Supporting Information

Self-assembly of DNA nanostructures in different cations

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MATERIALS AND METHODS

Materials

DNA strands were purchased from Integrated DNA Technologies (IDT) with standard desalting. M13mp18 single stranded circular DNA was purchased from IDT. Sequences of DNA strands used for the DX, three-point-star motif and tetrahedron are provided in **Tables S2** and **S3**. Sequences of DNA strands for the origami triangle are provided in **Table S4**. For different metal ions, the chemicals used were cadmium (II) nitrate tetrahydrate (Cd $(NO_3)_2 \cdot 4H_2O$), ≥98% (Fisher Scientific), calcium chloride dihydrate ($CaCl_2 \cdot 2H_2O$), ≥99% (Sigma-Aldrich), lithium chloride (LiCl), ≥99% (Sigma Aldrich), silver nitrate, ($AgNO_3$), (Millipore), nickel chloride hexahydrate, ($NiCl_2 \cdot 6H_2O$) (VWR, high purity), copper (II) sulfate pentahydrate ($CuSO_4 \cdot 5H_2O$), ≥98% (Sigma-Aldrich), barium chloride ($BaCl_2$), 99% (Sigma-Aldrich), lead (II) chloride ($PbCl_2$), 98% (Sigma-Aldrich), sodium chloride (NaCl), ≥99% (Sigma-Aldrich), zinc chloride anhydrous ($ZnCl_2$), 97% (Sterm chemicals), magnesium chloride ($MgCl_2$), ≥99% (Sigma-Aldrich), and potassium chloride (KCl), 99-100.5% (Sigma-Aldrich).

DNA nanostructure assembly

Double crossover (DX) motif. Component DNA strands (DX1, DX2, DX3 and DX4) were mixed in equimolar ratios in 1× Tris-Acetic-EDTA (TAE) buffer (40 mM Tris base, pH 8.0; 20 mM acetic acid, 2 mM EDTA) containing 10 mM of different cations (Mg^{2+}, Ca^{2+}, Ba^{2+}, Ni^{2+}, Cd^{2+}, Pb^{2+}, Zn^{2+}, Cu^{2+}, Na^{+}, K^{+}, Li^{+} and Ag^{+}). The final concentration of the DNA complex was 250 nM for polyacrylamide gel electrophoresis (PAGE) studies, 1 μM for UV melting studies and 5 μM for circular dichroism (CD) studies. The mixture was annealed from 90 °C to 20 °C over two hours in a T100 Thermal Cycler (Bio-Rad) using the following protocol: 90 °C for 5 min, 65 °C for 20 min, 45 °C for 20 min, 37 °C for 30 min, and 20 °C for 30 min.

3-point-star motif. Component DNA strands (L, M and S-blunt) were mixed in 1:3:3 ratio in 1× TAE containing 10 mM of different cations. Sequences of DNA strands are given in **Table S2**. The final concentration of the DNA complex was 250 nM. The mixture was annealed from 90 °C to 20 °C over two hours in a T100 Thermal Cycler (Bio-Rad) using the following protocol: 90 °C for 5 min, 65 °C for 20 min, 45 °C for 20 min, 37 °C for 30 min, and 20 °C for 30 min.

DNA tetrahedron. DNA strands L, M and S were mixed in 1:3:3 ratio at 30 nM in 1× TAE containing 10 mM of different cations. Sequences of DNA strands are given in **Table S3**. The DNA solution was slowly cooled down from 95°C to room temperature over 48 hours by placing the tubes in 2 liters of hot water in a beaker placed in a Styrofoam box.

DNA origami. M13mp18 scaffold strand and 208 staple strands were mixed in a 1:5 ratio (final DNA concentration of 5 nM) in 1× TAE buffer (40 mM Tris, 20 mM acetic acid, 1 mM EDTA) containing 10 mM or higher concentrations of a cation. The mixture was annealed from 80°C to room temperature over 16 hours in a Biometra TRIO Thermal Cycler.

Polyacrylamide gel electrophoresis (PAGE)

Non-denaturing gels containing 4-10% polyacrylamide (19:1 acrylamide/bisacrylamide) were run at 4 °C (100 V, constant voltage) in 1× TAE running buffer with or without 10 mM Mg^{2+} (see text for details). Samples were mixed with gel loading dye containing 50% glycerol, bromophenol blue and 1× TAE before loading on gels. Gels were stained in deionized water containing 0.5× GelRed (Biotium). Gels were imaged on a Bio-Rad Gel Doc XR+ imager using the default settings for GelRed with UV illumination. Gel images were exported as 12-bit images and quantified using ImageJ. Quantification was done using the highest exposure image that did not contain saturated pixels in the band of interest. For the DX assembly, we quantified the bands corresponding to the structure. For three-point-star assembly, we calculated the percentage of the band corresponding to the structure in the entire lane.

Agarose gel electrophoresis

The DNA origami triangles were run on 1% agarose gels in 1× TAE running buffer. The gels were pre-stained with SYBR-Green (Thermo Fisher), run at a constant voltage of 7.5 V/cm for 2 hours on ice and scanned using GelDoc (UVP GelStudio).

UV melting experiments

Experiments were performed in a Cary 3500 UV-Visible Spectrophotometer equipped with a temperature controller, using 1 μM DNA complexes assembled in 1× TAE buffer containing 10 mM metal ions. Melting curves were acquired at 260 nm by heating and cooling from 20 °C to 90 °C at a rate of 1 °C/min.

Circular dichroism experiments

CD spectra were collected on 5 μM DNA complexes assembled in 1× TAE buffer containing 10 mM metal ions. Experiments were performed on a Jasco-815 CD spectrometer at room temperature in a quartz cell with a 1 mm path length. CD spectra were collected from 350 to 200 nm with a scanning speed of 100 nm/min and with 3 accumulations. The bandwidth was 1.0 nm, and the digital integration time was 1.0 s. All CD spectra were baseline-corrected for signal contributions due to the buffer.

AFM imaging

The mica surface was washed with double distilled water and dried by compressed air. 5 µl of the annealed DNA sample (5 nM) was deposited onto the freshly-cleaved mica surface and incubated for 5 minutes. 40 µl of 1× TAE buffer with different cations (specific to the condition the DNA origami was annealed in) was then added and the AFM scan was performed under tapping mode in the fluid cell on Multimode AFM Asylum Research Cypher S with SNL-10 probe (Bruker Nano, Inc.). After the scan, raw AFM files were processed with Gwyddion V.2.6.1 software by using the flatten function to adjust the AFM images to reflect the actual height of the DNA origami nanostructures.

