Electronic Supplementary Material (ESI) for RSC Advances.


# The stability study of tubular DNA origami in the presence of protein crystallisation buffer

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## 1. Materials

All chemicals were obtained from Alfa Aesar (Tianjing, China) and used without further purification. All short oligo-DNA strands were purchased from Invitrogen. M13mp18 viral DNA was purchased from New England Biolabs. Water used in all experiments was Milli-Q deionized (18.2 MΩ.cm).

## 2. Method

### Preparation of tubular DNA origami

Detailed structures of tubular DNA origami used in this study are shown in Supplementary Fig. S1, and the sequences of the staple strands are listed at the end. DNA origami assembly was done by mixing scaffold and staples to a final concentration of 6.25 nM and 15.625 nM, respectively, in a 1×TAE-$Mg^{2+}$solution buffer (40 mM Tris, pH 8.0, 2 mM EDTA, 12.5 mM $Mg(OAc)_2$). This mixture was cooled from 90 to 25 °C at a rate of − 1.0 °C /min using a PCR thermal cycler.

The assembled structures were purified from the excess staple strands by centrifugation with Millipore's 100 kD molecule-cutoff Centricon spin-filter in three cycles at a speed of 3,000 g for 10 min at 4 °C in the same 1×TAE-$Mg^{2+}$ buffer. The assembled origami structures were then collected at the end of the third cycle of filtration.

### AFM measurements

For each measurement, 5 μL of the sample was deposited onto a freshly cleaved mica surface and left to adsorb for 3 min. 30 μL of 1×TAE-$Mg^{2+}$ buffer was added to the liquid cell and the sample was scanned under ScanAsyst model using a E scanner of AFM (Bruker Multimode 8). The proble used here was ScanAsyst Fluid+ (Olympus). All the images were only flattened by the AFM analysis program without other treatment.

