# Routing of individual polymers in designed patterns

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#### **Materials and Methods**

#### Reagents and equipment

All chemicals were purchased from Sigma-Aldrich and used without further purification unless otherwise stated. HPLC grade solvents were used and anhydrous solvents were purchased in Sure/Seal bottles with inert atmospheres or dried using an MBRAUN MB SPS-800 Solvent Purification System. Reactions were carried out under argon atmosphere unless otherwise stated (argon gas was dried over phosphorus pentoxide). Organic reactions were monitored by thin-layer chromatography (TLC) whenever possible and flash chromatography was carried out on Silica gel 60 (230 -400 mesh). NMR spectra were recorded on a Varian Gemini System connected to a 400 MHz Oxford magnet or on a Bruker Avance III HD system connected to a 400 MHz Bruker Ascend magnet. Chemical shifts are reported in ppm and corrected according to the solvent residual peak<sup>31</sup>. Mass spectra of small molecules were obtained on a Bruker Maxis Impact (ESI-TOF) using a Dionex Ultimate 3000 RS (HPLC) as interface. Melting points were obtained on a BÜCHI Melting Point B-540 system. Water used for DNA experiments was purified on a Milli-Q Biocel system by Millipore. DNA oligonucleotides used as staple strands in DNA origami structures were desalted by the manufacturer. DNA origami scaffold (M13mp18) was purchased from New England BioLabs. DNA oligonucleotides were purchased from Sigma-Aldrich or synthesized in house on a BioAutomation MerMade-12 automated oligonucleotide synthesizer. Preloaded standard 1000Å CPG columns were purchased from BioAutomation in the US and used for the synthesis of unmodified DNA oligos. Standard chemicals used in the automated DNA synthesis and preloaded 3000Å CPG were purchased from Link Technologies Ltd in Scotland: Deblock mix (3% trichloroacetic acid in dichloromethane), ETT activator (0.25 M 5-ethylthio-1H-tetrazole in anhydrous acetonitrile), cap mix A (tetrahydrofuran/lutidine/acetic anhydride), cap mix B (10% methylimidazole in THF), oxidizer (0.02 M lodine in tetrahydrofuran/pyridine/water). Acetonitrile was purchased as DNA synthesis grade from Sigma Aldrich and stored over molecular sieves purchased from BioAutomation in the US. Dichloromethane was purchased as HPLC grade and

stored over molecular sieves purchased from VWR. Synthesized oligonucleotides were cleaved from the solid-support either using 33% ammonium hydroxide solution or AMA (ammonia hydroxide 30-33% and aq. methylamine 40% v/v 1:1). Oligonucleotides were HPLC purified on an Agilent 1100 or 1200 Series HPLC systems equipped with a Phenomenex Clarity 3u Oligo-RP, 50 mm x 4.6 mm column running a gradient of MeCN in TEAA (100 mM, pH 7) buffer. All DNA concentrations were determined using a Nanodrop ND -1000 spectrophotometer. Mass spectra of oligonucleotides were either obtained on a Bruker Daltonics Autoflex Speed MALDI -TOF MS spectrometer using AnchorChip target plates, or on a Shimadzu LCMS-2020EV connected to a Shimadzu Prominence RP-UPLC system equipped with a Phenomenex Gemini 3u C18, 100 mm x 4.6 mm column and running a gradient of MeOH in 1,1,1,3,3,3-hexafluoroisopropanol/triethylamine buffer (HFIP, 100 mM / TEA, 8 mM). The matrix used for MALDI -TOF MS was 90% 3hydroxypicolinic acid (50 mg/mL) in water/MeCN 1:1 and 10% diammonium citrate (50 mg/mL) in water. Gel permeation chromatography (GPC) was performed on a system comprising an LC-20AD Shimadzu HPLC pump, a Shimadzu RID-10A refractive index detector and a DAWN HELEOS 8 LS detector. For polymers soluble in organic solvents, the system was equipped with an Mz-Gel SDplus Linear column with 5 µm particles length of 300 mm and an internal diameter of 8 mm from MZ-Analysentechnik providing an effective molecular weight range of 1,000-1,000,000. The eluent was DMF with 10 mM LiBr at 30 °C (flow rate: 1 mL min<sup>-1</sup>). For polymers soluble in water, the system was equipped with a HEMA-Bio Linear column with 10 µm particles, a length of 300 mm and an internal diameter of 8 mm from MZ-Analysentechnik providing an effective molecular weight range of 1,000–1,000,000. The eluent is 0.1 µm filtered PBS buffer (0.01 M phosphate, NaCI 0.138 M, KCI 0.027 M) with 300 ppm sodium azide to inhibit bacterial growth. XPS data acquisition was performed using a Kratos Axis UltraDLD instrument (Kratos Analytical Ltd., Telford, UK) equipped with a monochromated Alk $\alpha$  x-ray source (hv = 1486.6 electron volts, eV) operated at 15 kV and 10 mA (150 W). A hybrid lens mode was employed during analysis with an analysis area of approximately 700  $\mu$ m × 300  $\mu$ m. The XPS spectra for all samples were taken

at a photoemission angle of 0°, which has a probe depth of around 10 nm. Survey spectra (Binding Energy (B.E.) of 0 - 1100 eV with pass energy of 160 eV) were used for element identification and quantification. The acquired data were converted to VAMAS format and analysed using CASAXPS software. Absorbance spectra and DNA melting profiles were recorded at a Varian Cary 100 Bio UV-visible spectrophotometer using a Hellma Quartz Suprasil 4 mm x 10 mm, 1400 µL cuvette. For some of the absorption measurements we used a Cary 60 instrument from Agilent Technologies. Fluorescence measurements were recorded at a Horiba JobinYvon FluoroMax-3 instrument using a Hellma Quartz Suprasil 3 mm x 3 mm, 60 µL cuvette. DNA origami structures were annealed on an Eppendorf Mastercycler Personal thermal cycler.

For the 3D PAINT superresolution imaging, the non-modified DNA oligonucleotides were purchased from Integrated DNA Technologies (Coralville, IA). Fluorescently modified DNA oligonucleotides were purchased from Biosynthesis (Lewisville, TX). Streptavidin was purchased from Invitrogen (S-888, Carlsbad, CA). Bovine serum albumin (BSA), and BSA-Biotin was obtained from Sigma Aldrich (A8549, St. Louis, MO). Glass slides and coverslips were purchased from VWR (Radnor, PA). Trolox, PCA (protocatechuic acid), and PCD (protocatechuate 3,4-dioxygenase) were purchased from Sigma Aldrich (238813-1G, 03930590-50MG, P8279-25UN, St. Louis, MO).

#### Synthesis of monomer 3 used for polymerization via the dithiocarbamate precursor route

An overview of the synthesis of the monomer shown in Supplementary Fig. 1.



**Supplementary Fig. 1.** Detailed scheme of the synthesis of the monomer (**3**) used for the formation of poly(APPV-TBDPS) via the dithiocarbamate precursor route. The monomer was synthesized in 7 steps from commercially available triethylene glycol and 2,5-dihydroxy-terephthalic acid diethyl ester.

Synthesis of 2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecan-12-ol (5)<sup>46-48</sup>



To a flask were added triethylene glycol (24.3 mL, 182 mmol), TBDPSCI (9.46 mL, 36.4 mmol), imidazole (248 mg, 3.64 mmol), anhydrous DMF (50 mL) and anhydrous DIPEA (7.12 mL, 40

mmol). After stirring at rt for 3 hours, the solution was diluted with EtOAc (200 mL) and washed with H<sub>2</sub>O (2 x 80 mL) and sat. aq. NaCl (2 x 80 mL). The organic layer was dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (Et<sub>2</sub>O) afforded **(5)** as a clear oil (12.33 g, 87%). <sup>1</sup>H NMR (400 MHz, (CD<sub>3</sub>)<sub>2</sub>CO)  $\delta$  7.76 - 7.73 (m, 4H), 7.46 - 7.41 (m, 6H), 3.83 (dd, J = 4.6, 5.6 Hz, 2H), 3.64 - 3.60 (m, 8H), 3.54 - 3.49 (m, 3H), 1.05 (s, 9H).<sup>13</sup>C NMR (100 MHz, (CD<sub>3</sub>)<sub>2</sub>CO)  $\delta$  135.5, 133.6, 129.7, 127.7, 72.7, 72.2, 70.5, 70.3, 63.5, 61.1, 26.3, 18.9.HRMS (ESI): [M+K]; Calc.: 427.1701, found: 427.1703.

Synthesis of 2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecan-12-yl 4methylbenzenesulfonate (6)



To a flask were added (**5**) (9.10 g, 23.42 mmol), TsCl (4.46 g, 23.42 mmol) and anhydrous DCM (230 mL). To this solution was added finely powdered KOH (10.51 g, 187.35 mmol) in small portions. The solution was stirred at rt for 1 hour before the mixture was diluted with H<sub>2</sub>O (100 mL) and the aqueous layer extracted with DCM (3 x 100 mL). The combined organic layers were dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (pentane/Et<sub>2</sub>O 3:1 to 2:3) afforded (**6**)as a clear oil (11.32 g, 89%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.80 (d, *J* = 8.2 Hz, 2H), 7.70 (dd, *J* = 1.6, 7.9 Hz, 4H), 7.45 - 7.36 (m, 6H), 7.32 (d, *J* = 8.0 Hz, 2H), 4.16 (dd, *J* = 4.3, 5.4 Hz, 2H), 3.82 (dd, *J* = 5.0, 5.5 Hz, 2H), 3.69 (dd, *J* = 4.5, 5.2 Hz, 2H), 3.60 - 3.55 (m, 6H), 2.42 (s, 3H), 1.07 (s, 9H).<sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>)  $\delta$  144.8, 135.6, 133.7, 133.0, 129.8, 129.6, 128.0, 127.7, 72.5, 70.8, 70.7, 69.3, 68.7, 63.4, 26.8, 21.6, 19.2.HRMS (ESI): [M+Na]; Calc.: 565.2051 found: 565.2051.

Synthesis of diethyl 2-hydroxy-5-methoxyterephthalate (7)



To 2,5-dihydroxy-terephthalic acid diethyl ester (10.00 g, 39.33 mmol) were added acetone (130 mL) and anhydrous K<sub>2</sub>CO<sub>3</sub> (5.44 g, 39.33 mmol). The mixture was heated to reflux and then iodomethane (2.69 mL, 43.27 mmol) was added. The solution was refluxed for 24 hours before the solvent was removed *in vacuo*. The residue was dissolved in DCM (120 mL), H<sub>2</sub>O (60 mL) and sat. aq. NH<sub>4</sub>Cl (60 mL). The layers were separated and the aqueous phase extracted with DCM (2 x 100 mL). The combined organic layers were dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (pentane/Et<sub>2</sub>O 4:1 to 2:1) afforded (**7**) as a slightly yellow solid (4.55 g, 43%).<sup>1</sup>H NMR (400 MHz, (CD<sub>3</sub>)<sub>2</sub>CO)  $\delta$  10.38 (s, 1H), 7.48 (s, 1H), 7.17 (s, 1H), 4.47 (q, *J* = 7.1 Hz, 2H), 4.32 (q, *J* = 7.1 Hz, 2H), 3.83 (s, 3H), 1.42 (t, *J* = 7.1 Hz, 3H), 1.34 (t, *J* = 7.1 Hz, 3H).<sup>13</sup>C NMR (100 MHz, (CD<sub>3</sub>)<sub>2</sub>CO)  $\delta$  169.1, 164.8, 155.0, 150.3, 129.4, 118.8, 114.5, 112.5, 61.9, 60.9, 56.2, 13.6, 13.5.HRMS (ESI): [M+Na]; Calc.: 291.0839, found: 291.0840.M<sub>P</sub> (uncorr.) 52.5 - 53.8 °C.

Synthesis of diethyl 2-((2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecan-12-yl)oxy)-5methoxyterephthalate (2)



To a flask were added (7) (8.75 g, 16.12 mmol), (6) (4.54 g, 16.93 mmol) and anhydrous DMF (65 mL). The mixture was heated to 90 °C before K<sub>2</sub>CO<sub>3</sub> (4.46 g, 32.24 mmol) was added. The mixture became yellow and was stirred for 3 hours at 90 °C. After cooling to rt the mixture was diluted with EtOAc (150 mL) and the organic layer was washed with H<sub>2</sub>O (2 x 100 mL) and sat. aq. NaCl (2 x 50 mL). The organic layer was dried over Na<sub>2</sub>SO<sub>4</sub> and concentrated*in vacuo*. Flash chromatography on silica (pentane/Et<sub>2</sub>O 2:1 to Et<sub>2</sub>O) afforded (**2**) as a clear oil (9.72 g, 94%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.70 - 7.67 (m, 4H), 7.41 - 7.34 (m, 8H), 4.35 (tq, *J* = 0.9, 7.0 Hz, 4H), 4.16 (t, *J* = 5.0 Hz, 2H), 3.87 - 3.85 (m, 5H), 3.82 (t, *J* = 5.3 Hz, 2H), 3.72 - 3.65 (m, 4H), 3.61 (t, *J* = 5.3 Hz, 2H), 1.36 (dt, *J* = 0.8, 7.1 Hz, 6H), 1.05 (s, 9H).<sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>)  $\delta$  165.7, 165.3, 152.8, 151.5, 135.6, 133.7, 129.6, 127.6, 125.3, 124.3, 117.9, 115.2, 72.5, 71.0, 70.8, 70.0, 69.7, 63.4, 61.3, 61.3, 56.7, 26.8, 19.2, 14.3 (2H).HRMS (ESI): [M+K]; Calc.: 677.2543, found: 677.2541.

Synthesis of (2-((2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecan-12-yl)oxy)-5-methoxy-1,4phenylene)dimethanol (8)



To a flask were added (**2**) (9.72 g, 15.22 mmol) and anhydrous THF (150 mL). The solution was cooled to 0 °C and LiAlH<sub>4</sub> (2.31 g, 60.86 mmol) was slowly added. The reaction was stirred for 10 minutes before quenched with a mixture of H<sub>2</sub>O and THF 1:2. The mixture was diluted with H<sub>2</sub>O (250 mL) and sat. aq. NaCl (100 mL). The aqueous layer was extracted with DCM (3 x 200 mL). The combined organic layers were dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (Et<sub>2</sub>O to Et<sub>2</sub>O/acetone 10:2) afforded (**8**) as a clear oil (8.40 g, 99%).<sup>1</sup>H NMR (400 MHz, (CD<sub>3</sub>)<sub>2</sub>CO)  $\delta$  7.76 - 7.73 (m, 4H), 7.45 - 7.40 (m, 6H), 7.09 (s, 1H), 7.01 (s, 1H),

4.63 (t, *J* = 6.0 Hz, 4H), 4.11 (dd, *J* = 4.0, 5.5 Hz, 2H), 3.96 (q, *J* = 6.0 Hz, 2H), 3.84 (dd, *J* = 4.8, 5.4 Hz, 2H), 3.81 - 3.78 (m, 2H), 3.78 (s, 3H), 3.67 - 3.61 (m, 6H), 1.05 (s, 9H).<sup>13</sup>C NMR (100 MHz, (CD<sub>3</sub>)<sub>2</sub>CO) δ 150.7, 150.0, 135.5, 133.7, 130.2, 129.7, 129.6, 127.7, 112.3, 110.2, 72.2, 70.6, 70.5, 69.6, 68.7, 63.5, 59.6, 59.0, 55.2, 26.3, 8.9.HRMS (ESI): [M+Na]; Calc.: 577.2592, found: 577.2593.

Synthesis of 12-(2,5-bis(chloromethyl)-4-methoxyphenoxy)-2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecane (9)



To a flask was added anhydrous DCM (400 mL), which was cooled to 0 °C before SOCI<sub>2</sub> (7.37 mL, 101.6 mmol) was added. To this mixture was added a solution of (8) (9.40 g, 16.94 mmol) in anhydrous DCM (25 mL). The reaction was stirred at 0 °C for 2 hours and then diluted with H<sub>2</sub>O (200 mL) and sat. aq. NaCI (200 mL). The aqueous layer was extracted with DCM (2 x 200 mL). The combined organic layers were dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (pentane/Et<sub>2</sub>O 3:1 to 3:2) afforded (**9**) as a clear oil (7.36 g, 73%). <sup>1</sup>H NMR (400 MHz, CDCI<sub>3</sub>)  $\delta$  7.70 - 7.67 (m, 4H), 7.43 - 7.35 (m, 6H), 6.94 (s, 1H), 6.91 (s, 1H), 4.64 (s, 2H), 4.60 (s, 2H), 4.14 (dd, *J* = 4.7, 5.3 Hz, 2H), 3.86 - 3.81 (m, 7H), 3.72 - 3.66 (m, 4H), 3.62 (t, *J* = 5.4 Hz, 2H), 1.05 (s, 9H).<sup>13</sup>C NMR (100 MHz, CDCI<sub>3</sub>)  $\delta$  151.5, 150.4, 135.6, 133.7, 129.6, 127.6 (2C), 126.9, 115.4, 113.1, 72.5, 71.0, 70.9, 69.8, 69.3, 63.5, 56.2, 41.3, 41.2, 26.9, 19.2.HRMS (ESI): [M+Na]; Calc.: 613.1914, found: 613.1924.

# Synthesis of (2-((2,2-dimethyl-3,3-diphenyl-4,7,10-trioxa-3-siladodecan-12-yl)oxy)-5-methoxy-1,4phenylene)bis(methylene) bis(diethylcarbamodithioate) (**3**)



To a flask were added (9) (7.36 g, 12.44 mmol), anhydrous MeCN (125 mL) and sodium diethyldithiocarbamatetrihydrate (16.82 g, 74.64 mmol). The solution was stirred at rt for 1 hour and then diluted with H<sub>2</sub>O (100 mL) and sat. aq. NaCl (100 mL). The aqueous layer was extracted with DCM (2 x 300 mL). The combined organic layers were dried over Na<sub>2</sub>SO<sub>4</sub> and the solvent removed *in vacuo*. Flash chromatography on silica (pentane/EtOAc 19:1 to 3:1) afforded (**3**) as a clear oil (10.10 g, 99%).<sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.70 - 7.66 (m, 4H), 7.43 - 7.34 (m, 6H), 7.04 (s, 1H), 7.03 (s, 1H), 4.59 (s, 2H), 4.53 (s, 2H), 4.10 (dd, *J* = 4.9, 5.2 Hz, 2H), 4.03 (q, *J* = 7.0 Hz, 4H), 3.82 (q, *J* = 5.1 Hz, 4H), 3.79 (s, 3H), 3.71 - 3.64 (m, 8H), 3.61 (t, *J* = 5.4 Hz, 2H), 1.28 - 1.20 (m, 12H), 1.05 (s, 9H).<sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>)  $\delta$  196.1, 196.0, 151.8, 150.7, 135.7, 133.8, 129.7, 127.7, 125.6, 124.8, 115.6, 113.9, 72.6, 71.1, 71.0, 70.0, 69.1, 63.6, 56.3, 49.5, 46.7, 36.8, 36.8, 27.0, 19.3, 12.6, 11.8.HRMS (ESI): [M+K]; Calc.: 855.2786, found: 855.2793.

# Synthesis of APPV polymers





**Supplementary Fig. S2.** The monomer (**3**) is deprotonated using LHMDS in THF and then it polymerizes into the prepolymer (**10**). This prepolymer is converted into poly(APPV-TBDPS) (**4a**) via thermal elimination at 180 °C in 1,2-dichlorobenzene. To prepare the APPV-TBDPS polymer for DNA functionalization, a fraction of the TBDPS ethers is removed using HF-pyridine to afford the partially deprotected random-copolymer; poly[(APPV-TBDPS)-*ran*-(APPV-OH)] (**4b**).

Procedure for polymerization via the dithiocarbamate precursor route to afford the prepolymer (10)



The method is based on a report by J. Vandenbergh *et al*<sup>49</sup>. Monomer (**3**) was added to a flask that had been cleaned with methanol and thoroughly flame dried. The flask was evacuated for 2 hours before it was refilled with argon. Anhydrous THF (inhibitor free, volume specified in Supplementary Table 1) was added and the monomer was allowed to dissolve for 30 minutes, after which the mixture was degassed with argon for 20 minutes. The solution was heated to 35 °C, and then LHMDS (1.0 M in THF, 1.5 eq., volume specified in Supplementary Table 1) was added in one portion. The solution was stirred under argon flow for 60 min. The mixture was diluted with 2methyltetrahydrofuran (100 mL) and washed with H<sub>2</sub>O (2 x 100 mL). The organic layer was separated and the solvent removed *in vacuo* to afford a yellow foam. The crude prepolymer (**10**) was dried *in vacuo* for 16 hours before it was subjected to the following thermal elimination without further purification or characterization.

**Supplementary Table 1.** Final concentration of monomer and amount of monomer, solvent, and base added.

| Final concentration | Monomer (3) | THF     | LHMDS (1.0 M in THF) |
|---------------------|-------------|---------|----------------------|
| 0.08 M              | 966 mg      | 13.0 mL | 1.77 mL              |
| 0.10 M              | 839 mg      | 8.5 mL  | 1.54 mL              |
| 0.15 M              | 711 mg      | 4.5 mL  | 1.30 mL              |
| 0.20 M              | 724 mg      | 3.0 mL  | 1.33 mL              |

#### Procedure for thermal elimination of the TBDPS-prepolymer to afford the APPV-TBDPS polymer

(4a)



The method is based on a previous report by J. Vandenbergh *et al.*<sup>35</sup>. To a thoroughly flame-dried and argon filled three necked flask was added a solution of the prepolymer (10) in 1,2dichlorobenzene. Dissolvation and transfer of the prepolymer were performed under argon atmosphere and gentle heating to improve polymer solubility. Additional 1,2-dichlorobenzene was added until a volume of around 300 mL. It was important to keep the concentration of prepolymer low (below 3 mg per mL solvent) due to gelation issues in the reaction. The solution was degassed with argon for 1 hour before the mixture was refluxed for 3 hours at 180 °C in complete darkness using a heating mantle. The now orange solution was allowed to cool to rt, after which the solvent was removed in vacuo until approximately 10 mL remained (the temperature was set to 70 °C and the rotary evaporator was connected to a Schlenk line to achieve lower pressure). After the elimination reaction, light was avoided as much as possible. The resulting dark orange polymer residue was precipitated in MeOH (600 mL) directly from 1,2-dichlorobenzene to afford a dark red polymer. The polymer was dried in vacuo for 36 hours to yield the desired product (4a) as a red solid.<sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  7.66 (br d, J = 5.9, 4H), 7.46 (br s, 1H), 7.40 - 7.32 (br m, 6H), 7.16 (br s, 1H), 4.21 (br s, 2H), 3.92 (br s, 3H), 3.78 - 3.58 (m, 10H), 1.02 (s, 9H).<sup>13</sup>C-NMR (100 MHz, CDCl<sub>3</sub>) δ 135.6, 133.7, 129.6, 127.6, 77.2, 72.5, 71.0, 70.8, 70.0, 63.4, 26.8, 19.2. The observed broadening of the <sup>1</sup>H NMR signals and missing backbone signals in the <sup>13</sup>C NMR analysis, likely arise from inhomogeneous broadening due to for example aromatic ring stacking, aggregation, and inhomogeneity in the backbone.

**Supplementary Table 2.** Amount of prepolymer (**10**) added (estimated with 100% yield from the polymerization reaction), solvent, and yield over two steps.





Supplementary Fig. 3. <sup>1</sup>H NMR of poly(APPV-TBDPS) (4a) in CDCI<sub>3</sub>.

#### Supplementary Information



Supplementary Fig. 4. <sup>13</sup>C-NMR of poly(APPV-TBDPS) (4a) in CDCI<sub>3</sub>.

Procedure for partial removal of TBDPS ethers from poly(APPV-TBDPS) to provide the random copolymer poly[(APPV-TBDPS)-*ran*-(APPV-OH)] **(4b)**.



To the APPV-TBDPS polymer (**4a**) (75 mg, 145 µmol TBDPS groups) in a 50 mL Corning centrifuge tube (polypropylene tube) was added THF (22 mL, polymer concentration of 3.4 mg/mL)

and the polymer was allowed to dissolve for 48 hours. A mixture of HF-Pyridine 70%, THF and pyridine (3.1 mL, v/v 1:8:2, approx. 11 mmol HF, 75 eq.) was added, and the mixture was stirred at rt for 90 minutes before it was directly precipitated in MeOH (600 mL) to obtain (**4b**) as a red solid. The polymer was dried *in vacuo* for 16 hours before further use.

As an example, the naming of the resulting copolymer poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M was performed in correspondence to the starting material poly(APPV-TBDPS) 0.20 M.

As will be mentioned later, poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M was used for the synthesis of all poly(APPV-DNA) used.

The experiment was performed in plastic equipment, and HF solutions were handled with plastic pipettes to avoid corrosion and loss of active fluoride due to reaction with glassware. For the optimization of the partial deprotection reaction initial experiments were performed on low molecular weight polymers from the 0.08 M APPV-TBDPS polymerization. The partial deprotection could easily be observed by both ATR-IR and <sup>1</sup>H NMR, where the presence of an alcohol and the loss of the TBDPS ether were observed respectively. For the higher molecular weight (APPV-TBDPS) polymers, 0.15 M and 0.20 M polymerizations, the polymers had an increased tendency to aggregate upon removal of the protection groups.



<u>Supplementary</u> Fig. 5. ATR-FTIR data of poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.08 M (4b). Poly(APPV-TBDPS) 0.08 M (4a) was deprotected with HF using the procedure given above, and the reaction was quenched by precipitation in MeOH at different reaction times 0 (black), 30 (red), 60 (blue), 90 (cyan), 120 (magenta), and 150 (green) minutes. The resulting polymers were washed with MeOH and dried *in vacuo* for 16 hours before analysis (the arrow indicates the formation of alcohol groups during the reaction). The spectra have been normalized at 1111 cm<sup>-1</sup>.



**Supplementary** Fig. 6. <sup>1</sup>H NMR spectra of poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.08 M (4b). Poly(APPV-TBDPS) 0.08 M (4a) was deprotected with HF using the procedure given above, and the reaction was quenched by precipitation in MeOH at different reaction times of 0 (red), 30 (green), 60 (blue), and 90 (purple) minutes. The resulting polymers were washed with MeOH and dried *in vacuo* for 16 hours before analysis in CDCl<sub>3</sub>. The arrows indicate increasing reaction times. The removal of the silyl ether is evident by the decrease in the integral (indicated by arrows) relative to the ethers between 4.50 and 3.00 ppm. For reaction times of 120 and 150 minutes liquid state NMR was not possible.



**Supplementary Fig. 7.** a) <sup>1</sup>H NMR of poly(APPV-TBDPS) 0.20 M (**4a**) in CDCl<sub>3</sub>. b) <sup>1</sup>H-NMR of poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M (**4b**) in CDCl<sub>3</sub>. Based on the integral from the *tert*-butyl groups on the TBDPS moiety, it was estimated that 35% of the protective groups were removed. The analyzed poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M sample was prepared by treating poly(APPV-TBDPS) 0.20 M with HF for 90 minutes using the procedure given above. The viscosity of this sample was very high and aggregation was observed. To ease handling and avoid

precipitation, a degree of removal of TBDPS below 35% was generally persued. During deprotection some variation in the required reaction time was observed, probably due to the moisture sensitivity of the HF-pyridine mixture.

## Mass analysis of the APPV-TBDPS polymer by GPC

The APPV-TBDPS polymers were analyzed by GPC (gel permeation chromatography) at 30 °C using a mobile phase of DMF. Prior to analysis, polymers were allowed to dissolve for a minimum of 4 hours at 80 °C to obtain a well dispersed solution.

The specific refractive index increment (dn/dc) for poly(APPV-TBDPS) in DMF at 30 °C was estimated to  $0.2070 \pm 0.0048$  mL/g using the refractive index of various concentrations of poly(APPV-TBDPS) 0.08 M. The data is shown below in Supplementary Fig. 8.

The mass distributions of poly(APPV-TBDPS) polymerized at different monomer concentrations are summarized in Supplementary Table 3.



Supplementary Fig. 8. Determination of dn/dc of poly(APPV-TBDPS) in DMF using refractive

index. The (+) represents the data and the (-) represents the fit.

Supplementary Table 3. GPC analysis of fully intact poly(APPV-TBDPS) (0.08 M, 0.1 M, 0.15 M,

and 0.2 M).

| Sample                  | Mn           | Mw            | PDI           | Rz rms        | dn/dc  |
|-------------------------|--------------|---------------|---------------|---------------|--------|
|                         | (kDa)        | (kDa)         | (Mw/Mn)       | (nm)          | (mL/g) |
| poly(APPV-TBDPS) 0.08 M | 48.8 (±1.8%) | 69.7 (±0.5%)  | 1.440 (±1.8%) | 13.3 (±8.8%)  | 0.2070 |
| poly(APPV-TBDPS) 0.10 M | 51.4 (±3.0%) | 71.1 (±0.9%)  | 1.385 (±3.2%) | 16.3 (±10.3%) | 0.2070 |
| poly(APPV-TBDPS) 0.15 M | 59.1 (±2.1%) | 90.4 (±0.4%)  | 1.530 (±2.1%) | 17.9 (±3.4%)  | 0.2070 |
| poly(APPV-TBDPS) 0.20 M | 66.9 (±1.6%) | 100.4 (±0.4%) | 1.501 (±1.6%) | 19.2 (±2.9%)  | 0.2070 |

## Automated DNA synthesis on the APPV-polymer.



**Supplementary Fig. 9.** Synthetic scheme for the preparation of the APPV-DNA polymer. Step 1) CPG 3000 preloaded with thymidine is deprotected and the resulting alcohol group is converted into a phosphoramidite using 2-cyanoethyl *N*,*N*-diisopropylchlorophosphoramidite and DIPEA in DCM. Step 2) The phosphoramidite modified CPG allows for immobilization of poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M (**4b**) when added simultaneously with activator. Step 3) After

immobilization, polymer **4b** is deprotected with TBAF in THF to further expose the alcohol groups for DNA synthesis. Step 4) Using normal DNA synthesis, the alcohol groups on the APPV polymer can be functionalized with DNA, synthesized one nucleotide at a time (green strand). Step 5) After DNA synthesis, the APPV-DNA polymer is cleaved from the CPG 3000 and the protective groups removed using ultrafast deprotection conditions (AMA, 65 °C, 15 minutes) and the resulting poly(APPV-DNA) immediately purified using SEC CL-2B material and a mobile phase of TEAA (50 mM, pH 7).

# <u>General procedure for immobilization of poly[(APPV-TBDPS)-ran-(APPV-OH)]</u> 0.20 M (**4b**) on CPG 3000 and subsequent oligonucleotide synthesis directly on the immobilized polymers

The synthesis of DNA coated APPV polymer, poly(APPV-DNA) was solely performed on a MerMade 12 oligonucleotide synthesizer from Bioautomation using a fully automated procedure. This equipment is based on small columns loaded with CPG3000, and the different reagents are added to the column and eluted from the CPG using reduced pressure. Two amidite positions on the synthesizer, one containing a solution of 2-cyanoethyl N,N-diisopropylchlorophosphoramidite (200 µL) in anhydrous DCM (5 mL) and the other containing anhydrous DIPEA, were modified in such a way, that the two solutions were injected simultaneously to the synthesis column. This approach evades premixing of the chemicals prior to synthesis and allows for prolonged storage of the chemicals under argon atmosphere on the automated synthesizer. To functionalize the 3000Å CPG (preloaded with 200 nmol thymidine) as a phosphoramidite, the solid support was subjected to the following steps; 2 x deblock, 2 x MeCN wash, 3 x coupling steps with 2-cyanoethyl N,Ndisopropylchlorophosphoramidite in DCM added together with DIPEA, and then 5 x MeCN wash. The poly[(APPV-TBDPS)-ran-(APPV-OH)] 0.20 M (4b) (7 mg) was dissolved in anhydrous CHCl<sub>3</sub> (4 mL) and added to the column together with activator (0.25 M 5-ethylthio-1H-tetrazole in anhydrous acetonitrile). The following steps were performed in the immobilization of the polymer to the solid support; 1 x coupling steps with the poly[(APPV-TBDPS)-ran-(APPV-OH)] 0.20 M in

CHCl<sub>3</sub> added together with activator, 10 x DCM wash, 4 x MeCN wash. To remove the majority of remaining silyl ethers on the polymer, TBAF in THF (1 M) was added to the column without any additives. The following steps were used for this procedure; 2 x TBAF treatments, 4 x MeCN wash, 2 x DMF wash, 2 x TBAF treatments, 4 x MeCN wash, 2 x DMF wash, 2 x TBAF treatments, 4 x MeCN wash, 2 x DMF wash. The free alcohol groups on the immobilized polymer were used as handles for the DNA coating. The following steps in the automated synthesis were used for synthesis of each nucleotide on the polymer; 2 x deblock, 2 x MeCN wash, 2 x coupling of nucleoside phosphoramidite, 4 x MeCN wash, 2 x DMF wash, 4 MeCN wash, 2 x coupling of nucleoside phosphoramidite, 4 x MeCN wash, 2 x DMF wash, 4 MeCN wash, 2 x coupling of nucleoside phosphoramidite, 1 x MeCN wash, 1 x capping, 1 x oxidation, 2 x MeCN wash.

Deblock, capping, and oxidation steps were omitted before the first nucleotide was applied to the polymer since the OH groups on the polymer are already deprotected.

The following reaction times per addition were used in the reactions (number of vacuum pulses, wait time between vacuum pulses, and amount added): Nucleoside phosphoramidite (4 x 15 seconds, 70  $\mu$ L amidite, 85  $\mu$ L activator), phosphoramidite formation on CPG (8 x 75 seconds, 125  $\mu$ L 2-cyanoethyl *N*,*N*-diisopropylchlorophosphoramidite in CHCl<sub>3</sub>, 125  $\mu$ L DIPEA), polymer immobilization (8 x 75 seconds, 125  $\mu$ L polymer, 125  $\mu$ L activator), TBAF cleavage (8 x 75 seconds, 250  $\mu$ L 1.0 M TBAF in THF), MeCN wash (1 x 10 seconds, 250  $\mu$ L MeCN), DCM wash (1 x 60 seconds, 200  $\mu$ L DCM), DMF wash (8 x 75 seconds, 250  $\mu$ L DMF), deblock mix (4 x 10 seconds, 150  $\mu$ L deblock mix), capping (5 x 8 seconds, 75  $\mu$ L cap mix A, 75  $\mu$ L cap mix B), and oxidizer (3 x 15 seconds, 150  $\mu$ L oxidizer).