Nuclease degradation experiments

Annealed DX motif (at 0.5 µM) were first mixed with DNase I reaction buffer (final of 1×). DNase I enzyme was purchased from New England Biolabs (Catalog # M0303S), and according to the vendor, is isolated from a recombinant *E. Coli* strain carrying an MBP fusion clone of bovine pancreatic DNase I. Dilutions of DNase I enzyme to different units was made in nuclease-free water. For the DNase I assay, 1 µl of the enzyme was added to 10 µl of the sample containing DNase I reaction buffer. Samples were incubated at 37 °C for different time intervals. Incubated samples were mixed with gel loading dye and run on non-denaturing polyacrylamide gels to analyze degradation over time. A step-by-step protocol for our gel-based method of DNA nanostructure degradation analysis is provided in *Current Protocols in Nucleic Acid Chemistry*, 82: e115 (2020).

Stability test in FBS

Fetal bovine serum (FBS) was purchased from Thermo Fisher (Gibco, cat #: A4736301). FBS was added to annealed DNA complexes (DX motif or DNA origami triangle) to be at a final concentration of 10%. Typically, we added 1µl of FBS to 9 µl of the annealed samples and incubated them at 37 °C for different time intervals. Incubated samples were mixed with gel loading dye and run on non-denaturing polyacrylamide (for DX) or agarose gels (for DNA origami) to analyze degradation over time. Data was quantified using a minimum of two replicates for each condition tested.

STATISTICAL ANALYSIS

All experiments discussed in the manuscript were performed with at least two replicates and data are presented as mean and standard deviation of error propagated from replicates. Statistical details of experiments can be found in figure legends where applicable.

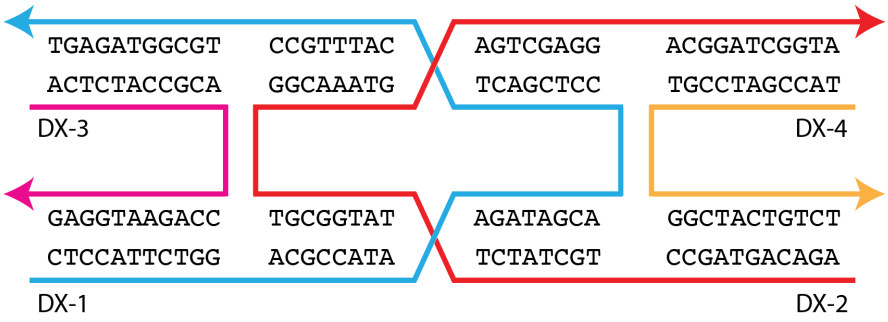

Figure S1. Schematic and sequence of the DX motif.

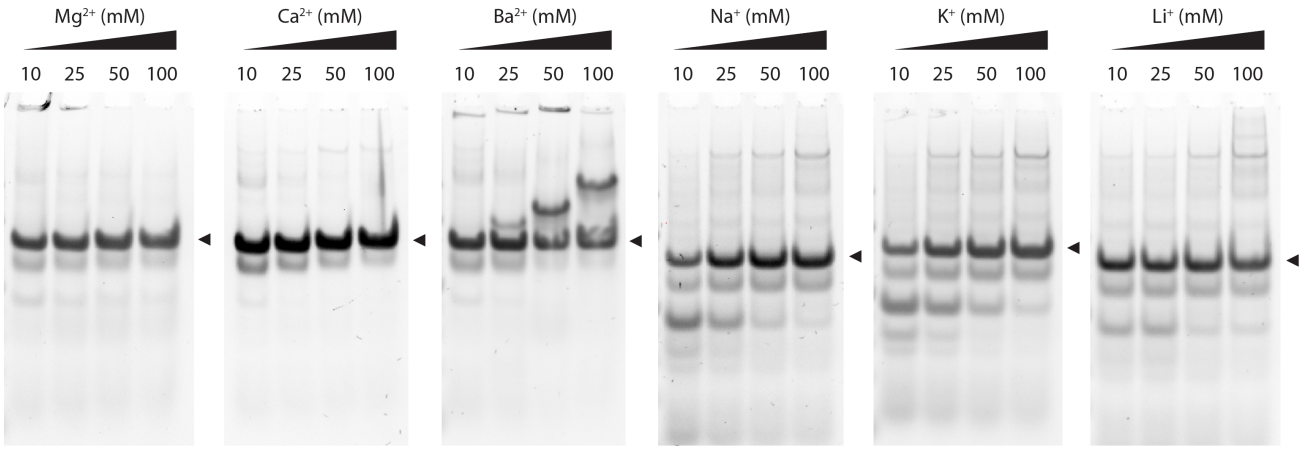

Figure S2. Assembly of DX in different metal ions. Full gels of images shown in Figure 1f.

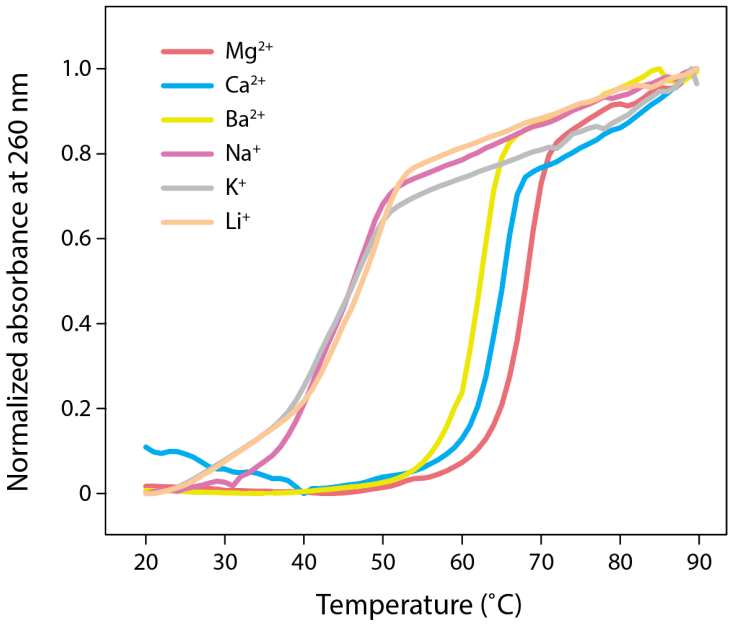

Figure S3. UV melting profiles of DX assembled in buffer containing different metal ions.