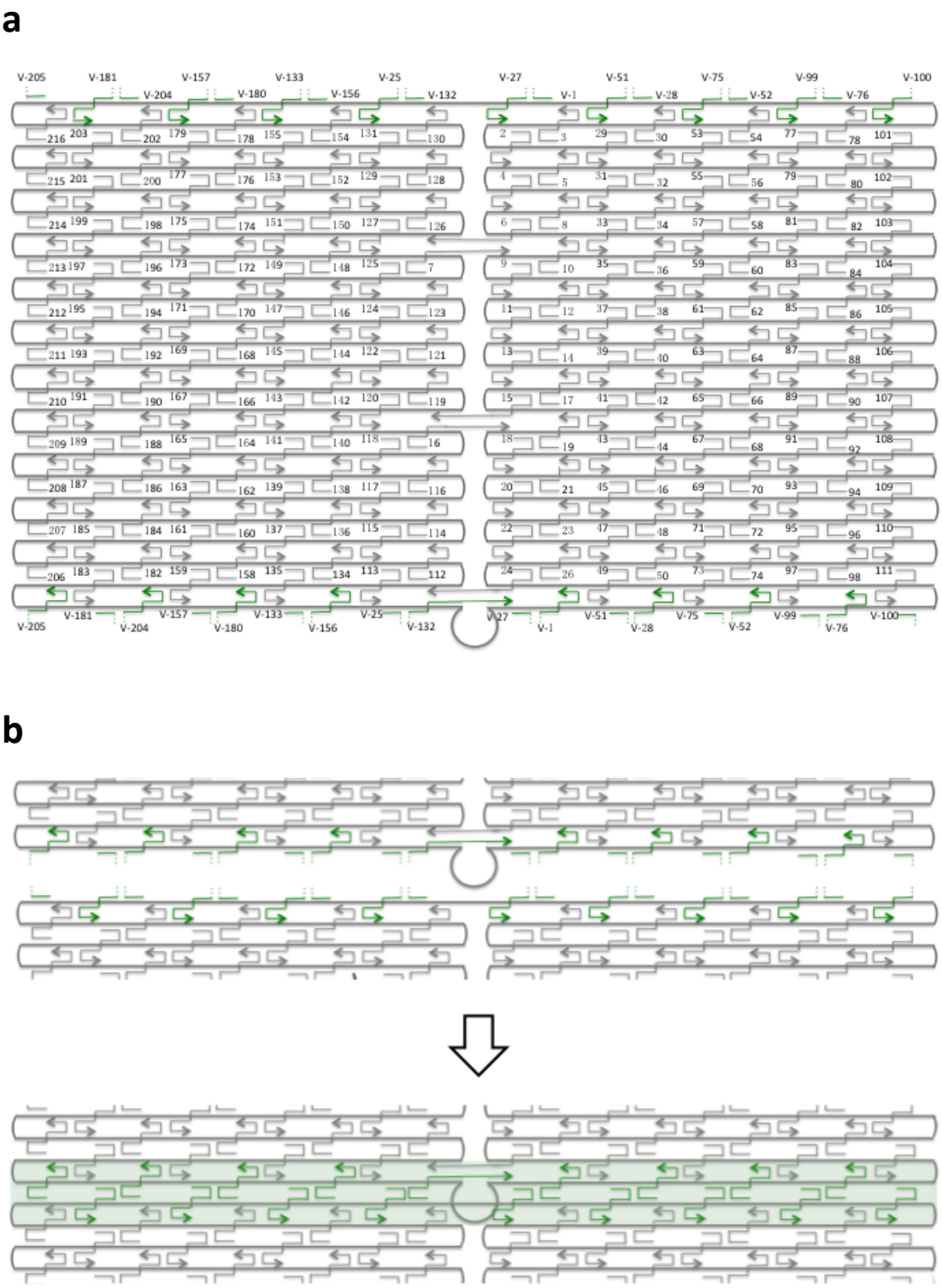


Fig. S1 (a) Design details of the tubular DNA origami with sticky ends between the top and bottom edges. The strand numbers are labeled at the 5’ terminal. The green lines were the sticky ends. (b) Design principle of the edge connections during the formation of tubular DNA origami.

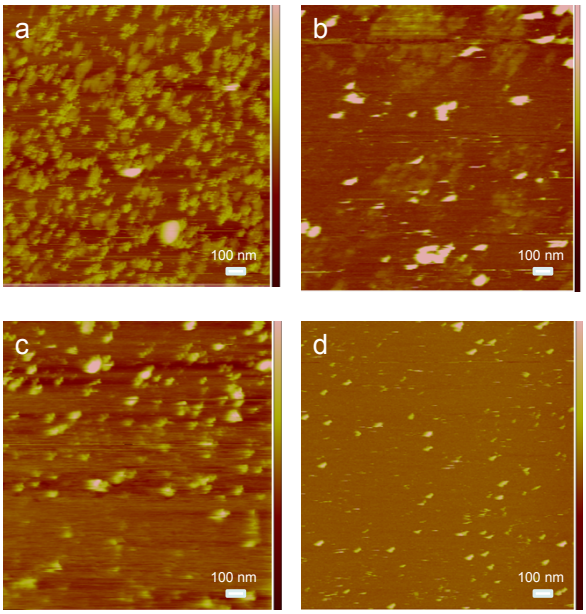


Fig. S2 AFM images of DNA origami assembled in protein crystallization cocktails of (a) lysozyme, (b) thaumatin, (c) human serum albumin, (d) catalase. All the samples are characterised after buffer exchange for at least 24 hrs.

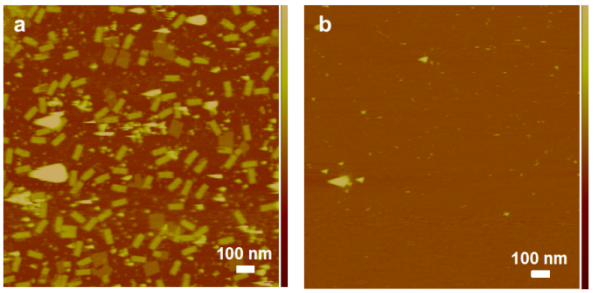


Fig. S3 AFM images of DNA origami after (a) gradient buffer exchange and (b) dialysis buffer exchange of catalase crystallization cocktails All the samples are characterised after buffer exchange for at least 24 hrs.

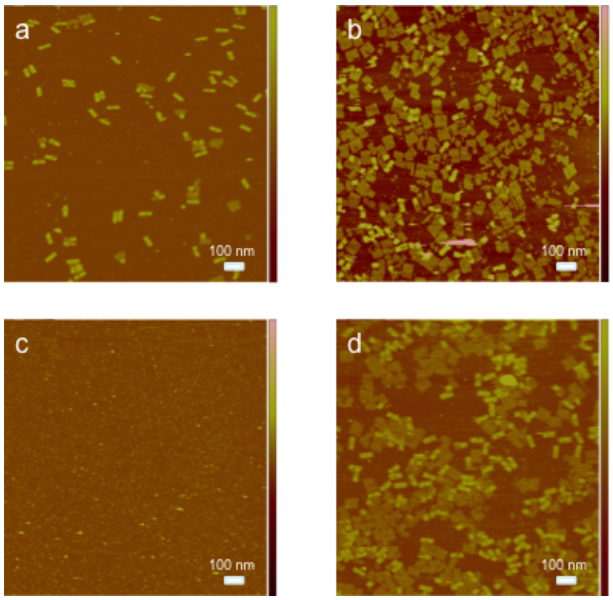


Fig. S4 AFM images of DNA origami in the DNA assembly buffer whose $Mg^{2+}$ was replaced with 200 mM (a) $Na^{+}$, (b) $K^{+}$, (c) $Ca^{2+}$ and (d) $NH_4^{+}$, respectively.