### Procedure for purification of poly(APPV-DNA)

The PPV-DNA was cleaved from the CPG by ultrafast deprotection conditions using AMA (ammonia hydroxide 30-33% and aq. methylamine 40% v/v 1:1) at 65 °C for 15 minutes. The

mixture was cooled and loaded onto a size exclusion column (PD-10 columns packed with Sepharose CL-2B material) and eluted with TEAA (50 mM, pH 7) buffer. Fractions containing poly(APPV-DNA) were lyophilized, dissolved in water, and again lyophilized before stored at -20 °C. Care was taken to avoid light during the purification and storage. Before use, the polymers were dissolved in water. Early fractions contain high molecular weight poly(APPV-DNA) while later fractions contain small molecules such as DNA strand, ammonia hydroxide, methyl amine, and protective groups. The polymers were analysed using GPC and the data is shown in Supplementary Table 4.

The poly(APPV-DNA) samples were named according to the fraction number from the purification, e.g. poly(APPV-DNA) fr. 3. The earliest fraction containing poly(APPV-DNA) was fraction 3. For the AFM imaging mentioned later, poly(APPV-DNA) fr. 3 was used, as this fraction contains polymers of highest molecular weight.

Several attempts were made to improve the quality and decrease the polydispersity of the APPV-DNA polymers. Prior to the DNA synthesis, attempts were made to purify the APPV-TBDPS polymers on Biorad SX-1 material using THF as the eluent. However, no significant improvements of the lengths or PDIs were observed by AFM of the resulting APPV-DNA polymers. In order to separate high molecular weight poly(APPV-DNA) from low molecular weight ones, gel electrophoresis using a 0.4% agarose gel was attempted. Samples taken before and after SEC purification on CL-2B material were analyzed and the resulting gel is shown in Supplementary Fig. 10. It is observed that the APPV-DNA polymers in early fractions tend to remain in the wells, while the lower molecular ones migrate in the gel.



**Supplementary Fig. 10.** Gel electrophoresis (0.4% agarose, 50 V, 2 hours, SYBR® Gold stain) of poly(APPV-DNA) before and after SEC purification. Lane 1 and 10: Before SEC purification. Lane 2 to 9: Selected fractions from SEC purification using CL-2B as solid phase.

Dialysis of the APPV-DNA polymers using Biotech CE tubing MWCO 1000 kDa proved unsuccessful since the polymers either could not penetrate the pores in the membrane material or simply adhered to the membrane due to potential presence of cellulose nitrate in the membrane composition.

### Mass analysis of the APPV-DNA polymer by GPC

The mass analysis of poly(APPV-DNA) was performed in PBS buffer using a dn/dc value of 0.1850 mL/g. The different fractions from the SEC purification were lyophilized, dissolved in water and lyophilized. The dry polymers were dissolved in PBS buffer before analysis.

**Supplementary Table 4.** GPC-MALS analysis of poly(APPV-DNA) resulting from DNA grafting on poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M. The analyses were performed in PBS buffer and on the different fractions after SEC purification. Due to the high molecular weight of the APPV-DNA polymers and the void volume of the column, no significant separation of the polymers were

observed, and the  $M_n$  values are therefore calculated to be close to the  $M_w$  values. This causes an artificially low PDI. The exceptions to this are fraction 7 and 8, containing large amounts of free DNA, probably arising from oligonucleotide synthesis on alcohol groups on the CPG 3000 which have not been functionalized with the APPV polymer.

| Sample               | Mn <sup>a</sup> | Mw             | PDI <sup>a</sup> | Rz rms       | dn/dc  |
|----------------------|-----------------|----------------|------------------|--------------|--------|
|                      | (kDa)           | (kDa)          | (Mw/Mn)          | (nm)         | (mL/g) |
| poly(APPV-DNA) fr. 3 | 2908.0 (±0.4%)  | 3344.5 (±0.6%) | 1.150 (±0.7%)    | 81.7 (±0.6%) | 0.1850 |
| poly(APPV-DNA) fr. 4 | 2663.1 (±0.5%)  | 3240.1 (±0.9%) | 1.217 (±1.0%)    | 88.7 (±1.0%) | 0.1850 |
| poly(APPV-DNA) fr. 5 | 1540.8 (±0.6%)  | 1906.2 (±0.6%) | 1.237 (±0.8%)    | 71.8 (±0.7%) | 0.1850 |
| poly(APPV-DNA) fr. 6 | 1046.1 (±0.7%)  | 1291.2 (±0.6%) | 1.234 (±1.0%)    | 62.7 (±0.7%) | 0.1850 |
| poly(APPV-DNA) fr. 7 | 347.6 (±4.6%)   | 724.8 (±1.0%)  | 2.085 (±4.7%)    | 49.7 (±1.7%) | 0.1850 |
| poly(APPV-DNA) fr. 8 | 54.9 (±6.8%)    | 343.9 (±1.1%)  | 6.260 (±6.9%)    | 46.1 (±2.1%) | 0.1850 |



**Supplementary Fig. 11.** The distribution analysis of APPV-DNA polymers after SEC purification. Black: poly(APPV-DNA) fr. 3, red: poly(APPV-DNA) fr. 4, orange: poly(APPV-DNA) fr. 5, blue: poly(APPV-DNA) fr. 6, pink: poly(APPV-DNA) fr. 7, green: poly(APPV-DNA) fr. 8. Fraction 7 and 8 are dominated by small molecular weight molecules, probably DNA strands synthesized on nonfunctionalized hydroxyl groups on the CPG 3000 material.



**Supplementary Fig. 12.** Elution and UV-vis profiles of GPC analyzed poly(APPV-DNA). a) poly(APPV-DNA) fr. 3 showing the polymer harbours UV from both DNA (261 nm) and the polymer backbone (496 nm). b) poly(APPV-DNA) fr. 8 shows free DNA oligomers clearly visible at a larger elution volume than the polymer. These DNA oligomers are not bound to the polymer as they do not co-elude.

**Supplementary Table 5.** Estimation of average theoretical molecular length of poly(APPV-DNA). The calculations are based on a repeating unit weight of 2999.8 Da for poly(APPV-DNA). The calculations assume a complete functionalization of each repeating unit with a 9mer DNA strand (5'-TCA TCT AAC, MW 2657.8 g/mol). The repeating unit length of 0.665 nm for APPV was estimated using ChemBio3D Ultra 13.0 on a minimized structure. For DNA functionalization, poly(APPV-TBDPS) 0.20 M was used. It should be noted that the lengths of the APPV-DNA polymers in fractions 3 and 4 appears shorter when characterized by AFM (See Supplementary Fig. 17).

| Sample               | <b>Mn</b><br>(kDa) | <b>Mw</b><br>(kDa) | Repeating<br>unit (Da) | Repeating<br>unit length<br>(nm) | Average<br>DP (Mn) | Average<br>DP (Mw) | Average<br>length in<br>nm (Mn) | Average<br>length in<br>nm (Mw) |
|----------------------|--------------------|--------------------|------------------------|----------------------------------|--------------------|--------------------|---------------------------------|---------------------------------|
| poly(APPV-DNA) fr. 3 | 2908.0             | 3344.5             | 2999.8                 | 0.665                            | 969                | 1115               | 644.6                           | 741.4                           |
| poly(APPV-DNA) fr. 4 | 2663.1             | 3240.1             | 2999.8                 | 0.665                            | 888                | 1080               | 590.4                           | 718.3                           |
| poly(APPV-DNA) fr. 5 | 1540.8             | 1906.2             | 2999.8                 | 0.665                            | 514                | 635                | 341.6                           | 422.6                           |
| poly(APPV-DNA) fr. 6 | 1046.1             | 1291.2             | 2999.8                 | 0.665                            | 349                | 430                | 231.9                           | 286.2                           |
| poly(APPV-DNA) fr. 7 | 347.6              | 724.8              | 2999.8                 | 0.665                            | 116                | 242                | 77.1                            | 160.7                           |
| poly(APPV-DNA) fr. 8 | 54.9               | 343.9              | 2999.8                 | 0.665                            | 18                 | 115                | 12.2                            | 76.2                            |

# XPS elemental analysis of the APPV-DNA polymer

XPS (X-ray photoelectron spectroscopy) was performed on the different polymer samples to estimate the degree of DNA functionalization of the polymers. The polymer samples were coated on a titanium surface by evaporation of the solvent under ambient conditions.

The data are associated with some degree of uncertainty and are mainly suitable for qualitative indications. As an example, the amount of silicon in poly(APPV-TBDPS) appears to be higher after the partial deprotection, poly[(APPV-TBDPS)-*ran*-(APPV-OH)]. However, the data for poly(APPV-TBDPS) agrees well with the theoretical values, poly(APPV-TBDPS) theoretical. Theoretical values are calculated based on a complete functionalization of each repeating unit of the APPV with the corresponding structure (TBDPS, DNA, or dT). Based on the ratios of P/C and N/C in the

poly(APPV-DNA) sample compared to the calculated value, the DNA coverage of the polymer is roughly estimated to 63%.

**Supplementary Table 6.** XPS analysis and theoretical values of selected functionalized APPV polymers. The standard deviations (SD) were calculated from samples analyzed in triplicate. The poly(dT-APPV) resembles the situation where all alcohol groups from the APPV polymer have been attached to the 5' alcohol group on the dT preloaded CPG 3000 material. ND – not detected. The unexpectedly high silicon content in poly[(APPV-TBDPS)-*ran*-(APPV-OH)] may be due to a contamination.

| Sample                           | С     | 0     | Р    | Ν     | Si   | Ti   | S    | Na   | F    |
|----------------------------------|-------|-------|------|-------|------|------|------|------|------|
| poly(APPV-TBDPS)                 | 83.85 | 13.22 | ND   | ND    | 2.19 | 0.46 | 0.28 | ND   | ND   |
| SD                               | 3.28  | 2.70  |      |       | 0.36 | 0.40 | 0.17 |      |      |
| poly[(APPV-TBDPS)-ran-(APPV-OH)] | 83.80 | 12.79 | ND   | ND    | 3.25 | 0.16 | ND   | ND   | ND   |
| SD                               | 0.10  | 0.25  |      |       | 0.22 | 0.14 |      |      |      |
| poly(APPV-DNA)                   | 57.44 | 25.93 | 2.90 | 11.82 | 0.60 | 0.28 | 0.05 | 0.36 | 0.62 |
| SD                               | 2.79  | 2.49  | 0.19 | 0.71  | 0.55 | 0.48 | 0.09 | 0.11 | 0.58 |
| poly(APPV-TBDPS) theoretical     | 83.80 | 13.50 | 0    | 0     | 2.70 | 0    | 0    | 0    | 0    |
| poly(APPV-DNA) theoretical       | 51.00 | 29.50 | 4.50 | 15.00 | 0    | 0    | 0    | 0    | 0    |
| poly(APPV-dT) theoretical        | 62.50 | 30.00 | 2.50 | 5.00  | 0    | 0    | 0    | 0    | 0    |

# Yield determination of oligonucleotide synthesis on the poly(APPV) backbone

The yields of the synthesis of oligonucleotide brushes on the poly(APPV) backbone are determined based on the amount of single stranded DNA attached to the polymer as measured by UV-absorbance (260 nm). The synthesis is performed on 200 nmol CPG columns and the product is isolated by size exclusion chromatography (SEC). Typically poly(APPV-DNA) is isolated in 1 mL fractions during SEC and the product typically elutes in fraction 3 to 8. Single stranded DNA also elutes in fractions 7 and 8, and therefore the isolated yield of poly(APPV-DNA) is based on the added amounts from fraction 3 to 6.

**Supplementary Table 7.** Calculated amounts of single stranded DNA in poly(APPV-DNA) from seven different synthesis batches. The results are based on UV (260 nm) measurements and extinction coefficients determined using IDT oligoanalyzer software.

| Synthesis number | Isolated yield (nmol ssDNA in<br>poly(APPV-DNA) |
|------------------|---|
| 1                | 58.2  |
| 2                | 112   |
| 3                | 102   |
| 4                | 9.7   |
| 5                | 15.1  |
| 6                | 10.1  |
| 7                | 15.9  |

It is observed that the yields vary from around 10 nmol to above 100 nmol of ssDNA in the poly(APPV-DNA). Although varying, the yields are comparable to the yields obtained from standard solid phase oligonucleotide synthesis on 200 nmol solid supports. It should also be noted that the amount of poly(APPV-DNA) required for one DNA-origami experiment is typically in the range from 20 pmol to 1 nmol dependent on the kind of experiment. Therefore, the amount of isolated poly(APPV-DNA) from one synthesis column is sufficient for several experiments.

Finally, the percentage yield of oligonucleotide synthesis on the poly(APPV) can be roughly estimated based on the amount of injected polymer, and the DNA-coverage of the resulting product. These estimations give yields of 3.1% to 35%, and the details of the calculations can be found below.

Determining the percentage yield of the oligonucleotide synthesis on the poly(APPV) polymer is not straightforward, and in general, only rough estimates of the percentage yields can be made. This is due to the fact that the structure of poly(APPV-DNA) cannot be characterized at the atomic level. Moreover, the shortest fractions of the synthesized DNA-APPV cannot be completely separated from single stranded DNA synthesized along with the poly(APPV-DNA) synthesis. Typically, the poly(APPV-DNA) is purified by gravity size exclusion chromatography where fractions of approximately 1 mL are collected. Fractions 3 to 6 contain poly(APPV-DNA) isolated from single stranded DNA. We here give a representative example of the determination of the percentage yield based on the amount of poly(APPV-DNA) isolated in fraction 3-6 during purification. The absorbance at 260 nm is used as a measure of the amount of isolated DNA-APPV. Moreover, the DNA-coverage of 63% as determined by XPS has to be taken into account when calculating the yields. It shall be noted that we have no means of estimating the number of attachment sites to the solid support. In these calculations, we therefore do not take attachment sites into account.

For the synthesis of one batch of DNA-APPV, 125 µL of partly deprotected poly(TBDPS-APPV) (1.75 mg/mL) is added to the synthesis column.

$$0.125 \ mL \cdot 1.75 \ \frac{mg}{mL} = 0.219 \ mg$$

During the partial deprotection of the poly(TBDPS-APPV) approximately 35% of the protection groups are removed. The protecting group makes up 46% of the mass of the repeating unit. From this we can calculate the percentage of mass lost during the partial deprotection:

$$mass loss(\%) = 0.35 \cdot 0.46 = 0.16 = 16\%$$

The  $M_N$  of the poly(TBDPS-APPV) batch was 66.9 kDa. The amount of added polymer can now be calculated:

$$66.9 kDa - (66.9 kDa \cdot 16\%) = 56.2 kDa$$

$$n_{poly(APPV)} = \frac{0.219 \ mg}{149.0 \ kDa} = 3.90 \ nmol$$

From these figures the maximum theoretical amount of single stranded DNA synthesized on the polymers based on a 63% coverage can be calculated.

The degree of polymerization for the described batch was 129 (66.9 kDa/518.73 Da). With a 63% coverage of DNA this corresponds to an average of 81 molecules of single stranded DNA grafted to each poly(APPV) backbone. The maximal amount of single stranded DNA synthesized on poly(APPV) can therefore be determined:

$$n_{max,DNA} = 3.90 \ nmol \cdot 81 = 316 \ nmol$$

Based on these calculations, the estimated percentage yield of the DNA oligonucleotide synthesis varies from 3.1% to 35%:

$$\frac{9.7 \ nmol}{316 \ nmol} \cdot 100\% = 3.1\% \quad \frac{112 \ nmol}{316 \ nmol} = 35\%$$

## **Optical properties of poly(APPV-DNA)**

The optical properties of the material have been investigated in terms of UV-Vis absorption and fluorescence. Moreover, the possibility to turn on fluorescence of small-molecule fluorophores by Förster Resonance Energy Transfer (FRET) from the polymer to acceptor fluorophores on DNA-origami, has been investigated.





**Supplementary Fig. 13.** UV-vis absorption spectra of poly(APPV-TBDPS) in THF, red (----) and poly(APPV-DNA) in water, green (----). The light source is shifted at 350 nm between UV and visible light.



**Supplementary Fig. 14.** Fluorescence spectra of poly(APPV-TBDPS) in THF and poly(APPV-DNA) in water.

Solid red (----): Excitation spectrum of poly(APPV-TBDPS) with a fixed emission wavelength at 580 nm. Dashed red (- - -): Emission spectrum of poly(APPV-TBDPS) with a fixed excitation wavelength at 500 nm. Solid green (----): Excitation spectrum of poly(APPV-DNA) with a fixed emission wavelength at 600 nm. Dashed green (- - -): Emission spectrum of poly(APPV-DNA) with a fixed excitation wavelength at 475 nm. Front entrance and exit slits were set at 2 nm. The poly(APPV-DNA) shows a significantly higher absorption in the region around 260 nm than the poly(APPV-TBDPS). The peaks at 290 and 300 nm are artefacts arising at half the detected emission wavelength.

#### FRET from the PPV polymer to a fluorophore on DNA origami

Fluorescence of the polymer is also observed after specific immobilization on DNA origami as shown in Supplementary Fig. 15a. We demonstrate how the positioning of the polymer on origami

can be used to obtain Förster Resonance Energy Transfer ( (FRET) between the polymer and a single acceptor co-localized on the origami. An Alexa647 dye was conjugated to one of the polymer-binding extended staple strands on the DNA origami. Thus specific polymer binding onto the DNA-origami board is expected to occur in close proximity to the Alexa647 acceptor position. Before addition of poly(APPV-DNA) to the fluorophore-labelled DNA origami sample, very low acceptor emission was observed upon excitation at 525 nm (Supplementary Fig. 15b). After addition of the polymer to the sample, however, a ~20x signal enhancement of acceptor fluorophores on DNA-origami. Fluorescence from a control measurement with no acceptor fluorophore incorporated to the DNA origami, shows only signal arising from polymer fluorescence (Supplementary Fig. 15b).


**Supplementary Fig. 15.** FRET between the polymer and a single fluorophore. a) Illustration of the set-up for precise positioning of poly(APPV-DNA) and Alexa647 (red sphere). The poly(APPV-DNA) is aligned on rectangular DNA-origami with an Alexa647 dye attached to one of the polymerbinding extended staple strands. b) Fluorescence spectra for: Alexa647 and poly(APPV-DNA) immobilized on the origami (blue curve), poly(APPV-DNA) on DNA-origami without acceptor fluorophore (purple dashed curve), Alexa647 labelled DNA-origami without poly(APPV-DNA) (cyan curve), and fluorophore excited at 575 nm (black dashed curve). Apart from the latter example the samples were excited at 525 nm and the fluorescence measured from 550 nm to 800 nm. Background spectra were subtracted.

### Experimental description of fluorescence measurements

For FRET experiments poly(APPV-DNA) with a 9mer ssDNA complementary to the extended staple strands on DNA-origami was used. The applied sequence was:

### 5'-ACG AGA CAG-APPV

DNA-origami was folded at a 0.20 pmol scale to a final volume of 20  $\mu$ L TAE(x1) buffer with 12.5 mM MgCl<sub>2</sub>. Alexa647 was incorporated by labelling of an amino modified extended staple strand with the following sequence:

## 5'-CTGTCTCGT(c6-N-Alexa647)-TTT-CCAGGCGCGAGGACAGATGAACGGGTAGAAAA

The part of the sequence denoted in bold is the polymer binding part of the sequence.

Before measurements the samples were diluted to 80 µL buffer. In general, fluorescence spectra were obtained using 80 µL samples. A spectrum of the origami without polymer was obtained, and then the polymer was added. Polymer addition was carried out from a concentrated solution of poly(APPV-DNA) in milliQ water and the resulting dispersion was mixed thoroughly by pipette. Typically, 1 uL of a 50 µM polymer solution based on the concentration of ssDNA on poly(APPV-DNA) was added. The samples were excited at 525 nm, and the emission was measured from 550 nm to 800 nm. Background spectra were obtained by exciting a DNA-origami sample without any dyes at 525 nm and measuring the emission from 550 nm to 800 nm. To obtain a spectrum of the poly(APPV-DNA) on origami without any fluorophores, a separate DNA-origami sample was prepared. The spectrum was obtained using the same protocol as described above. All measurements were performed at 25 °C.

#### Fluorescense quantum yield of poly(APPV-DNA)

The polymer fluorescence quantum yield  $\Phi_{PPV}$  was determined using absorption and fluorescence measurements of both sample and a reference using:

$$\Phi_{\rm PPV} = \Phi_{ref} \frac{I_{PPV} \cdot Abs_{Ref}}{I_{ref} \cdot Abs_{PPV}} \frac{n_{PPV}^2}{n_{ref}^2}$$

where the subscripts PPV and ref stand for the PPV sample and the reference standard. The parameter *Abs* is the absorbance at the fluorescence excitation wavelength and *I* is the integrated area under the fluorescence spectrum. The square of the refractive index, *n*, is employed to make the correction due to the difference in media of the standard and the polymer sample. Sulforhodamine 101 (Reference dye sample kit, Life technologies) in ethanol was used as a reference (with fluorescence quantum yield  $\Phi_{ref} = 1$ ).<sup>50</sup> A quartz cuvette with 1 cm path length was used for both absorption and fluorescence measurements. The absorbance of both sample and reference was kept below 0.05. We estimated an uncertainty of ~20% on our quantum yield measurements by further using 5-carboxytetramethylrhodamine (CMTR, Reference dye sample kit, life technologies) in methanol as a reference ( $\Phi_{CTMR}=0.68$ ).<sup>51</sup> The polymer sample was prepared by dilution of the stock concentration in 20 mM Tris-acetate-EDTA buffer with pH 8.3. Prior to measurements, this sample was heated to 95 degrees for 5 minutes and left to cool down slowly to room temperature overnight.

## DNA melting temperatures of the poly(APPV-DNA) DNA sequences

The hybridization properties of the attached DNA on the polymer was investigated by measuring the melting profiles of the APPV-DNA polymers with complementary ssDNA oligonucleotides, ODN1 together with ODN1\*, and APPV-DNA polymers without any complementary DNA oligoes. ODN1 denotes the 9mer DNA sequence coated on the APPV-DNA polymer used in the majority of this study, including origami experiments. ODN1\* is complementary to ODN1. The melting profiles are shown in Supplementary Fig. 16. The experiments were carried out in the presence of MgCl<sub>2</sub>, NaCl, or both. In some cases, precipitation was observed when MgCl<sub>2</sub> was present, but precipitation was never observed at isothermic conditions over a time period of 12 hours. Melting points for hybridized strands are given in Supplementary Table 8.

#### Supplementary Information



**Supplementary Fig. 16.** Melting temperature determination of poly(APPV-DNA) with complementary ssDNA in TAE buffer (1x). All samples were monitored at an absorbance wavelength of 260 nm. MgCl<sub>2</sub> and NaCl concentrations were 12.5 mM and 100 mM, respectively. ODN1 and ODN1\* are depicted as blue and orange respectively. a) poly(APPV-DNA) ODN1 fr. 5, ssDNA ODN1\*, and MgCl<sub>2</sub>. b) poly(APPV-DNA) ODN1 fr. 5, ssDNA ODN1\*, and MgCl<sub>2</sub>. b) poly(APPV-DNA) ODN1 fr. 5, ssDNA ODN1\*, and NaCl. c) poly(APPV-DNA) ODN1 fr. 5, ssDNA ODN1\*, fr. 5, ssDNA ODN1\*, ssDNA ODN1\*, mgCl<sub>2</sub>, and NaCl. d) ssDNA ODN1, ssDNA ODN1\*, and MgCl<sub>2</sub>. e) ssDNA ODN1, ssDNA ODN1\*, and NaCl. f) ssDNA ODN1\*, mgCl<sub>2</sub>

and NaCl. g) poly(APPV-DNA) ODN1 fr. 4 and MgCl<sub>2</sub>. h) poly(APPV-DNA) ODN1 fr. 4 and NaCl. i) poly(APPV-DNA) ODN1 fr. 4, MgCl<sub>2</sub>, and NaCl.

**Supplementary Table 8.** Summarized melting temperatures (degrees Celsius) between poly(APPV-DNA) ODN1 & ODN1\* and between ODN1 & ODN1\*. The listed melting temperatures are average values extracted from six temperature ramps. MgCl<sub>2</sub> and NaCl concentrations were 12.5 mM and 100 mM.

|                             | MgCl <sub>2</sub> | NaCl | MgCl <sub>2</sub> & NaCl |
|-----------------------------|-------------------|------|--------------------------|
| poly(APPV-DNA) ODN1 & ODN1* | 27.2              | 17.6 | 27.2                     |
| ODN1 & ODN1*                | 29.3              | 24.0 | 28.3                     |

# AFM imaging of single polymers

APPV-DNA polymers were analysed by AFM revealing isolated polymers with only a small amount of aggregation observed. The analysed APPV-DNA polymers were obtained from DNA grafting on poly[(APPV-TBDPS)-*ran*-(APPV-OH)] 0.20 M. After SEC purification, the first fraction containing APPV-DNA polymers, named poly(APPV-DNA) fr. 3, was used for the AFM imaging. The APPV-DNA polymers were adsorbed to a freshly cleaved mica surface for 2 min and imaged in TAE buffer (1x) with MgCl<sub>2</sub> (12.5 mM) and NiCl<sub>2</sub> (1 mM).



**Supplementary Fig. 17.** AFM images of poly(APPV-DNA) fr. 3 on a mica surface. The polymers observed by AFM are up to more than 200 nm long which is significantly shorter than the theoretical average lengths of 640-740 nm derived from GPC (Supplementary Table 5). The longer polymers may be lost during handling as it is observed that the polymers stick to plastic tubes and pipettes and the longer polymers may also be mechanically cleaved during handling and imaging.

# Scanning probe microscopy measurements of nanomechanical and conductivity properties of the APPV-DNA polymer

### Quantitative nanomechanical microscopy

The quantitative nanomechanical mapping mode was operated under ambient conditions, which allowed control of the applied force during the measurement. Commercial silicon tips with a nominal spring constant of 20 N/m were used in the experiment, and the substrate used in AFM experiments is silicon. The following formula derived for a spherical tip indenting a semi-infinite planar sample was used to estimate a local reduced elastic modulus.

$$F_{interaction} = \left(\frac{4}{3}\right) E^* \sqrt{R} (d - d_0)^{\frac{3}{2}} + F_{adh} \qquad (1)$$

where  $F_{\text{interaction}}$  is the tip-sample force,  $E^*$  the reduced elastic modulus of the tip and the sample, R the tip radius,  $d_0$  the surface rest position,  $d - d_0$  the depth of indentation and  $F_{\text{adh}}$  the constant adhesion force during the contact. The topography, elastic modulus and force maps were processed using SPIP<sup>TM</sup> software.

#### Surface Potential measurements with Kelvin probe force microscopy

The surface potential measurements were performed on an atomic force microscope (Multimode VIII, Bruker) with a Co/Cr-coated tip (MESP) using a two-pass scan technique. Topography information was acquired using a tapping mode on the first pass. During the second pass, the probe was lifted at 15nm with respect to the sample topography, while an oscillating voltage was applied to generate the vibration of the probe. The feedback controller monitored the vibrating amplitude of probe and recorded the potential difference to construct the surface potential image. The result of the well-known mathematical treatment is that the force felt by the vibrating capacitor is proportional to the difference in voltage between the probe and the substrate

$$F_{cap} \approx F_{cap}(\omega) = -\frac{dy}{dx} \Delta V_{Dc} \Delta V_{Ac} \sin \omega t$$
 (2)

where C is capacitance, Z is separation, VDC and VAC are the DC and AC voltage differences between the probe and substrate, and  $\omega$  is the resonant frequency of the Kelvin probe. The applied DC voltage is adjusted until the magnitude of the oscillating deflection of the probe is minimized. This is the voltage where the capacitor plates are applying a minimum force on one another and corresponds to the voltage equal to the difference in work function between the two

plates. It is instructive to note that the force is proportional to the magnitude of the AC voltage, providing a simple way to increase the sensitivity of the KPFM.



**Supplementary Fig. 18.** The stiffness of different species measured by quantitative nanomechanical microscopy. The stiffness map and histogram of, a) DNA origami, b) poly(APPV-DNA) fr. 3, c) Au nanowire, and d) and SiO<sub>2</sub>. e) The summary of stiffness of different species.



**Supplementary Fig. 19.** The surface potential measurement of different species. a) The topography map of poly(APPV-DNA) fr. 3. b) The surface potential map of poly(APPV-DNA) fr. 3. c) Topography and surface potential maps of poly(APPV-DNA) fr. 3 on DNA origami. The surface potential and line profiles of d) poly(APPV-DNA) fr. 3, e) gold nanowire, and f) DNA origami. g) The summary of surface potential of different species.

## DNA origami

### Origami annealing protocol

Rectangular DNA origami was formed according to a modified version of Rothemund's original protocol (*18*). The M13mp18 scaffold (10 nM) was mixed with unpurified staple strands (100 nM) in TAE buffer (1x) with MgCl<sub>2</sub> (12.5 mM). The mixture was annealed on an Eppendorf Mastercycler Personal machine (Ramp: 80 to 55 °C over 10 min. and 55 to 4 °C over 80 min.). After annealing excess staples were removed using Amicon centrifugal filter units (100,000 MWCO, 6000 g, 10 min.) and washed twice with TAE-Mg<sup>2+</sup>-buffer (1x, 12.5 mM).

A detailed illustration and a list of the DNA oligo sequences for the self-assembly of the different DNA origami structures are listed at the end of this document.

## General procedure for AFM Scanning of DNA Origami

The APPV-DNA polymer binding to the DNA origami was visualized by atomic force microscope (AFM) (Multimode VIII, Bruker). The purified DNA origami solution (2  $\mu$ L) was deposited onto a freshly-cleaved mica surface, immediately followed by addition of diluted polymer solution (10  $\mu$ l). After incubation (0.5-5 min.), sufficient TAE buffer (1x) with MgCl<sub>2</sub> (12.5 mM) was added for the AFM scanning. For some experiments the origami was allowed to immobilize first for 1 min. followed by addition of the APPV-DNA polymer (Fig. 3c and Supplementary Fig. 21).

## Self-assembly of poly(APPV-DNA) on DNA origami



**Supplementary Fig. 20.** AFM images of poly(APPV-DNA) fr. 3 positioned on 2D DNA origami rectangles showing full control of the positioning of poly(APPV-DNA) on DNA origami depending on DNA sequence. a) Plain origami with two linear lanes of extended staple strand sequences: ODN1\* (Black in inset) and ODN2 (Blue in inset). The lane closest to the origami edge is complementary to poly(APPV-DNA)-ODN1, while he lane closer to the middle is not complementary to poly(APPV-DNA)-ODN1. Faint lines of the ssDNA extensions are observed. b) Poly(APPV-DNA) ODN1 is hybridized to the complementary lane closest to the edge and lines of polymer are only observed on the line closest to the edge.



**Supplementary Fig. 21.** Illustrations of patterns and AFM images of poly(APPV-DNA) fr. 3 positioned on 2D DNA origami rectangles in circular, wave and staircase line pattern.

## High speed AFM imaging

The assembly process of the APPV-DNA polymer binding to the DNA origami was monitored via high speed AFM (Fast-Scan, Bruker). The purified DNA origami solution of 2  $\mu$ L was deposited onto a freshly-cleaved mica surface, and after incubation (around 30 seconds), 100  $\mu$ L TAE buffer (1x) with MgCl<sub>2</sub> (12.5 mM) was added. Next, 2  $\mu$ L poly(APPV-DNA) fr. 3 solution (30  $\mu$ M ssDNA on the polymer) was carefully placed on the top of a fast-scan tip, which was then rapidly lowered onto the mica surface. Images where then captured sequentially.

#### Supplementary Information



**Supplementary Fig. 22.** Direct visualization of the dynamic assembly process for the poly(APPV-DNA) fr. 3 on the DNA origami. The AFM images were recorded in up to ~21 second per image and a wait-time of around 1-3 minutes between selected images. As shown by the red arrows, it's clear to see a polymer was initially attaching on the edge of the DNA origami. Then, the polymer was gradually zippering up on the DNA origami along the extended staple strand path.



**Supplementary Fig. 23.** Immobilization of poly(APPV-DNA) fr. 3 on DNA origami containing the U-shaped pattern.

## 3D DNA-PAINT super-resolution imaging of the APPV-DNA polymer

### **Optical setup**

Fluorescence imaging was carried out on an inverted Nikon Eclipse Ti microscope (Nikon Instruments, Melville, NY) with the Perfect Focus System, applying an objective-type TIRF configuration using a Nikon TIRF illuminator with an oil-immersion objective (CFI Apo TIRF 100×, NA 1.49, Oil). A total magnification of 100× was used, yielding a pixel-size of 160 nm. A 561 nm laser (200 mW nominal, Coherent Sapphire) was used for excitation. The laser beam was passed through a cleanup filter (ZET561/10, Chroma Technology, Bellows Falls, VT) and coupled into the microscope objective using a beam splitter (ZT561rdc, Chroma Technology). Fluorescence light was spectrally filtered with an emission filter (ET600/50m, Chroma Technology) and imaged on an EMCCD camera (iXon X3 DU-897, Andor Technologies, North Ireland).

#### Super-resolution DNA-PAINT imaging

For sample preparation, a piece of coverslip (No. 1.5, 18 mm × 18 mm,  $\approx$ 0.17 mm thick) and a glass slide (3" × 1", 1 mm thick) were sandwiched together by two strips of double-sided tape to form a flow chamber with inner volume of  $\approx$ 5 µl. First, 20 µl of biotin-labeled bovine serum albumin (1 mg/ml, dissolved in buffer A) was flown into the chamber and incubated for 2 min. The chamber was then washed using 40 µl of buffer A. 20 µl of streptavidin (0.5 mg/ml, dissolved in buffer A) was then flown through the chamber and allowed to bind for 2 min. After washing with 40 µl of buffer A and subsequently with 40 µl of buffer B. To increase the density of structures on the surface, the chamber was incubated with the undiluted biotin-labeled DNA structures three times and incubated for 5 min each time. The chamber was washed using 20 µl of buffer B.

*Direct imaging of DNA Origami structures.* The final imaging buffer solution contained 2 nM Cy3blabeled imager strand in buffer B with Trolox, PCA and PCD. The chamber was sealed with epoxy before imaging. Imaging was performed under the following conditions: The CCD readout bandwidth was set to 1 MHz at 16 bit and 5.1 pre-amp gain. No EM gain was used. 15000 frames were acquired with an integration time of 300 ms. The Nikon N-STROM package, including a cylindrical astigmatism lens, was used to acquire 3D images.

DNA-PAINT of polymer on DNA origami structures. To the chamber containing biotinylated DNA nanostructures the purified polymer was added at a 1:40 dilution and incubated for 10 min. The chamber was washed with 20 µl of buffer B and the imaging buffer solution was added (1 nM Cy3b-labeled imager strand in buffer B with Trolox, PCA and PCD). The chamber was sealed with epoxy before imaging. Imaging conditions as described in the paragraph above.