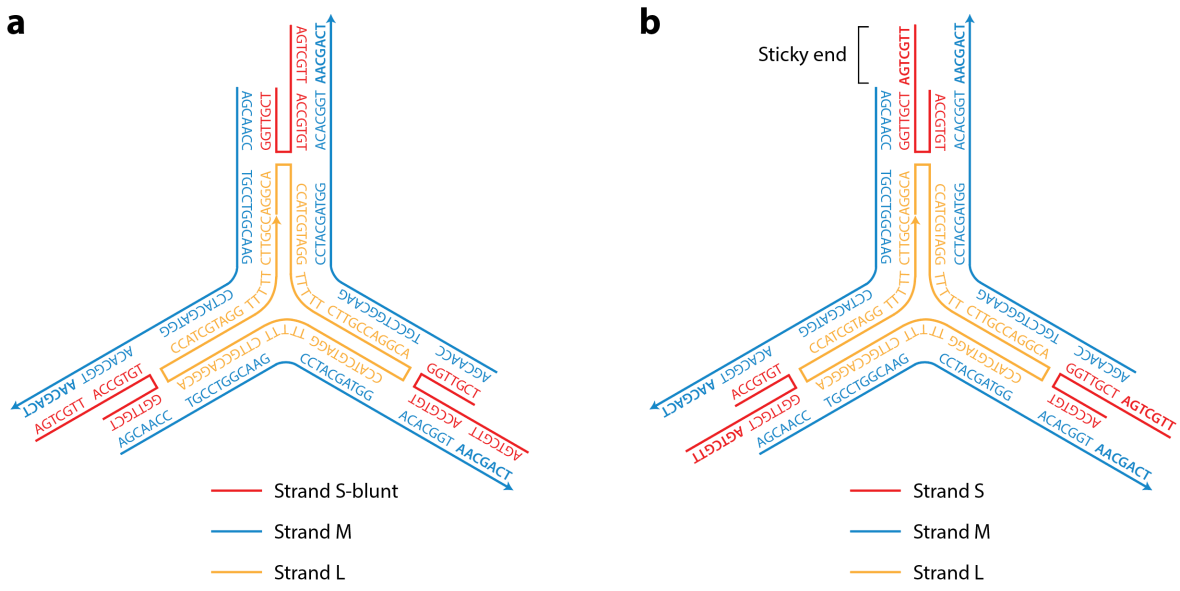

Figure S4. (a) Design of the 3-point star motif without sticky ends to assemble the motif. (b) 3-point-star motif with sticky ends that allows hierarchical assembly into a DNA tetrahedron.

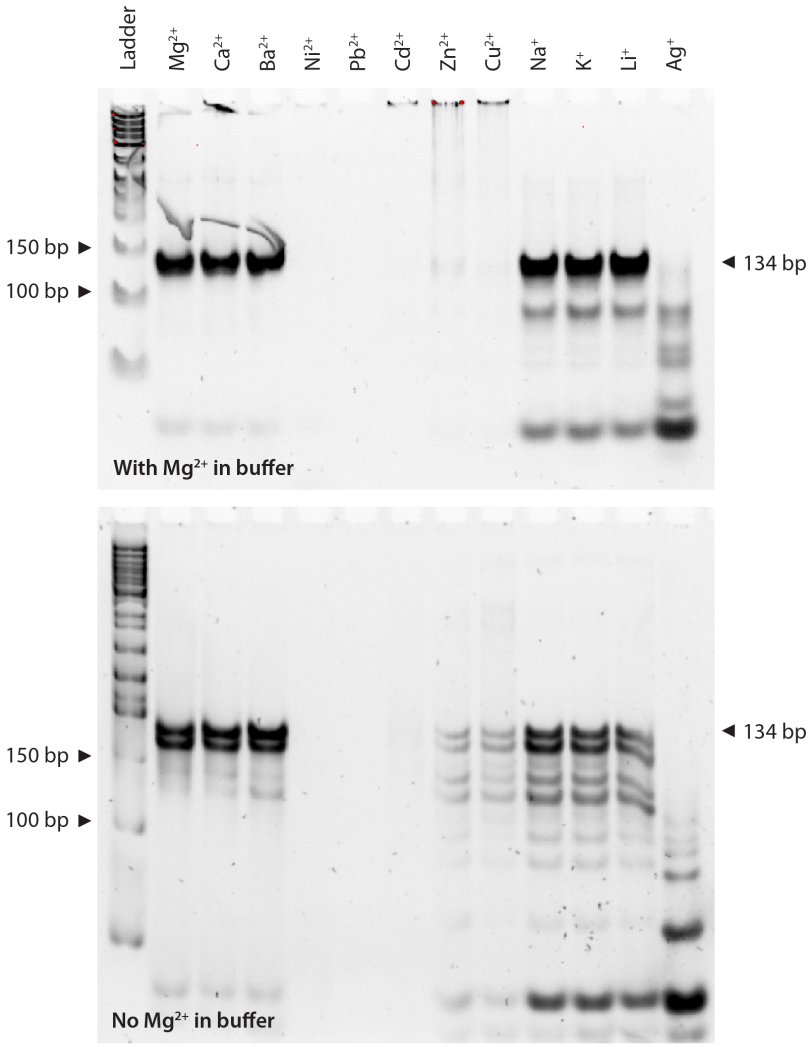

Figure S5. Three-point star motif assembled in different ions and run in gels with or without Mg^{2+}.