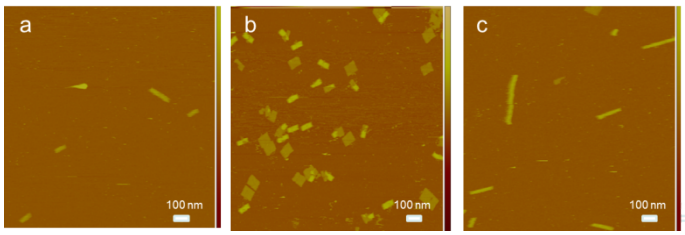


Fig. S5 AFM images of DNA origami in the DNA assembly buffer, whose 40 mM Tris was replaced with 100 mM (a) HEPES, (b) PEPES and (c) MES, respectively.

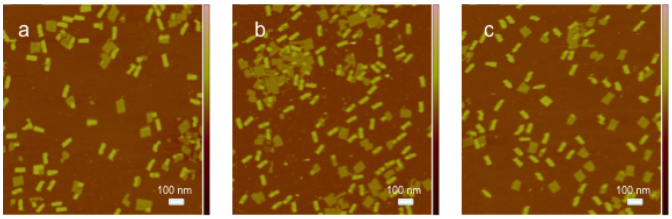


Fig. S6 AFM images of DNA origami with 10 % (v/v) (a) ethanol, (b) MPD, (c) glycerol in the DNA assembly buffer, respectively.

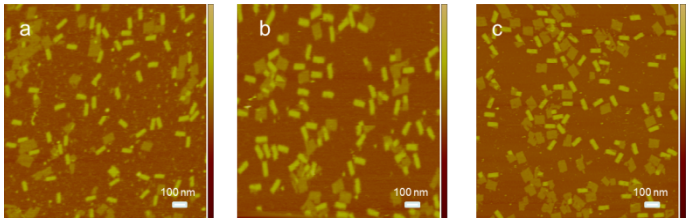


Fig. S7 AFM images of DNA origami with 30 % (w/v) (a) $PEG_{2000}$, (b) $PEG_{4000}$, (c) $PEG_{8000}$ in the DNA assembly buffer, respectively.

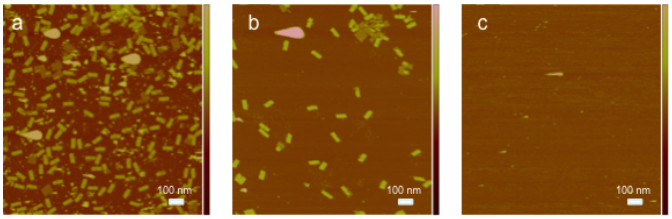


Fig. S8 AFM images of DNA origami with (a) 2 M NaCl, (b) 3 M NaCl, (c) 4 M NaCl in the DNA assembly buffer, respectively.

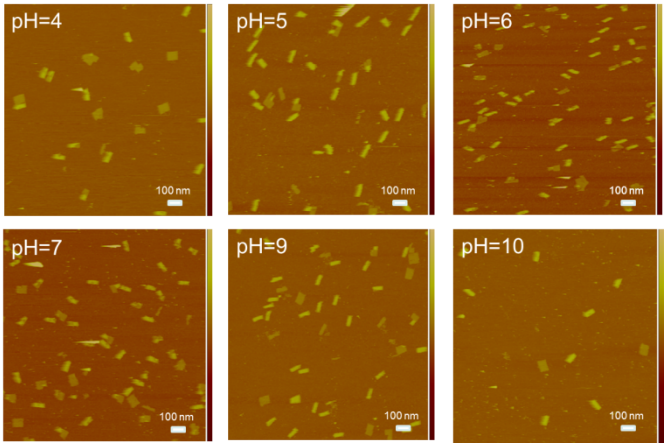


Fig. S9 AFM images of DNA origami assembled at different pH conditions.