Super-resolution reconstruction was performed using the N-STORM package and a custom MATLAB software. EMAN2<sup>52</sup> was used for EM-type class averaging of DNA-PAINT super-resolution images. DNA-PAINT localization data was binned with a bin size of 2.66 nm/px and imported in EM2 for subsequent classification, alignment, and averaging. Distance measurements using intensity line profiles on class-averaged datasets was performed with ImageJ, LabVIEW, and

Origin.

## 3D Visualization and helix fitting software

An x-y-projection of the helix is used to fit an ellipse to the localizations with a least square algorithm described by Fitzgibbon *et al*<sup>53</sup>. The orientation and radius of the ellipse determines the amplitude of a sinusoidal function that is fitted when projecting the point cloud sidewise in the YZ-Plane with a nonlinear least square model. Accordingly, a projection in the XZ-Plane is fitted with a sinusoidal function with phase shift of  $\pi/2$  (hence a cosinusoidal function). The height of the helix is calculated as the difference of the mean values of the minimum and maximum z position of the sinusoidal functions with a length of  $2\pi$ . The fit values of the sinusoidal and cosinusoidal function determine the helix as it may be described in Cartesian Coordinates as  $[X,Y,Z] = [a^*\cos(t),b^*\sin(t),t]$ 

#### **DNA-PAINT** sequences.

Docking strand on DNA Origami: 5' – ATCCATTAT – staple Imager strand sequence for polymer imaging: 5' – GATCCATTAT – Cy3b Imager strand sequence for guide strand (origami) imaging: Cy3b – ATAATGGATC – 3'

Polymer sequence for Poly(APPV-DNA-)-PAINT experiments: 5' TTAGGTAAAG-polymer (10 nt)-ATAATGGAT-Polymer

## Trolox, PCA and PCD preparation.

*Trolox* was prepared as 100x stock solution with 100mg Trolox, 430 μl 100% methanol, 3.2 ml H2O, 345 μl 1 N NaOH.

PCA was prepared as 40x stock solution with 154 mg PCA in 10 ml H<sub>2</sub>O. NaOH was used to adjust

# pH = 9.0.

*PCD* was prepared as 100x stock solution with 9.3 mg PCD in 13.3 ml buffer (50% glycerol in 50 mM KCl, 1 mM EDTA and 100 mM Tris-HCl pH 8).

Stocks were stored at -20C. To prepare imaging buffers, stock solutions were brought to 1x by dilution in buffer B.

## Buffers.

Buffer A (10 mM Tris-HCl, 100 mM NaCl, 0.05 % Tween-20, pH 7.5).

Buffer B (5 mM Tris-HCl, 10 mM MgCl2, 1 mM EDTA, 0.05 % Tween-20, pH 8).

## DNA sequences and DNA origami design

DNA-polymer sequences:

poly(APPV-DNA)-ODN1: 5' TCATCTAAC-polymer

ODN1\*: 5' GTTAGATGA 3'

ODN2: 5' TTATGCACC 3'

ODN3: 5' CTGTCTCGT 3'

Poly(APPV-DNA)-PAINT: 5'-ATAATGGAT-Polymer

Poly(APPV-DNA)-FRET: 5'-ACGAGACAG-Polymer

The poly(APPV-DNA)-ODN1 was used for all experiments except the DNA PAINT on a 3D nanostructure and the FRET on DNA-origami experiments. ODN1\*, ODN2 and ODN3 are used as 5' staple strand extensions for 2D DNA origami experiments. A 3T spacer is incorporated between the origami and the extension. Poly(APPV-DNA)-ODN1 binds to ODN1\* and ODN2 serves as a sequence specificity reference. Poly(APPV-DNA)-FRET binds to ODN3.

Origami with two linear paths:

#### Supplementary Information

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| TAACATC AATAAA                          | CATACAGECAAEGCAA GAATTAECAAAATTA   | AGCANTANAGCETCA  | C G G T T G T A C C A A A A A C A C A A A T A T A T  | AATTTCATCTTCTGAG TAAATTTAATGGTT  | GAAATACCGACCGTGT ATAAATA\GGCGTTA   | AATAAGAATAAACACO GAATCATAATTACTA   |     |
| 1941141341341351441151455114111         | 1V15133511335111311VV1351111VV   | 0511V111055V5101051V11105V111V   | 574574155111115, p111414144444154  | .144491454854315541114441145344  | 11114155315534343141114113353444   | 1411311411191955511451411441541  | 1   |
|   |  |  |  |  |  | 1  | /   |
| CTTTACCTACACATTACTCAGGCATTGCATT         | AAATATATGAGGGTTCTAAAAATTTTTATC   | TGCGTTGAAATAAAGGCTTCTCCCGCAAAAI  | TATTACAGGGTCATAAAAAAGTTTTCTCGC   | TTCTTTGTCTTGCGATTGGATTTGCATCAGC.   | TTACATATAGTTATATAACCCAACCTAAGCC  | GAGGTTAAAAAGGTAGTCTCTCAGACCTATC  |     |
|   |  |  |  |  | A  | 1  |     |
|   |  |  |  |  |  |  |     |
|   |  |  |  |  |  |  | ~   |
| 144211113334313111332333131313134       | 114212214214141421442112224424   | 1242141114411432222121222341224  | *****)1)1)1*5*1505**)5**5*3*111  | 2342322414411441144444232244131142   | ** JIIIIJIVIJJJIVIJJVVIJIVVIJIV  | ** 31 31 31 31 34 31 14 1 34 31 14 44 14 31 11 14  | 1   |
|   |  |  |  |  |  | 1 /  | /   |
| GETTTTETSATTATEAACCOSCOTACATATE.        | TEACATSCINSTITUACEATTACCETTEAT   | ATTETETTETTECTECASACTETCASGEA  | CALCINATASCETT TATTCACTCACATA  | ATTENTTATETACTOTTTCCATTAAAAAAG   |  | TTOTTTC TOATOTTC TTCATCATCTTC  |     |
| 5555554151V1V3.                         | AA2121A22A12AAAA 221AA1222AA21A2   | 2144242442244224 212124242122211   | 142122A2141222AAAAAA1AA212A2121A1  | 1442144414241242   | ATTAA211142211144 AATTIA2ATTAATTA  | 4443444494431434431434443143143143143  |     |
| T GT AT A A C C A A A T A               | TTAAATTGTAAACGT AATATTTI CTTAAAAT  | I COCATTAAATITITA TAAATCAGCTCATT   | TTTTAACCAATAGGAACAACAGTACCTTTTAC   | TCGGGAGAAACAATAA GGATTCGCCTGATT  | CTTTGAATACCAAGT ACAAAATCCCCCAGAG   | GCGAATTATTCATTTCAATTACCT CAGCAAAA  | _   |
| 2021111101021101AA0A1A1102111A1         | ATTTAACANTTAACGTTTACAAAAAAAAAAAAAAAAAAAA   | AATGAGCTGATTTAACAAAAATTTTAATOOAAAAAA   | AAAAAGGTACTCT CTTCCTATTGGAAAAATG   | AATCAGGGAATCCGTTATTGTTTCTCCCG  | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   | 11111001040014411044109401091111   | /   |
|   |  |  |  | 11   |  | 11   | /   |
| GETCAATCCGCCGTTTGTTCCCACGGAGAAT         | GACGGGTTGTTACTCGCTCACATTTAATGT   | ATGAAAGCTEGETACAGGAAGGCCAGACGC   | ATTATTTTGATGGC CTGTATATTCATCT  | ACGTTAAACCTGAAAATCTACGCAATTTCTT  | TTTCTGTTTTACGTGCAAATAATTTTGATAT  | GTAGGTTCTAACCCTTCCATTATTCAGAAGT  |     |
|   |  | 1 Y 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  |  | 1 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9  |  | 1-10-1-100 for 1-1-1-1   |     |
| GTTGGTGTAGATGG                          | COCATCO TAACCOTO TO TOTOCCACTITICACO   | LGATGATGATAGTATTEGTTTTAGGAAGATC  | CALL ACCESCITE ACATTALCATING   | CAACAAAGAAACCACCACCAGCGAGCGGAATT   | TCATCATATTCCTCAT ATCACATS ATCCC  | TTCATCAATATAATCA CATTCTTTCCATTA  |     |
|   |  |  |  |  |  |  | 7   |
| 741147771417742122A422A2A121A22         | **************************************   | 1123123121341433335545133113143  | 1124221322132441231441431444432  | 0110111J111001001311031303311WV  | 214214144234314V149131431433311  | A 3 T 4 3 T 4 T 4 T 4 3 3 M 3 T M 3 M M 3 3 T M M 1 M  | /   |
|   | II   |  | II   | II   |  | ///  | 1   |
| GCCAGCTEGCETAATAGCGAAGAGGCCCCGCA        | GATCGCCCTTCCCAACAGTTGCGCAGCCTG   | TESCEANTESCECTITECCTESTITECESC   | CAGAAGCGETGECEG ACTCAAACTTTTAA   | ATTAATAACGTTCGGGGCAAAGGATTTAATAC   | GTTGTCCAATTGTTTGTAAAGTCTAATACT   | TARATCCTCARATGTATTATCTATTGACGGC  |     |
| 33113133999991                          | 22142222344522112124422221222423   | 1422221142222244 2222422244422222  | 192121129 2242522415451112444411   | 1441141192442222011122144411412  | 1244242211442444 4411124241141244  | (2ATTEA22 A2TTEA24 AATA2ATAA2T2222   |     |
| CAAGGCGATTAAGT                          | EGGTAACGCCAGGGT TCCCAGTCACGACGT  | L GTAAAACGACGGCCA TGCCAAGCTTGCAT   | CCTGCAGGTCGACTCTCAAATATCAAACCCT  | AATCAATATCIGGTCA TIGGCAAATCAACA  | TTGAAAGGAATTGAGGAAGGTTAT: TAAAATA  | TCTTTAGGAGCACTAA AACTAATAGATTAGA   | _   |
| 211122222142428428122221441134          | 1224110200122244440001240102102  | 041111001000001040001100440014   | 043013340312404 011141431110304  | 140114140403401044330111401101   | A01110011A001001100A0160A1111A1  | 9444133139194119119411413144131  | /   |
|   |  |  |  | 11   |  | 11   | 1   |
| CTTTATECTTCCGGCTCGTATETTCTCTGGA.        | T T G T G A G C G G A T A A C A A T T T C A C A C A G G A A A  | GC TAT GACCAT GAT TACGAAT TC GAGC TC GI  | ACCCEGEGATECTET AGETTEASCAAGETE  | Teetttagatttttcatttgcteeteetet   | GCGTGGCACTGTTGCAGGCGGTGTTAATAC   | ACCECCTCACCTCTETTTTATCTTCTECTEC  |     |
| C                                       | WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW   |  |  | CONTRACT PROPERTY INCOMENTATION  | TATATA A ANTINA ANT   | 1  |     |
| CTAATCALTCACT.                          | ACTCACATTAATTGCATTGCGCTCACTGCCC  | TTTTCASTCSSSAA CTSTCSTSTCASCT  | CLATTAATCAATCCCCCACCTCAAACCCTAAC   | ATACGTGGCACAGACATATTTTTGAATGGC   | ATTACTUTTAATCCC CAACTCALACCCCT   | AAAFATCSCCATTAAA ATACCSAACSAACC  |     |
|   | the second se  |  | 1  | Contraction of the second seco | The second s   | in the second seco   | -   |
| *************************************** |  | ****>>>>>  | **************************************   | ***************************************  | ***************************************  |  | 1   |
|   | II   |  | II   | 11   |  | 11   | /   |
| I SU AAU I UTOTOAGGGCCAGGCGGTGAAGGG     | ATLASTIGTTECCCETCTCACTEETEAAAA   | AAAALLACCCTGGCGCCCAATACGCAAACCI  | LILILLCCCCCCCTT CAGAAGGETTCTATC  | 191199CCAGAATGTCCCTTTTATTACTGG   | SISISACTEGTGAATCTECCAATETAAATAA  | LLAIIICAGACGATTGAGCGTCAAAATGTAG  |     |
| 010000000000000000000000000000000000000 | 211401004 2440000 1 64010400 11111   | TTTT20120040001000114100011100   | 22242422222222244212112224424142   | A 2 4 2 4 4 5 2 5 2 1 2 1 1 4 2 4 2 5 4 4 4 4 1 4 4 1 5 4 2 5 5 1 2 1 4 2 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5  | 0343431843343114 439911434111411   | 1001111010101010101010111100010  |     |
| GTTTGCC: CAGCAG                         | COARANTCCTOTTES GOTOGT CCOARATO  | S GCARAATCCCTTATA ATCARAGAATAGC  | C C G A G A T A G G G T T G A G T G T G A G A  | CCTGAGTAGAAGAACT AAACTAT CGGCCTT   | CTGGTAATATCCAGAA CAATATTA: CGCCAGO   | CATTGCAACAGGAAAA CGCTCAT SGAAATAC  |     |
| 201120224001020040204442000012012       | 2111122272744014224224234  | 2211114222441411142111721172144  | A DIDIATODOAADION BATTATTUNANA   | AA66444661116461116461161161646  | A0041141400101101141441441441441441441441  | 14400110100111110009019111110  | - 7 |
|   |  |  |  |  |  | 1  | 1   |
| ATTTGGGTGATGGTTCACGTAGTGGGCCATC         | CCTGATAGACGGTTTTTCGCCCTTTGACGT   | GAGTCCACGTTCTTTAATAGTGGACTCTTG   | CCARACTGGARCARCTARTCARAGARGTAT   | CTACAACGGTTAATTTGCGTGATGGACAGA   | CTTTTACTCGGTGGCCTCACTGATTATAAAA  | CACTTOTOAGGATTOTGGCGTACCGTTCCTC  |     |
|   |  | 1  | 1  |  | 1  | /  |     |
| 93413433399149                          | 100041141110114444400000444010044  | 1011400101404441141040010404401  | **>>1113*3311313*11451113113*14  | *324121123344114 *32243143312131   | **************************************   | 101044040101014444000001000440040  |     |
| EACGTGCCCTAAAGC.                        | ALIAAAILUUAALULI <b>A</b> AAGGGAGCCCCCGAT3   | I AUAUL I I UALUUUUAAAGCCCGCCAACGTG  | DIGAGAAAGGAAGGGAAATGCGCCGCTACAGGG;   | LOCOTACTATION FOR TEACEAGCACETAT.  | AALGIGLIIIILLILGI <b>A</b> GAATCAGAGCGGGA  | CIARALAUUAUULUATTAAAGGGATTTTAGA  |     |

### Purple line sequences:

GTTAGATGATTTCCAAATCATTACTTAGCCGGAACGTACCAAGC GTTAGATGATTTTTCATTTCTGTAGCTCAACATGTTTAGAGAG GTTAGATGATTTGCGAAACAAGAGGGCTTTGAGGGACTAGGGAGTT GTTAGATGATTTCAAAATTAGGATAAAAATTTTTAGGATATTCA GTTAGATGATTTGTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT GTTAGATGATTTTTTCAACTACGGAACAACATTATTAACACTAT GTTAGATGATTTTCACGACGTGTTTCCTGTGTGAAATTTGCGCTC GTTAGATGATTTTGTAGCATAACTTTCAACAGTTTCTAATTGTA GTTAGATGATTTCATAACCGCGTCCAATACTGCGGTATTATAG GTTAGATGATTTTGCAACTAGGTCAATAACTTGCGGTATTATAG GTTAGATGATTTTGCAACTAGGTCAATAACCTGTTTAGAATTAG GTTAGATGATTTTAAAGGCCGCTCCAAAAGGAGCCTTAGCAGAGT GTTAGATGATTTTAAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT **GTTAGATGATTTGGCGATCGCGCATCGTAACCGTGCGAGTAACA GTTAGATGATTTACCCGTCGTTAAATTGTAAACGTTAAAACTAG GTTAGATGATTTTATATTTTCATACAGGCAAGGCAAAGCTATAT GTTAGATGATTTAGCTGATTACTCACATTAATTGCGTGTTATCC GTTAGATGATTTTACCTTTAAGGTCTTTACCCTGACAATCGTCA GTTAGATGATTTACGGTCAATGACAAGAACCGGATATGGTTTAA GTTAGATGATTTGTTAAAATAACATTAAATGTGAGCATCTGCCA** GTTAGATGATTTAAAGATTCTAAATTGGGCTTGAGATTCATTAC **GTTAGATGATTTTCAGAAGCCTCCAACAGGTCAGGATTTAAATA GTTAGATGATTTACCGTTCTGATGAACGGTAATCGTAATATTTT** GTTAGATGATTTACTGCCCGCTTTTCACCAGTGAGATGGTGGTT GTTAGATGATTTTATCAGGGCGAAAATCCTGTTTGACGGGCAAC GTTAGATGATTTTCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT GTTAGATGATTTGCTCACAAGGGTAACGCCAGGGTTTTGGGAAG **GTTAGATGATTTCATGTCAAAAATCACCATCAATATAACCCTCA GTTAGATGATTTTAAATATTGAGGCATAGTAAGAGCACAGGTAG** 

Green line sequences:

TTATGCACCTTTATCAACAGGAGAGCCAGCAGCAGCAAAATATTTTT TTATGCACCTTTCCTGATTGAAAGAAGAAGTGCGTAGAAGAAGGAG TTATGCACCTTTGAATGGCTACCAGTAATAAAAGGGCAAACTAT TTATGCACCTTTGCCTTGACAGTCTCTGAATTTACCCCTCAGA TTATGCACCTTTCCTAATTTAAGCCTTAAATCAAGAATCGAGAA TTATGCACCTTTTAAAGTACCAGTAGGGCTTAATTGCTAAATTT TTATGCACCTTTTTAACGTTCGGGAGAAACAATAACAGTACAT TTATGCACCTTTTGAACAAAGATAACCCACAAGAATAACAGTACAT TTATGCACCTTTTGAACAAAGATAACCCACAAGAATAAGACTCC TTATGCACCTTTCATATTTATTTCGAGCCAGTAATAAATCAATA TTATGCACCTTTTCATATTTATTTCGAGCCAGTAATAAATCAATA **TTATGCACCTTT**AAATCAATCGTCGCTATTAATTAAATCGCAAG **TTATGCACCTTT**CGGAATTACGTATTAAATCCTTTGGTTGGCAA **TTATGCACCTTT**AATGGTTTTGCTGATGCAAATCCATTTTCCCT **TTATGCACCTTT**GCCACCACTCTTTTCATAATCAAATAGCAAGG **TTATGCACCTTT**GCCAACAGATACGTGGCACAGACATGAAAAAT **TTATGCACCTTT**CAAGCAAGCGAGCATGTAGAAACCAGAGAATA TTATGCACCTTTTTATTACGTAAAGGTGGCAACATACCGTCACC **TTATGCACCTTT**GTTGTAGCCCTGAGTAGAAGAACTACATTCTG **TTATGCACCTTT**ATCGGCTGACCAAGTACCGCACTCTTAGTTGC **TTATGCACCTTT**ACAAAGAAAATTTCATCTTCTGACAGAATCGC **TTATGCACCTTT**CCGGAAACTAAAGGTGAATTATCATAAAAGAA **TTATGCACCTTTCTAAAGCAAATCAATATCTGGTCACCCGAACG TTATGCACCTTT**GACTTGAGGTAGCACCATTACCATATCACCGG **TTATGCACCTTT**TATTTTGCACGCTAACGAGCGTCTGAACACCC **TTATGCACCTTT**TTATTAATGAACAAAGAAACCACCTTTTCAGG **TTATGCACCTTT**GCCCAATAGACGGGAGAATTAACTTTCCAGAG **TTATGCACCTTTAACCAGAGACCCTCAGAACCGCCACGTTCCAG TTATGCACCTTT**ACGCAAAGAAGAACTGGCATGATTTGAGTTAA

Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC TTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

Additional sequences:

TACTCAGGAGGTTTAGATAGTTAG TATAAGTATAGCCCGGAATAGGTGTATCACCG CACCACCCTCATTTTCCGTAACAC GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC ACCAGGCGGATAAGTGGGGGTCAG GAAGGATTAGGATTAGAAACAGTT GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG ACCGCCACCCTCAGAAACAACGCC GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG CTAAATCGGAACCCTAAAACCGTC ATCACTTGAATACTTCTTTGATTAGTTGTTCC ACGTGCTTTCCTCGTTGCCACCGA TAGAGCTTGACGGGGAAAAGAACG CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT GCGTACTATGGTTGCTAATTAACC CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CTAAACAGGAGGCCGAGAATCCTG CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC AAACCCTCTCACCTTGCTGAACCTAGAGGATC AAAAAAGGCTTTTGCGGGATCGTCGGGTAGCA TCATAGCTTGTAAAACGACGGCCAAAGCGCCA AGTGTACTATACATGGCTTTTGATCTTTCCAG GCGCATTAATAAGAGCAAGAAACAATAACGGA

TTTTAATTGCCCGAAAGACTTCAACAAGAACG CCAGACGACAAATTCTTACCAGTAGATAAATA TACATACACAGTATGTTAGCAAACTGTACAGA CTGTAATAGGTTGTACCAAAAACACAAAATATA CTTTTACACAGATGAATATACAGTGCCATCAA AGTTTGGACGAGATAGGGTTGAGTGTAATAAC GCAAATATGATTCTCCGTGGGAACCGTTGGTG ATACGTAAGAGGCAAAAGAATACACTGACCAA CTCATCTTGGAAGTTTCCATTAAACATAACCG GCGTTATACGACAATAAACAACATACAATAGA ATATAATGGGGGCGCGAGCTGAAATTAACATC ACGAACTATTAATCATTGTGAATTTCATCAAG TCGCAAATAAGTACGGTGTCTGGACCAGACCG AATCACCACCATTTGGGAATTAGACCAACCTA GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA TCAGGTCATTTTTGAGAGATCTACCCTTGCTT GCAATAGCAGAGAATAACATAAAAACAGCCAT CACCAGAGTTCGGTCATAGCCCCCTCGATAGC GGACGTTGAGAACTGGCTCATTATGCGCTAAT CTAAAATAAGTATTAACACCGCCTCGAACTGA TGGACTCCGGCAAAATCCCTTATACGCCAGGG GGAATTACCATTGAATCCCCCTCACCATAAAT CGTAACGAAAATGAATTTTCTGTAGTGAATTT CTGTAAATATATGTGAGTGAATAAAAAGGCTA GCTCCATGACGTAACAAAGCTGCTACACCAGA ATTTTGCGTTTAAAAGTTTGAGTACCGGCACC GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG GCGCAGAGATATCAAAATTATTTGTATCAGAT ATTAAGTTTTCCACACAACATACGCCTAATGA

TTAAGACGATTAATTACATTTAACACAAAATC ACGAGTAGATCAGTTGAGATTTAGCGCCAAAA GAGCCGCCCCACCACCGGAACCGCTGCGCCGA GAAATGGAAAACATCGCCATTAAACAGAGGTG TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA AGCACCGTAGGGAAGGTAAATATTTTATTTG CTTAAACAACAACCATCGCCCACGCGGGTAAA ATATATTCTCAGCTTGCTTTCGAGTGGGATTT TCACAATCCCGAGGAAACGCAATAATGAAATA GTAAAAGACTGGTAATATCCAGAAATTCACCA AGGCGGTCTCTTTAGGAGCACTAAACATTTGA CCAGGCGCGAGGACAGATGAACGGGTAGAAAA AGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA TCCATATATTTAGTTTGACCATTAAGCATAAA TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG CAAAAATCATTGCTCCTTTTGATAATTGCTGA GCTTCTGGCACTCCAGCCAGCTTTACATTATC ACTGGATATCGTTTACCAGACGACTTAATAAA TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA ACAGAAATCTTTGAATACCAAGTTAATTTCAT AAATAATTTTTAACCAATAGGAACAACAGTAC AGAGAATCAGCTGATAAATTAATGCTTTATTT AGGTTTTGGCCAGTTACAAAATAAACAGGGAA AGTAATCTTCATAAGGGAACCGAACTAAAACA TGAGTTTCAAAGGAACAACTAAAGATCTCCAA TATGTAAAGAAATACCGACCGTGTTAAAGCCA GAAGATCGTGCCGGAAACCAGGCAGTGCCAAG TTGAATTATTGAAAACATAGCGATTATAACTA

CTTTCATCTCGCATTAAATTTTTGAGCAAACA CGATTTTAGGAAGAAAAATCTACGGATAAAAA AATGCCCCATAAATCCTCATTAAAAGAACCAC GGATTTAGTTCATCAATATAATCCAGGGTTAG AACCTACCGCGAATTATTCATTTCACATCAAG AAAACAAACTGAGAAGAGTCAATATACCTTTT TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG CAATGACAGCTTGATACCGATAGTCTCCCTCA GGGAGAGGCATTAATGAATCGGCCACCTGAAA CCCGGGTACCTGCAGGTCGACTCTCAAATATC AGAGGCATACAACGCCAACATGTATCTGCGAA CTTGCATGCCGAGCTCGAATTCGTCCTGTCGT CGAGTAGAACAGTTGATTCCCAATATTTAGGC TAGCCCTATTATTTACATTGGCAGCAATATTA ATTATTATTAGCGAACCTCCCGACGTAGGAA CAATAAATAAATGCAATGCCTGAGAAGGCCGG AAACGAAATGCCACTACGAAGGCAGCCAGCAA GCCACGCTTTGAAAGGAATTGAGGAAACAATT GATGGCAAAAGTATTAGACTTTACAAGGTTAT ATACCCAAACACCACGGAATAAGTGACGGAAA TCATTACCGAACAAGAAAAATAATAATTCTGT ATCAGAGAGTCAGAGGGTAATTGAACCAGTCA CCAAAATAAGGGGGTAATAGTAAAAAAAGATT CTTTGAAAATAGGCTGGCTGACCTACCTTATG ACGGCTACAAGTACAACGGAGATTCGCGACCT TTCGCCATGGACGACGACAGTATCGTAGCCAG AGACAGTCTCATATGTACCCCGGTTTGTATAA GAAGCAAAAAAGCGGATTGCATCAATGTTTAG CTTTACAGTATCTTACCGAAGCCCAGTTACCA

CGACAACTTCATCATATTCCTGATCACGTAAA TTATTCATGTCACCAATGAAACCATTATTAGC CTAATTTACCGTTTTTATTTTCATCTTGCGGG GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG GCGTAAGAAGATAGAACCCTTCTGAACGCGCG AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT AGAAGTGTCATTGCAACAGGAAAAAATCGTCT TTTTAGTTCGCGAGAAAACTTTTTTTTATGACC GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC **TCTTACCAACCCAGCTACAATTTTAAAGAAGT** GAGGCGTTTCCCAATCCAAATAAGATAGCAGC TAACCTCCAATAAGAATAAACACCTATCATAT GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT GTCACACGATTAGTCTTTAATGCGGCAACAGT GGTATTAATCTTTCCTTATCATTCATATCGCG ACGCTCAACGACAAAAGGTAAAGTATCCCATC CAACGCAAAGCAATAAAGCCTCAGGATACATT AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT TGGATTATTTTTGCCGTCAATAGATAATCAACTAAT TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG AATTACTATTTCATAGGTCTGAGAGACGTGAATTT ATCAAAATTTTTGAAGATGATGAAACAAAATTACCT TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT