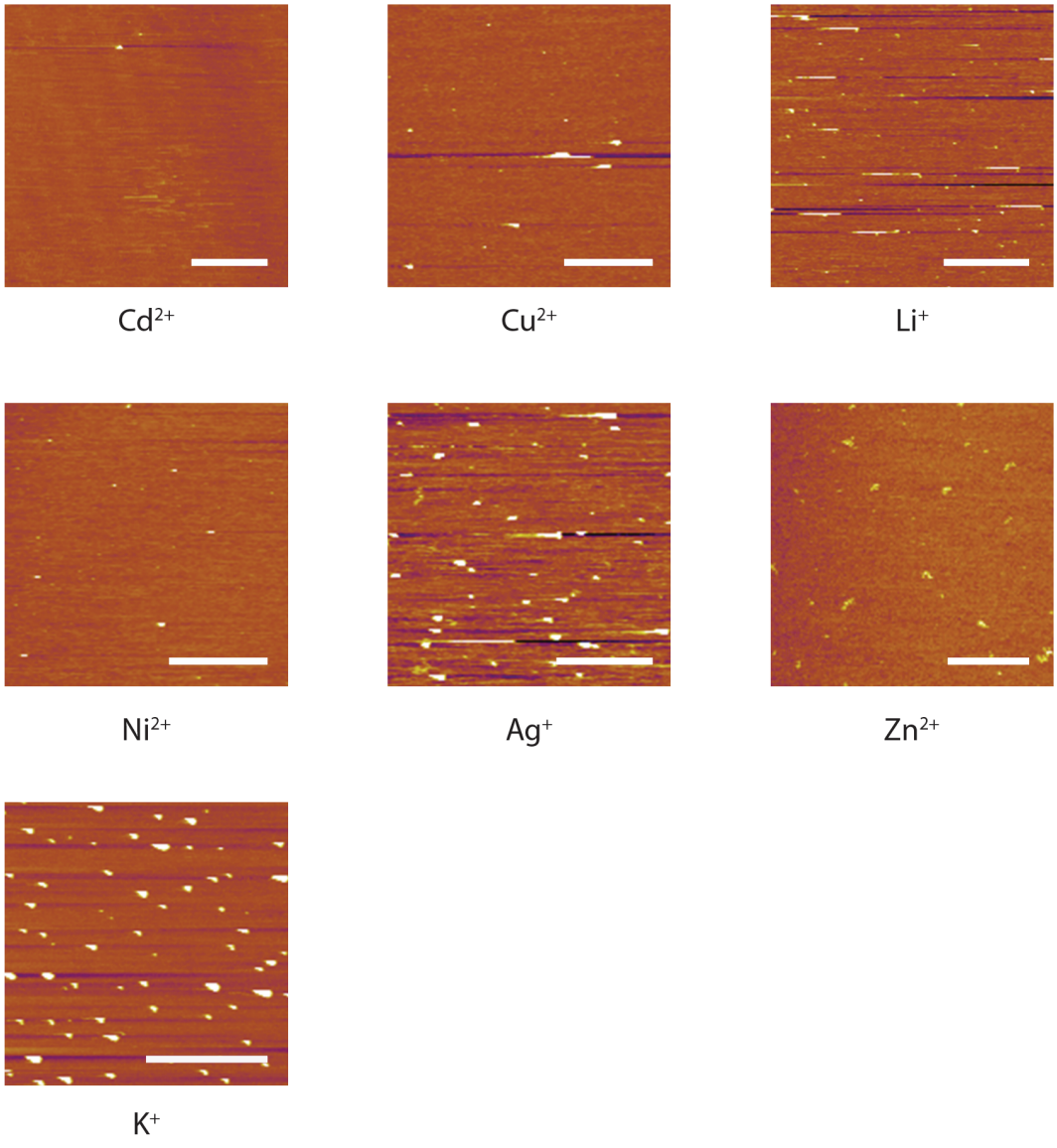

Figure S6. AFM analysis of DNA origami triangles assembled in 10 mM of different ions. Scale bars in insets are 100 nm.

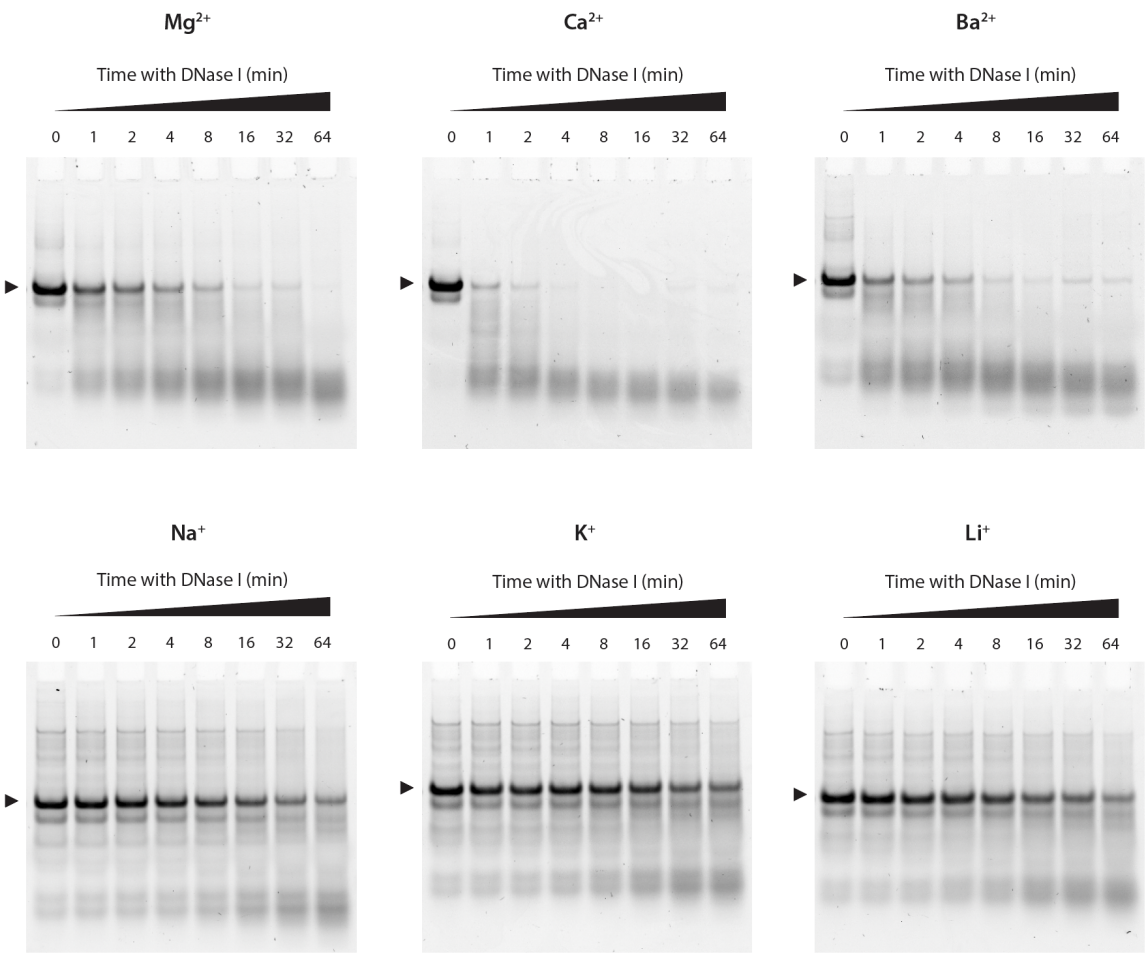

Figure S7. Nuclease degradation analysis of DX motif assembled in different ions. Full gels of images shown in Figure 4b.