Sequences

V-1 CGGCCTTGATAGGAACCCATGTACAAACAGTT

2 AATGCCCCGTAACAGTGCCCGTATCTCCCTCA

3 TGCCTTGACTGCCTATTTCGGAACAGGGATAG

4 GAGCCGCCCCACCACCGGAACCGCGACGGAAA

5 AACCAGAGACCCTCAGAACCGCCAGGGGTCAG

6 TTATTCATAGGGAAGGTAAATATTCATTCAGT

7 CATAACCCGAGGCATAGTAAGAGCTTTTTAAG

8 ATTGAGGGTAAAGGTGAATTATCAATCACCGG

9 AAAAGTAATATCTTACCGAAGCCCTTCCAGAG

10 GCAATAGCGCAGATAGCCGAACAATTCAACCG

11 CCTAATTTACGCTAACGAGCGTCTAATCAATA

12 TCTTACCAGCCAGTTACAAAATAAATGAAATA

13 ATCGGCTGCGAGCATGTAGAAACCTATCATAT

14 CTAATTTATCTTTCCTTATCATTCATCCTGAA

15 GCGTTATAGAAAAAGCCTGTTTAGAAGGCCGG

16 GCTCATTTTCGCATTAAATTTTTGAGCTTAGA

17 AATTACTACAAATTCTTACCAGTAATCCCATC

18 TTAAGACGTTGAAAACATAGCGATAACAGTAC

19 TAGAATCCCTGAGAAGAGTCAATAGGAATCAT

20 CTTTTACACAGATGAATATACAGTAAACAATT

21 TTTAACGTTCGGGAGAAACAATAATTTTCCCT

22 CGACAACTAAGTATTAGACTTTACAATACCGA

23 GGATTTAGCGTATTAAATCCTTTGTTTTCAGG

24 ACGAACCAAAACATCGCCATTAAA TGGTGGTT

V-25 TGAGTTTCCGAGAAAGGAAGGGAACAAACTAT

26 TAGCCCTACCAGCAGAAGATAAAAACATTTGA

V-27 CAAGCCCACTGGTAATATCCAGAACGAACTGA

V-28 CCGCCAGCCACCACCCTCATTTTCCTATTATT

29 CTGAAACAGGTAATAAGTTTTAACCCCTCAGA

30 AGTGTACTTGAAAGTATTAAGAGGCCGCCACC

31 GCCACCACTCTTTTCATAATCAAACCGTCACC

32 GTTTGCCACCTCAGAGCCGCCACCGATACAGG

33 GACTTGAGAGACAAAAGGGCGACAAGTTACCA

34 AGCGCCAACCATTTGGGAATTAGATTATTAGC

35 GAAGGAAAATAAGAGCAAGAAACAACAGCCAT

36 GCCCAATACCGAGGAAACGCAATAGGTTTACC

37 ATTATTTAACCCAGCTACAATTTTCAAGAACG

38 TATTTTGCTCCCAATCCAAATAAGTGAGTTAA

39 GGTATTAAGAACAAGAAAAATAATTAAAGCCA

40 TAAGTCCTACCAAGTACCGCACTCTTAGTTGC

41 ACGCTCAAAATAAGAATAAACACCGTGAATTT

42 AGGCGTTACAGTAGGGCTTAATTGACAATAGA

43 ATCAAAATCGTCGCTATTAATTAACGGATTCG

44 CTGTAAATCATAGGTCTGAGAGACGATAAATA

45 CCTGATTGAAAGAAATTGCGTAGACCCGAACG

46 ACAGAAATCTTTGAATACCAAGTTCCTTGCTT

47 TTATTAATGCCGTCAATAGATAATCAGAGGTG

48 AGATTAGATTTAAAAGTTTGAGTACACGTAAA

49 AGGCGGTCATTAGTCTTTAATGCGCAATATTA

50 GAATGGCTAGTATTAACACCGCCTCAACTAAT

V-51 CTCAGAGCCATTGCAACAGGAAAAATATTTTT

V-52 GGAAATACACCGCCACCCTCAGAACTGAGACT

53 CCTCAAGAATACATGGCTTTTGATAGAACCAC

54 TAAGCGTCGAAGGATTAGGATTAGTACCGCCA

55 CACCAGAGTTCGGTCATAGCCCCCGCCAGCAA

56 TCGGCATTCCGCCGCCAGCATTGACGTTCCAG

57 AATCACCAAATAGAAAATTCATATATAACGGA

58 TCACAATCGTAGCACCATTACCATCGTTTTCA

59 ATACCCAAGATAACCCACAAGAATAAACGATT

60 ATCAGAGAAAGAACTGGCATGATTTTATTTTG

61 TTTTGTTTAAGCCTTAAATCAAGAATCGAGAA

62 AGGTTTTGAACGTCAAAAATGAAAGCGCTAAT

63 CAAGCAAGACGCGCCTGTTTATCAAGAATCGC

64 AATGCAGACCGTTTTTATTTTCATCTTGCGGG

65 CATATTTAGAAATACCGACCGTGTTACCTTTT

66 AATGGTTTACAACGCCAACATGTAGTTCAGCT

67 TAACCTCCATATGTGAGTGAATAAACAAAATC

68 AAATCAATGGCTTAGGTTGGGTTACTAAATTT

69 GCGCAGAGATATCAAAATTATTTGACATTATC

70 AACCTACCGCGAATTATTCATTTCCAGTACAT