# TTTTTGAAAGTATTAAGAGGCTATTATT

## Origami with 90 degree curve:

| TEGECTTECTATCCCTEAAAATEAEGETEET        | GGCTCTGAGGGTGGCGGTTCTGAGGGT             | TEECESTTCTEAGEGTEECESTACTAAACCTCCT               | GAGTACGGTGATACACCTATICCGGGCTATACTTA      | TATCAACCCTCTCGACGGCACTTATCCGCCTGG  | TACTGAGCAAAACCCCGCTAATCCTAATCCTT        | CTCTTGAGGAGTCTCAGCCTCTTAATACTTTC              | Δ.       |
|--|---|--|--|--|---|---|----------|
| 01111401000400W                        | 20404010004000014404010004              | ADD0004A0407000400000410411004004                | 212412222421410100414400222041410441     | 1140110004040001003010441400000000   | A 10A010011110000 \$ A11A00A11A00AA     | 24244212212424013 00004114124440              | -        |
| CETAACACIGAETTT                        | CGTCACCAGTACAAACTACAACGCCTC             | GTAGCATTCCACAGACAGCCCTCATAGTTAGCG1               | AACGATCTAAAGTTTTGTCGTGATACAGGAGTGTA      | CTGGTAATAAGTTTTAA GGGGTCAGTGCCTTC  | ASTAACAGTGCCCGTATAAACAGTTAATGCCC        | CCTGCCTATTTCGGAAC TATTATT: TGAAAC             | 4        |
| 1413311959143419534119194313444        | V010010V101110V10110000V                | ACCC1AACTATCACCCCTCTCTCTCCC                      | 1193. 99111399993939 01910133139391      |  | V11913V355551V1V111513VV11V3555         | V355V1VVV5331155V1VV1V5V31115                 | 1 /      |
|  |   |  |  |  |   |   | 1        |
| ITATTATICGCAATTCCTTTAGTTGTTCCTT        | CTATTCTCACTCCGCTGAAACTGTTC              | GAAAGTTETTTAGCAAAATCCCATACAGAAAATT               | CATTINCTAACGTCTGGAAAGATCAAAAGCCATGT      | AT ACCCTTACTGGAACGGTAAATTCAGAGACI  | GCTTTCCATTCTGGCTTTAATGAGGATTTA          | TGTTTGTGAATATCAAGGCCAATCGTCTGA                | 4        |
| AAAT2AA2AA22AA                         | AACAGETTA AGGGGAGE GAGAATAG             | 2111344 24441321 \$1149323 \$131311144           | 91944 19411939 9433111314911113991434    | A 2122244194221123 \$41114421212134  | 22224442214424223444114212214441        | 44244424 <u>3114142</u> 22221142242431        |          |
| ATCTCCAA VAAAAAG                       | CTCCAAAAGGAGCCTTTAATTGTATC              | CGGTTTATCAGCTTGCTTTCGAG TGAATTICTT               | AAACAGCTTGATACCGATAGTCTCCCTCAGAGCCG      | CONCEPTENDANCEDECT COTTAGA DECACES   | C: CTCAGAGCCGCCACCAGAACCAC: ACCAGA      | CCCCCCCCACCATTCA CAGCACCT TCACCCA             | <u> </u> |
| AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | VADDITTTDDDDDDAATTAADATA                | AAGAAATTCACCTCGAAAGCAAGCTG                       | 1110.00401410001410404050401010000       | 001000101000001000000000000000000000000  | 10100100100100100100100100100101        | 100000000000000000000000000000000000000       | 3 /      |
|  |   |  |  |  |   |   | 1        |
| TTTCGCTGCTGAGGGTGACGATCCCGCAAAA        | GGCCTTTAACTCCCTGCAAGCCTCA               | AGCGACCEANTATATCGGTTATGCGTGGGCGATG               | STTETETCATTETCEGCECA CCESTTCCGETGET      | CONTENDED TECEGORGATITICATTATEAAAAA  | GGCAAACGCTAATAAGGGGGCTATGACCGA          | ATECCEATEAAAACECECTACAETCTEACE                | 4        |
| 010010000001111                        | 2222244411242224011222421               | 1202100211414143224414302422202142               | 24424 4242144242222222222224422224224    | 22242422448222421484421441421111   | 14222111232411414222222414212221        | 114200214211103 020410124042102               | 1        |
| COTAGCALCOCTA                          | AGAGGETTTGAGGACTAAAGACTITT              | TTCATGAGGAAGTTTCCATTAAA GGGTAAAATA               | CETAATECCACTACGAAGECAGCCAECAAAATCAC      | CAGTAGCACCATTACCAT TAGCAAGGCCGGAAA   | CSTCACCAATGAAACCATCGATAGCAGCACCG        | TAATCAGTAGCGACAGA ATCAAGTJ TGCCTTT            | 4        |
| 146000110011001000110011000110         | 0100044401001041110104444               | TATTTTACCCGTTTAATGGAAACTTC                       | 01041111001001001000100100101010000      | 111CCCCCC11CC1VV1CC1VV1CC1CC1V   | A010011A0111001A001A1001001000.         | AAAGGCAAACTTGATTCTGTCGCTACTGAT                | 1 /      |
|  |   |  |  |  |   |   | 1        |
| ATCAGGCGATGATACAAATCTCCGTTGTACT        | TGTTTCGCGCTTGGTATAATCGCTGG              | GGGGTCA AGATGAGTGTTTTAGTGTATTCTTT                | GCCTOTITEGTITIAGGTIGGTCTAATICCCAAAT      | CONTRACTORGET GARGET GATAATTCACCTTI  | TGAATAATTICCGTCAATATTTACCTTCCC          | CCTCAATCGGTTGAATGTCGCCCTTTTGTC                | 4        |
| 14242224424124                         | A2AAA22222AA22A3ATTA222A3               | 222240111214212426464612426466666                | 39949 44493444 4133443349411449991114    | 12 24211242 22421222 2141144212244   | 114211411444892243 14144419244922       | 1222A2TT4222AA2T1 2A22222AAAA2A2              | 4        |
| COCOACCE SCIECAL                       | TTACTTAGCCGGAACGAGGCGCAGAG              | CEETCANTCATANGEGANCCEAN LIGACCANCIT              | T CAAA GAGGACAGAT GAACGGGT AGAAAA TACATA | CATAAAGGTGGCAACATATAAAAGAAACGCAAA  | GACACCACCGAATAAGT TATTTTCCACAAT         | CANTAGAAAATTCATAT GETTTACCAGCGCCA             | 4        |
| 1114434343311143333313343343343        | A12A41322331123133231313                | 000001001011000110001100010000                   | A2111 122121212122 0 4121111412141       | 9.VIII33V339II9IVIVIII1311311939II1  | 101001000110110000100000000010110       | 141311114401414334441001303001                | 1 /      |
|  |   |  |  |  |   |   | 1        |
| CTTATTCACTGAATGAGCAGCTTTGTTACG         | TGATTTGGGTAATGAATATCCGGTTC              | CTTGTCA GATTACTCTTGATGAAGGTCAGCCAG               | CCTATACGCCTGGTCTGTACA CTTTGCTAACATAC     | TO GTAATAAGGAGTCTTAATCATGCCAGTTCI  | T TEEETATTCCETTATTATTCCETTTCCTCE        | TTTCCTTCTGGTAACTTTGTTCGGCTATCTG               | 4        |
| 10010044044100                         | A21AAA222A11A213 1A2222AA2              | 0110101101101010101001000100010                  | 004140000000040404000004400041101410     | 10 50VIIVII 0010V0V 1V0IV00910VV0V   | AAA222ATA4222AATA4TAA222AAA222A2        | 244493449433341194443449333414343             |          |
| CACCAGALCGAGTA                         | TAAATTGGGCTTGAGATGGTTTAATI              | ITCAACITTAATCATTETEAATTACCTTATECEA               | TTTTAAGAACTEGCTCATTATECECTAAJ ATCAGA     | <u>GAGATAACCCACAAGAA TGAGTTAAGCCCAA</u> T  | AATAAGAGCAAGAAACA TGAAATA 2 CAATAG      | CTATCTTACCGAAGCCG TTTTTAAGAAAAGTA             | 4        |
| 24632222431231311121221311231341       | ATTTAA22228AA2T2TA22AAATTA4             | WA2112 MATLA21AA2A211AA122AA1A2221               | AAAA1 0110A000A01AA14 0000A11A1A0101     |  | VII010011011011011001110100010010       | *1149441993113999444441131111341              | 1 /      |
|  | 1                                       | II   |  | 11   |   | 11  | 1        |
| STTGAATGTGGTATTCCTAAATCTCAACTGA        | CAATCTTTCTACCTGTAATAATGTTC              | GTTCCG AGTTCGTTTTATTAACGTAGATTTTT                | CTTC: AACGTCCTGACTGGT CAATTACCCTCTG      | A TTETTCAGGETETTCAETTAATTCTCCCET   | CAATGCGCTTCCCTGTTTTTATGTTATTCTC         | TGTAAAGGCTGCTATTTTCATTTTTGACGT                | 4        |
| V111V5V5115V51                         | 211626662666666666666666666666666666666 | 2442224 41244224 4441441 52412144444             | <u> </u>                                 | 194443449132343444 3441144949933   | 2411422224452224544444414244144242      | 19A3A1113 20A30A14 AA01AAAAA3103A             | 1        |
| ESCCARA SEGATTA                        | GAGGCATAGTAAGAGGAACACTAJ : A            | ATAACCEICETTTACCAGACGAC ATAAAAACCA               | AAATAGCGAGAGGCTTTTGCAATCCTGA& TCTTAC     | CARCECTARCERECETCT TCCRERECCTART   | TRECASTINGAMATAA CASCCALLIATIT          | ATCCCAATCCAAATAAS AAACGATJ TITIGIT            | ÷        |
| VIIV39131V101V11030911113311VV1        | 01000101001101001101001001              | TATTOD: ADDAAA100101001001A11111001              | 11141 001010000444001 4004011404410      | 011030411031303404460013130941141  | 19913VV191111V111913991V1VVV            | 000011000111011100100000000                   | 1 /      |
|  |   |  |  |  |   |   | 1        |
| AACTGTTTAAAGCATTTGAGGGGGGATTCAAT       | ATATTTATGACGATTCCGCAGTATT               | TEGACEC ATCCAGTCTAAACATTTTACTATTAC               | CCCCT TEECAAAACTTCTTTAAAATTETAECTEE      | GT CAAAATAGCAACTAATCTTGATTTAAGGC1  | AAAACCTCCCGCAAGTCGGGAGGTTCGCTA          | ACCCCTCCCGTTCTTAGAATACCGGATAAG                | 4        |
| 11104010000100                         | TIATAAAIASTOJIAA DODIJATAA              | ADDIDODATAGENER ACTOCATA CCCTCCA                 | 000040404001111044044011114404100400     | A 201111A1 20112A11 8 20021AAA112222   | A0111100400000110400001004400041        | 11100004000040044044001011410000014110        |          |
| CATAGAT CAGAGAT                        | AGGTCTTTACCCTGAGTATTATAGTC              | CAGAAGCAAAGCGGATTGCATCA                          | AGGAAGCCCGAAAGACTTCAACAAGAACGGGTATT      | AAACCAAGTACCGCACT ATCGAGAACAAGCAA  | GC GETTETTATTETCAT GTAGGAALCATTAC       | COCOCCANTAGCANOS ANATCAGATATAGAN              | 4        |
| 5151111551511451551411145111114        |   | 010110 11000010V0001V0111101VV110                | 1001.00001110104401101101100004144       | 1.001101101000104014001010110011   | 00000000000000000000000000000000000000  | 000001101001100111001010101010101             | 1 /      |
|  |   |  |  |  |   |   | 1        |
| GCAAAAATGACCTCTTATCAAAAGGAGCAA         | TAAAGGTACTCTCTAATCCTGACCTC              | GTTGGACTTTGCTTCCGGTCTGGTTCGCTTTGAA               | GCTCC ATTAAAACGCGATAT CAATGATAAGGAAA     | CALAGECEATTATTEATTEETTEETACATECTC  | CAAATTAGGATGGGATATTATTTTCTTGTT          | GGACTTATCTATTGTTGATAAACAGGCGCG                | 1        |
| 114211112212211                        | ATTT55AT545A5AT1455A5T55A5              | 28422128882288822222828228882211                 | 22422114411112222141421142141122111      | 1010000144144014460440941014004  | 241114412214222141441444444544244       | 21001044140414004401411101000000              | 4        |
| ATTGCTGALTATAAT                        | GCTGTAGCTCAACATGT TTTAAATATC            | GCAACTAAAGTACGGTGTCTGGA <mark>AGTTTCAJTCC</mark> | ATATAACAGTTGATTCCCAATATTTAGGCAGAGGG      | ATTTTCGAGCCAGTAATA GAGAATATAAAGTA  | C: GACAAAAGGTAAAGTAATTCTGT: CAGACG      | ACGACAATAAACAACAT STTCAGCJAATGCAG             | 4        |
| 2102220012122001100250211010110        | VVJVIJJVJIJJVJVVVVIIIVIV.               | 391194 134193343494333113444914495               | 1414.0313443144555114.4441335131335      | IV VV90109910VIIVII01011VIVII10V   | **************************************  | 01011V1101101V0V0100V11V0010                  | 1 /      |
|  |   |  |  |  |   |   | 1        |
| AGAATTGATGCCACCTTTTCAGCTCGCGCCC        | AATGAAAATATAGCTAAACAGGTTA               | ATTGACCO TTTGCGA AATGTATCTAATGGTCAAA             | CTAR/ CTACTCOTTCOCAGE TACATOTTGOCOTT     | CT AAATATGGCGATTCTCAATTAAGCCCTACI  | TTGAGCGTTGGCTTTATACTGGTAAGAATTT         | TATAACGCATATGATACTAAACAGGCTTTTT               | 4        |
| AAA0732A0303020                        | 11143111 [4141354 115133441             | 14421221444222121424140 <mark>4114224211</mark>  | 041114041040044400010141014044000044     | AATTIATA2 20214404 \$11441120204104  | 24421222442224441412422411211444        | 241411939 [414314 ] 41119133944444            | •        |
| TAACATC AATAAA                         | TCATACAGGCAAGGCAA GAATTAG 7             | AAAATTAAGCAATAAAGCCTCACAGCATAAAGCT               | AAATC GETTETACCAAAAACACAAATATA TTTTAG    | TTAATTTCATCTTCTGAC TAAATTTAATGGTT  | T SAMATACCOACCOTO CATAAATA SOCOTT       | AAATAAGAATAAACACO GGAATCAJAATTACT             | 4        |
| 1041141041041001441101400114111        | 1419100011000111011441001               | 111144 00114111000401010014111004                | 1114/ 00404190111110 01114141444410      | AACCATTAAATTTAGGTCAGAAAGATGAAATTAJJAA  | AACCCCTTATTTATCACACGGGGGGGGAATTTA       | 1011011011011010000011100101100100            | 1 /      |
|  |   |  |  |  |   |   | 1        |
| TTTACCTACACATTACTCAGGCATTGCATT         | AAATATATGAGGGTTCTAAAAATTI               | TTTATCO TGCGTTGAAATAAAGGCTTCTCCCGC               | AAAAGTATTACAGGGTCATAA AAAAGTTTTCTCG      | CONTENTITETETTECENTIEGATTIECATEAGE   | TTTACATATAGTTATATAACCCAACCTAAGC         | CAGGTTAAAAAGGTAGTCTCTCAGACCTAT                | 4        |
| A013331AA331AA                         | 1111VIVI #31333VV PV11111VVV            | ******   | 1111 VIVVI913 53V91V11111113VVVV9V93     | *********  | 14441014141344141411000110041130        | 222122AA1 11122A1 AAAAAA12122A1A              |          |
| AGECCEPIEACAET                         | CANATCACCATCAATAT CATATTCAAC            | CCOTTCTAGCTGATAAATTAATC CGGAGAGGGT               | AGCTATTTTTGAGAGATCTACCCTTGCTT CTGTAA     | ATCOTOCOTATTAATTA TTTTCCCTTAGAATS  | CTTGAAAACATAGCGATAGCTTAGALTAAGAC        | <u>CCT CACAACACT CAATA CT CAATT TAT CAAAA</u> | 1        |
| 1440111100040101110000001010104        | 1114010014011414014140111               | ACCCTCCCCCATTAATTTAACCACC                        | 1004 444401010140410 004000400404041     | 1 Y 1 C 1 Y Y C C C Y Y Y L I Y Y I I Y Y I Y Y Y Y Y Y Y Y  | 4101111919100019100994101999            | A 21 21 21 21 24 21 141 24 21 1444 14 21 11 1 | ₹ /      |
|  |   |  |  |  |   |   | 1        |
| CTITICIGATIATCAACCOGGGTACATAIG         | TGACATGCTAGTTTTACGATTACCC               | GTTCATO ATTCTCTTGTTTGCTCCAGACTCTCA               | GECAN GACCTGATAGCCTTT TATTCACTCACAT      | A TATTGATTTATGTACTGTTTCCATTAAAAAA  | CAATTCAAATGAAATTGITAAATGIAATTAA         | I TETTICIEATETTETTCATCATCI                    | 4        |
| 00000001010101                         | 4421214234124444 221441222              | 244214221442424424244224                         | 22211 02122001 012220000000000000000000  | A 144214441424124124144422144111111  | 24114421114421114454111424114411        | ****  | 1        |
| T GTATAA SCAAATA                       | ITTAAATTETAAACETTAATATTTI 1             | TTANAN I COCATTANATITITO TANATCASCI              | CATTLETTAACCAATAGGAACAACAGTAC CITTEA     | CATCOGGAGAAACAATAACGGATTCGCCTGATI  | G: TTTGAATACCAAGTTACAAAATC2CGCAGA       | SECENATIATICATITE NATIACCI MACCANA            | 4        |
| 22211111212211214A2A1A1122111A1        | ATTIAASATTISSAATTATAAAASA               | AA11114A0001AA1111AAAA0004A111A0100A             | 01444 441100114100119 1010410044441      | 0140000101110114110001440000040144   | AAAA3114133113AA131111433333131         | 9931144144914449114419943139111.              | 1 /      |
|  | 11                                      |  |  | 11   |   | 11  | 1        |
| COTCAATCCGCCGTTTGTTCCCACGGAGAAT        | GACGGETTETTACTCECTCACATTI               | TAATGTTCAAAAGCTGGCTACAGGAAGGCCAG                 | ACCCONTRATTITICATOC ACTOTATATICATC       | TO ACGITA AACCIGA AAATCIACGCAATTICII   | TTTCTGTTTTACGTGCAAATAATTTTGATA          | GTAGGTTCTAACCCTTCCATTATTCAGAAG                | 4        |
| WV55515551511W                         | 22722224 426472645 5262727644           | ALLAND TAPELLE AND DATE TO THE DOLLARD           | 1939311001000 (031033919030101009109     | TO IS STATED AND IN THE REAL PROPERTY AND INTERVAL PROPE | VIVV99939 VVVISOV 011141144493141       | 122412244 0V112224 021441442121122            | 1        |
| COTTOGTO LAGATOS                       | SC CATCOTAACCOTO ATCTOCCA 21            | TTTGAGGGGACGACGACAGTATO GCCTCAGGAA               | GATES CACTOCASCCASCTITACATTATE ATTITS    | CEGAACAAAGAAACCACC <mark>AGAAGGA</mark> GCEGAATI   | ATCATCATATTCCTGAT ATCAGAT LATGGCA       | ATTCATCAATATAATCO IGATTETI IGGATTA            | 1        |
| 241142221412242122442242342121422      | 0301602611003630160630101               | AAA0101 010010010104140000004010011              | 0140-0104001000100444 00144140144440     | 0 0 1191110111991991011001090011W  | 10210210101000000000000000000000000000  |   | 1 /      |
|  |   |  |  |  |   |   | 1        |
| CCAGCTEGCETAATAGCGAAGAGECCCGCA         | GATEGEEETTEECAACAGTTGEGEA               | AGCCTGA TGGCGAATGGCGCTTTGCCTGGTTTC               | CGGCA CAGAAGCGGTGCCGG ACTCAAACTTTTA      | A . TTAATAACGTTCGGGCAAAGGATTTAATAO   | GTTGTCGAATTGTTTGTAAAGTCTAATACT          | TAAATCCTCAAATGTATTATCTATTGACGG                | 4        |
| 000110100000001                        | 22762262666666666666666666666666666666  |  | 00001001010000000000000000000000000000   | 111441141192448223 011122144411415   | 21244242211442444641112424114124        | APATTIAPP APTIAPA AATAPATAAPTPPP              | 1        |
| CAAGGCELTTAAGT                         | ISCOLARCECCASES TATCCCASE IN            | ACGACGTTGTAAAACGACGGCCA TGCCAAGCTT               | GCATECOTECASETCEACTOTCAAATATE AAACCO     | ICANTCANTATCIGGICA STIGGCANATCANCI   | GTTGANAGGANTTGAGGAAGGTTAT: TAANAT       | ATCTITAGGAGCACTAA CAACTAAJ AGATTAG            | 4        |
| 2111222221424224221122221441124        | 03341103001333444400013401              | 1931934 34111193193399134399113944               | 2014.002010240210404 01114140111000      | ***I40114140400401044000111401101  | A01110011460100110046160411114          | **************************************        | 1 /      |
|  | 11                                      | 11   |  | 11   | 1                                       | 11  | 1        |
| TTTATECTTCCGGCTCGTATGTTGTGTGGA         | TGTGAGCGGATAACAATTTCACACA               | AGGAAAGAGCTATGACCATGATTACGAATTCGAG               | CTCGC ACCCGGGGATCCTCT AGGTTCAGCAAGGT     | GATGCTTTAGATTTTTCATTTGCTGCTGGCTC1  | AGCGTGGCACTGTTGCAGGCGGTGTTAATAC         | ACCECCTCACCTCTETTTTATCTTCTECTE                | 9        |
| 00414044040400000                      | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  | 10011101004140100140144 0011440010               | 0400041000000 2140040410044010011004     | 10000000000000000000000000000000000000   | 01000000000000000000000000000000000000  | 2122226421224243434444442428282               | 1        |
| CTAATGASTGAGCT                         | ACTEACATTAATTGES TECCETEAC              | CTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCC              | AGCTGCATTAATGAATCGGCCACCTGAAAGCGTAA      | GANTACGTOGCACAGACA TATTTT GAATGG   | TATTAGTETTTAATGEGGAACTGATAGECET         | AAAACATCGCCATTAAA AATACCGAACGAACC             | 4        |
| A3A111332A33332A322A11A312A3132A       |   | 003050 00005130533311155034550395                | 1394.4144114311493399 0943111393411      | 1 VI03V3301013101VIVVVVV311V33   | WWIDVOVVIIVD0000110V01V10000V           | 110140300144111114100311031100                | 1 /      |
|  | 11                                      | 11   |  | 11   | 1                                       | 11  | 1        |
| TGCAACTCTCTCAGGGCCAGGCGGTGAAGGG        | ATCASCISTICCCGTCTCACTSS                 | TGAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA          | AACCONCTCTCCCCGCGCGTT CAGAAGGGTTCTAT     | CT TGTTGGCCAGAATGTCCCTTTTATTACTG   | GTGTGACTGGTGAATCTGCCAATGTAAATA          | CCATTICAGACGATTGAGCGTCAAAATGTA                | 4        |
| \$2100000011000                        | TTADTOA 2400000 4040104004              | ************************************             | 1100200404000000000401011000440414       | A 24244222221211424 22444441441242   | A224242124224211484222114241141         | 14001444010100144 10004011114041              | 1        |
| GETTTGCC: CAGCAG                       | CCGAAAATCCTGTTTGA FGGTGGTT              | CGANATEGGEARAATEEETTATAAATEAAAAAGAA              | TAGCCCGAGATAGGGTTGAGTGTAATAACATCACT      | TECCTENETAGANGANCE ANACTATCESCCTT  | GET GET AATATCCAGAA CAATATTACCGCCAG     | CCATTECAACAGGAAAAACGCTCATIGAAATA              | 4        |
| 3911393346919394334443939913913        | 011111055V0VVV01V00V059                 | 001111V 0011111V0000VV1V1111V01111011            | V105 0101V1000W010 V11V1191V919V         | V 000000000000000000000000000000000000   | TV05V11V1V591511911V1V19555915          | 1111000110100111110009101000111111            | * 7      |
|  | 11                                      |  |  | 11   |   | 11  | 1        |
| ATTTGGGTGATGGTTCACGTAGTGGGCCATC        | CCTGATAGACGGTTTTTCGCCCTTT               | TGACGT GAGTCCACGTTCTTTAATAGTGGACT                | CTTGT CCANACTGGANCANC TAATCANAGAAGTA     | TTACAACGGTTAATTTGCGTGATGGACAGA   | CTTTTACTCGGTGGCCTCACTGATTATAAA          | CACTTCTCAGGATTCTGGCGTACCGTTCCT                | 4        |
| 100410400000140                        | 222721V1 212220VV \$ V22222VVV          | *219344221249914344944411413433194               | 9443449911194 \$311911941149111311341    | V 29VI9II9 29VVIIV 299V9IV9919191  | 242444415452342238845134214414111       | 119194494 01001440 00004199044994             | 1        |
| AGGTGCCGTAAAGC                         | ACTANATOGGANCOOTA ANGEGANCOO            | CCCGATTTAGAGCTTGACGGGGA AAGCCGGCGAA              | COTOSCOACAAAGCAAGGCAATGCGCCGCTACAGG      | CC GC GT A CT A T G G T T G A C G A G C A C G T A T  | AACGTGCTTTCCTCGTTAGAATCAGAGCGGGA        | CTARACAGGAGGCCGA TTARAGGGATTTTAG              | 1        |
|  | 201120201000000000000000000000000000000 |  | ********                                 | 2222241241422442244224422222   | 110000000000000000000000000000000000000 |   | <b>a</b> |

## Purple 90degree curve sequences:

GTTAGATGATTTATCAACAGGAGAGCCAGCAGCAAAATATTTT GTTAGATGATTTGCGAAACAAGAGGGCTTTGAGGACTAGGGAGTT GTTAGATGATTTAAATAATTTTTAACCAATAGGAACAACAGTAC GTTAGATGATTTCCAAATCATTACTTAGCCGGAACGTACCAAGC GTTAGATGATTTGCCACGCTTTGAAAGGAATTGAGGAAACAATT GTTAGATGATTTTACCTTTAAGGTCTTTACCCTGACAATCGTCA GTTAGATGATTTCGACAACTTCATCATATTCCTGATCACGTAAA GTTAGATGATTTTAAATATTGAGGCATAGTAAGAGCACAGGTAG GTTAGATGATTTGGTAGCTATTGCCTGAGAGTCTGGTTAAATCA GTTAGATGATTTCAGGTCATTTTCGAGAGATCTACCCTTGCTT **GTTAGATGATTTCTAAAATAAGTATTAACACCGCCTCGAACTGA GTTAGATGATTTGGATTTAGTTCATCAATATAATCCAGGGTTAG GTTAGATGATTTCAACGCAAAGCAATAAAGCCTCAGGATACATT** GTTAGATGATTTTTTCATGATGACCCCCAGCGATTAAGGCGCAG **GTTAGATGATTTTGTAGCATAACTTTCAACAGTTTCTAATTGTA GTTAGATGATTTTGCAACTAGGTCAATAACCTGTTTAGAATTAG GTTAGATGATTTGATGGCAAAAGTATTAGACTTTACAAGGTTAT** GTTAGATGATTTTTTCAACTACGGAACAACATTATTAACACTAT **GTTAGATGATTTGCTTCTGGCACTCCAGCCAGCTTTACATTATC GTTAGATGATTTAAAGATTCTAAATTGGGCTTGAGATTCATTAC** GTTAGATGATTTTTATTAATGAACAAAGAAACCACCTTTTCAGG **GTTAGATGATTTTCAGAAGCCTCCAACAGGTCAGGATTTAAATA** GTTAGATGATTTGCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG **GTTAGATGATTTAGGCGGTCTCTTTAGGAGCACTAAACATTTGA GTTAGATGATTTCTAAAGCAAATCAATATCTGGTCACCCGAACG GTTAGATGATTTCATAACCCGCGTCCAATACTGCGGTATTATAG** GTTAGATGATTTTCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT **GTTAGATGATTTAAACCCTCTCACCTTGCTGAACCTAGAGGATC** GTTAGATGATTTTCGCAAATAAGTACGGTGTCTGGACCAGACCG **GTTAGATGATTTACGGTCAATGACAAGAACCGGATATGGTTTAA** GTTAGATGATTTGCTAAATCCTTTTGCGGGGAGAAGCCCCGGAGAG GTTAGATGATTTAAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT GTTAGATGATTTATTTTGCGTTTAAAAGTTTGAGTACCGGCACC **GTTAGATGATTTGAAGCAAAAAAGCGGATTGCATCAATGTTTAG** 

Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC

ATTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

Additional sequences:

GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG TGGATTATTTTTGCCGTCAATAGATAATCAACTAAT ATCAAAATTTTTGAAGATGATGAAACAAAATTACCT TTTTTGAAAGTATTAAGAGGCTATTATT AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT AATTACTATTTCATAGGTCTGAGAGACGTGAATTT AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA ACAAAGAAAATTTCATCTTCTGACAGAATCGC TGAACAAAGATAACCCACAAGAATAAGACTCC CTTTGAAAATAGGCTGGCTGACCTACCTTATG GGGAGAGGCATTAATGAATCGGCCACCTGAAA TGCCTTGACAGTCTCTGAATTTACCCCTCAGA CAATGACAGCTTGATACCGATAGTCTCCCTCA GTAAAAGACTGGTAATATCCAGAAATTCACCA AAAACAAACTGAGAAGAGTCAATATACCTTTT

ACTGGATATCGTTTACCAGACGACTTAATAAA CCAAAATAAGGGGGTAATAGTAAAAAAAGATT CATGTCAAAAATCACCATCAATATAACCCTCA AAATCAATCGTCGCTATTAATTAAATCGCAAG TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC AGGTTTTGGCCAGTTACAAAATAAACAGGGAA CAATAAATAAATGCAATGCCTGAGAAGGCCGG AGACAGTCTCATATGTACCCCGGTTTGTATAA CACGACGTGTTTCCTGTGTGAAATTTGCGCTC CGTAACGAAAATGAATTTTCTGTAGTGAATTT ATATAATGGGGGCGCGAGCTGAAATTAACATC TTGAATTATTGAAAACATAGCGATTATAACTA TTATTCATGTCACCAATGAAACCATTATTAGC ATCAGAGAGTCAGAGGGTAATTGAACCAGTCA TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG CTAATTTACCGTTTTTATTTTCATCTTGCGGG CTTAAACAACAACCATCGCCCACGCGGGTAAA CATATTTATTTCGAGCCAGTAATAAATCAATA TATGTAAAGAAATACCGACCGTGTTAAAGCCA ATTAAGTTTTCCACACAACATACGCCTAATGA GCTCCATGACGTAACAAAGCTGCTACACCAGA CCGGAAACTAAAGGTGAATTATCATAAAAGAA TATTTTGCACGCTAACGAGCGTCTGAACACCC AGTAATCTTCATAAGGGAACCGAACTAAAACA ACCCGTCGTTAAATTGTAAACGTTAAAACTAG TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA TTCGCCATGGACGACGACAGTATCGTAGCCAG AGAGGCATACAACGCCAACATGTATCTGCGAA ACAGAAATCTTTGAATACCAAGTTAATTTCAT

TACATACACAGTATGTTAGCAAACTGTACAGA CCAGGCGCGAGGACAGATGAACGGGTAGAAAA TAAAGTACCAGTAGGGCTTAATTGCTAAATTT GCGTAAGAAGATAGAACCCTTCTGAACGCGCG TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG ACGGCTACAAGTACAACGGAGATTCGCGACCT TCCATATATTTAGTTTGACCATTAAGCATAAA CTTTACAGTATCTTACCGAAGCCCAGTTACCA TGGACTCCGGCAAAATCCCTTATACGCCAGGG GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA GCCACCACTCTTTTCATAATCAAATAGCAAGG GCCCAATAGACGGGAGAATTAACTTTCCAGAG ATACGTAAGAGGCAAAAGAATACACTGACCAA ACGCAAAGAAGAACTGGCATGATTTGAGTTAA CCTGATTGAAAGAAATTGCGTAGAAGAAGGAG ACCGTTCTGATGAACGGTAATCGTAATATTTT CTTTCATCTCGCATTAAATTTTTGAGCAAACA GAGGCGTTTCCCAATCCAAATAAGATAGCAGC GTCACACGATTAGTCTTTAATGCGGCAACAGT AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT GGCGATCGCGCATCGTAACCGTGCGAGTAACA TCATTACCGAACAAGAAAAATAATAATTCTGT TTAAGACGATTAATTACATTTAACACAAAATC CACCAGAGTTCGGTCATAGCCCCCTCGATAGC AGCACCGTAGGGAAGGTAAATATTTTATTTG GCCAACAGATACGTGGCACAGACATGAAAAAT CGAGTAGAACAGTTGATTCCCAATATTTAGGC GAGCCGCCCCACCACCGGAACCGCTGCGCCGA TTTCATTTCTGTAGCTCAACATGTTTAGAGAG

GTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT GCTCACAAGGGTAACGCCAGGGTTTTGGGAAG AGCTGATTACTCACATTAATTGCGTGTTATCC GAAGATCGTGCCGGAAACCAGGCAGTGCCAAG TGAGTTTCAAAGGAACAACTAAAGATCTCCAA TCTTACCAACCCAGCTACAATTTTAAAGAAGT CCCGGGTACCTGCAGGTCGACTCTCAAATATC GTTAAAATAACATTAAATGTGAGCATCTGCCA CAAAATTAGGATAAAAATTTTTAGGATATTCA ATTATTATTAGCGAACCTCCCGACGTAGGAA GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT AGTGTACTATACATGGCTTTTGATCTTTCCAG CCTAATTTAAGCCTTAAATCAAGAATCGAGAA CGATTTTAGGAAGAAAAATCTACGGATAAAAA TATCAGGGCGAAAATCCTGTTTGACGGGCAAC AGAAGTGTCATTGCAACAGGAAAAAATCGTCT AATGGTTTTGCTGATGCAAATCCATTTTCCCT ACGAGTAGATCAGTTGAGATTTAGCGCCAAAA CTGTAATAGGTTGTACCAAAAACACAAAATATA AACCTACCGCGAATTATTCATTTCACATCAAG CTCATCTTGGAAGTTTCCATTAAACATAACCG GGAATTACCATTGAATCCCCCTCACCATAAAT GGACGTTGAGAACTGGCTCATTATGCGCTAAT TAGAATCCCCTTTTTTAATGGAAACGGATTCG CAAGCAAGCGAGCATGTAGAAACCAGAGAATA ATACCCAAACACCACGGAATAAGTGACGGAAA AATGCCCCATAAATCCTCATTAAAAGAACCAC AAAAAGGCTTTTGCGGGATCGTCGGGTAGCA AATCACCACCATTTGGGAATTAGACCAACCTA

CTTTTACACAGATGAATATACAGTGCCATCAA TTTTAGTTCGCGAGAAAACTTTTTTTATGACC GCGCAGAGATATCAAAATTATTTGTATCAGAT TAGCCCTATTATTTACATTGGCAGCAATATTA GTTGTAGCCCTGAGTAGAAGAACTACATTCTG AACCAGAGACCCTCAGAACCGCCACGTTCCAG GCAATAGCAGAGAATAACATAAAAAACAGCCAT GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC GCGTTATACGACAATAAACAACATACAATAGA AGTTTGGACGAGATAGGGTTGAGTGTAATAAC ACGAACTATTAATCATTGTGAATTTCATCAAG GCAAATATGATTCTCCGTGGGAACCGTTGGTG CTGTAAATATATGTGAGTGAATAAAAAGGCTA GAAATGGAAAACATCGCCATTAAACAGAGGTG GAATGGCTACCAGTAATAAAAGGGCAAACTAT TATATTTTCATACAGGCAAGGCAAAGCTATAT ACTGCCCGCTTTTCACCAGTGAGATGGTGGTT CAAAAATCATTGCTCCTTTTGATAATTGCTGA TCACAATCCCGAGGAAACGCAATAATGAAATA GGTATTAATCTTTCCTTATCATTCATATCGCG CTTGCATGCCGAGCTCGAATTCGTCCTGTCGT ACGCTCAACGACAAAAGGTAAAGTATCCCATC AAACGAAATGCCACTACGAAGGCAGCCAGCAA TCATAGCTTGTAAAACGACGGCCAAAGCGCCA ATATATTCTCAGCTTGCTTTCGAGTGGGATTT AGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA TAACCTCCAATAAGAATAAACACCTATCATAT TTTTAATTGCCCGAAAGACTTCAACAAGAACG GACTTGAGGTAGCACCATTACCATATCACCGG

TTTAACGTTCGGGAGAAACAATAACAGTACAT GCGCATTAATAAGAGCAAGAAACAATAACGGA CCAGACGACAAATTCTTACCAGTAGATAAATA TTATTACGTAAAGGTGGCAACATACCGTCACC ATCGGCTGACCAAGTACCGCACTCTTAGTTGC AGAGAATCAGCTGATAAATTAATGCTTTATTT CATTCAACTTTTCTTGCCCTGACGAGAACATTCAGT CGCCTGATTTTTGACAGCATCGGAACGAACCCTCAG GATTGACCTTTTCCCAAAAACAGGAAGATGATAATC TTTTCAAGTTTTTTGGGGTCGAACCATC CAGCGAAATTTTTTTTTCACGTTGAAAGAATTGCG AGAAAAGCTTTTATTCAAAAGGGTGAGATAATGTGT AAACAGTTTTTTTAATGCAGATACATAAGAATACCA AATAATAATTTTATAGGAACCCATGTACAGGGATAGCAAGCCCA GAATAAGGTTTTAAATTGTGTCGAAATCTGTATCAT CAGCTGGCTTTTGTAATGGGATAGGTCAAAACGGCG TCAATTCTTTTGATGGCTTAGAGCTTAAGAGGTCA ACCCAAATTTTTGCAAGCGGTCCACGCTCCCTGAGA GAGTTGCATTTTTGTAAAGCCTGGGGTGAGCCGGAA GCATAAAGTTTTGAAAGGGGGGATGTGCTTATTACGC TTTTTGCGTTTTCAGAAAACGAGAATGAAATGCTTT AGGTAAAGTTTTACTAATAGTAGTAGCAAGGTGGCA TAGAGCTTGACGGGGAAAAGAACG CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG ATCACTTGAATACTTCTTTGATTAGTTGTTCC CTAAATCGGAACCCTAAAACCGTC ACGTGCTTTCCTCGTTGCCACCGA CTAAACAGGAGGCCGAGAATCCTG

CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG GCGTACTATGGTTGCTAATTAACC CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT TACTCAGGAGGTTTAGATAGTTAG ACCGCCACCCTCAGAAACAACGCC GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA GAAGGATTAGGATTAGAAACAGTT ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC ACCAGGCGGATAAGTGGGGGTCAG TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA TATAAGTATAGCCCGGAATAGGTGTATCACCG CACCACCCTCATTTTCCGTAACAC TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA
## Origami with 180 degree curve:

| SSSCIISCIAICCCISAAAAISASSSISSI                     | GECTETEAGETEGEGETT  | CIERCECICECCE                           | ICIGAGGEIGGEGGIACIAAACC  | ICCI GAGIA  | CGGIGATACACCTATI                        | CUSSSCIATACITATA  | ILAACCETCICSACGS    | CACITATCOCCISEI           | ACTEACCAAAACCCCCGCTAATCCTAATCCTTG  | ICTIGAGGAGICICAGCCICITAATACII   |
|--|---|---|--|-------------|---|---|---------------------|---------------------------|--|---|
| 011114010004004                                    | 2 2040407000400000  | ACCOCCACCOCCC                           | A0A01000A00000A10A11100  | A00A010A1   | 200A01A10100A1AA                        | 0000004141044141  | 401100040400100:    | 0104414000004004          | 104010011110000; 041140041140044;  | A0443133134242130242441141244   |
| LOTANCAL IVALITI                                   | COLONG LAGE ACTACIANA CONTRACTOR  | AACECS ISTANCA                          | CCACAGACAGECCE IN TAST IA  | COLUMN CON  | CIAAAGIIIIIGICG                         | CATACAGEAGISTAC   | S 14414451111449    | A STORY ISCOUTER          | A ACADINE CONTRACTOR OF COLOR  | LIGCCIAL INCOMMUNICATION CIGAN  |
| 10011000140410004110104010444                      | 149139134191119419.   | 11000040410014                          | 33131313133333431413441  | )))//II))/  | 12411124444234234                       | 114101001040410   | 1241141124444112    | 11111421141224411         | ***************************************  | **>>>*******>>>*****************  |
|  | TATTCTCACTCCCCTCAL  | AACTGTTCAAAGT                           | TTTAGCAAAATCCCATACAGAA.  | ATTCATT     | CTARCETCICCARAC                         | TCAAAAGCCATGTAT   | CALCUTTACTOCAACO    | CTAAATTCACACACT           | CONTRACTOR CONTRACTOR CALL   | TETTETENATATCANES/CANTEST   |
|  | COLUMN PARATOR  |   | WWW.DOI CHARGEST   |             | AVI 1438 (1433)                         |   |                     |                           | Constant Provide States and States   | The second s  |
| TCTCCAAAAAAAA                                      | GCTCCAAAAGGAGCCTTAA   | ATTGTATCGGTTTA                          | I CASCITISCITICGAS I GAATT   | TETTAAACA   | SCTTGATACCGATAGT                        | CTCCCTCAGAGCCGCG  | ACCETCAGAACCGCCA    | CCTCAGAGCCACCAC           | CTCAGAGCCGCCACCAGAACCACCACCAGA   | COCCOCCASCATTOA AGGAGGTTGAG   |
|  |   | 1 8 8 9 8 1 8 9 7 7 8 8 8 1             | 211222222222222222222222222222222222222  | 22XX1112    |   | 1x2222412122222   | 00000010110000001   | 222221212221221           | 222121222222222222222222222222222222222  |   |
|  |   |   |  |             |   |   |                     |                           |  |   |
| TTCGCTGCTGAGGGTGACGATCCCGCAAAA                     | GECCTTTAACTCCCTGC   | AAGCCTCAGCGAC                           | AATATATCGGTTATGCGTGGGC   | SATGGTTG    | GTCATTGTCGGCGCA                         | CGETTCCGETGETG  | TETESTICESSTEAT     | TTTGATTATGAAAAG           | GGCAAACGCTAATAAGGGGGCTATGACCGA   | ATGCCGATGAAAACGCGCTACAGTCTGA  |
| 10014000001111                                     | 100000000000000000000000000000000000000                                 | 110001000100                            | 21141414 9224414 9242228   | 21V22VV3V   | *2*51**3*5225251                        |   | 20202266 002200     | VVV31VV1V3111131          | ADDRITTO QANTERI DODODAREADIDADI   | 11435531431111515354151345431   |
| GGTAGCA ACGGCTA                                    | AGAGGETTTGAGGACTAA  | AGACTITITCATGA                          | GAAGTTTCCATTAAS GGGTAA   | ATACCTAN    | L GCCACTACGAAGGCA                       | GCCAGCADAATCACCA  | STAGCACCATTACCAT    | AGCAAGECCEGAAAG           | STCACCAATGAAACCA CGATAGCAGCACCG  | AATCAGTAGCGACAGA ATCAAGTJ TGCCI   |
| 191391493311931333413911933941                     | 101005444010015911  | 1313444445143                           | 0110VVV001VV1110000V11   | 114155411   | 399194193113391                         | 000100111100100   | ¥1001001¥¥1001¥     | VI0011000000111           | V010011V0111001V001V10010000   | 105130135315131105113000355   |
|  |   |   |  |             |   |   |                     |                           |  |   |
| TCAGGCGATGATACAAATCTCCGTTGTACT                     | TETTTCGCGCTTGGTATA  | ATCOCTOGOGOTC/                          | AGATGAGTGTTTTAGTGTATTC   | TTTSCCT     | TICCITITAGETIGE                         | CTAATTCCCAAATG  | TCAAGTCGGTGACGG     | TGATAATTCACCTTT           | ATGAATAATTTCCGTCAATATTTACCTTCCC  | CCTCAATCGGTTGAATGTCGCCCTTTTG  |
| 14242224424124                                     | A344493938443341  | 14030433333401                          | 11214212424444134241442  | ****>>>>*>  | AAA22AAA 4722AA22                       | A241144222111423  | 2421134222451533    | C1411440100441            | 1421141144662242114144412264222  | 22242TTA 2224A2T1 242222224AAA  |
| CGCGACCTGCTCCAT                                    | CTTACTTAGCCGGAACGAG   | GEGEAGAEGETEAA                          | CATAAGGGAACCGAA TGACCA   | ACTITGAAA   | SAGGACACATGAACGO                        | GTAGAAAATACATACI  | TAAAGGTGGCAACATA    | AAAAGAAACGCAAAA           | ACACCACGGAATAAGT TATTTTCTCACAAT  | AATAGAAAATTCATAT GTTTACCAGCG  |
| TTAADADADTTTTADDDDDTTDDADDAD                       | AA10AA1000000110010   | 000010100004011                         | 0141100011000110401001   | 194443111   | 10010101010000000                       | 041011114101410   | 111004000110141     | V11110111939111           | 010010001000110110000000000000000000000  | 1413111144914143344413913935  |
|  |   |   |  |             |   |   |                     |                           |  |   |
| CTTATTCACTGAATGAGCAGCTTTGTTACG                     | GATTIGGGTAATGAATA   | ICCGGITCTIGIC/                          | GATTACTCTTEATEAAGETCAE   | CAGCCTAT    | COCCTONTOTACE                           | TTTGCTAACATACT  | GTAATAAGGAGTCTT     | AATCATGCCAGTTCT           | TEGETATICCETTATIATIECETTICCICE   | TICCITCIGGTAACITIGTIC6GCTATC  |
| 120122444244102                                    | ADIAAAD224AIIADI1   | ************                            | 12144124 24421421 224212   | 991399VIV   | 2020042240424701                        |   | 22A11A1122212A2AA   | .149143991344844          | 4433341442334414414433344432423  | 44422442423241124 (424422224143   |
| ACACCAGAACGAGTA                                    | CTANATTEEECTTEACA CO  | GTTT AN TIT CAACT                       | TAATCATTGIGAATI CCITAL   | C GATTITA   | A GAACIGGCICATIA                        | SCECTARJATCAGAG   | ATAACCCACAAGAAT     | GAGTTAAGCCCCAATA          | A TAAGAGCAAGAAACA TGAAATA GCAATAG  | ATCTTACCEASECCO TITTAAFAAAAA  |
| AA3322A31231311 <u>1313213111231341</u>            | 11114A00004A0101A0  | DAAATTAAADTTDA                          | ATTA2TA2A211AA122AA1A  | DDDTAAAA.   |   | 0000411414010101  | 01011000010110110   | ADTOAATT000011A           | A11010011011101140111410011410   | 11424412221132224444411311113   |
|  |   |   |  |             |   |   |                     |                           |  |   |
| · · · · · · · · · · · · · · · · · · ·              | PARTCH I CLACCIGTAA   | CARIELIELICCE                           | ANTICOLLIA LIAACGTAGAT   |             | MACHICCISACT661                         | SAATTALCETCTGA  | IICASSSIGTTC        | ANTIAATICICCCGT           | ARTICS COLLECTION COLLECTION COLLECTION  | IN ARABELISCIALITICALITICA  |
| VVIIIV5V5115V31                                    | A 311434443412343411  | ATTADAA <u>DAADDDA</u>                  | AT24A224A4444110241214   | ****        | 0110040040104004                        | A011AA1000A0A012  | AAA3AA3T223A3AA2    | DAATTAADADDDDDA2          | ATTACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   | 2A2A111322A22A1AAA21AAAAA21   |
| EGCCAAAAGGGAATTA                                   | CAUSE A LASTAACACINA  | CALLAR LATAACCC                         | COLLARSACGA ATAAAA   | o LLAAAATA  | C GAGAGECTTTTGC/                        | ATTE ISAN TETTACCI  | LOCI ANCONCETCI     | CTAATTI                   | CASCING AND A CASCCAPATIATIT   | CLEARING AND ANCEAN THE   |
| 114331314131411933911113311441                     | 1100014104101010011   | 01041401V11000                          | 23444122131031031V1111   | 199111141   | 123123133264444323                      | . #33#J11¥5¥¥155.   | 1010411001000404    | *************             | 201344101114111010001V1VV1VV.  | 222114221114112111221444444   |
| ACTGTTTAAAGCATTTGAGGGGCC*****                      | ATATTTATCACCATTCC   | CONSTATTOOP                             | ATCCASTC TABACATT TACAT  | TACCOL      | TEECAAAACTTCTTT                         | AAATTGTAGCTCCC  | CAAAATAGCAACTAA     | TOTIGATITAACCOT           |  | ACCOUNTS CONTENTS CANTACTAN   |
|  | A   |   |  |             | ANT THE OWNER OF                        |   | *******             | CARACTER STORE            | den se den s   | The second descent and the second second  |
| CATABATCAAAAAT                                     | CAGGICITTACCCIGACTA   | TATACTCAGAACC                           | AAGCCCATTCCATCA AAACAT   | **100000*   | 50000000000000000000000000000000000000  | CARGAACGGGTATTA   | ACCANCTACCECACT     | TCGAGAACAAGCAAG           | COTTETTATETTCAT CTACCAATCATTAC   |   |
| Contracting Contraction                            |   |   |  |             |   |   |                     |                           | Contraction of Contra | Contraction of the second s   |
| 10111100101140100141114011114                      | 1                                 | **1*13*5131133                          | 1112221442214211111214   | **********  | 0000011101044011                        | 011011000041441   |                     | 140010110110011           |  | ······································  |
|  | TARAGETACTCTCTAATC  | TEACCTETTEEAC                           | TTACTICCASTCISSITCSCIT:  | GAAGCTC     | ATTAAAACGCGATAT                         | AATCATAACCAAAC  | ACCCCATTATTCATT     | COTTO TACATO TO           | A A A T T A G A T C C C A T A T T A T T T T T T T T T  | CONCEPTION CONTRACTOR CONCEPTION  |
|  | ALL STAT PARAMETERS   |   | and the second second second   |             |   |   |                     | EXPERIMENTAL PROPERTY AND | the second se  | Sector Sector Sector Sector Sector  |
| ATTCCTCAATATAAT                                    | CTGTASCTCAACATCTT   | TAAATATGCAACTA                          | AAGTACGGTGTCTGGA GTTTCA  | TTCCATATA   | ACAGTTGATTCCCAAT                        | ATTTACCCACACCCA   | TTTCGAGCCAGTAATA    |                           | CALABAAGCTAAACTAATTCTGTCCAGACC   | CACAATAAACAACAT TTCACCTAATG   |
|  |   |   |  |             |   |   |                     |                           |  |   |
|  | 1   |   |  |             |   |   |                     |                           |  |   |
| GAATTGATGCCACCTTTTCAGCTCGCGCCC                     | AATGAAAATATAGCTAA   | ACAGGTTATTGAC                           | TTTGCGAAATGTATCTAATGGT   | CAAACTAAA   | CTACTCGTTCGCAGA                         | ACATGTTGGCGTTG  | TAAATATGGCGATTCT    | CAATTAAGCCCTACT           | TEACCOTTECTTTATACTECTAAGAATTT  | ATAACGCATATGATACTAAACAGGCTTT  |
| 11121222222222                                     | COLUMN THE PROPERTY OF A  | 10100441440100                          | WWW.SOLEWARD   | 211127111   | **************************************  | VI51V3VV33552VV3V   | VIIIVIV3 72214424   | 011001102220120           | 10010000 (000000 (0000000 (000000000000  | THE REPORT OF THE PARTY OF THE |
| TTAACATC CAATAAA                                   | TCATACAGGCAAGGCAA   | AATTASCAAAATTA                          | AGCANTANAGCCTCAC GCATAN  | AGCTAAATC   | SETTETACCAAAAACA                        | CARATATATITTAGTI  | ATTTCATCTTCTGA      | TAAATTJAATGGTTT           | SAMATACCGACCGTGT ATAMATAAGGCGTT  | AATAAGAATAAACACC GAATCATAATTA   |
| 241141241241221441121422114111                     |   | 1177122111177                           | 0211111022242101021411   | 122711173   | 000000000000000000000000000000000000000 |   | 1111121121121121212 | 241114441142244           | 111111222122272272171117112222777  | 11110101010101010200101010101010  |
|  |   |   |  |             |   |   |                     |                           |  |   |
| TTTACCTACACATTACTCAGGCATTGCATT                     | AAATATATGAGGGTTCT   | AAAAATTTTTATCO                          | TECETTEAAATAAAGECTTCTC   | CCCCAAAA    | ATTACAGGGTCATAA                         | AAAAGTTTTCTCGC  | TETTTGTETTGEGAT     | TGGATTTGCATCAGC           | TTACATATAGTTATATAACCCAACCTAAGC   | GAGGTTAAAAAGGTAGTCTCTCAGACCT  |
| V010001V001VV                                      | 11114141431333344 PA1   | 1111100001055                           | AA222AA2 LITATIL DAA22AA   | 993911113   | VIVVI513 55V51V11                       | 1111134444545355  | *******             | 00010000001001001         | AAA101A1A10AA1A1A110001100A1100  | 22122AA111122A1 AA2A2012122   |
| AAGGCCGGAGACAGT                                    | CANATCACCATCANTAT CA.   | TATTCAACCETTCI                          | ACCEGATAAATTAATS COGAGA  | GESTARCTA   | TTTTGAGAGATCTAC                         | COTTOCT J CTOTANAT  | GICGCTATTAATTA      | TTTCCCJ TAGAATCO          | I TGAAAACATAGCGATAGCTTAGATTAAGAC   | TGAGAAGAGTCAATA TGAATTJATCAA  |
| AA21111333A3131113332333131213A                    | 1110313510511011010   | V1VV011000VV0V                          | 3242141114411422222121   | 2224122¥:   | AAAAAJIJIJIAGAIS                        | 0.04#30##9#3#111  | 0.040004144114411   |                           | VADITITATATOODIA102AA101AA11012  | A21211212A211A12A211AAA1A211  |
|  |   |   |  |             |   |   |                     |                           |  |   |
| CTTTTCTGATTATCAACCGGGGTACATATG                     | A TGACATGCTAGTTTTACI  | GATTACCETTCAT                           | ATTCTCTTGTTTGCTCCAGACT   | CTCAGGCAI   | GACCTGATAGCCTTT                         | TATTCACTCACATA  | TTGATTTATGTACTG     | TTTCCATTAAAAAAG           | AATTCAAATGAAATTGTTAAATGTAATTAA   | TIGTTTTCTTGATGTTTGTTTCATCATC  |
| 100000041014140                                    | 1440101400410444410   | 01441000440140                          | 21442424 42444324 5212124  | 11600153646 | AD100AD1 41000AAA                       | AA1AA010A0101A1A  | 14431444 14341243   | VVV001VV111111100         | ATTAADIT LADITTAA MAATTAADATTAATTA   | ***************************************   |
| <b>TIGTATAAGCAAATA</b>                             | TTAAATTGTAAACGT AA  | LALILI GILAAAAI                         | COCATTAAATTTTT TAAATC  | ACTUALL     | TTAACCAATAGGAAC                         | AACAGTACCTITIACA  | CGGGAGAAACAATAA     | GGATICSCCIGATIC           | TTTGAATACCAAGTT ACAAAATCGCGCAGA  | CGAATTATICATIT  |
| 221111121221121662616112211141                     | VIIIIVV5VIII55VVII  | ATAAAA2AA11111                          | 22221441114444454411142  | 122421444   | AA112211A122113                         | 10104100444410.   | (533313111511911V11 | 93316666666666666         | AAAA211A122112AA121111A22222121  | 2211441442144421144122421221  |
|  | II  |   | I  |             |   |   |                     |                           |  |   |
| STEARTERSEEST TETTECCACGEAGAAT                     | STRACESS FIGTTACTORCI   | I SASALI TAATGTI                        | A I SAAASC I SECTACACEAACE   | LUAGACECI   | ATTATTTGATEGO                           | SISTATATTCATCT  | ASSILABACCIGAAAA    | ICTACSCARTITETT!          | ATTICIST TRACETOCA AATAATTITCATA   | CTARCTICIAACCCTTCCATTATTCAG   |
| WV55515551311W                                     | 2 3 3 1 2 3 3 3 W 4 7 W 4 7 9 W 5 9 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 | *3131444114344                          | J14J113503350191331133   | 991010000   | 114414444401 <u>4005</u>                | 1040414144014043  | 1994011159051111    | 1041030114440444          | 14442434444415343111411444443141   | 33413344241133348391841443131   |
| Correctly Incarios                                 | CACHICAL MACCHINE AT  | -19-50 x1116869                         | A REAL PROPERTY AND A REAL | VARAATUS    | ACTOCASCIASCITI                         | ASALIA19 81111903   | AASAAAAAAACCACG     | Canage Contract           | A CARACTER A CARACTER A CARACTER A   | Concentration of the second second  |
| ATTADDDTATDDA0T00A0000A0101A00                     | 100140041100040014  | 0.0000000.00000000000000000000000000000 | 0100100101041400000401   | 221121421   | 124221222122444                         | 21841421444433  | 110111011100100     | 101100100001144           | 212212121212222222222222222222222222222  | 421421141411422421442442214   |
|  |   |   |  |             |   |   | ******              |                           |  |   |
| CANCERNESS AND | Columnation of the second second  | ANNAL AND ADDRESS                       | IN THE OWNER OF THE OWNER OWNER OF THE OWNER OWNE  |             | CANADA CANADA CANADA                    | A CONTRACTOR OF | Teerrer Augerre     |                           |  | de la caracteria de la car   |
| CAAGGCGATTAAGT                                     | 1000TAACCCCACCTTET  | CCCACTCACCACCT                          | TOTAAAACGACGCCCALTGCCAA  |             | CTGC AGGTCGACTCT                        | CARATATCARACCCT   | ATCAATATCTGGTCA     | TIGGCABATCAACAC           | TTGAAACCAATTCACCAACCTTATCTAAAAT  | CTTTAGGAGGAGTAA AACTAATAGAT   |
|  |   | 100100000000000000000000000000000000000 |  | 10001010    |   |   |                     |                           |  |   |
|  |   |   |  |             |   |   |                     |                           |  |   |
| TTATECTTCCSGCTCGTATETTGTGTGGA                      | TETEAGEGGATAACAAT   | TTCACACAGGAAAA                          | G CTATGAC CATGATTAC GAATT  | GAGETCO     | ACCCGGGGATCCTCT                         | GGTTCAGCAAGGTC  | GCTTTAGATTITTCA     | TTTGCTGCTGGCTCT           | GC GT G G C A CT G T T G C A G G C G G T G T T A AT A C 1  | ACCECCTCACCTCTETTTATCTTCTG  |
| 011100000000000000000000000000000000000            | 1 44242128 22141181   | AA212121221112                          | 100VIV01 001V01V1 0011VV   | 221224222   | ¥1000000 f1400404                       | 1000001001100000  | CONTRACT PROPERTY   | ****************          | 1000000 for the local back of  | 212222221 21222221 10101 1210212  |
| CTAATGAGTGAGCT                                     | AACTCACATTAATTGC  | CCCTT ACTOCCC                           | TTTCCAGTCGGGAAA CTGTCG   | GCCAGCTO    | ATTAATGAATCGGCC                         | ACCTGANAGCGTANG   | A TACGTGGCACAGACA   | TATTTTJGAATGGCT           | ATTAGTETTTAATGET GAACTGATAGECET  | AAACATCGCCATTAAAAATACCGAACGAA   |
| **************************************             | 1000101001001000000   | 0000401040000                           | ¥¥¥2212¥222211123¥3¥3  | V222122V3   | 111111111111111111111111111111111111111 | 199701110907110   | ¥190¥0091919191     | 1717777777117777          | AATOAOAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   | 1101900019910111191000110011  |
|  | 1   |   |  |             |   |   |                     |                           |  |   |
| GCAACTCTCTCAGGGCCAGGCGGTGAAGGG                     | ATCASCISTICCCCGTC   | TCACTGGTGAAAA                           | AAAACCACCCTGGCGCCCAATA   | GCAAACCO    | CTCTCCCCCCCCCTT                         | AGAAGGETTETATET   | TETTEGCCAGAATET     | CCCTTTTATTACTGG           | GTGTGACTGGTGAATCTGCCAATGTAAATAI  | CCATTTCAGACGATTGAGCGTCAAAATG  |
| 001010000000000000000000000000000000000            | 211421224 2442222 1421  | 1010V22V211112                          | 11111201 2007000 1001111   | 225111552   | 201010000000000000000000000000000000000 | 2121122224941494  | 20200223551211020   | 22777717127227            | 22121210 (221211) 122221122111   | 10011110 for 001011111  |
| GETTIGGEGGAGGAG                                    | SCGAAAATCCTGTTTGA   | STEETJCCGAAATC                          | SCANAATCCCTTATA ATCAAA   | GAATAGEC    | GAGATAGGETTGAGT                         | STAATAACATCACTT   | CTGAGTAGAAGAACT     | AAACTAJCESCCTT            | TEGTANTATCCAGAN ANTATTACCECCAS   | ATTGCAACAGGAAAAACGCTCAJGGAAA  |
| 211222242212224224422222212212                     | 21111422424442142   | CALIFIC CARACTAC                        | 221111122227414111122101   | 121111223   | 010141000440104                         | PV11V1121V212VV   | 9993139131131139    | 9111991993399999          | ¥227411414221211211414412222212  | 11110010010001000000000000000000000000  |
|  |   |   |  |             |   |   |                     |                           |  |   |
| TTTGGGTGATGGTTCACGTAGTGGGCCATC                     | CCTGATAGACGGTTTTT   | CGCCCTTTGACGT                           | GAGTCCACGTTCTTTAATAGTG   | SACTOTIC    | CCAAACTEEAACAAC                         | AATCAAAGAAGTAT  | CTACAACGGTTAATT     | TGCGTGATGCACAGA           | CTTTTACTCGGTGGCCTCACTGATTATAAA   | CACTTOTCAGGATTOTGGCGTACCGTTO  |
| 1004104000000140                                   | 2222421412122244444   | ***********                             | 2212422122442444   | 112424477   | ¥991119¥ 50119115                       | ¥114511101104144  | 2241211222041144    | 00000100010101010         | *9****15*50000050*915*01**1*11.  | 101044040100144040000041000440  |
| CACCTOCCTAAAACC                                    | ACTABATCEEAACCCT  | CCCACTTTCCCCCATT                        | TAGAGETTGACGGGGG AGECGG  | CAACGTES    |   | TELECCOLTACASES   | SCOTACTATESTTSC     | TGACGAGCACGTATA           | ACCTOCTTTCCTCCTT CAATCACACCCCCCA   | TAAAACACGACCCCCA TAAACCCATTT  |

## Purple 180 degree curve sequences:

GTTAGATGATTTCACGACGTGTTTCCTGTGTGAAATTTGCGCTC GTTAGATGATTTTTCAACTACGGAACAACATTATTAACACTAT GTTAGATGATTTGCGTAAGAAGATAGAACCCTTCTGAACGCGCG GTTAGATGATTTGCGCAGAGATATCAAAATTATTTGTATCAGAT GTTAGATGATTTCACCAGAGTTCGGTCATAGCCCCCCTCGATAGC GTTAGATGATTTGATGGCAAAAGTATTAGACTTTACAAGGTTAT GTTAGATGATTTGGGAGAGAGGCATTAATGAATCGGCCACCTGAAA GTTAGATGATTTCTAAAGCAAATCAATATCTGGTCACCCGAACG GTTAGATGATTTTGTAGCATAACTTTCAACAGTTTCTAATTGTA GTTAGATGATTTTGTAGCATAACTTTCAACAGTTTCTAATTGTA GTTAGATGATTTCCAAATCATTACTTAGCCGGAACGTACCAAGC GTTAGATGATTTCAAAGATTCTAATTGGGCTTGAGATCCAAGC GTTAGATGATTTAAAGATTCTAAATTGGGCTTGAGATTCATTAC GTTAGATGATTTACCGTTCTGATGAACGGTAATCGTAATATTTT **GTTAGATGATTTAGGTTTTGGCCAGTTACAAAATAAACAGGGAA GTTAGATGATTTAGCACCGTAGGGAAGGTAAATATTTTATTTTG GTTAGATGATTTCGACAACTTCATCATATTCCTGATCACGTAAA GTTAGATGATTTTTATTAATGAACAAAGAAACCACCTTTTCAGG** GTTAGATGATTTTCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT **GTTAGATGATTTTCAGAAGCCTCCAACAGGTCAGGATTTAAATA GTTAGATGATTTTTTCATTTCTGTAGCTCAACATGTTTAGAGAG** GTTAGATGATTTTTCGCCATGGACGACGACAGTATCGTAGCCAG **GTTAGATGATTTTACCTTTAAGGTCTTTACCCTGACAATCGTCA GTTAGATGATTTGTTAAAATAACATTAAATGTGAGCATCTGCCA GTTAGATGATTTACGCTCAACGACAAAAGGTAAAGTATCCCATC GTTAGATGATTTTTAAGACGATTAATTACATTTAACACAAAATC GTTAGATGATTTAATGCCCCATAAATCCTCATTAAAAGAACCAC GTTAGATGATTTTCATAGCTTGTAAAACGACGGCCAAAGCGCCA GTTAGATGATTTACGGTCAATGACAAGAACCGGATATGGTTTAA GTTAGATGATTTGCGCATTAATAAGAGCAAGAAACAATAACGGA GTTAGATGATTTTAAATATTGAGGCATAGTAAGAGCACAGGTAG** GTTAGATGATTTCTTGCATGCCGAGCTCGAATTCGTCCTGTCGT **GTTAGATGATTTACCCGTCGTTAAATTGTAAACGTTAAAACTAG GTTAGATGATTTCATAACCCGCGTCCAATACTGCGGTATTATAG** GTTAGATGATTTTCACAATCCCGAGGAAACGCAATAATGAAATA **GTTAGATGATTTTTATTCATGTCACCAATGAAACCATTATTAGC GTTAGATGATTTTTGAATTATTGAAAAACATAGCGATTATAACTA** GTTAGATGATTTGCCAGCTGCGGTTTGCGTATTGGGAATCAAAA **GTTAGATGATTTTCATTACCGAACAAGAAAAATAATAATTCTGT GTTAGATGATTTATCAACAGGAGAGCCAGCAGCAAAATATTTT GTTAGATGATTTATACCCAAACACCACGGAATAAGTGACGGAAA GTTAGATGATTTATTATTATTAGCGAACCTCCCGACGTAGGAA** 

**GTTAGATGATTTAAACCCTCTCACCTTGCTGAACCTAGAGGATC** GTTAGATGATTTGTTTGCCACCTCAGAGCCGCCACCGCCAGAAT **GTTAGATGATTTTATATTTTCATACAGGCAAGGCAAAGCTATAT GTTAGATGATTTACAGAAATCTTTGAATACCAAGTTAATTTCAT GTTAGATGATTTCCCGGGTACCTGCAGGTCGACTCTCAAATATC** GTTAGATGATTTTTTCATGATGACCCCCAGCGATTAAGGCGCAG GTTAGATGATTTGGCGATCGCGCATCGTAACCGTGCGAGTAACA GTTAGATGATTTGCGAAACAAGAGGCTTTGAGGACTAGGGAGTT GTTAGATGATTTCTAATTTACCGTTTTTATTTTCATCTTGCGGG **GTTAGATGATTTTATGTAAAGAAATACCGACCGTGTTAAAGCCA** GTTAGATGATTTAGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA **GTTAGATGATTTAAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT GTTAGATGATTTTGCAACTAGGTCAATAACCTGTTTAGAATTAG** GTTAGATGATTTGTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT **GTTAGATGATTTCAAAATTAGGATAAAAATTTTTAGGATATTCA GTTAGATGATTTGCAATAGCAGAGAATAACATAAAAAACAGCCAT GTTAGATGATTTCCAGACGACAAATTCTTACCAGTAGATAAATA GTTAGATGATTTCATGTCAAAAATCACCATCAATATAACCCTCA** 

## Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC ATTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

Additional sequences:

AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT TGGATTATTTTTGCCGTCAATAGATAATCAACTAAT AATTACTATTTCATAGGTCTGAGAGACGTGAATTT TTTTTGAAAGTATTAAGAGGCTATTATT AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA ATCAAAATTTTTGAAGATGATGAAAACAAAATTACCT AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT TTTAACGTTCGGGAGAAACAATAACAGTACAT ACAAAGAAAATTTCATCTTCTGACAGAATCGC TCAGGTCATTTTTGAGAGATCTACCCTTGCTT TGCCTTGACAGTCTCTGAATTTACCCCTCAGA TTTTAATTGCCCGAAAGACTTCAACAAGAACG GCGTTATACGACAATAAACAACATACAATAGA ATTAAGTTTTCCACACAACATACGCCTAATGA CTTTACAGTATCTTACCGAAGCCCAGTTACCA ACTGGATATCGTTTACCAGACGACTTAATAAA GTAAAAGACTGGTAATATCCAGAAATTCACCA GCCCAATAGACGGGAGAATTAACTTTCCAGAG ATACGTAAGAGGCAAAAGAATACACTGACCAA AAAAAAGGCTTTTGCGGGATCGTCGGGTAGCA CTTAAACAACCAACCATCGCCCACGCGGGTAAA CAAGCAAGCGAGCATGTAGAAACCAGAGAATA GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG

ATATAATGGGGGCGCGAGCTGAAATTAACATC GTCACACGATTAGTCTTTAATGCGGCAACAGT TAGAATCCCCTTTTTTAATGGAAACGGATTCG AAATAATTTTTAACCAATAGGAACAACAGTAC AATGGTTTTGCTGATGCAAATCCATTTTCCCT GCCAACAGATACGTGGCACAGACATGAAAAAT ATATATTCTCAGCTTGCTTTCGAGTGGGATTT TGAACAAAGATAACCCACAAGAATAAGACTCC ACTGCCCGCTTTTCACCAGTGAGATGGTGGTT TGAGTTTCAAAGGAACAACTAAAGATCTCCAA CTTTTACACAGATGAATATACAGTGCCATCAA CAATAAATAAATGCAATGCCTGAGAAGGCCGG ACGCAAAGAAGAACTGGCATGATTTGAGTTAA TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG GGATTTAGTTCATCAATATAATCCAGGGTTAG CAACGCAAAGCAATAAAGCCTCAGGATACATT TAGCCCTATTATTTACATTGGCAGCAATATTA AAATCAATCGTCGCTATTAATTAAATCGCAAG GCCACCACTCTTTTCATAATCAAATAGCAAGG AGTTTGGACGAGATAGGGTTGAGTGTAATAAC TACATACACAGTATGTTAGCAAACTGTACAGA AGCTGATTACTCACATTAATTGCGTGTTATCC TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG CCAGGCGCGAGGACAGATGAACGGGTAGAAAA CTAAAATAAGTATTAACACCGCCTCGAACTGA CTCATCTTGGAAGTTTCCATTAAACATAACCG GGAATTACCATTGAATCCCCCTCACCATAAAT ATTTTGCGTTTAAAAGTTTGAGTACCGGCACC CGATTTTAGGAAGAAAAATCTACGGATAAAAA

GAAGATCGTGCCGGAAACCAGGCAGTGCCAAG TCCATATATTTAGTTTGACCATTAAGCATAAA CCTAATTTAAGCCTTAAATCAAGAATCGAGAA AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT AATCACCACCATTTGGGAATTAGACCAACCTA AGAAGTGTCATTGCAACAGGAAAAAATCGTCT GAGCCGCCCCACCACCGGAACCGCTGCGCCGA TATCAGGGCGAAAATCCTGTTTGACGGGCAAC TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA CTGTAATAGGTTGTACCAAAAACACAAAATATA TAACCTCCAATAAGAATAAACACCTATCATAT CAATGACAGCTTGATACCGATAGTCTCCCTCA AGACAGTCTCATATGTACCCCGGTTTGTATAA CATATTTATTTCGAGCCAGTAATAAATCAATA TCGCAAATAAGTACGGTGTCTGGACCAGACCG CCTGATTGAAAGAAATTGCGTAGAAGAAGGAG ACGGCTACAAGTACAACGGAGATTCGCGACCT GCAAATATGATTCTCCGTGGGAACCGTTGGTG GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC AGAGAATCAGCTGATAAATTAATGCTTTATTT GAAATGGAAAACATCGCCATTAAACAGAGGTG TAAAGTACCAGTAGGGCTTAATTGCTAAATTT TGGACTCCGGCAAAATCCCTTATACGCCAGGG CTTTGAAAATAGGCTGGCTGACCTACCTTATG AAAACAAACTGAGAAGAGTCAATATACCTTTT AACCTACCGCGAATTATTCATTTCACATCAAG CGTAACGAAAATGAATTTTCTGTAGTGAATTT GGACGTTGAGAACTGGCTCATTATGCGCTAAT CAAAAATCATTGCTCCTTTTGATAATTGCTGA

AAACGAAATGCCACTACGAAGGCAGCCAGCAA TATTTTGCACGCTAACGAGCGTCTGAACACCC GAGGCGTTTCCCAATCCAAATAAGATAGCAGC GCTCACAAGGGTAACGCCAGGGTTTTGGGAAG GACTTGAGGTAGCACCATTACCATATCACCGG AGGCGGTCTCTTTAGGAGCACTAAACATTTGA TCTTACCAACCCAGCTACAATTTTAAAGAAGT CTTTCATCTCGCATTAAATTTTTGAGCAAACA CCAAAATAAGGGGGGTAATAGTAAAAAAAGATT CTGTAAATATATGTGAGTGAATAAAAAGGCTA GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG GCTCCATGACGTAACAAAGCTGCTACACCAGA ATCAGAGAGTCAGAGGGTAATTGAACCAGTCA ACGAACTATTAATCATTGTGAATTTCATCAAG GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC ACGAGTAGATCAGTTGAGATTTAGCGCCAAAA AACCAGAGACCCTCAGAACCGCCACGTTCCAG GCTTCTGGCACTCCAGCCAGCTTTACATTATC AGAGGCATACAACGCCAACATGTATCTGCGAA AGTAATCTTCATAAGGGAACCGAACTAAAACA GAATGGCTACCAGTAATAAAAGGGCAAACTAT GCCACGCTTTGAAAGGAATTGAGGAAACAATT GTTGTAGCCCTGAGTAGAAGAACTACATTCTG GAAGCAAAAAAGCGGATTGCATCAATGTTTAG CGAGTAGAACAGTTGATTCCCAATATTTAGGC TTTTAGTTCGCGAGAAAACTTTTTTTATGACC ATCGGCTGACCAAGTACCGCACTCTTAGTTGC GGTATTAATCTTTCCTTATCATTCATATCGCG

AGTGTACTATACATGGCTTTTGATCTTTCCAG CCGGAAACTAAAGGTGAATTATCATAAAAGAA TTATTACGTAAAGGTGGCAACATACCGTCACC TTTTCAAGTTTTTTGGGGGTCGAACCATC TCAATTCTTTTGATGGCTTAGAGCTTAAGAGGTCA AATAATAATTTTATAGGAACCCATGTACAGGGATAGCAAGCCCA CAGCGAAATTTTTTTTTTCACGTTGAAAGAATTGCG CGCCTGATTTTTGACAGCATCGGAACGAACCCTCAG AGGTAAAGTTTTACTAATAGTAGTAGCAAGGTGGCA AAACAGTTTTTTTAATGCAGATACATAAGAATACCA GATTGACCTTTTCCCAAAAACAGGAAGATGATAATC ACCCAAATTTTTGCAAGCGGTCCACGCTCCCTGAGA GAATAAGGTTTTAAATTGTGTCGAAATCTGTATCAT GAGTTGCATTTTTGTAAAGCCTGGGGTGAGCCGGAA CATTCAACTTTTCTTGCCCTGACGAGAACATTCAGT GCATAAAGTTTTGAAAGGGGGGATGTGCTTATTACGC TTTTTGCGTTTTCAGAAAACGAGAATGAAATGCTTT AGAAAAGCTTTTATTCAAAAGGGTGAGATAATGTGT CAGCTGGCTTTTGTAATGGGATAGGTCAAAACGGCG CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CTAAACAGGAGGCCGAGAATCCTG CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG GCGTACTATGGTTGCTAATTAACC CTAAATCGGAACCCTAAAACCGTC GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG ATCACTTGAATACTTCTTTGATTAGTTGTTCC TAGAGCTTGACGGGGAAAAGAACG CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA

CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC ACGTGCTTTCCTCGTTGCCACCGA ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG TATAAGTATAGCCCGGAATAGGTGTATCACCG ACCAGGCGGATAAGTGGGGGGTCAG TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA GAAGGATTAGGATTAGAAACAGTT TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA TACTCAGGAGGTTTAGATAGTTAG CACCACCCTCATTTTCCGTAACAC ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC

## Origami with circle-pattern:

| GTAACACTGAGTTT                      | 1949401000400900 (18401000400900)<br>GTCACCAGTACAAAC (CAACGCCLGTAGCA   | Υσυστοσουσοσου ντι το συσσυτου<br>Ττα και και τη στη τ | SCOVERNMENT OF COMPANY OF COMPANY. | YSTESSYSYSSESE (LSYVEYSSESYS)<br>ISTAATAAGTTITAAT GGGTCAGTGCCTTG   | TANCAGT CCCCGTAL MACAGT TAAT CCCC        | THE CONTRACT OF THE CONTRACT. THE CONTRACT OF |
|-------------------------------------|--|---|--|--|--|---|
| 11111110001030103301131503133000    |  | A21212121222224214124444444444444444444   | ALTANCETCICEANNENTCANNECCATETA   | CALCULATIONANAN CONTRACTOR CONTRA | CLITICATIC CCLITICATION CARD             | ******  |
| TETECA                              |  |   |  | SISSEVUL SUSSELSE VILLIVISISIONS   |  |   |
| ******                              | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   |   | 044074700747010404004070700000   | 100101010100100100040101001001   | 04010100000010010110010010010111         | 10000100100100101001000000000000000000  |
| 1100016016AGGGTGACGATCCCGCAAAAA     | 55155VVV 115V555V 511555V5155115   |   | V3V51VV3 \$53553513533VV5533V33V3  | TCTGGTTCCGGTGATTITGATTATGAAAAG   |  | ATGCCGATGAAAACGCGCTACAGTCTGACGC   |
| 101001400011001001000110000011      | 010000000000000000000000000000000000000  | 101111400111140000111114100011  | AD2010A100110001 00010011111A0100.   | ATCODEDIATESTATCOTTCCCCC   | 10100110111001001010100000000000000000   | .1401041000101011101100440000441  |
| TCAGGCGATGATACAAATCTCCGTTGTACT      | **************************************   | AGATGAGTGTTTTAGTGTATTCTTTTGCCTG   | TTEGTTTTAGGTTGG CTAATTCCCAAATG   | TCAAGTCGGTGACGGTGATAATTCACCTTT   | 19311911999999999999999999999999999999   | CCTCAATCGGTTGAATGTCGCCCTTTTGTCT   |
| 1144343435511149335315343545514     | VISWISSSISIISSISSSISISSS   | V91V1133311993119V3199119VV3111   | 13315131313131355 PVI31111V191V19  | VIII33V335II5IVIVIIII3III535III  | ACACCACGGAATAAG TATTITETCACAATG          | AATAGAAAATICATATGGIITACCAGCGCCA   |
| CITATICACIGAAIGAGCAGCITIGITACG      |  | AGATTACTCTTGATGAAGGTCAGCCAGCCTA   | CCCCTGGTCTGTACA CTTTGCTAACATACT  | GTAATAAGGAGTCTTAATCATGCCAGTTCT   |  | TITCCTTCTGGTAACTITGTTCGGCTATCTGC  |
| CACCAGAACGAGTA                      | TANATISSECTIENEN ISETTAN LITEANE   | VILVELVENDELEVELESSWEEDSELWIVE  | AGAACTEGETEATTATECGETAATATEAGAG  | CATALCCCACALGAAT GAGTTAAGCCCAAT  | ATANGAGCANGANACA TGANATAGCANTAG          | TATCTTACCGAAGCCO TITTAAGAAAAGTAA  |
| TTGAATGTGGTATTCCTAAATCTCAACTGA      | AATCITICIACCIGIAATAATGITGITCCG   | TAGTICGTITIATIAACGTAGATTITICTIC   | AACGTCCTGACTGGT CAATTACCCTCTGA   | TITETTCAGESTGITCASTTAATTCTCCCGT  | TAATGCGCTICCCTGTTTTTATGTTATTCTC          | I GTAAAGGETGETATTTTCATTTTTGAEGTT  |
|                                     |  | TCGTTTACCAGACGAG ATAAAA CCAAAAT   | CCGAGAGGCTTTTGCAATCCTGAATCTTACC  | ACCTAACGAGCGTCI TCCAGAGCCTAATT   | GCCAGTTACAAAATAA ACAGCCAJATTATTT         | ICCCAATCCAAATAAGAAACGATJITTIGTT   |
| ACTETTTAAAGCATTTGAGGGGGATTCAAT      | ATATTTATGACGATTCCGCAGTATTGGACG   | TATCCAGTCTAAACATTTTACTATTACCCCC   | A TEECAMAA CTTCTTT AAAATTETAECTEEE   |  | TAAAACCTCCCGCAAGTCGGGAGGTTCGCTAA         | ACCCCTCGCGTTCTTAGAATACCGGATAAGC   |
| 51555551995119<br>[CATAAAJ] AAAAATS | ACCULATION CONTRACTOR AND A CARACTER | VIVSSISV SVIIISI VVISVIVVISSSSS   | 5V555111 55V55VV11111VV3V155V5555  | ACCANGTACCOCACTO   | 01111050 (0000111 (000011000000000000000 | 1103094930344944311410533141139<br>90900000000000000000000000000000000  |
| 1311115313114313514111451111145     | TAAAGGTACTCTCTAATCCTGACCTGTTGGAC   |   | 199991111119999110119119339944941  | CAGCCGATTATTGATTGGTTTCTACATGCTC  | 5559999991999919519519519519519519519519 | 99999911V1991199111V9191V1V1919119  |
| ATTGCTGATATAAT                      | УППОРУГ ФУЗУЗУЛ (1937) ГОЗУЛДЗУУЛУЛОГ.<br>СТОТАССТСААСАТС: ПТТАААТ <mark>Д І ССААСТ</mark> І   | ANGTACGGTGTCTGGA GTTTCATTCATATA   | ACAGTTGATTCCCAATATTTAGGGAGAGGCA  | SISSESIWING AND A CARACTATA ANALY TANAGTA  | COACAAAAGGTAAAGT AATTCTGTCCAGACG         | 13313441434144344314111513353535<br>GGACAATAAACAACATTTCAGCTAATGCAGA   |
| 143324413132441144324311414114      | 9V3V139V91191V3VVVV111V1V39119V  | 139153393959331139995199551919  | 913443144999114 (44413391313391  | VV45313551341141131311414111341  | 9319111133V1113V114V9V3V9913193          | 3191141119119143449139411439131   |
| TAACATE: AATAAA                     |  | IVVVDDDI FIVDVIV TIVDDVDIIIDVII<br>AGCAATAAAGCCTCACAGCATAAAGCTAAATC   | VOVIDVOD WVODDIDIVIDIVDVVDDDDVVD   | VIIIVIVS SSIVVSV SIIVVIISSSSVISV<br>AATTTCATCTTCTGAS TAAATTJAATGGTT  |  | VIVILOJO EVIVOLVI VIILOIDODVVVVO  |
| 241141241241251441151455114111      | 91V1910091100911011VV1091111VV   |   |  | .144451454454515541114441145344  | 0111101000100010010111101000000          | .141131141191993311491411441941   |
| TITACCTACACATTACTCAGGCATTGCATT      |  | VV305VV3 F11V111 0VV0V0005301111  | VIVVISIS SVSIVILIIIIISVVVSVSIS   | **************************************   | 1111ACATATAGTTATATAACCCAACCTAAGCC        | 331339V1111133V 8V8V8V813185V1V   |
| AA01111000A010111000000101010A      | 11149199149114141491414911999449   |   | *****  | A240204144114411444400044121140  | wollingivi.com/lowici.wilois             | ******  |
| CTTTTCTGATTATCAACCGGGGTACATATG      | TTGACATECTACTTTTACGATTACCGTTCATC   | ATTCTCTTGTTTGCTCCAGACTCTCAGGCA  | SACCTGATAGCCTTT TATTCACTCACATA   | TTGATTTATGTACTGTTTCCATTAAAAAAG   | TAATTCAAATGAAATTGTTAAATGTAATTAA          | TTETTTCTTEATETTTETTTCATCATCTTC  |
| TGTATA <u>, CAAATA</u>              |  | **************************************  | VV119911V19911V  | A000010111011A110001AA0000A01AA  | VVV011V100110VV101111V0000001010         | 00011441440144401144100401001111  |
| CTCAATCCGCCGTTTGTTCCCACGGAGAAT      | GACGGGTTGTTACTCGCTCACATTTAATGTT  | CATGAAAGCTGGCTACAGGAAGGCCAGACGCO  | ATTATTTTTGATGGCACTGTATATTCATCT   | ACGTTAAACCTGAAAATCTACGCAATTTCTT  | ATTTCTGTTTTACGTGCAAATAATTTTGATA          | GTAGGTTCTAACCCTTCCATTATTCAGAAGT   |
| ETTEETFTAGATGE                      | CECATCETAACCETCO ATCTGCCA 2TTTGAG  | 0.010.010.010.010.010.000.000.001.00110.0100  | TOADDTODDTODAAA DTAATAOTAAAADD   | 211911131119191991311331393311VV   | TCATCATATTCCTGA ATCAGATGATGGCA           | VOIVOITVITVITVOOVOITVOVVOOTVVIV   |
| CCASCTESCETAATAGCGAAGAGGCCCCCCA     | CGATEGECETTECCAACAGTTGEGEAGECTG  |   | CLAGAAGEGGTGEEEGTACTEAAAETTTTAA  | ATTAATAACGTTCGGGCAAAGGATTTAATAC  | GTTGTCGAATTGTTTGTAAAGTCTAATACT           | TAAATCCTCAAATGTATTATCTATTGACGGC   |
| CAAGGC ATTAAGT                      | GEGTAACGCCAGGGT TTCCCAGT ACGACG  | TETAAAACEACEGECCA TECCAAFCTTECAT  | CTECAGETCEACTCTCAAATATEAAACCCT   | AATCAATATCIGGICA TIGGCA/ ATCAACA   | TTGAAAGGAATTGAGGAAGGTTAJCTAAAAT          | TETTTAGGAGCACTAN AACTAAJAGATTAGA  |
| TTTATGCTTCCGGCTCGTATGTTGTGTGGAA     | TTGTGAGCGGATAACAATTTCACACAGGAAAA   | ACCTATGACCATGATTACGAATTCGAGCTCGG  | TACCCORRECTCETCET  | IGCTTTAGATTTTTCATTTGCTGCTGGCTCT  | ACCOTOCCACTOTTCCACCCCCTCTTAATACT         | ACCECCTCACCTCTETTTTATCTTCTECTEC   |
| CTAATGA2TGAGCTI                     | ACTEACATTAATTGES TGEGETELETGEEE  | CTETCCAGTCGGGAAA CTETCG GCCAGCTC  | VIDDDDDD SIVDDVDVD DDVVDLDDLLDDVD<br>CATTAATGAATCGGCCACCTGAAAGCGTAAG   | ADDAAADD LAAAAAAAA TATTTTJGAATGGC  | ATTAGTCTTTAATGCS CGAACTGATAGCCCT/        | 10000010010010110110100100100000000000  |
| GCAACTETETEAGGGCCAGGCGGTGAAGGG      | ATCAGCTETTECCCETCTCACTEETEAAAAA  | WAAAACCACCCTGGCGCCCAATACGCAAACCC  | CTCTCCCCGCGCGTT AGAAGGGTTCTATC   | CIGTIGGCCAGAATGICCCTTTTATTACTGG  | GTGTGACTGGTGAATCTGCCAATGTAAATA           | ICCATTTCAGACGATTGAGCGTCAAAATGTAG  |
| GETTIGGT CAGCAGE                    | 11001000 00000000 00010000000000000000   | 11111001 000100 001111000   | 50404000 0303030440131133344041491   | 50300335551311030 55000010015033<br>   | CTGGTAATATCCAGAA CAATATTACCGCCAG         | CATTOCAACAGGAAAAACGCTCAJ SGAAATAC   |
| 911393399919399339933993399513513   |  | ****  | 1010141000440104 041141191491944.  | **************************************   | ***************************************  |   |
| 53913933355195                      | 10000101010000000000000000000000000000   | 55159991 5399999 19199351899999   | VS51115V SS115115V11VS1115115VIV   | SEVIELES POVILEY POSTOLEVOLOUS   | ACGTGCTTTCCTCGT AGAATCAGAGCGGGA          | 10100000001001000000000000000000000000  |

Turquoise circle-pattern sequences:

GTTAGATGATTTCTAATTTACCGTTTTTATTTTCATCTTGCGGG **GTTAGATGATTTTTATTACGTAAAGGTGGCAACATACCGTCACC GTTAGATGATTTTATGTAAAGAAATACCGACCGTGTTAAAGCCA GTTAGATGATTTCAAGCAAGCGAGCATGTAGAAACCAGAGAATA** GTTAGATGATTTTTATTAATGAACAAAGAAACCACCTTTTCAGG **GTTAGATGATTTCTTTCATCTCGCATTAAATTTTTGAGCAAACA GTTAGATGATTTCCCGGGTACCTGCAGGTCGACTCTCAAATATC GTTAGATGATTTCCTGATTGAAAGAAATTGCGTAGAAGAAGGAG GTTAGATGATTTTACCTTTAAGGTCTTTACCCTGACAATCGTCA GTTAGATGATTTTCAGAAGCCTCCAACAGGTCAGGATTTAAATA GTTAGATGATTTAGTAATCTTCATAAGGGAACCGAACTAAAACA GTTAGATGATTTACGCTCAACGACAAAAGGTAAAGTATCCCATC GTTAGATGATTTGTTAAAATAACATTAAATGTGAGCATCTGCCA GTTAGATGATTTTTGAATTATTGAAAAACATAGCGATTATAACTA GTTAGATGATTTTTTAACGTTCGGGAGAAACAATAACAGTACAT GTTAGATGATTTGCTTCTGGCACTCCAGCCAGCTTTACATTATC GTTAGATGATTTCCTAATTTAAGCCTTAAATCAAGAATCGAGAA GTTAGATGATTTACGAACTATTAATCATTGTGAATTTCATCAAG GTTAGATGATTTCATAACCCGCGTCCAATACTGCGGTATTATAG** GTTAGATGATTTATTTTGCGTTTAAAAGTTTGAGTACCGGCACC **GTTAGATGATTTATCAGAGAGTCAGAGGGTAATTGAACCAGTCA** GTTAGATGATTTAGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA **GTTAGATGATTTAAACCCTCTCACCTTGCTGAACCTAGAGGATC GTTAGATGATTTCAATAAATAAATGCAATGCCTGAGAAGGCCGG GTTAGATGATTTCTTGCATGCCGAGCTCGAATTCGTCCTGTCGT** 

Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC ATTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

# Additional sequences:

ACCGTTCTGATGAACGGTAATCGTAATATTTT GCGTTATACGACAATAAACAACATACAATAGA GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT TCCATATATTTAGTTTGACCATTAAGCATAAA TCATAGCTTGTAAAACGACGGCCAAAGCGCCA GCTCACAAGGGTAACGCCAGGGTTTTGGGAAG AGAAGTGTCATTGCAACAGGAAAAAATCGTCT AAATCAATCGTCGCTATTAATTAAATCGCAAG GGATTTAGTTCATCAATATAATCCAGGGTTAG TTTCATGATGACCCCCAGCGATTAAGGCGCAG ACTGGATATCGTTTACCAGACGACTTAATAAA CACCAGAGTTCGGTCATAGCCCCCTCGATAGC GATGGCAAAAGTATTAGACTTTACAAGGTTAT AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT CAATGACAGCTTGATACCGATAGTCTCCCTCA ACCCGTCGTTAAATTGTAAACGTTAAAACTAG AAAGATTCTAAATTGGGCTTGAGATTCATTAC ATACGTAAGAGGCAAAAGAATACACTGACCAA

CTTTTACACAGATGAATATACAGTGCCATCAA GCTCCATGACGTAACAAAGCTGCTACACCAGA GCCCAATAGACGGGAGAATTAACTTTCCAGAG TAGAATCCCCTTTTTTAATGGAAACGGATTCG AAATAATTTTTAACCAATAGGAACAACAGTAC CCAAATCATTACTTAGCCGGAACGTACCAAGC AATGCCCCATAAATCCTCATTAAAAGAACCAC ACAGAAATCTTTGAATACCAAGTTAATTTCAT TTTTTGAAAGTATTAAGAGGCTATTATT GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG CGACAACTTCATCATATTCCTGATCACGTAAA CTAAAGCAAATCAATATCTGGTCACCCGAACG TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC AGAGAATCAGCTGATAAATTAATGCTTTATTT GCGAAACAAGAGGCTTTGAGGACTAGGGAGTT GGACGTTGAGAACTGGCTCATTATGCGCTAAT ACAAAGAAAATTTCATCTTCTGACAGAATCGC GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT CACCACCCTCATTTTCCGTAACAC AGCTGATTACTCACATTAATTGCGTGTTATCC CTCATCTTGGAAGTTTCCATTAAACATAACCG ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA TGCCTTGACAGTCTCTGAATTTACCCCTCAGA GCGTACTATGGTTGCTAATTAACC ATCACTTGAATACTTCTTTGATTAGTTGTTCC CCAAAATAAGGGGGTAATAGTAAAAAAAGATT TCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT CTTTACAGTATCTTACCGAAGCCCAGTTACCA CAAAATTAGGATAAAAATTTTTAGGATATTCA

TTATTCATGTCACCAATGAAACCATTATTAGC GCCACGCTTTGAAAGGAATTGAGGAAACAATT AGAGGCATACAACGCCAACATGTATCTGCGAA AATTACTATTTCATAGGTCTGAGAGACGTGAATTT TGGACTCCGGCAAAATCCCTTATACGCCAGGG TTTTAGTTCGCGAGAAAACTTTTTTTTTGACC GCAATAGCAGAGAATAACATAAAAAACAGCCAT AATCACCACCATTTGGGAATTAGACCAACCTA CACGACGTGTTTCCTGTGTGAAATTTGCGCTC GAGCCGCCCCACCACCGGAACCGCTGCGCCGA CTAAATCGGAACCCTAAAACCGTC AATGGTTTTGCTGATGCAAATCCATTTTCCCT GTAAAAGACTGGTAATATCCAGAAATTCACCA TAGCCCTATTATTTACATTGGCAGCAATATTA ATATATTCTCAGCTTGCTTTCGAGTGGGATTT AGTGTACTATACATGGCTTTTGATCTTTCCAG CTTAAACAACAACCATCGCCCACGCGGGTAAA CGAGTAGAACAGTTGATTCCCAATATTTAGGC GCGCAGAGATATCAAAATTATTTGTATCAGAT AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA GAATGGCTACCAGTAATAAAAGGGCAAACTAT GCCAACAGATACGTGGCACAGACATGAAAAAT AGACAGTCTCATATGTACCCCGGTTTGTATAA AACCTACCGCGAATTATTCATTTCACATCAAG AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT GGAATTACCATTGAATCCCCCTCACCATAAAT TGCAACTAGGTCAATAACCTGTTTAGAATTAG TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA GGGAGAGGCATTAATGAATCGGCCACCTGAAA

TGGATTATTTTTGCCGTCAATAGATAATCAACTAAT ATCAAAATTTTTGAAGATGATGAAAAAAAAATTACCT GCCACCACTCTTTTCATAATCAAATAGCAAGG GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT **TCTTACCAACCCAGCTACAATTTTAAAGAAGT** ATTATTATTAGCGAACCTCCCGACGTAGGAA GTTGTAGCCCTGAGTAGAAGAACTACATTCTG AGCACCGTAGGGAAGGTAAATATTTTATTTG CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CCAGACGACAAATTCTTACCAGTAGATAAATA ATACCCAAACACCACGGAATAAGTGACGGAAA TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA GCAAATATGATTCTCCGTGGGAACCGTTGGTG TGTAGCATAACTTTCAACAGTTTCTAATTGTA GAAGGATTAGGATTAGAAACAGTT GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC ACGTGCTTTCCTCGTTGCCACCGA TATCAGGGCGAAAATCCTGTTTGACGGGCAAC TAAATATTGAGGCATAGTAAGAGCACAGGTAG CAACGCAAAGCAATAAAGCCTCAGGATACATT AAAACAAACTGAGAAGAGTCAATATACCTTTT ATCGGCTGACCAAGTACCGCACTCTTAGTTGC CATATTTATTTCGAGCCAGTAATAAATCAATA CCGGAAACTAAAGGTGAATTATCATAAAAGAA GAAGCAAAAAAGCGGATTGCATCAATGTTTAG GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG ACGGCTACAAGTACAACGGAGATTCGCGACCT AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT TTTTAATTGCCCGAAAGACTTCAACAAGAACG

GCGTAAGAAGATAGAACCCTTCTGAACGCGCG ACGAGTAGATCAGTTGAGATTTAGCGCCAAAA AACCAGAGACCCTCAGAACCGCCACGTTCCAG GTCACACGATTAGTCTTTAATGCGGCAACAGT ATCAACAGGAGAGCCAGCAGCAAAATATTTT GAAATGGAAAACATCGCCATTAAACAGAGGTG GGTATTAATCTTTCCTTATCATTCATATCGCG ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT TCACAATCCCGAGGAAACGCAATAATGAAATA ATTAAGTTTTCCACACAACATACGCCTAATGA CTAAAATAAGTATTAACACCGCCTCGAACTGA TCAGGTCATTTTTGAGAGATCTACCCTTGCTT TATAAGTATAGCCCGGAATAGGTGTATCACCG AAAAAGGCTTTTGCGGGATCGTCGGGTAGCA CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG ACGGTCAATGACAAGAACCGGATATGGTTTAA GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA ATATAATGGGGGCGCGAGCTGAAATTAACATC TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA TAACCTCCAATAAGAATAAACACCTATCATAT CTGTAAATATATGTGAGTGAATAAAAAGGCTA ACCGCCACCCTCAGAAACAACGCC TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC TATTTTGCACGCTAACGAGCGTCTGAACACCC CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA TTTCAACTACGGAACAACATTATTAACACTAT TTAAGACGATTAATTACATTTAACACAAAATC

TACTCAGGAGGTTTAGATAGTTAG ACTGCCCGCTTTTCACCAGTGAGATGGTGGTT CTAAACAGGAGGCCGAGAATCCTG AGGTTTTGGCCAGTTACAAAATAAACAGGGAA TGAGTTTCAAAGGAACAACTAAAGATCTCCAA TAGAGCTTGACGGGGGAAAAGAACG ACCAGGCGGATAAGTGGGGGTCAG TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT GCGCATTAATAAGAGCAAGAAACAATAACGGA TAAAGTACCAGTAGGGCTTAATTGCTAAATTT CGTAACGAAAATGAATTTTCTGTAGTGAATTT GACTTGAGGTAGCACCATTACCATATCACCGG TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC TCGCAAATAAGTACGGTGTCTGGACCAGACCG ACGCAAAGAAGAACTGGCATGATTTGAGTTAA TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG TCATTACCGAACAAGAAAAATAATAATTCTGT CTGTAATAGGTTGTACCAAAAACACAAAATATA ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG AGGCGGTCTCTTTAGGAGCACTAAACATTTGA GAGGCGTTTCCCAATCCAAATAAGATAGCAGC AAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT GGCGATCGCGCATCGTAACCGTGCGAGTAACA CAAAAATCATTGCTCCTTTTGATAATTGCTGA AGTTTGGACGAGATAGGGTTGAGTGTAATAAC

## Origami with staircase pattern:

| STAACACIGASTIT                          | STCACCAGTACAAACT ACAACGCC               | E TELVECULICCUCUEUCUEUCUE        | TAGTTAGCGTAACGAT      | CTARAGITITETCET    | ATACAGGAGIGIACI   | CTAATAACTITIAA    | COOLCAPION 200                          | CTAACAGTGCCCGTAT AACAGTJAATGCC  | CCTECCTATTICEEAA                        | LIATTATZ CIGA                          |
|---|---|----------------------------------|-----------------------|--------------------|-------------------|-------------------|---|---|---|--|
| 10001404100041101040104010444           | A010010A101110A10110000                 | 24241221442212121212222          | 014104410004110014    | 241112444242224    | 14191331343434194 | 2241141124444115  | 000000000000000000000000000000000000000 | ATT010A0000ATATT010AATTA000   | 228432224144422211                      | 2281881882821                          |
| IICGCAATICCITTAGTIGTICCIT               | TATICICACICCGCIGAAACIGI                 | TTGAAAGT TTTTAGCAAAATCC          | ATACAGAAAATICATI      | CTAACGTCTGGAAAG    | TCAAAAGCCATGTA1   | ACGCTTACTGGAACO   | GTAAATTCAGAGACTO                        | SCITTCCATTCTGGCTTTAATCAGGATIT   | TOTTICICANTATC                          | AAGGCCAATCGTC                          |
| TCTCCA AAAAAAA                          | STEERAAAAGAAGGAGGET TAATTET             | A TOGOTTIATONECTICOTITO          | IN TEADTIFCTIANACAS   | CITEATACCEATAGT    | TECCTEREASCESS    | ****              | CCTCASE CCACCAC                         |   | ACCOCCOCCASCATTS                        | ALAGGAGGT TOAG                         |
| 19244211114242211111112                 | 242211112212224441144241                | 14000444.40100440044400          |                       | 244214122214124    | A000A0T0T000000   | .999V91011990991  | 10004010100010010                       | 24212122222212212112212212212   | 110000000001001440                      | 1913313384313                          |
| GCTGAGGGTGACGATCCCGCAAAA                | GGCCTTTAACTCCCTGCAAGCCT                 | TCAGCGACCEAATATATCGGTTA          | GCGTGGGCGATGGTTGT     | STCATTOTCOCCCC     | CGGTTCCGGTGGTG    | TCTEGTTCCEETEAT   | TTTGATTATGAAAAGA                        | GGCARACGCTRATRAGGGGGCTATGACCG   | AAATGCCGATGAAAAC                        | GCGCTACAGTOTG                          |
| CGTAGC ACCECTAC                         | AGAGGETTTGAGGACTAAAGACT                 | ITTCATES SEARCETTICCATTA         | GEGTANAATACETAAT      | GCCACTACGAAGGCA    | CCAGCADANTCACCA   | TAGCACCATTACCAT   | AGCANGE: COGANAC                        | STCACCAATGAAACCATCGATAGCAGCACC  | ETANICAGI AGCGACAG                      | A TCAAGT TOCC                          |
| 400011001000410011000041                | 101000444010010411101044                | AAAA2140.0110AAA221AA1           | 19000411114100410     | 22212A122112221    | 000100111140100.  | AT201001AA10011   | W100110000001110                        | A212211A3111221A231A132132132   | 04.14010410001010                       | 1140110444000                          |
| GATGATACAAATCTCCGTTGTACT                | GTTTCGCGCTTGGTATAATCGCT                 | TEEGETCANAGATEAGTETTTT           | GTGTATTCTTTTGCCTC     | TTEETTTTAGETTGE    | CTAATTCCCAAATG    | TCAAGTCGGTGACG    | TGATAATTCACCTTT                         | TGAATAATTTCCGTCAATATTTACCTTCC   | CTECCTCAATCGGTTGA                       | ATSTOSCOTTTT                           |
| CIVSVSSSVVSVISVA<br>GCGACCIGCTCCATO     | TTACTINGCCGGAACGAGGCGCAG                | ACCETCANTCATANGEGAACCE           | TGACCAACTTTGAAAG      | AGGACAGATGAACGG    | TAGAAAATACATACA   | 5V5113V5 33V31533 | AAAAGAAACGCAAAG                         | ACACCACGGAATAAG TTATTTTGTCACAA  | TCAATAGAAAATTCATA                       | GTTTACE AGEG                           |
| A100111140000010040040014               | VIIIVII0000011001000001                 | 01000001. 01V110001.             | 19431951194443111     | 100101014011000    | VIJIIIVIJIVIJ     | 111334339119141   | VIIII3III3391113                        | 91991933114113444144443491911   | ******                                  | ADDAAAT001000                          |
| CACTGAATGAGCAGCTTTGTTACG                | GATTTGGGTAATGAATATCCGGT                 | TTCTTGTCALGATTACTCTTGAT          | AAGGTCAGCCAGCCTAT     | COCCTONTOTACA      | TTTGCTAACATACT    | GTAATAAGGAGTCTT   | AATCATGCCAGTTCT                         | TGGGTATTCCGTTATTATTGCGTTTCCTC   | GOTTECCTECTEGETAAC                      | TTTGTTCGGCTAT                          |
|   | 4214442234114211 1162221                | *****                            | 12242122212224142     | 0000400404041010   | ****              | 22411411 32126244 | 140143001344044                         | A222414 42224414 11442224442243   |   | 41455555414                            |
| CACCAC ACCACTAC                         | VILLEVEDDDDVVDIDIVDDVVVIL               | 14440110444114014404011          | VISSVVIVSSSIVVVVI     | 0110V000V01VV1V    | 000001101001010   | INTRACCCACAAGAAT  | VOIDVVIID55511V                         | V11010010011011011V0111V10011V  | 50 1V9VV195511595                       | STATISTICS AND STATES                  |
|   |   |                                  |                       |                    |                   |                   |   |   |   |  |
| VIIIV9V9119V31                          | 31119111 SV19913 111113                 | *****************                | 1 2012100000000000    | 1100400 401040044  | 01100100000000000 | *******           |   | 41143939 44392434 44441434414434  |   | ALAA21444431                           |
| GCCAAAAGGAATTAC                         | CASSCATASTAASASS ACACTA                 | CATAACCETCETTTACCAGACG           | Id LATAAAAA CCAAAATAR | CEAGAGECTTTTECA    | ITECTOR ICTTACCA  | ACGETAACGAGEGTEI  | TTEEAGAGE CTAATT                        | CCASTIACAAAATAA CASCCAJATIATI   | TATCCCAATCCAAATAA                       | daaceati iiii                          |
|   | 1100014104110100101010414               | *51*11555*55***155151555         | .9.91411111991111414  | 5313133354444353   |                   | .535411531353451  | *******                                 | 55154415111141115155514144144   | *                                       |  |
| TAAAGCATTTGAGGGGGATTCAAT                | ATATTTAIGACGATTCCGCAGT                  | ATTGGACGETATCCAGTCTAAAC          | TTTTACTATTACCCCC      | IGGCARARCTICITI    | AAATTGTAGCTGGGT   | CAAAATAGCAACTAA   | TCITGATITAAGGCT                         | AAAACCTCCCCCAAGTCGGGAGGTTCGCT   | AACGCCTCGCGTTCT                         | TAGAATACCGGAT                          |
| CATAAAT CAAAAATS                        | AGGICTITACCCIGAS                        | TCAGAAGCAAAGCGGATTGCAT           | AAAGATJ AAGAGGAAG     | CCCGAAAGACTTCAAS   | AAGAACEGETATTAA   | ACCANGTACCOCACTO  | TCGAGAD CAAGCAAG                        | CGITTITATITICAT GTAGGAAICATTA   | COCCCCANTAGCANG                         | AATCAGA TATA                           |
| 901011401991411149111114                |   | 040101100.1100001440014          | 111113199113133133    | 000011101044011    | 1121122222414411  | .99113419939194   | 01400101101100110                       | 222444441444421422412211421441  | 9999999114199113                        | 0111401014141                          |
| ATGACCTCTTATCAAAAGGAGCAA                | TAAAGGTACTCTCTAATCCTGACC                | CTETTEEACTITECTICCEETCI          | GTTCGCTTTGAAGCTCCA    | ATTAAAACGCGATAT    | AATGATAAGGAAAGA   | AGCCGATTATTGATT   | GETTTCTACATECTCO                        | AAATTAGGATGGGATATTATTTTTCTTGT   | TEAGGACTTATCTATTG                       | TTGATAAACAGGC                          |
| ATT6CT6AATATAATO                        | VIIISSVISVSVSVI VSSVSIS                 | <u>A 16CAACTAAAGTAC66161016</u>  | GTTTCAJTCCATATA       | CASTIGATICCCAATA   | TTTAGGE AGAGGE AT | 5135531941993199  | 544454151435455<br>GAGAATATAAAGTAC      | CGACAAAAGGTAAAGTAATTCTGJCCAGAC  | VSISSISVVI VSVIVVS<br>GACGACAATAAACAACA | TTCAGCIAATG                            |
| *10100**11**00*011*1*1*                 | *************************************** | 1422112411241022424242           | 11344451445514141     | 010000100000110    |                   | V44501055104114   | 1212114141112413                        | 010111100411104114404040991013  | ). 931911V11191191                      | ADAADTDDATTAD                          |
| ATECCACCTITICAGCTCGCGCCC                | AATGAAAATATAGCTAAACAGGT                 | TTATTGACCONTINGCGARATGTA         | CTAATGGTCAAACTAAA     | CTACTOSTTOSCASA    | ACATGTTGGCGTTG    | AAATATGGCGATTCI   | CAATTAAGCCCTACTO                        | TGAGCGTTGGCTTTATACTGGTAAGAATT   | TOTATAACGCATATGAT                       | ACTAAACAGGCTT                          |
| 440130403030000                         | 11103111 (0101350 1151330               | *****31551***35511****           | 114334911194111       | 5915955999551319   | 191434433934434   | VIIIVIV3 SOLIVION | 0110011333301303                        | V31353V (335VVV) (15V33V11311V  | *3*1411939[*14314                       | VIII31335VV                            |
| 201201201001001000000000000000000000000 | 101010001100011011011001                | 391111VV 3911V111399V9.          | 01001011100011100     | 344341991111191    |                   | 114445145445451   | 05011100011055000                       | 111419931993434546101111  | ******                                  | 33311V91V11VV                          |
| TACACATTACTCASSCATTSCATT                |   | TTTTTATCOTTCCTTCAAATAA           | CONTRACTOR            | ATTACASSSTCATAA    |                   | TETTTGTETTGEGAT   | TEGATTTECATCAECA                        |   |   | AGTETETEAGACE                          |
| A010201A0201AA0                         | 11114141 (5155549 (F11111               | ***********************          |                       | 1991010 509019111  |                   | ********          | 222100222102222                         | ***************************************   |   | ************************************** |
| AGGCCGGAGACAGT                          | AAATCACCATCAATA CATATIC                 | ACCETTCIASCISATAAATTAA           | CEGAGAGEGEAGCTA       | TTTTGAGAGATCTAC    |                   | <u> </u>          | TITICCC TAGAATCC                        |   | 2 2 2 2 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 | A LIGANTIN ATCA                        |
|   |   |                                  |                       |                    |                   |                   |   |   |   |  |
| 2222222410141421                        | 442121428412444413214418                | 99344914931449494 <b>6</b> 34443 | 10010100000100011     | JISSAJI &IJSSAAA   | V1VV515V5151V1V   | TVOLVEY PVOVIOVO  | VV551VV11111155                         | TITLE POLICY WITH THE POLICY  | TANAL STATES                            | A2444214214                            |
| TIGTATAAGCAAATAT                        | TANATISTAAASSIMATATTI                   | J STIAAAA TESSATIAAATTIT         | IN TANALSPECTEMETER   | TTAACCAATAGGAAC    | ACASTASCITITACA   | CGGGAGAAACAATAA   | CONTROPTORIES                           | CTTTGAATACCAAGTT ACAAAATFGCGCAG   | AGECGAATTATICATIT                       | ATTACCI GASC                           |
| 1010011010400414110011141               | ******                                  | A2AATTTTAA22221AATTTAAAA         | CAATTTADTDDADTAAA     | ¥¥115511¥155115    | 10104100444101    | V933313111911V11  | 10001440000401440                       | AAA211A122112AA121111A2222212   | 12222114414421444                       | 5114415545155                          |
| CCECCETTETTCCCACGEAGAAT                 | GACGGGTTGTTACTCGCTCACAT                 | TTTAATGTTCATGAAAGCTGGCT          | CAGGAAGGCCAGACGCC     | ATTATTTTTGATGG     | CTGTATATTCATCT    | CGTTAAACCTGAAAA   | TCTACGCAATITCTT                         | TTICIGITITACGIGCAAATAATITIGAT   | ATCGTAGGTICTAACCC                       | TTCCATTATICAS                          |
| GTTGGTGTAGATGG                          | COCATCOTAACCOTOCATCTOCC                 | AGTTTEAGEGEACEACEACAETA          | GECTEAPEAAEATES       | ACTECAGECAGETTT    | CATTAICATTIECS    | AACAAAGAAACCAC    | GANGEAS GEANTIA                         | ICATCATATICCIGAT TATCAGAJ GAIGGO  | ANTICATCANTATAATC                       | GATTOTI TOGA                           |
| 214133491034433434131433                | 0.2014024110024202140420201             | 13444313333133133133131341       | 000004010011014000    | 104001000100444    | 014414014444000   | 11911191119919    | 01011001000011441                       | 21421414422421441421214214322   | 11,4401401141414140                     | 2421442444321                          |
| GGEGTAATAGEGAAGAGGEEEGEA                | GATEGECETTECEAACAGTTGE                  | GEAGECTEA TEGEGAATEGEGE          | TTGCCTGGTTTCCGGC      | CAGAAGEGGTGCCGG    | ACTCARACTTTTRA    | TTAATAACGTTCGGG   | CAAAGGATTTAATAC                         | GTIGICGAATIGTITGTAAAGICTAATAC   | TT TAAATCCTCAAATG                       | TATTATCTATIGA                          |
| CAAGGCEATTAAGT                          | 531453555445551161344355                | 301305V311V330311V33030          | A TECCAMECTTECATEC    | 5131135 33V35533V  | AAATATEAAACCCTC   | AATCAATATCTGGTC   | TTGGCAAATCAACAG                         | TTGAAAGGAATTGAGGAAGGTTAJCTAAA   | VV SVIIIVSSVSIIIVS<br>TATCITIAGGAGCACTA | CAACTAAJAGAT                           |
| 2214242626251122221441124               | 000011000010000000000000000000000000000 | A0100100 A011110010000           | 10000011000000100     | 242212242212424    | 111111051115550   | .149114149499999  |   | A211122114A21221122AA1A2A1111   | ********                                | 191190110191                           |
| CTTCCGGCTCGTATGTTGTGTGGAA               | TGTGAGEGGATAACAATTTEACA                 | ACAGGANAG AGCTATGACCATGA         | TACGAATTCGAGCTCGO     | ACCCGGGGATCCTCT    | IGETTCAGCAAGGTGA  | GCTTTAGATTTTTC    | TTTGCTGCTGGCTCTO                        | GCGTGGCACTGTTGCAGGCGGTGTTAATA   | CTRACEGUCTURECTUT                       | GITTIATCTICTE                          |
| 0341434434343211                        | **************************************  | 191331119 3941431 991431         | 1001100001000000      | 1999333 \$1999999  |                   | *******           | **************                          | 11111111111111111111111111111111111111  | ******                                  | *********                              |
| LUIAATGAGTGAGCTV                        | SVOIDINNIINNODNNODDNA                   | SISVSSSS WWWSSISWSSSS            | LIGITIG CCACCIEC      | IVVIIVOIIVOIDO     | 05V0111050V110    | VISOVOSSISIONS    | IVIVVVVVJIIV555                         | VV13V5VVV11V35353115V31V13555   | ¥111514535514411                        | 111V100011001                          |
|   |   |                                  |                       |                    |                   |                   |   |   |   | ********                               |
| 101030500000000000000000000000000000000 | 11401304 3443000 0 0401043              | 33V3111131111991999V33           | 3011410301110030      | 9494999 \$39393445 | 131133344541454   | 94344339 #1311434 | \$22444144124224                        | A STORAGE AND A | LIVESIVVE PIEST                         | 1353¥51111¥                            |
| COTTOCCCCA CAN                          | CONNANT COLOTITICA COLOGI               | CCGARATCESCARAATCCCTTA           | IN ATCANAGENATABLE    | GAGATAGGETTGAGT    | TAATAAFATCACTIS   | CTGAGTAGAAGAACI   | LAAACTAJ: SECTTS                        | CTEETAATATCCAEAA AATATTACCECCI  | STATTSCAACAGGAAA                        | ACCETCATORA                            |
| 7422723243344453222273273               | 17TTT422474A40T422423A                  | 4000111410000441                 | 11140111011410019     | )1)141)JJVVJJV     | ************      | 224212412112121   | 131113414333322AA3                      | **>>*11*1*>>>>10118181900000  | Jan 44 Jan 19133111                     | 1100040140011                          |
| TGATGGTTCACGTAGTGGGCCATC                | CCTGATAGACGGTTTTTCGCCCT                 | TITGACGT GAGTCCACGTTCT           | TAATAGTEGACTCTTGT     | CCAAACTEGAACAAC    | AATCAAAGAAGTAT    | CTACAACGGTTAATI   | TECETEATEEACAGA                         | CTITTACTOGGTGGCCTCACTGATTATAA   | AAACACTTCTCAGGATT                       | CTEECETACCETT                          |