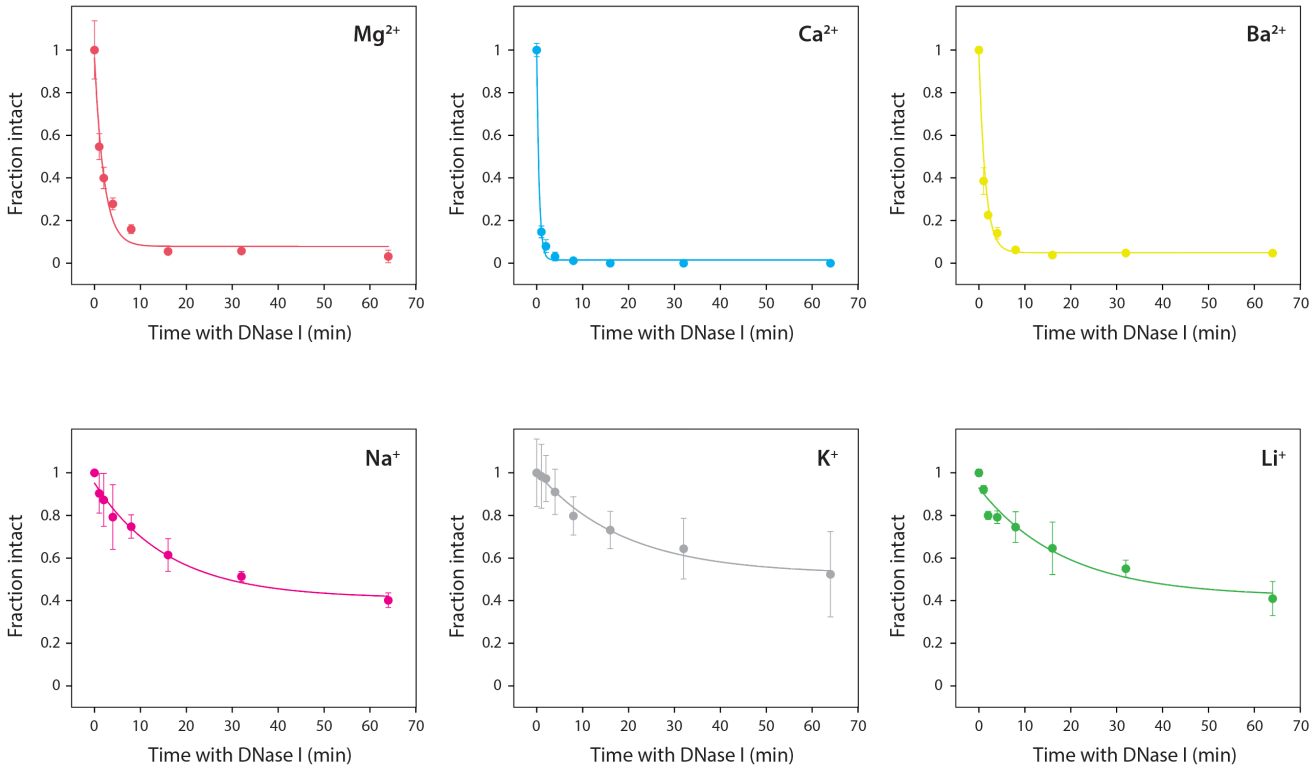

Figure S8. Quantitative analysis of nuclease degradation of DX motif assembled in different ions.

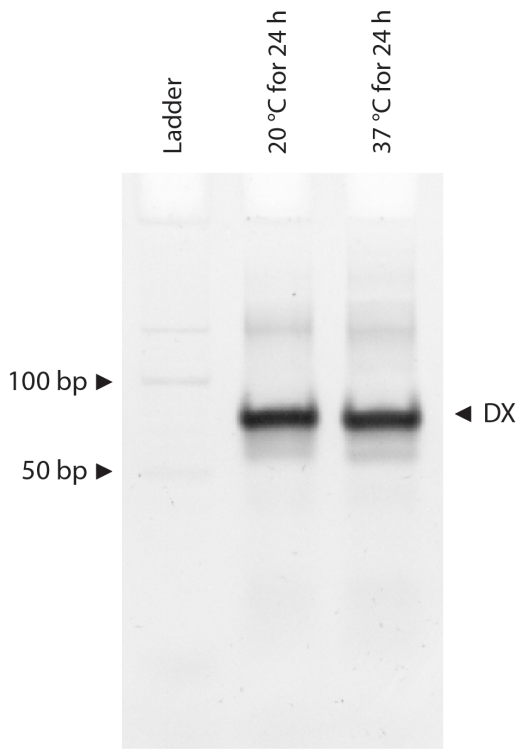

Figure S9. Stability of DX motif at 37 °C for 24 h.