71 ATTTTGCGTCTTTAGGAGCACTAAGCAACAGT

72 CTAAAATAGAACAAAGAAACCACCAGGGTTAG

73 GCCACGCTATACGTGGCACAGACAACGCTCAT

74 GCGTAAGAGAGAGCCAGCAGCAAAAAGGTTAT

V-75 CCCTCAGACTACATTTTGACGCTCACCTGAAA

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78 GGAAAGCGACCAGGCGGATAAGTGAATAGGTG

79 TGAGGCAGGCGTCAGACTGTAGCGTAGCAAGG

80 TGCCTTTAGTCAGACGATTGGCCTGCCAGAAT

81 CCGGAAACACACCACGGAATAAGTAAGACTCC

82 ACGCAAAGGTCACCAATGAAACCAATCAAGTT

83 TTATTACGGTCAGAGGGTAATTGAATAGCAGC

84 TGAACAAACAGTATGTTAGCAAACTAAAAGAA

85 CTTTACAGTTAGCGAACCTCCCGACGTAGGAA

86 GAGGCGTTAGAGAATAACATAAAAGAACACCC

87 TCATTACCCGACAATAAACAACATATTTAGGC

88 CCAGACGAGCGCCCAATAGCAAGCAAGAACGC

89 AGAGGCATAATTTCATCTTCTGACTATAACTA

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91 TATGTAAACCTTTTTTAATGGAAAAATTACCT

92 TTGAATTATGCTGATGCAAATCCACAAATATA

93 GAGCAAAAACTTCTGAATAATGGAAGAAGGAG

94 TGGATTATGAAGATGATGAAACAAAATTTCAT

95 CGGAATTATTGAAAGGAATTGAGGTGAAAAAT

96 ATCAACAGTCATCATATTCCTGATTGATTGTT

97 CTAAAGCAAGATAGAACCCTTCTGAATCGTCT

98 GCCAACAGTCACCTTGCTGAACCTGTTGGCAA

V-99 TATCACCGTTATTTACATTGGCAGACATTCTG

V-100

GTCACACGTTTTTATAAGTATAGCCCGGCCGTCGAG

101

AGGGTTGATTTTATAAATCCTCATTAAATGATATTC

102

ACAAACAATTTTAATCAGTAGCGACAGATCGATAGC

103

AGCACCGTTTTTTAAAGGTGGCAACATAGTAGAAAA

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TACATACATTTTGACGGGAGAATTAACTACAGGGAA

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GCGCATTATTTTGCTTATCCGGTATTCTAAATCAGA

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TATAGAAGTTTTCGACAAAAGGTAAAGTAGAGAAT

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107

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116 TTCGCCATTGCCGGAAACCAGGCATTAAATCA

117 GCTTCTGGTCAGGCTGCGCAACTGTGTTATCC

118 GTTAAAATTTTAACCAATAGGAACCCGGCACC

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140 AAATAATTTTAAATTGTAAACGTTGATATTCA

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142 ACCGTTCTAAATGCAATGCCTGAGAGGTGGCA

143 TATATTTTAGCTGATAAATTAATGTTGTATAA

144 TCAATTCTTTTAGTTTGACCATTACCAGACCG

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154 CAATGACACTCCAAAAGGAGCCTTACAACGCC

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V-156 CCCCGATTTCCACAGACAGCCCTCATCTCCAA

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192 CAAAATTAAAGTACGGTGTCTGGAAGAGGTCA

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194 TTTTTGCGCAGAAAACGAGAATGAATGTTTAG

195 AAACAGTTGATGGCTTAGAGCTTATTTAAATA

196 ACTGGATAACGGAACAACATTATTACCTTATG

197 ACGAACTAGCGTCCAATACTGCGGAATGCTTT

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202 AAAGGCCGAAAGGAACAACTAAAGCTTTCCAG

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