| 158 | TGCACCCAAGCGCATTAGACGGAGGGTATGCC | 32 |
| 159 | GTTGGAGGTTGAGCATGAAAATAA | 24 |
| 160 | ATCATTACCGCAAATAAACAGC | 22 |
| 161 | TCATCGAAGCAAGCAAATCAGGAGCCTA | 28 |
| 162 | GTATTAAAGGCTTATCCGGTAACGCTAA | 28 |
| 163 | CCAGAACGCGTTAACAAGGAATCA | 24 |
| 164 | TCCTTATAACGCGAGGCGTTTATTTTAT | 28 |
| 165 | CAATCAACCTCCCGACTTGCGGCTATTT | 28 |
| 166 | AAGGTAAAGTAATTCAAGCCG | 21 |
| 167 | TTTCGAGGACGACGACAATAAACCGCAC | 28 |
| 168 | ATGTAATGTTCAGCTAATGCAAGAACGG | 29 |
| 169 | GCCATATCCTGTTTATCAACACTGTCTT | 28 |