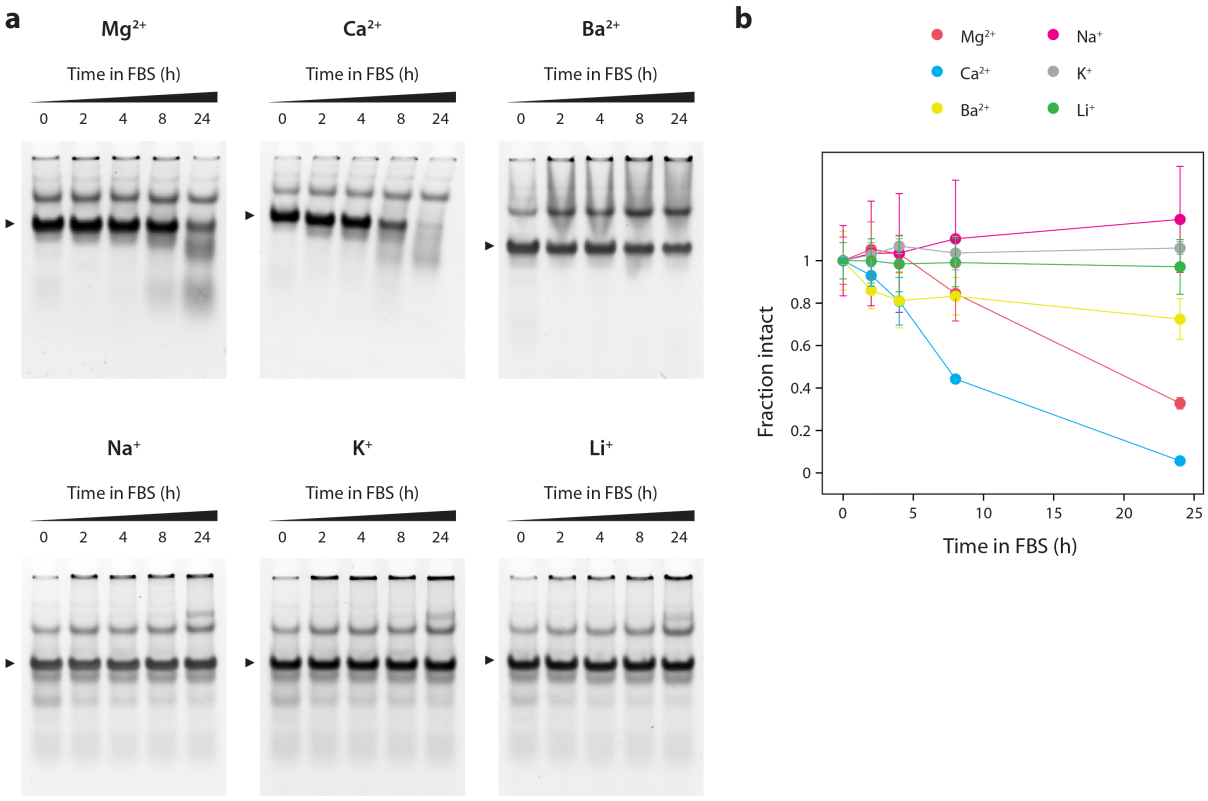

Figure S10. DX biostability in FBS. (a) PAGE analysis of DX degradation in FBS. Full gels of images shown in Figure 4e. (b) Quantified results from gels shown in (a). Fraction intact at the 24-hour time point is shown in Figure 4f. Components in FBS also get stained in the gel and appear as a higher mobility band.

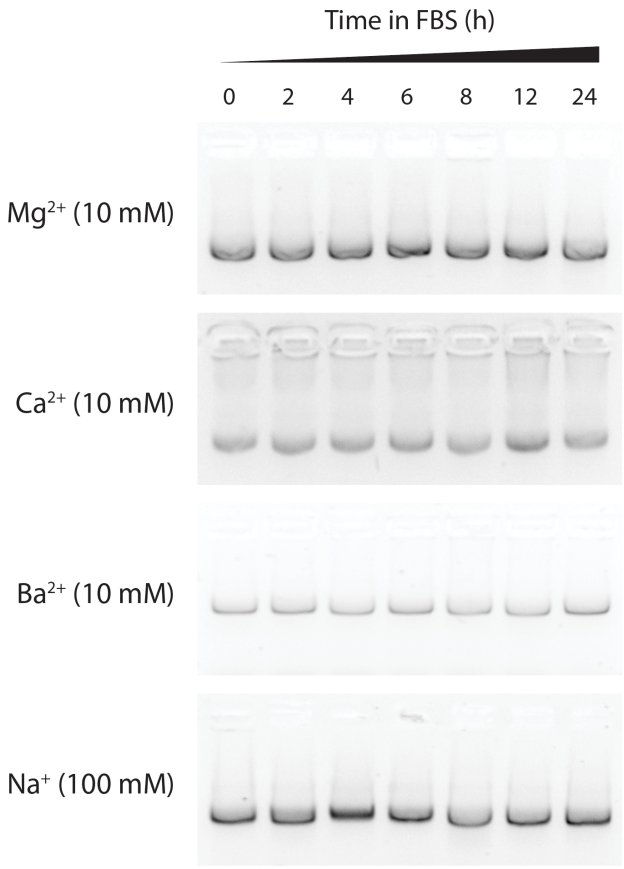

Figure S11. Agarose gel analysis of DNA origami triangle degradation in 10% FBS.

Table S1. Time constants for nuclease degradation analysis of DX motif in different ions.

Metal ion	Time constant (τ)	R square
Mg^{2+}	2.03 ± 0.35	0.9639
Ca^{2+}	0.52 ± 0.05	0.9950
Ba^{2+}	1.41 ± 0.28	0.9480
Na^{+}	16.04 ± 3.20	0.9731
K^{+}	18.85 ± 3.48	0.9791
Li^{+}	18.42 ± 6.82	0.9183

Table S2. Sequences of DNA strands used for DX motif.

Strand	Sequence	Length
DX1	CTCCATTCTGGACGCCATAAGATAGCACCTCGACTCATTTGCCTGCGGTAGAGT	54
DX2	AGACAGTAGCCTGCTATCTTATGGCGTGGCAAATGAGTCGAGGACGGATCGGTA	54
DX3	ACTCTACCGCACCAGAATGGAG	22
DX4	TACCGATCCGTGGCTACTGTCT	22

Table S3. Sequences of DNA strands used for three-point-star motif (strands L, M and S-blunt) and the DNA tetrahedron (strands L, M and S).

Strand	Sequence	Length
Strand L	AGGCACCATCGTAGGTTTTTCTTGCCAGGCACCATCGTA GGTTTTTCTTGCCAGGCACCATCGTAGGTTTTTCTTGCC	78
Strand M	AGCAACCTGCCTGGCAAGCCTACGATGGACACGGTAACGACT	42
Strand S	ACCGTGTGGTTGCTAGTCGTT	21
Strand S-blunt	AGTCGTTACCGTGTGGTTGCT	21

Table S4. Staple DNA oligos used for self-assembly of DNA triangle origami.

Strand	Sequence
A_01	CGGGGTTTCCTCAAGAGAAGGATTTTGAATTA
A_02	AGCGTCATGTCTCTGAATTTACCGACTACCTT
A_03	TTCATAATCCCCTTATTAGCGTTTTTCTTACC
A_04	ATGGTTTATGTCACAATCAATAGATATTAAAC
A_05	TTTGATGATTAAGAGGCTGAGACTTGCTCAGTACCAGGCG
A_06	CCGGAACCCAGAATGGAAAGCGCAACATGGCT
A_07	AAAGACAACATTTTCGGTCATAGCCAAAATCA
A_08	GACGGGAGAATTAACTCGGAATAAGTTTATTTCCAGCGCC
A_09	GATAAGTGCCGTCGAGCTGAAACATGAAAGTATACAGGAG
A_10	TGTACTGGAAATCCTCATTAAAGCAGAGCCAC
A_11	CACCGGAAAGCGCGTTTTCATCGGAAGGGCGA
A_12	CATTCAACAAACGCAAAGACACCAGAACACCCTGAACAAA
A_13	TTTAACGGTTCGGAACCTATTATTAGGGTTGATATAAGTA
A_14	CTCAGAGCATATTCACAAACAAATTAATAAGT
A_15	GGAGGGAATTTAGCGTCAGACTGTCCGCCTCC
A_16	GTCAGAGGGTAATTGATGGCAACATATAAAAGCGATTGAG
A_17	TAGCCCGGAATAGGTGAATGCCCCCTGCCTATGGTCAGTG
A_18	CCTTGAGTCAGACGATTGGCCTTGCGCCACCC
A_19	TCAGAACCCAGAATCAAGTTTGCCGGTAAATA
A_20	TTGACGGAAATACATACATAAAGGGCGCTAATATCAGAGA
A_21	CAGAGCCAGGAGGTTGAGGCAGGTAACAGTGCCCG
A_22	ATTAAAGGCCGTAATCAGTAGCGAGCCACCCT
A_23	GATAACCCACAAGAATGTTAGCAAACGTAGAAAATTATTC
A_24	GCCGCCAGCATTGACACCACCCTC
A_25	AGAGCCGCACCATCGATAGCAGCATGAATTAT
A_26	CACCGTCACCTTATTACGCAGTATTGAGTTAAGCCCAATA
A_27	AGCCATTTAAACGTCACCAATGAACACCAGAACCA
A_28	ATAAGAGCAAGAAACATGGCATGATTAAGACTCCGACTTG
A_29	CCATTAGCAAGGCCGGGGGAATTA
A_30	GAGCCAGCGAATACCCAAAAGAACATGAAATAGCAATAGC
A_31	TATCTTACCGAAGCCCAAACGCAATAATAACGAAAATCACCAG
A_32	CAGAAGGAAACCGAGGTTTTTAAGAAAAGTAAGCAGATAGCCG
A_33	CCTTTTTTCATTTAACAATTTCATAGGATTAG
A_34	TTTAACCTATCATAGGTCTGAGAGTTCCAGTA
A_35	AGTATAAAATATGCGTTATACAAAGCCATCTT
A_36	CAAGTACCTCATTCCAAGAACGGGAAATTCAT
A_37	AGAGAATAACATAAAAACAGGGAAGCGCATTA
A_38	AAAACAAAATTAATTAAATGGAAACAGTACATTAGTGAAT
A_39	TTATCAAACCGGCTTAGGTTGGGTAAGCCTGT
A_40	TTAGTATCGCCAACGCTCAACAGTCGGCTGTC

A_41	TTTCCTTAGCACTCATCGAGAACAATAGCAGCCTTTACAG
A_42	AGAGTCAAAAATCAATATATGTGATGAAACAAACATCAAG
A_43	ACTAGAAATATATAACTATATGTACGCTGAGA
A_44	TCAATAATAGGGCTTAATTGAGAATCATAATT
A_45	AACGTCAAAAATGAAAAGCAAGCCGTTTTTATGAAACCAA
A_46	GAGCAAAAGAAGATGAGTGAATAACCTTGCTTATAGCTTA
A_47	GATTAAGAAATGCTGATGCAAATCAGAATAAA
A_48	CACCGGAATCGCCATATTTAACAAAATTTACG
A_49	AGCATGTATTTCATCGTAGGAATCAAACGATTTTTTGTTT
A_50	ACATAGCGCTGTAAATCGTCGCTATTCATTTCAATTACCT
A_51	GTTAAATACAATCGCAAGACAAAGCCTTGAAA
A_52	CCCATCCTCGCCAACATGTAATTTAATAAGGC
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A_54	TCCCTTAGAATAACGCGAGAAAACTTTTACCGACC
A_55	GTGTGATAAGGCAGAGGCATTTTCAGTCCTGA
A_56	ACAAGAAAGCAAGCAAATCAGATAACAGCCATATTATTTA
A_57	GTTTGAAATTCAAATATATTTTAG
A_58	AATAGATAGAGCCAGTAATAAGAGATTTAATG
A_59	GCCAGTTACAAAATAATAGAAGGCTTATCCGGTTATCAAC
A_60	TTCTGACCTAAAATATAAAGTACCGACTGCAGAAC
A_61	GCGCCTGTTATTCTAAGAACGCGATTCCAGAGCCTAATTT
A_62	TCAGCTAAAAAAGGTAAAGTAATT
A_63	ACGCTAACGAGCGTCTGGCGTTTTAGCGAACCCAACATGT
A_64	ACGACAATAAATCCCGACTTGCGGGAGATCCTGAATCTTACCA
A_65	TGCTATTTTGCACCCAGCTACAATTTTGTTTTGAAGCCTTAAA
B_01	TCATATGTGTAATCGTAAAACTAGTCATTTTC
B_02	GTGAGAAAATGTGTAGGTAAAGATACAACTTT
B_03	GGCATCAAATTTGGGGCGCGAGCTAGTTAAAG
B_04	TTCGAGCTAAGACTTCAAATATCGGGAACGAG
B_05	ACAGTCAAAGAGAATCGATGAACGACCCCGGTTGATAATC
B_06	ATAGTAGTATGCAATGCCTGAGTAGGCCGGAG
B_07	AACCAGACGTTTAGCTATATTTTCTTCTACTA
B_08	GAATACCACATTCAACTTAAGAGGAAGCCCGATCAAAGCG
B_09	AGAAAAGCCCCAAAAAGAGTCTGGAGCAAACAATCACCAT
B_10	CAATATGACCCTCATATATTTTAAAGCATTAA
B_11	CATCCAATAAATGGTCAATAACCTCGGAAGCA
B_12	AACTCCAAGATTGCATCAAAAAGATAATGCAGATACATAA
B_13	CGTTCTAGTCAGGTCATTGCCTGACAGGAAGATTGTATAA
B_14	CAGGCAAGATAAAAATTTTTAGAATATTCAAC
B_15	GATTAGAGATTAGATACATTTCGCAAATCATA
B_16	CGCCAAAAGGAATTACAGTCAGAAGCAAAGCGCAGGTCAG
B_17	GCAAATATTTAAATTGAGATCTACAAAGGCTACTGATAAA
B_18	TTAATGCCTTATTTCAACGCAAGGGCAAAGAA

B_19	TTAGCAAATAGATTTAGTTTGACCAGTACCTT
B_20	TAATTGCTTTACCCTGACTATTATGAGGCATAGTAAGAGC
B_21	ATAAAGCCTTTGCGGGAGAAGCCTGGAGAGGGTAG
B_22	TAAGAGGTCAATTCTGCGAACGAGATTAAGCA
B_23	AACACTATCATAACCCATCAAAAATCAGGTCTCCTTTTGA
B_24	ATGACCCTGTAATACTTCAGAGCA
B_25	TAAAGCTATATAACAGTTGATTCCCATTTTTG
B_26	CGGATGGCACGAGAATGACCATAATCGTTTACCAGACGAC
B_27	TAATTGCTTGGAAGTTTCATTCCAAATCGGTTGTA
B_28	GATAAAAACCAAAATATTAAACAGTTCAGAAATTAGAGCT
B_29	ACTAAAGTACGGTGTCGAATATAA
B_30	TGCTGTAGATCCCCCTCAAATGCTGCGAGAGGCTTTTGCA
B_31	AAAGAAGTTTTGCCAGCATAAATATTCATTGACTCAACATGTT
B_32	AATACTGCGGAATCGTAGGGGGTAATAGTAAAATGTTTAGACT
B_33	AGGGATAGCTCAGAGCCACCACCCCATGTCAA
B_34	CAACAGTTTATGGGATTTTGCTAATCAAAAGG
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B_36	GCGCAGACTCCATGTTACTTAGCCCGTTTTAA
B_37	ACAGGTAGAAAGATTCATCAGTTGAGATTTAG
B_38	CCTCAGAACCGCCACCCAAGCCCAATAGGAACGTAAATGA
B_39	ATTTTCTGTCAGCGGAGTGAGAATACCGATAT
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Link-A3C	CTGTCCAGACGTATACCGAACGA
Link-A4C	TCAAGATTAGTGTAGCAATACT
Link-B1A	TGTAGCATTCCTTTTATAAACAGTT
Link-B2A	TTTAATTGTATTTCCACCAGAGCC
Link-B3A	ACTACGAAGGCTTAGCACCATTA
Link-B4A	ATAAGGCTTGCAACAAAGTTAC
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Link-C2B	CGGTGCGGGCCTTCCAAAAACATT
Link-C3B	ATGAGTGAGCTTTTAAATATGCA
Link-C4B	ACTATTAAAGAGGATAGCGTCC
Loop	GCGCTTAATGCGCCGCTACAGGGC
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C_02	CCTGATTAAAGGAGCGGAATTATCTCGGCCTC
C_03	GCAAATCACCTCAATCAATATCTGCAGGTCGA
C_04	CGACCAGTACATTGGCAGATTCACCTGATTGC
C_05	TGGCAATTTTTAACGTCAGATGAAAACAATAACGGATTCG
C_06	AAGGAATTACAAAGAAACCACCAGTCAGATGA
C_07	GGACATTCACCTCAAATATCAAACACAGTTGA
C_08	TTGACGAGCACGTATACTGAAATGGATTATTTAATAAAAG
C_09	CCTGATTGCTTTGAATTGCGTAGATTTTCAGGCATCAATA
C_10	TAATCCTGATTATCATTTTGCGGAGAGGAAGG
C_11	TTATCTAAAGCATCACCTTGCTGATGGCCAAC
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C_16	AGAATCAGAGCGGGAGATGGAAATACCTACATAACCCTTC
C_17	GCGCAGAGGCGAATTAATTATTTGCACGTAAATTCTGAAT
C_18	AATGGAAGCGAACGTTATTAATTTCTAACAAC
C_19	TAATAGATCGCTGAGAGCCAGCAGAAGCGTAA
C_20	GAATACGTAACAGGAAAAACGCTCCTAAACAGGAGGCCGA
C_21	TCAATAGATATTAAATCCTTTGCCGGTTAGAACCT
C_22	CAATATTTGCCTGCAACAGTGCCATAGAGCCG
C_23	TTAAAGGGATTTTAGATACCGCCAGCCATTGCGGCACAGA
C_24	ACAATTCGACAACTCGTAATACAT
C_25	TTGAGGATGGTCAGTATTAACACCTTGAATGG
C_26	CTATTAGTATATCCAGAACAATATCAGGAACGGTACGCCA

C_27	CGCGAACTAAAACAGAGGTGAGGCTTAGAAGTATT
C_28	GAATCCTGAGAAGTGTATCGGCCTTGCTGGTACTTTAATG
C_29	ACCACCAGCAGAAGATGATAGCCC
C_30	TAAAACATTAGAAGAACTCAAACTTTTTATAATCAGTGAG
C_31	GCCACCGAGTAAAAGAACATCACTTGCCTGAGCGCCATTAAAA
C_32	TCTTTGATTAGTAATAGTCTGTCCATCACGCAAATTAACCGTT
C_33	CGCGTCTGATAGGAACGCCATCAACTTTTACA
C_34	AGGAAGATGGGGACGACGACAGTAATCATATT
C_35	CTCTAGAGCAAGCTTGCATGCCTGGTCAGTTG
C_36	CCTTCACCGTGAGACGGGCAACAGCAGTCACA
C_37	CGAGAAAGGAAGGGAAGCGTACTATGGTTGCT
C_38	GCTCATTTTTTAACCAGCCTTCCTGTAGCCAGGCATCTGC
C_39	CAGTTTGACGCACTCCAGCCAGCTAAACGACG
C_40	GCCAGTGCGATCCCCGGGTACCGAGTTTTTCT
C_41	TTTCACCAGCCTGGCCCTGAGAGAAAGCCGGCGAACGTGG
C_42	GTAACCGTCTTTCATCAACATTAAAATTTTTGTTAAATCA
C_43	ACGTTGTATTCCGGCACCGCTTCTGGCGCATC
C_44	CCAGGGTGGCTCGAATTCGTAATCCAGTCACG
C_45	TAGAGCTTGACGGGGAGTTGCAGCAAGCGGTCATTGGGCG
C_46	GTTAAAATTCGCATTAATGTGAGCGAGTAACACACGTTGG
C_47	TGTAGATGGGTGCCGGAAACCAGGAACGCCAG
C_48	GGTTTTCCATGGTCATAGCTGTTTGAGAGGCG
C_49	GTTTGCGTCACGCTGGTTTGCCCCAAGGGAGCCCCCGATT
C_50	GGATAGGTACCCGTCGGATTCTCCTAAACGTTAATATTTT
C_51	AGTTGGGTCAAAGCGCCATTCGCCCCGTAATG
C_52	CGCGCGGGCCTGTGTGAAATTGTTGGCGATTA
C_53	CTAAATCGGAACCCTAAGCAGGCGAAAATCCTTCGGCCAA
C_54	CGGCGGATTGAATTCAGGCTGCGCAACGGGGGATG
C_55	TGCTGCAAATCCGCTCACAATTCCCAGCTGCA
C_56	TTAATGAAGTTTGATGGTGGTTCCGAGGTGCCGTAAAGCA
C_57	TGGCGAAATGTTGGGAAGGGCGAT
C_58	TGTCGTGCACACAACATACGAGCCACGCCAGC
C_59	CAAGTTTTTTGGGGTCGAAATCGGCAAAATCCGGGAAACC
C_60	TCTTCGCTATTGGAAGCATAAAGTGTATGCCCGCT
C_61	TTCCAGTCCTTATAAATCAAAAGAGAACCATCACCCAAAT
C_62	GCGCTCACAAGCCTGGGGTGCCTA
C_63	CGATGGCCCACTACGTATAGCCCGAGATAGGGATTGCGTT
C_64	AACTCACATTATTGAGTGTTGTTCCAGAAACCGTCTATCAGGG
C_65	ACGTGGACTCCAACGTCAAAGGGCGAATTTGGAACAAGAGTCC