Turquoise staircase pattern sequences:

GTTAGATGATTTAAAAAAGGCTTTTGCGGGATCGTCGGGTAGCA GTTAGATGATTTTTTCAACTACGGAACAACATTATTAACACTAT GTTAGATGATTTCCAAAATAAGGGGGGTAATAGTAAAAAAAGATT GTTAGATGATTTCCAAAATAAGGGGGGTAATAGTAAAAAAAGATT GTTAGATGATTTAACCTACCGCGAATTATTCATTTCACATCAAG GTTAGATGATTTGGTATTAATCTTTCCTTATCATTCATATCGCG GTTAGATGATTTGGAATTACCATTGAATCCCCCTCACCATAAAT GTTAGATGATTTACGGCTACAAGTACAACGGAGATTCGCGACCT GTTAGATGATTTCCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGGAG GTTAGATGATTTTTTAATTGCCCGAAAGACTTCAACAAGAACG GTTAGATGATTTAAATCAATCGTCGCTATTAATTAAATCGCAAG GTTAGATGATTTAAATCAATCGTCGCTATTAATTAAATCGCAAG GTTAGATGATTTTAGCCCTATTATTTACATTGGCAGCAATATTA **GTTAGATGATTTACGAACTATTAATCATTGTGAATTTCATCAAG GTTAGATGATTTTAAATATTGAGGCATAGTAAGAGCACAGGTAG GTTAGATGATTTTCAGGTCATTTTTGAGAGATCTACCCTTGCTT** GTTAGATGATTTGCGAAACAAGAGGCTTTGAGGACTAGGGAGTT GTTAGATGATTTGGATTTAGTTCATCAATATAATCCAGGGTTAG **GTTAGATGATTTTGAGTTTCAAAGGAACAACTAAAGATCTCCAA** GTTAGATGATTTGGACGTTGAGAACTGGCTCATTATGCGCTAAT GTTAGATGATTTGAAATGGAAAACATCGCCATTAAACAGAGGTG GTTAGATGATTTAAAGATTCTAAATTGGGCTTGAGATTCATTAC **GTTAGATGATTTCTGTAATAGGTTGTACCAAAAACACAAAATATA GTTAGATGATTTCTAAAATAAGTATTAACACCGCCTCGAACTGA GTTAGATGATTTTCTTACCAACCCAGCTACAATTTTAAAGAAGT GTTAGATGATTTACAAAGAAAATTTCATCTTCTGACAGAATCGC GTTAGATGATTTCCAAATCATTACTTAGCCGGAACGTACCAAGC GTTAGATGATTTAATGGTTTTGCTGATGCAAATCCATTTTCCCT GTTAGATGATTTAAAACAAACTGAGAAGAGTCAATATACCTTTT** GTTAGATGATTTTTTTAGTTCGCGAGAAAACTTTTTTTTATGACC **GTTAGATGATTTCTGTAAATATATGTGAGTGAATAAAAAGGCTA GTTAGATGATTTAGAAGTGTCATTGCAACAGGAAAAAATCGTCT GTTAGATGATTTACGAGTAGATCAGTTGAGATTTAGCGCCAAAA GTTAGATGATTTTTGAATTATTGAAAAACATAGCGATTATAACTA** GTTAGATGATTTTTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA GTTAGATGATTTGATGGCAAAAGTATTAGACTTTACAAGGTTAT **GTTAGATGATTTCGAGTAGAACAGTTGATTCCCAATATTTAGGC GTTAGATGATTTAGAGGCATACAACGCCAACATGTATCTGCGAA GTTAGATGATTTCATAACCCGCGTCCAATACTGCGGTATTATAG** GTTAGATGATTTGAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC **GTTAGATGATTTTTAAGACGATTAATTACATTTAACACAAAATC GTTAGATGATTTTATGTAAAGAAATACCGACCGTGTTAAAGCCA** 

GTTAGATGATTTAGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA GTTAGATGATTTTAACCTCCAATAAGAATAAACACCTATCATAT GTTAGATGATTTTAGAATCCCCTTTTTTAATGGAAACGGATTCG GTTAGATGATTTCGATTTTAGGAAGAAGAAAATCTACGGATAAAAA GTTAGATGATTTGCTCCATGACGTAACAAAGCTGCTACACCAGA GTTAGATGATTTAAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT GTTAGATGATTTAGGCGGTCTCTTTAGGAGCACTAAACATTTGA GTTAGATGATTTACTGGATATCGTTTACCAGACGACTTAATAAA GTTAGATGATTTGCGCAGAGATATCAAAATTATTTGTATCAGAT

## Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC ATTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

# Additional sequences:

CATATTTATTTCGAGCCAGTAATAAATCAATA GTTGTAGCCCTGAGTAGAAGAACTACATTCTG AAATAATTTTTAACCAATAGGAACAACAGTAC GCCAACAGATACGTGGCACAGAACATGAAAAAT CCGGAAACTAAAGGTGAATTATCATAAAAGAA GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG TCATAGCTTGTAAAACGACGGCCAAAGCGCCA GCAATAGCAGAGAATAACATAAAAACAGCCAT CAAAAATCATTGCTCCTTTTGATAATTGCTGA CACGACGTGTTTCCTGTGTGAAATTTGCGCTC TACCTTTAAGGTCTTTACCCTGACAATCGTCA GCCCAATAGACGGGAGAATTAACTTTCCAGAG GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA TCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT CTTAAACAACAACCATCGCCCACGCGGGTAAA TTTCATGATGACCCCCAGCGATTAAGGCGCAG TGGATTATTTTGCCGTCAATAGATAATCAACTAAT TATCAGGGCGAAAATCCTGTTTGACGGGCAAC ATTAAGTTTTCCACACAACATACGCCTAATGA CTAAACAGGAGGCCGAGAATCCTG CACCAGAGTTCGGTCATAGCCCCCTCGATAGC TCCATATATTTAGTTTGACCATTAAGCATAAA ACGCTCAACGACAAAAGGTAAAGTATCCCATC GACTTGAGGTAGCACCATTACCATATCACCGG ACAGAAATCTTTGAATACCAAGTTAATTTCAT GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA CCCGGGTACCTGCAGGTCGACTCTCAAATATC ACGGTCAATGACAAGAACCGGATATGGTTTAA GCGTACTATGGTTGCTAATTAACC ATACCCAAACACCACGGAATAAGTGACGGAAA ATCACTTGAATACTTCTTTGATTAGTTGTTCC CTTTGAAAATAGGCTGGCTGACCTACCTTATG GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT GGCGATCGCGCATCGTAACCGTGCGAGTAACA CTAAAGCAAATCAATATCTGGTCACCCGAACG GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC

GCGTTATACGACAATAAACAACATACAATAGA ATCAGAGAGTCAGAGGGTAATTGAACCAGTCA CAATGACAGCTTGATACCGATAGTCTCCCTCA GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA TCACAATCCCGAGGAAACGCAATAATGAAATA AGTGTACTATACATGGCTTTTGATCTTTCCAG ACCAGGCGGATAAGTGGGGGTCAG GAATGGCTACCAGTAATAAAAGGGCAAACTAT CAAAATTAGGATAAAAATTTTTAGGATATTCA GAAGGATTAGGATTAGAAACAGTT TGGACTCCGGCAAAATCCCTTATACGCCAGGG TATTTTGCACGCTAACGAGCGTCTGAACACCC CTTGCATGCCGAGCTCGAATTCGTCCTGTCGT AGAGAATCAGCTGATAAATTAATGCTTTATTT GAAGATCGTGCCGGAAACCAGGCAGTGCCAAG AGTTTGGACGAGATAGGGTTGAGTGTAATAAC TGAACAAAGATAACCCACAAGAATAAGACTCC ATACGTAAGAGGCAAAAGAATACACTGACCAA TTTAACGTTCGGGAGAAACAATAACAGTACAT GCAAATATGATTCTCCGTGGGAACCGTTGGTG CAACGCAAAGCAATAAAGCCTCAGGATACATT TATATTTCATACAGGCAAGGCAAAGCTATAT TTATTCATGTCACCAATGAAACCATTATTAGC AATCACCACCATTTGGGAATTAGACCAACCTA AAACGAAATGCCACTACGAAGGCAGCCAGCAA TGTAGCATAACTTTCAACAGTTTCTAATTGTA TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT GTAAAAGACTGGTAATATCCAGAAATTCACCA ATCAAAATTTTTGAAGATGATGAAACAAAATTACCT

TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA TACTCAGGAGGTTTAGATAGTTAG CATGTCAAAAATCACCATCAATATAACCCTCA GAGCCGCCCCACCACCGGAACCGCTGCGCCGA ATTTTGCGTTTAAAAGTTTGAGTACCGGCACC TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG TTATTACGTAAAGGTGGCAACATACCGTCACC AGTAATCTTCATAAGGGAACCGAACTAAAACA TCAGAAGCCTCCAACAGGTCAGGATTTAAATA ACCCGTCGTTAAATTGTAAACGTTAAAACTAG TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC ATATAATGGGGGGCGCGAGCTGAAATTAACATC TGCCTTGACAGTCTCTGAATTTACCCCTCAGA ATCAACAGGAGAGCCAGCAGCAAAATATTTT AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG CTTTTACACAGATGAATATACAGTGCCATCAA TTTTTGAAAGTATTAAGAGGCTATTATT GTCACACGATTAGTCTTTAATGCGGCAACAGT GTTAAAATAACATTAAATGTGAGCATCTGCCA CAATAAATAAATGCAATGCCTGAGAAGGCCGG ACGTGCTTTCCTCGTTGCCACCGA GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT TATAAGTATAGCCCGGAATAGGTGTATCACCG AATGCCCCATAAATCCTCATTAAAAGAACCAC ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA CTTTCATCTCGCATTAAATTTTTGAGCAAACA

AATTACTATTTCATAGGTCTGAGAGACGTGAATTT TCATTACCGAACAAGAAAAATAATAATTCTGT CAAGCAAGCGAGCATGTAGAAACCAGAGAATA TGCAACTAGGTCAATAACCTGTTTAGAATTAG AGGTTTTGGCCAGTTACAAAATAAACAGGGAA ACCGCCACCCTCAGAAACAACGCC TAGAGCTTGACGGGGGAAAAGAACG GGGAGAGGCATTAATGAATCGGCCACCTGAAA ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG TCGCAAATAAGTACGGTGTCTGGACCAGACCG CTCATCTTGGAAGTTTCCATTAAACATAACCG TTCGCCATGGACGACGACAGTATCGTAGCCAG CACCACCCTCATTTTCCGTAACAC TTATTAATGAACAAAGAAACCACCTTTTCAGG CCAGACGACAAATTCTTACCAGTAGATAAATA AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG CGTAACGAAAATGAATTTTCTGTAGTGAATTT AACCAGAGACCCTCAGAACCGCCACGTTCCAG GCTCACAAGGGTAACGCCAGGGTTTTGGGAAG CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT GCCACCACTCTTTTCATAATCAAATAGCAAGG ATATATTCTCAGCTTGCTTTCGAGTGGGATTT CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT CTAATTTACCGTTTTTATTTTCATCTTGCGGG ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT ACTGCCCGCTTTTCACCAGTGAGATGGTGGTT CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA GCTTCTGGCACTCCAGCCAGCTTTACATTATC

CTAAATCGGAACCCTAAAACCGTC AAACCCTCTCACCTTGCTGAACCTAGAGGATC AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT GTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT ATTATTATTAGCGAACCTCCCGACGTAGGAA GAAGCAAAAAAGCGGATTGCATCAATGTTTAG TACATACACAGTATGTTAGCAAACTGTACAGA GCGTAAGAAGATAGAACCCTTCTGAACGCGCG CCTAATTTAAGCCTTAAATCAAGAATCGAGAA CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CTTTACAGTATCTTACCGAAGCCCAGTTACCA ATCGGCTGACCAAGTACCGCACTCTTAGTTGC TTTCATTTCTGTAGCTCAACATGTTTAGAGAG AGCTGATTACTCACATTAATTGCGTGTTATCC CGACAACTTCATCATATTCCTGATCACGTAAA CCAGGCGCGAGGACAGATGAACGGGTAGAAAA GAGGCGTTTCCCAATCCAAATAAGATAGCAGC AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT CCTGATTGAAAGAAATTGCGTAGAAGAAGGAG GCGCATTAATAAGAGCAAGAAACAATAACGGA TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA ACGCAAAGAAGAACTGGCATGATTTGAGTTAA GCCACGCTTTGAAAGGAATTGAGGAAACAATT ACCGTTCTGATGAACGGTAATCGTAATATTTT CGGAATTACGTATTAAATCCTTTGGTTGGCAA AGCACCGTAGGGAAGGTAAATATTTTATTTG AGACAGTCTCATATGTACCCCGGTTTGTATAA TAAAGTACCAGTAGGGCTTAATTGCTAAATTT

TCGGCATTCCGCCGCCAGCATTGATGATATTC ATTGAGGGAATCAGTAGCGACAGACGTTTTCA GAAGGAAAAATAGAAAATTCATATTTCAACCG TGCCTTTATTTTAGACAAAAGGGCGACAGGTTTACC CTGAAACATTTTGTCAGACGATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGACTGTAGCGATCAAGTT

#### Origami with zigzag pattern:

|   | 20000000000000000000000000000000000000   | V9V31333V303333V1 V11133V393313V1   | 5004014101004144000000414104444  |  |  | V9VV313313V9V91305V9VV11V19VVV9   |
|---|--|---|--|--|--|---|
| 14133112221424122341121243134313444   | A010010A101110A1011000A0A1001  | ADDIDIDIDIDDDDDDDDDDDDDDDDDDDDDDDDDDDD  | ADATTTOAAAADADAA   | 2241141124444110222240134200442  | A11010400000A1A111010AA1140000.  | 101111040001000010000000000000000000000   |
| ITATTATTCGCAATTCCTTTAGTTGTTCCTT   | CTATTCT CACTCCGCTGAAACTGTTGAAAGT   |   | A CTARCETCIGGARAGAT CARRAGC CATETA   | CACECTTACTEGAACEETAAATTCAEAEACT  | GCTTTCCATTCTGGCTTTAATGAGGATTTA   | T G T T T G T G A A T A T C A A G G C C A A T C G T C T G A C   |
| **************************************  | 0V1VV0V010V000000001110V0V001110V0   |   | 19411934 84331113149111139514341   |  | 22244422 [4424222   44114212214441   | AA2AAA2A211A1A21222211A22A2A212   |
| TCTCCAAAAAAAG   | TCCAAAAGAGCCT AATTGTATCGGTTT   | TEAGETTGETTTEGA TEAATT CTTAAAC  |  |  | CTCAGAGCCGCCAC   | CCGCCGCCAGCATTG AGGAGGTTGAGGCAG   |
|   |  |   |  |  |  |   |
| 100100000000000000000000000000000000000   | 23355744 1545554 21135545135315  |   |  | TANK TANK TANK TANK TANK TANK TANK TANK  | V3391115 J9V11V1 0333300 IN 159311   | 112000100101010100001010000000000000000   |
| GGTAGCAACGGCTA  | AGAGGETTTGAGGAC AAAGACTJTTTCATG  | COASTTTCCATTAA COCTAASATACOTA   | TECCACTACGAAGGCAGCCAGCAAAATCACC  | TAGCACCATTACCA ACCAACP: CGGAAAC  | TCACCANTGANACCA CGATAGE SCACCOT  | AATCAGTAGCGACAGATCAAGTJTGCCTTTA   |
| 212122142221122122241221122281  |  | 221124AA221AA1112222A1111A122A11  | A32212A1231133215221321111A2122  | 0413212214412214412211232233111  | 04010011401110014001410010010000   | 11421241222121211421124442224441  |
| ATCAGGCGATGATACAAATCTCCGTTGTACT   | GTTTCGCGCTTGGTATAATCGCTGGGGGTC   | AGAIGAGIGITITAGIGIATICTITIGCCI  | TITEGTTITAGGITGO CTAATTCCCAAATG  | TCAAGTCGGTGACGGTGATAATTCACCTTT   | TGAATAATTTCCGTCAATATTTACCTTCCC   |   |
| GCGACCTGCTCCAT  | TTACTTAGCCGGAACCAGGCGCAGACGGTCA  | TCATAAGGGAACCGAACTGACCAACTTTGAA   | AGGACAGATGAACGGGTAGAAAA TACATAC  | ATAAAGGTGGCAACATATAAAAGAALCGCAAAG  | ACACCACGGAATAAGTTATTTTCCACAATC   | AATAGAAAATTCATATGGTTTACCAGCGCCAA  |
| 1114424242311142222212242242214   | VVI9VVI399331193133939131933V91.   |   | 122121212122222222222222222222222222222  | YIII33Y339II9IVIYIIII3III939III.   | 2122122211411244414444242121143  | 111010111100010100000010000011  |
| CTTATICACTGAATGAGCAGCTTTGTTACG  | CATTICGGTAATCAATATCCGGTTCTTGTC   | AGATTACTCTTGATGAAGGTCAGCCAGCCTAT  | COCCTOOTCTOTACA CTTTOCTAACATACT  | C GTAATAAGGAGTCTTAATCATGCCAGTTCT   | TEGETATICCETTATTATTECETTICCICE   | TTECTTCTGGTAACTITGTTCGGCTATCTGC   |
|   | TAAATTGGGCTTGAGATGGTTTAATTTCAAC  | TTAATCATIGTGAATTACCTTATCCGATTTT   | 333559933459939151399935911519159<br>Agaactggctcattatgcgctaajatcagag   | 5559119115515959911951955159999<br>A SATAACCCACAAGAAT GAGTTAASCCCAATA  | 4455541445534414144553444554535<br>ATAAGAGCAAGAAACAATGAAATA; CAATAGC   | TATCTTACCGAAGCCGTTTTTAAGAAAAGTAA  |
| 044300001011010101010101010101  | AITTAA33338A3131A33AAATTAAA3113  | AATTADIAADADIIAAIDDAAIADDDIAAAA   | *211242224414145556  |  | ¥113139113111911¥3111¥13911¥13   | 1799491999911999994444411911119411  |
| ********************************  | CANTETTTETACCTETANTANTETTETTEES  |   | ********   | TTGTTCAGGGTGTTCAGTTAATTCTCCCGT   | TAATGCGCTTCCCTGTTTTTATGTTATTCTC  | TGTAAAGGCTGCTATTTTCATTTTTGACGTT   |
| VIIIV5V5115V51  | 51145444 50155039 114114544545555  | 41344224 (ALTAL 24131444442442  | 9119362242126226621166192266263  | 244424421322424491244114424222343  | 41143232 44222434 4444143441442424   | 2424111232422414444214444212244   |
| VIIV35131V191V11335511113311VV1   | 100014104110100110104140141100   | A14444 CT4444   | 100101000444400 140040114044100  | 232011231223245462512132541144   |  |   |
|   |  |   |  |  |  |   |
| ATT6AATCCCCCC   | 110100010010010000000000000000000000000  | 10000104001010 F101001041000000   | 22222211112222222222222222222222222222   | 1001111111 3011041 1 004011404110004   | 211112242022113  | 110300402030344044 2311410033141130   |
| CATAAAJ CAAAAAT   | AGGTETTTACCETGAS ATTATASTCAGAAG  | AAAGCEGATICCATCA AAAGATJ AAGAGGA  | COCCANAGACTICAACAAGAACG GETATTA  | ACCANGTACCECACTO TCEAGAD AAGCAAS   | COTTITIATITICA CIAGGANICATIACO   | CCCCCCAATACCAAC   |
|   |  |   |  |  |  | /   |
|   |  |   | AATTAAAACGCGATAT AATGATAAGGAAAG  | AGCCGATTATTGATTGGTTTCTACATGCTC   | AAATTAGGATGGGATATTATTTTTTTTTTTTTT  | GGACTTATCTATTGTTGATAAACAGGCGCGT   |
| ATTECTEANTATAAT   | TETASCICAACATET TTAAATA TECAACT  | AAGTACGGTGTCTGGA GTTTCATTCCATAT   |  | TTTCGAGCCAGTAATA GAGAATALAAAGTAC   | GACAAAAGGTAAAGTAATTCTGJ CAGACG   | C GACAATAAACAACATETTCASCJAATSCAS  |
| 21433284413138441144324311414114  | 0424122421121424444111414231124:   |   | 1010400144000114 (44410001010001   | *****  | 212111122A1112A11AA2A2A262121223   | 10101111011011010000100011000100  |
| AGAATTGATGCCACCTTTTCAGCTCGCGCCC   | AAATGAAAATATAGCTAAACAGGTTATTGACI   | ATTTGCGARATGTATCTAATGGTCARACTAAJ  | TCTACTCGTTCGCAGA FACATGTTGGCGTTG   | TAAATATGGCGATTCTCAATTAAGCCCTACT  | TGAGCGTTGGCTTTATACTGGTAAGAATTTG  | TATAACGCATATGATACTAAACAGGCTTTTTC  |
| VV0100V0000000  | 0111401111414100411010044144010  | 144439311143414   | MANIA A 2 4 4 2 2 2 2 2 2 1 2 1 4 1 2 1 4 2 4 4 2 2 2 2  | VIIIVIV33531VV5 011VV113555V15V3   | 442122244222444  | ATATT0001ATA01A10ATT101000AAAAA   |
|   | ICATACAGGCAAGGCAA AGAATTAGCAAAATTI   | AND AND ANALY CITERS  | A ST TATACCARA A A CACAGA A A TATA   |  | A REAL PROPERTY AND A REAL | AATAAGAATAAACACOEGAATCATAATTACTA  |
| 1041141041041001441101400114111   | 14191939119391193911191144199111144  |   |  |  |  |   |
| 19VIIVIDVIDVID0IVVII0IV59IIVIII   | ATACAGGGAAGGGAAGGGAAGTAG<br>1141913331133311131144139111144<br>AAATATATGAGGGTTCTAAAAATTTTTATCI   | 1331141113559913135141113541114<br>15665116AAATAAAG6CTTCTCCCGGAAAAA   | YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY<br>Yattacagggtcataa aaaaagtiittcicgc   | 114449149499991999111449149999<br>1167176767766687766877766877766  | 21114122212224244<br>TTTACATATAGTTATATAACCCAACCTAAGC   | A ATTA A GAATAA A A GAA GAATAA TA CTA<br>1 VII 221 I VII 121 23 23 23 11 V21 VII VVI 29 VI<br>1 GAAGATTAA A A A A GGTA GTA CTA CTA GAACATAT   |
|   | ATACAGGCAAGGCAAGGAATTAGCAAAATT<br>YYYYYJJJJJSSIIJJIIIYYYJ<br>AAATAATAGGGGTTCTAAAAATTTTTATC<br>YYYYYYYYYYYYYYYYYY<br>AAATCACCGTC  |   | DVVDV100111132 D111V1VVVV1DV<br>TATTACAGGGCATAALAAAAGTTTTCCCC<br>VIVI013 DV01VIIIIIIS  | LIVVVSIVSVVSVSISSVIIIVVVIIVSSVV<br>TECTTECTTECEATEGEATTEGEATEGEA<br>VVSVVSVVSVVSSLVSISSI<br>TECTECEATEATEAT        | 21114120212029999999914114112320344<br>TTTACATATAGTTATATAACCCAACCTAAGC<br>WYDDYI (159474)<br>TTTACATATACTACAT  | ATTAGGATTAACAE SCATCE ATTACT<br>IVIISIIVIII91995511V9IVIIV9VI<br>caacataaaacotattactattacaacatat<br>23133VVI 11133V PV9V9V912103VIC<br>caacataa   |
|   | LTARAGECAAGECAAGECAATTLE     CAAATTLE       LTARSIDSSILSSILSSILSSILVUSDELLUVE     AAATAATAAGAGECTICAAAAAATTTTTAACA       AAATAATAAGAGECTICAAAAAATTTTTAACA     AAATAATAAGAGECTICAAAAAATTTTTAACA       LILVUVSSILSSINVEVENENENENENENENENENENEN     AAATAAGCAATAATAATAATAATAATAATAATAATAATAATAATAAT | 135114111355949131355441113544411       155114111355949131355441115544411       1561471111555441115544411       15614711111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       1561471111       15614711111       15614711111       1561471111111       1561471111111111111111111111111111111111 | DWWVIDDIIIID<br>ATTACAGGETCATAA<br>AAAAGTTTTCCCC<br>VIWIDJ<br>TTTGGGGGGCTCATAA<br>WWVDDIDIIWVID<br>WWVDDDDIIWVID<br>BOWDWVVID  | LIWYSIYSYYSISISYYIIIWYIIYS<br>TICTTIGTCTTGCATTGCATTGCATCAGO<br>WWWYSYYYSYYII<br>SIGGCATAATAATAA<br>SIGGCATAATAATAA |  | ATTACATTACAT BEARTCH ANTACTA<br>IVIISIINIISISSSSIVSIVIIVIVIVI<br>CAASSTTAAAAASSTASTICTICAAACCTAT<br>SUSSWIICIISSY PSYNYISISSSYIV<br>CIGAGAAGAGTAAT<br>VIISIIISISSIIVIIVIVIVIIVIIVI  |
|   | LITERAGECALCECCAL CALITY CALANTI<br>IN 1913513511351111131111151111115111111<br>IN 191351135111111111111111111111111111111   | 1011111100000101000 1011100000101000 10100000000  | VVVVVISSIIIIIS DIIIVIVVVVISV<br>ATTACAGGGCCATAA AAAAGTTTTCCGC<br>VIVISIS SVSIVEIIIIISVVVOISSS<br>ITTIGAGAGATCTACCTTGCI CIGAAA<br>VVVVSISISVVIISVIISSVVVVVVIII<br>CACCTGATAGCCTT TATTGACTGACATA |  | STITUTES STANDARD STATEMENT STATEMEN | ATTAKATTAACCCECAATCATAATTACT<br>VII SIIVII SISSSSI VISI VII VVII VVI<br>AAGSTTAAAAGCTASTCCCCAGACCTAT<br>CIGACAAAAACAATACTAGATTAACAAT<br>CIGACAAAAACAATACTAGATTAACAAT<br>VII SII VII SIIVII VVII SIIIII<br>VII SII VII SIIVII SIIVII VVII SIIIII<br>VII SII VII SIIVII SIIVII VVII SIIIII<br>VII SII VII SIIVII SIIVII VVII SIIIII |
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| ЗУПЛУТОУ БУЛУТОУ ПУЛИТВУТОУЛ ПУЛИТ<br>ТИТАССТАСАСНАЯ СТОРИТВУТОУЛ ПУЛИТ<br>ИЗСТОРИСТВИИ<br>ИЗСТОРИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИ<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТИКА<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТИ<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТНИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТНИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТИ<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТСЯ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТВИТОВИ<br>ПОЛИТНИТОВИ<br>ПОЛИТВИ<br>ПОЛИТВИТНИ<br>ПОЛИТНИ<br>ПОЛИТНИ<br>ПО ПОЛИТНИ<br>ПОЛИТНИ |  |   |  |  |  |   |
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## Turquoise zigzag pattern sequences:

GTTAGATGATTTGCTCACAAGGGTAACGCCAGGGTTTTGGGAAG GTTAGATGATTTACTGGATATCGTTTACCAGACGACTTAATAAA GTTAGATGATTTACTGCCCGCTTTTCACCAGTGAGATGGTGGTT **GTTAGATGATTTAGAGGCATACAACGCCAACATGTATCTGCGAA GTTAGATGATTTGAAGCAAAAAAGCGGATTGCATCAATGTTTAG GTTAGATGATTTACAAAGAAAATTTCATCTTCTGACAGAATCGC** GTTAGATGATTTGAAGATCGTGCCGGAAACCAGGCAGTGCCAAG GTTAGATGATTTGGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT **GTTAGATGATTTAGTAATCTTCATAAGGGAACCGAACTAAAACA** GTTAGATGATTTAAAGATTCTAAATTGGGCTTGAGATTCATTAC GTTAGATGATTTCATATTTATTTCGAGCCAGTAATAAATCAATA GTTAGATGATTTCTTGCATGCCGAGCTCGAATTCGTCCTGTCGT GTTAGATGATTTAATGGTTTTGCTGATGCAAATCCATTTTCCCT **GTTAGATGATTTGCTTCTGGCACTCCAGCCAGCTTTACATTATC GTTAGATGATTTAAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT GTTAGATGATTTAGCTGATTACTCACATTAATTGCGTGTTATCC GTTAGATGATTTTTTCAACTACGGAACAACATTATTAACACTAT GTTAGATGATTTCTTTTACACAGATGAATATACAGTGCCATCAA GTTAGATGATTTACGGTCAATGACAAGAACCGGATATGGTTTAA GTTAGATGATTTTCCATATATTTAGTTTGACCATTAAGCATAAA GTTAGATGATTTAATCACCACCATTTGGGAATTAGACCAACCTA** GTTAGATGATTTTCATAGCTTGTAAAACGACGGCCAAAGCGCCA GTTAGATGATTTCGAGTAGAACAGTTGATTCCCAATATTTAGGC GTTAGATGATTTGTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC GTTAGATGATTTTAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGGTTGA **GTTAGATGATTTTTGAATTATTGAAAAACATAGCGATTATAACTA** GTTAGATGATTTCCAAATCATTACTTAGCCGGAACGTACCAAGC **GTTAGATGATTTTGCCTTGACAGTCTCTGAATTTACCCCTCAGA GTTAGATGATTTAAATAATTTTTAACCAATAGGAACAACAGTAC** GTTAGATGATTTTTTTAGTTCGCGAGAAAACTTTTTTTATGACC

**GTTAGATGATTTTATGTAAAGAAATACCGACCGTGTTAAAGCCA** GTTAGATGATTTATTTTGCGTTTAAAAGTTTGAGTACCGGCACC **GTTAGATGATTTTCAGAAGCCTCCAACAGGTCAGGATTTAAATA** GTTAGATGATTTGAGCCGCCCCACCACCGGAACCGCTGCGCCGA **GTTAGATGATTTGCCACCACTCTTTTCATAATCAAATAGCAAGG GTTAGATGATTTAAATCAATCGTCGCTATTAATTAAATCGCAAG** GTTAGATGATTTAACCAGAGACCCTCAGAACCGCCACGTTCCAG **GTTAGATGATTTCAATGACAGCTTGATACCGATAGTCTCCCTCA GTTAGATGATTTCTCATCTTGGAAGTTTCCATTAAACATAACCG GTTAGATGATTTCCTGATTGAAAGAAATTGCGTAGAAGAAGGAG** GTTAGATGATTTTTCGCCATGGACGACGACAGTATCGTAGCCAG **GTTAGATGATTTCATAACCCGCGTCCAATACTGCGGTATTATAG GTTAGATGATTTTAGAATCCCCTTTTTTAATGGAAACGGATTCG GTTAGATGATTTATACGTAAGAGGCAAAAGAATACACTGACCAA GTTAGATGATTTTTTAACGTTCGGGAGAAACAATAACAGTACAT GTTAGATGATTTCACGACGTGTTTCCTGTGTGAAATTTGCGCTC** 

Index sequences:

TCGGCATTCCGCCGCCTCCTCTTTTGAGGAACAAGTTTTCTTGTAGCATTGATGATATTC ATTGAGGGAATCAGTATCCTCTTTTGAGGAACAAGTTTTCTTGTGCGACAGACGTTTTCA GAAGGAAAAATAGAAATCCTCTTTTGAGGAACAAGTTTTCTTGTATTCATATTTCAACCG CTGAAACATTTTGTCAGACGTCCTCTTTTGAGGAACAAGTTTTCTTGTATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGATCCTCTTTTGAGGAACAAGTTTTCTTGTCTGTAGCGATCAAGTT TGCCTTTATTTTAGACAAAATCCTCTTTTGAGGAACAAGTTTTCTTGTGGGCGACAGGTTTACC

Additional sequences:

TTATTAATGAACAAAGAAACCACCTTTTCAGG CCAGACGACAAATTCTTACCAGTAGATAAATA AGGCGGTCTCTTTAGGAGCACTAAACATTTGA ATCACTTGAATACTTCTTTGATTAGTTGTTCC TCAGGTCATTTTTGAGAGATCTACCCTTGCTT GCCAACAGATACGTGGCACAGACATGAAAAAT GAGCAAAATTTTACTTCTGAATAATGGATGATTGTT CTAAACAGGAGGCCGAGAATCCTG ACGCTCAACGACAAAAGGTAAAGTATCCCATC CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC TGGATTATTTTGCCGTCAATAGATAATCAACTAAT GGAAATACTTTTCAGGAACGGTACGCCATTAAAGGGATTTTAGA GCGAAACAAGAGGCTTTGAGGACTAGGGAGTT ATACCCAAACACCACGGAATAAGTGACGGAAA CAACGCAAAGCAATAAAGCCTCAGGATACATT GTAAAAGACTGGTAATATCCAGAAATTCACCA ACGAACCATTTTCTACATTTTGACGCTCACGCTCAT GGCGATCGCGCATCGTAACCGTGCGAGTAACA TATAAGTATAGCCCGGAATAGGTGTATCACCG CTAAAATAAGTATTAACACCGCCTCGAACTGA ATCGGCTGACCAAGTACCGCACTCTTAGTTGC TACCTTTAAGGTCTTTACCCTGACAATCGTCA GGTATTAATCTTTCCTTATCATTCATATCGCG GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG TAGCCCTATTATTTACATTGGCAGCAATATTA TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA ATATATTCTCAGCTTGCTTTCGAGTGGGATTT

TCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT AGTGTACTATACATGGCTTTTGATCTTTCCAG CGATTTTAGGAAGAAAAATCTACGGATAAAAA TAACCTCCAATAAGAATAAACACCTATCATAT GAGGCGTTTCCCAATCCAAATAAGATAGCAGC TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC ACCGTTCTGATGAACGGTAATCGTAATATTTT TCGCAAATAAGTACGGTGTCTGGACCAGACCG TTATTCATGTCACCAATGAAACCATTATTAGC TACTCAGGAGGTTTAGATAGTTAG TCACAATCCCGAGGAAACGCAATAATGAAATA ATCAAAATTTTTGAAGATGATGAAAACAAAATTACCT AGATTAGATTTTCCAGCAGAAGATAAAAAATACCGA ACCCGTCGTTAAATTGTAAACGTTAAAACTAG AACCTACCGCGAATTATTCATTTCACATCAAG CTTAAACAACAACCATCGCCCACGCGGGTAAA CTGTAAATATATGTGAGTGAATAAAAAGGCTA AATGCCCCATAAATCCTCATTAAAAGAACCAC GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC GCAATAGCAGAGAATAACATAAAAAACAGCCAT TTTTGTTTTTTGCTTATCCGGTATTCTAAATCAGA AGCACCGTAGGGAAGGTAAATATTTTATTTG TTTTTGAAAGTATTAAGAGGCTATTATT CCGGAAACTAAAGGTGAATTATCATAAAAGAA AGAAGTGTCATTGCAACAGGAAAAAATCGTCT CCAGGCGCGAGGACAGATGAACGGGTAGAAAA GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA TAGAGCTTGACGGGGAAAAGAACG GCGCAGAGATATCAAAATTATTTGTATCAGAT

AGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA GTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT CAAGCAAGCGAGCATGTAGAAACCAGAGAATA CTTTACAGTATCTTACCGAAGCCCAGTTACCA CCTAATTTAAGCCTTAAATCAAGAATCGAGAA CAATAAATAAATGCAATGCCTGAGAAGGCCGG AGCGCCAATTTTGCAGATAGCCGAACAATTTTTAAG AAACCCTCTCACCTTGCTGAACCTAGAGGATC AATGCAGATTTTGAAAAAGCCTGTTTAGGGAATCAT CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA GGAATTACCATTGAATCCCCCTCACCATAAAT CTAATTTACCGTTTTTATTTTCATCTTGCGGG TGAACAAAGATAACCCACAAGAATAAGACTCC GCCACGCTTTGAAAGGAATTGAGGAAACAATT CATGTCAAAAATCACCATCAATATAACCCTCA GCAAATATGATTCTCCGTGGGAACCGTTGGTG CTAAAGCAAATCAATATCTGGTCACCCGAACG CTGTAATAGGTTGTACCAAAAACACAAAATATA ATCAACAGGAGAGCCAGCAGCAAAATATTTT CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT GGATTTAGTTCATCAATATAATCCAGGGTTAG CGTAACGAAAATGAATTTTCTGTAGTGAATTT AAAAAAGGCTTTTGCGGGATCGTCGGGTAGCA GGACGTTGAGAACTGGCTCATTATGCGCTAAT ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG AGAGAATCAGCTGATAAATTAATGCTTTATTT CGGAATTACGTATTAAATCCTTTGGTTGGCAA AAAACAAACTGAGAAGAGTCAATATACCTTTT TATAGAAGTTTTACGCGCCTGTTTATCAGTTCAGCT

GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG TTTCATGATGACCCCCAGCGATTAAGGCGCAG AGTTTGGACGAGATAGGGTTGAGTGTAATAAC TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG ACAGAAATCTTTGAATACCAAGTTAATTTCAT ACGTGCTTTCCTCGTTGCCACCGA GCCCAATAGACGGGAGAATTAACTTTCCAGAG GAAATGGAAAACATCGCCATTAAACAGAGGTG TAAATATTGAGGCATAGTAAGAGCACAGGTAG GCGCATTAATAAGAGCAAGAAACAATAACGGA GGGAGAGGCATTAATGAATCGGCCACCTGAAA ATTATTATTAGCGAACCTCCCGACGTAGGAA TTAAGACGATTAATTACATTTAACACAAAATC GTTGTAGCCCTGAGTAGAAGAACTACATTCTG TGCAACTAGGTCAATAACCTGTTTAGAATTAG TACATACACAGTATGTTAGCAAACTGTACAGA TTTCATTTCTGTAGCTCAACATGTTTAGAGAG GAATGGCTACCAGTAATAAAAGGGCAAACTAT ACGAACTATTAATCATTGTGAATTTCATCAAG CCCGGGTACCTGCAGGTCGACTCTCAAATATC GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG GCTCCATGACGTAACAAAGCTGCTACACCAGA ATATAATGGGGGCGCGAGCTGAAATTAACATC CTAAATCGGAACCCTAAAACCGTC GTTAAAATAACATTAAATGTGAGCATCTGCCA TCATTACCGAACAAGAAAAATAATAATTCTGT GACTTGAGGTAGCACCATTACCATATCACCGG

ACGCAAAGAAGAACTGGCATGATTTGAGTTAA ATTAAGTTTTCCACACAACATACGCCTAATGA GCGTTATACGACAATAAACAACATACAATAGA AGACAGTCTCATATGTACCCCGGTTTGTATAA ACCGCCACCCTCAGAAACAACGCC ACCAGGCGGATAAGTGGGGGTCAG GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA AAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT GAAGGATTAGGATTAGAAACAGTT AGGTTTTGGCCAGTTACAAAATAAACAGGGAA CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG CTTTCATCTCGCATTAAATTTTTGAGCAAACA GTCACACGATTAGTCTTTAATGCGGCAACAGT ACGGCTACAAGTACAACGGAGATTCGCGACCT TCTTACCAACCCAGCTACAATTTTAAAGAAGT GCGTACTATGGTTGCTAATTAACC GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT ACGAGTAGATCAGTTGAGATTTAGCGCCAAAA TTATTACGTAAAGGTGGCAACATACCGTCACC CAAAAATCATTGCTCCTTTTGATAATTGCTGA TATTTTGCACGCTAACGAGCGTCTGAACACCC TATATTTCATACAGGCAAGGCAAAGCTATAT TAAAGTACCAGTAGGGCTTAATTGCTAAATTT CGACAACTTCATCATATTCCTGATCACGTAAA CCAAAATAAGGGGGTAATAGTAAAAAAAGATT GCGTAAGAAGATAGAACCCTTCTGAACGCGCG CAAAATTAGGATAAAAATTTTTAGGATATTCA CACCACCCTCATTTTCCGTAACAC TGTAGCATAACTTTCAACAGTTTCTAATTGTA

CACCAGAGTTCGGTCATAGCCCCCTCGATAGC TATCAGGGCGAAAATCCTGTTTGACGGGCAAC TGAGTTTCAAAGGAACAACTAAAGATCTCCAA AATTACTATTTTCATAGGTCTGAGAGACGTGAATTT ATCAGAGAGTCAGAGGGTAATTGAACCAGTCA TGGACTCCGGCAAAATCCCTTATACGCCAGGG AAAAGTAATTTTAACGTCAAAAATGAAAAAACGATT GATGGCAAAAGTATTAGACTTTACAAGGTTAT

Origami for FRET experiment with polymer line and one Alexa647 fluorophore:

| RELLEVOLOGOVO BOVENDLOGINODOS VONDLOGOVOSOD<br>Istancas teactiti storcostaciaaco casocostatos  | VENELECCIONECCIU NILLESUSSUSLEUL                          | SCONDENISIOSNENNSSCCCONINISNNEN<br>TETAAASTITTSICSTGATACASSASTSTACT   | COLLODVOVOCION PLOVVIVOSCOVCOV  | TOVOLOGILLOGOG EVELVOSVILVOSVO<br>GIAACAGIGGGGGTA AARCAGIJAAIGGGG  | FORVOIDDEDROVOUDE<br>DIGGETATIOCOGANI CIGARACA   |
|--|---|---|---|--|--|
|  | 1012345282888888888888888888888888888888888               |   | 1.0012012000001000000000000000000000000   | COLTOCOLOGO COLTOCOLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLOGO COLTOCOLTOCOLTOCOLTOCOLTOCOLTOCOLTOCOL |  |
| VICTOCAN VANAVES CLOCANVEGABOOL AVALLET I COSTILI<br>MAATCAASAASSAASSAASSAASSASSAA TITETA LOSSILI  | CASCINGUITICGAS CIGANITZCITARACA                          | CONTRATACOGAINGTOTOCOTON GABOODO  | ACCOUNT BADDIES PAILANDIDIDES   | CTCAGAGCCGCCACS GAACCAPCACCAGAG  | CONCERCIPTION CONCERCIPTICA CONCERCIPACICA    |
|  | CANTATATOGETTATECOTGESCENTESTTC.                          | GTCATTGTCGSCGC/ CCGGTTCCGGTGGTG   | TTCTGETTCCCCCCCATTOTCATTATCAAAAC  | COCKARCOCTARTALOGOGOCTATOACCOAL  | ATECCENTERARACECECTACAETOTEACE   |
| I DELEVERE LITERES ENTERNAL AND  |   | TECLACTACEASECASECASEAAAATCACCA   | STARCACCATTACCAT ACCAASCCCCCAAA   |  |  |
|  | ACATOACTOCITIAN CONTRACTOCITICO                           |   | TEASTERTSACOTOATAATTEACETT  | TOATTAL TYPE CONTRACT TO CONTRACT.   | COTOAATOROTTGAATOTOROCOTTTETC  |
| COCOLOGICATESTICTICSCALCE COCCLE COCCLE  | TCATAAGGGAACCGAA TGACCAA CTTTGAAA                         | <u>CAGGACAGATGAACGEGTAGAAAATACA</u>   | TAAAGGTGGCAACATA <mark>TAAAAGAA</mark> ACGCAAAG   | ACACCACOGAATAAGI TATTIGTCACAATC  | AATAGAAAATTCATAT <mark>COTTACC</mark>  |
| LOSTIDEIDEN ANDERANDER CONVERNE CONTREES CONTREE | CONTRACTOTIONICARCOTCACCONCOCTAL                          |   | COTALLASSACTOTTALTCATCCCACTOTT  | TODOTATIOCOTTATIATIOCOTTACION  | **************************************   |
| LEALERS ACCASE AS TARATICESCITERS & CENTRES III CAACI  | VIIVELVOVELIVELESVELVESELVOVE                             |   | CATAACCCACAAGAA CASTTAPCCCCAAT  | ATAAGAGCAAGAAACS ATGAAATS CCAATAGC   | TATCTIACCGAAGCC  |
| PRIIVER ALTERNATE AND A ANTONIA  | TOTATO TTATIAA COLAGATITTTAT                              | AACCTCCTCACTCCT   | ***************************************   |  | TETRALIGUTETATTTCATTTTCATETT   |
|  |   |   |   |  |  |
| CONTRACTOR CONTRA   | VINCENTICAL CALLS AND | 20000000000000000000000000000000000000  | CAAAA7AGCAACTAATCTTGATCTAAGCCT<br>553222343 5510540 FORVOLVOLOOV  | CONTRACTOR CONCERNMENT OF CALCONTROLOGY  | ACCOUNTED CONTENTACE AT ACCOUNTER  |
| 1131121051311355054111401311344.33404445504320414414534013113  |   |   |   | 0.0000000000000000000000000000000000000  |  |
| LUBLICSEBIU VILLSULAUBUUT EBUULUUVESE<br>NITECTE ATATAATECTETAGETCAACATE   | ANTACONTATIONAL ANTACATATA                                |   |   | CALINALS FITTERS AND ANTICIDE CONSISTER  | CONCENTRAL CONCENTRAL  |
|  | ATTTESSAAATSTATSTAATSTCAAASTAA                            | CTACTOSITESCASA CACATETTSSECTTS   | ***************************************   |  | 151511V11151151404V5155411V55151   |
| TANCALS CARTANAT CATACAGE CANCERAL MANTANE CARTAN  | ACCANTANAGE CICAN ACCATANA CETANATE                       | COVIDUDD EVOLDED LVIDEVOVOLDED VOV  | ALITCATOTICS AN TAAATISAATOOTT  | CARATACCOACCOTO CATANATA ACCCOTTA  | VIVLIGES EVIVLIVI<br>RATARGRATRARCACI  |
|  | TTGCGTOGAAAZAAAGGCTZCTCCCCGCAAAA                          |   |   | TTACATATAGTTATATAACCCAACCTAAGC   | CARESTAAAAARGTAGTOOOTCAGACCTAO   |
|  | AGCIGATAARTTEATS COGRAGE COTACTA                          | TTITTGAGAGATOTACOUTTOTT   | COTOCCTATTANTIAN TITICCO  | TIGANAACATAGOGA AGOTTAGATTAAGAG  | TEAGAAGAGICAATA  |
| EDESCENTISTICS AND A CONTRACT AND A CONT   |   |   | AND INVESTIGATION PRODUCTION  |  | **************************************   |
| LISTATAP CCAAATATTTAAATTETAAACSI AATATTIP SITAAAAT   | TOUGATTANATITITI TANATOPUSTATIT                           | TTTAACCAATAGGAACAACAETAG CTITTACA   | CONTRACTANTAS CONTESCOTONES   | CTTTEAATACCAAST ACAAAATPSCCCASA  | CERATIATICATITI<br>Socievity Structure |
| LAASSESSEETAALASSESSEETAALASSESSEA<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE<br>LAASSESSEETAALASSESSEETAALASSESSE   | CATGARAGETEGETACAGERAGGECAGEGEG                           | ATTATTTTTGATES CTGTATATTCATCT   | CETTARASSISARATGIASESARTIGIT  | TTTGTGT TTTGGTGGAAATAATTTTGATA   | CTACGTTCTAACCCTTCCATTATTCACAACT  |
| ACTASSTATSSARSSAASASATSTASA<br>DSTATSSTATSSARSSARSSASATSTASA<br>DSTATSSTATSSARSSARSSARSSASATSTASASAS   | CALCACCACASTATI DECOTOAD CAACATOO                         |   | CAACAAACAAACCACI MCAAGCAPCOCAACTA   | CARCATATTECTEAL ATCAEAL GATEGEAA   | 105495142451455451445445534455   |
| AND  | TOTANACCACCOCCA TOCCARCTTCCCA                             | CAGAAGESSTECCS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLDLOS<br>DOLD<br>DOLDLOS<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD<br>DOLD | CTRATANGOTTOPOGGRAAGGACTTAATAG<br>CVVCLVLI<br>SCVCLVLI<br>SCVCLVLI<br>SCVCCCALATATCTGGTCA<br>CALCGATATCTGGTCA<br>CALCGATATCTGGTCA<br>CALCGATATCTGGTCA | CONTRACTOR OF CONTRACTOR AND CONTRACTOR  | TAAAAGGETGAAAGGTATTATGTATGAGGGG<br>SVILLNSS VSILLNSV<br>TCTTTAGGAGGAGTAA   |
|  |   |   |   | ***************************************  | ***************************************  |
| ISTATES CONSISTANT ANTICON TREES ANTICON   | CONTACT DESCRIPTION CONTRACTOR CONTRACTOR                 | VIDEDCCC DIVEDVENICOVALIDIZCOVCI<br>CATTAATGAATGESCERCETEAAA SCETAAGA   | **************************************  | LOBONDO FONONNO EDDEDONONNELNEN<br>ATTAUTUTTAATUUT ERAAUTUP TAUGUUTA   | AAACATCOCCATTAA  |
|  | **************************************                    | CTCCCCCCCCCCT \AGAAGGG70C7A70   |   |  |  |
| 2311205 CONCAS LUMUNICOLO21304 002023 CONVAS<br>231205 CONCENC LUMUNICOLO21304 002023 CONVAS<br>2312222040112222 1431204 4402224 143224  | LILLISSI SERVICE PERIVISIONILLESS                         | STATES CONTRACTOR STATES  |   | CONTRACTOR CONTRACTOR CONTRACTOR   | TESEVVES COLOCIES  |
|  | CONSTRUCTOR CONSTRUCTOR CONSTRUCTOR                       |   | CTACAACEGTTAATTTGCGTGATEGACAGA  |  |  |
| LOSVIENDEBLANDERL  | TAGAGCTTGACGGGGA AGCCGCGAACGTG                            | • 0011110490110110414011101104140<br>CEAGAAA3GAAGEGAATECGCCGCTACAEGG  | CONTRACTATEGATECH TEACGAECACETAT  | ACGESCITECTEGET GAATCAGAGEGGGA   | LELDVYDVDIDIDIVY<br>CTAAATAGGAGGCCGG<br>SVILISISSISSESSIVVILLSSSIVVVIJS  |

Polymer binding extended staple strands (Green in figure):

**CTGTCTCGTTTTTTATTCATGTCACCAATGAAACCATTATTAGC CTGTCTCGTTTTATTGAGGGAATCAGTAGCGACAGACGTTTTCA CTGTCTCGTTTTGCTCCATGACGTAACAAAGCTGCTACACCAGA CTGTCTCGTTTTACGGTCAATGACAAGAACCGGATATGGTTTAA CTGTCTCGTTTTTACATACACAGTATGTTAGCAAACTGTACAGA CTGTCTCGTTTTACGCAAAGAAGAACTGGCATGATTTGAGTTAA CTGTCTCGTTTTTCACAATCCCGAGGAAACGCAATAATGAAATA CTGTCTCGTTTTCCAAATCATTACTTAGCCGGAACGTACCAAGC CTGTCTCGTTTTAGTAATCTTCATAAGGGAACCGAACTAAAACA CTGTCTCGTTTTTTATTACGTAAAGGTGGCAACATACCGTCACC CTGTCTCGTTTTATACCCAAACACCACGGAATAAGTGACGGAAA CTGTCTCGTTTTGAAGGAAAAATAGAAAATTCATATTTCAACCG CTGTCTCGTTTTACGAGTAGATCAGTTGAGATTTAGCGCCAAAA CTGTCTCGTTTTTTTCAACTACGGAACAACATTATTAACACTAT CTGTCTCGTTTTCGATTTTAGGAAGAAAATCTACGGATAAAAA CTGTCTCGTTTTATCAGAGAGTCAGAGGGTAATTGAACCAGTCA CTGTCTCGTTTTGCCCAATAGACGGGAGAATTAACTTTCCAGAG CTGTCTCGTTTTGCAATAGCAGAGAATAACATAAAAACAGCCAT** 

Index sequences:

CTGAAACATTTTGTCAGACGATTGGCCTCAGGAGGT TGAGGCAGTTTTGCGTCAGACTGTAGCGATCAAGTT TCGGCATTCCGCCGCCAGCATTGATGATATTC TGCCTTTATTTTAGACAAAAGGGCGACAGGTTTACC Acceptor strand:

CTGTCTCGT(c6-N-Alexa647)TTTCCAGGCGCGAGGACAGATGAACGGGTAGAAAA

Additional sequences:

CACCACCCTCATTTTCCGTAACAC ACCGCCACCCTCAGAAACAACGCC TACTCAGGAGGTTTAGATAGTTAG TATAAGTATAGCCCGGAATAGGTGTATCACCG ACCAGGCGGATAAGTGGGGGTCAG GAAGGATTAGGATTAGAAACAGTT TGAGTTTCAAAGGAACAACTAAAGATCTCCAA TGTAGCATAACTTTCAACAGTTTCTAATTGTA CGTAACGAAAATGAATTTTCTGTAGTGAATTT AGTGTACTATACATGGCTTTTGATCTTTCCAG TGCCTTGACAGTCTCTGAATTTACCCCTCAGA AATGCCCCATAAATCCTCATTAAAAGAACCAC GAGAATAGGTCACCAGTACAAACTCCGCCACCCTCAGAGC TGCTAAACTCCACAGACAGCCCTCTACCGCCACCCTCAGA ACGTTAGTTCTAAAGTTTTGTCGTGATACAGG TAAGCGTCGGTAATAAGTTTTAACCCGTCGAGAGGGTTGA GGAAAGCGGTAACAGTGCCCGTATCGGGGTTTTGCTCAGT ACAAACAACTGCCTATTTCGGAACCTGAGACTCCTCAAGA AAAAAAGGCTTTTGCGGGATCGTCGGGTAGCA TCGGTTTAGGTCGCTGAGGCTTGCAAAGACTT CTTAAACAACAACCATCGCCCACGCGGGTAAA
GAGCCGCCCCACCACCGGAACCGCTGCGCCGA GCCACCACTCTTTTCATAATCAAATAGCAAGG CACCAGAGTTCGGTCATAGCCCCCTCGATAGC AAAGGCCGCTCCAAAAGGAGCCTTAGCGGAGT ATATATTCTCAGCTTGCTTTCGAGTGGGATTT CAATGACAGCTTGATACCGATAGTCTCCCTCA AACCAGAGACCCTCAGAACCGCCACGTTCCAG GTTTGCCACCTCAGAGCCGCCACCGCCAGAAT ACGGCTACAAGTACAACGGAGATTCGCGACCT TTTCATGATGACCCCCAGCGATTAAGGCGCAG ATACGTAAGAGGCAAAAGAATACACTGACCAA AATCACCACCATTTGGGAATTAGACCAACCTA CCGGAAACTAAAGGTGAATTATCATAAAAGAA AGCACCGTAGGGAAGGTAAATATTTTATTTG AAAGATTCTAAATTGGGCTTGAGATTCATTAC ACGAACTATTAATCATTGTGAATTTCATCAAG GGACGTTGAGAACTGGCTCATTATGCGCTAAT TGAACAAAGATAACCCACAAGAATAAGACTCC GCGCATTAATAAGAGCAAGAAACAATAACGGA CTTTACAGTATCTTACCGAAGCCCAGTTACCA GGAATTACCATTGAATCCCCCTCACCATAAAT CATAACCCGCGTCCAATACTGCGGTATTATAG CCAAAATAAGGGGGTAATAGTAAAAAAAGATT TCTTACCAACCCAGCTACAATTTTAAAGAAGT CCTAATTTAAGCCTTAAATCAAGAATCGAGAA ATTATTATTAGCGAACCTCCCGACGTAGGAA

TAAATATTGAGGCATAGTAAGAGCACAGGTAG ACTGGATATCGTTTACCAGACGACTTAATAAA TTTGCCAGGCGAGAGGCTTTTGCAATCCTGAA TATTTTGCACGCTAACGAGCGTCTGAACACCC AGGTTTTGGCCAGTTACAAAATAAACAGGGAA GAGGCGTTTCCCAATCCAAATAAGATAGCAGC CAAAAATCATTGCTCCTTTTGATAATTGCTGA TCAGAAGCCTCCAACAGGTCAGGATTTAAATA AAGAGGAACGAGCTTCAAAGCGAAAGTTTCAT GGTATTAATCTTTCCTTATCATTCATATCGCG CAAGCAAGCGAGCATGTAGAAACCAGAGAATA TCATTACCGAACAAGAAAAATAATAATTCTGT TACCTTTAAGGTCTTTACCCTGACAATCGTCA GAAGCAAAAAAGCGGATTGCATCAATGTTTAG TTTTAATTGCCCGAAAGACTTCAACAAGAACG ATCGGCTGACCAAGTACCGCACTCTTAGTTGC CTAATTTACCGTTTTTATTTTCATCTTGCGGG TAAGTCCTGCGCCCAATAGCAAGCAAGAACGC ATATAATGGGGGCGCGAGCTGAAATTAACATC TGCAACTAGGTCAATAACCTGTTTAGAATTAG TCCATATATTTAGTTTGACCATTAAGCATAAA AGAGGCATACAACGCCAACATGTATCTGCGAA TAAAGTACCAGTAGGGCTTAATTGCTAAATTT CCAGACGACAAATTCTTACCAGTAGATAAATA TTTCATTTCTGTAGCTCAACATGTTTAGAGAG TCGCAAATAAGTACGGTGTCTGGACCAGACCG

CGAGTAGAACAGTTGATTCCCAATATTTAGGC CATATTTATTTCGAGCCAGTAATAAATCAATA ACGCTCAACGACAAAAGGTAAAGTATCCCATC GCGTTATACGACAATAAACAACATACAATAGA CAATAAATAAATGCAATGCCTGAGAAGGCCGG CAAAATTAGGATAAAAATTTTTAGGATATTCA GCTAAATCCTTTTGCGGGAGAAGCCCGGAGAG TTTTAGTTCGCGAGAAAACTTTTTTTTATGACC AATGGTTTTGCTGATGCAAATCCATTTTCCCT AGGCGTTAGGCTTAGGTTGGGTTAAGCTTAGA TATATTTTCATACAGGCAAGGCAAAGCTATAT CAACGCAAAGCAATAAAGCCTCAGGATACATT CTGTAATAGGTTGTACCAAAAACACAAAATATA ACAAAGAAAATTTCATCTTCTGACAGAATCGC TATGTAAAGAAATACCGACCGTGTTAAAGCCA TAACCTCCAATAAGAATAAACACCTATCATAT AGACAGTCTCATATGTACCCCGGTTTGTATAA ACCGTTCTGATGAACGGTAATCGTAATATTTT GGTAGCTATTGCCTGAGAGTCTGGTTAAATCA CTGTAAATATATGTGAGTGAATAAAAAGGCTA TAGAATCCCCTTTTTTAATGGAAACGGATTCG TTAAGACGATTAATTACATTTAACACAAAATC CATGTCAAAAATCACCATCAATATAACCCTCA AGAGAATCAGCTGATAAATTAATGCTTTATTT TCAGGTCATTTTTGAGAGATCTACCCTTGCTT AAATCAATCGTCGCTATTAATTAAATCGCAAG

TTGAATTATTGAAAACATAGCGATTATAACTA AAAACAAACTGAGAAGAGTCAATATACCTTTT GCAAATATGATTCTCCGTGGGAACCGTTGGTG GTTAAAATAACATTAAATGTGAGCATCTGCCA GCTCATTTCGCGTCTGGCCTTCCTGGCCTCAG CTTTTACACAGATGAATATACAGTGCCATCAA CCTGATTGAAAGAAATTGCGTAGAAGAAGGAG GCGCAGAGATATCAAAATTATTTGTATCAGAT ACCCGTCGTTAAATTGTAAACGTTAAAACTAG CTTTCATCTCGCATTAAATTTTTGAGCAAACA AAATAATTTTTAACCAATAGGAACAACAGTAC TTTAACGTTCGGGAGAAACAATAACAGTACAT ACAGAAATCTTTGAATACCAAGTTAATTTCAT AACCTACCGCGAATTATTCATTTCACATCAAG TAGATGGGGTGCGGGCCTCTTCGCGCAAGGCG GTTTGAGGTCAGGCTGCGCAACTGTTCCCAGT GAAGATCGTGCCGGAAACCAGGCAGTGCCAAG ATTTTGCGTTTAAAAGTTTGAGTACCGGCACC CGGAATTACGTATTAAATCCTTTGGTTGGCAA GATGGCAAAAGTATTAGACTTTACAAGGTTAT GGCGATCGCGCATCGTAACCGTGCGAGTAACA TTCGCCATGGACGACGACAGTATCGTAGCCAG GCTTCTGGCACTCCAGCCAGCTTTACATTATC TTATTAATGAACAAAGAAACCACCTTTTCAGG CGACAACTTCATCATATTCCTGATCACGTAAA GGATTTAGTTCATCAATATAATCCAGGGTTAG

ATTAAGTTTTCCACACAACATACGCCTAATGA CACGACGTGTTTCCTGTGTGAAATTTGCGCTC CTTGCATGCCGAGCTCGAATTCGTCCTGTCGT AAACCCTCTCACCTTGCTGAACCTAGAGGATC ATCAACAGGAGAGCCAGCAGCAAAATATTTT CTAAAATAAGTATTAACACCGCCTCGAACTGA GCTCACAAGGGTAACGCCAGGGTTTTGGGAAG TCATAGCTTGTAAAACGACGGCCAAAGCGCCA CCCGGGTACCTGCAGGTCGACTCTCAAATATC CTAAAGCAAATCAATATCTGGTCACCCGAACG GCCACGCTTTGAAAGGAATTGAGGAAACAATT AGGCGGTCTCTTTAGGAGCACTAAACATTTGA GTGAGCTAGCCCTTCACCGCCTGGGGTTTGCC ACTGCCCGCTTTTCACCAGTGAGATGGTGGTT GCCAGCTGCGGTTTGCGTATTGGGAATCAAAA GCGTAAGAAGATAGAACCCTTCTGAACGCGCG GAATGGCTACCAGTAATAAAAGGGCAAACTAT TAGCCCTATTATTTACATTGGCAGCAATATTA AGCTGATTACTCACATTAATTGCGTGTTATCC TGGTTTTTCTTTCCAGTCGGGAAAAATCATGG GGGAGAGGCATTAATGAATCGGCCACCTGAAA GCCAACAGATACGTGGCACAGACATGAAAAAT GTCACACGATTAGTCTTTAATGCGGCAACAGT GAAATGGAAAACATCGCCATTAAACAGAGGTG CCAGCAGGCGATGGCCCACTACGTGAGGTGCCGTAAAGCA CCGAAATCAACGTCAAAGGGCGAAAAGGGAGCCCCCGATT

GAATAGCCACAAGAGTCCACTATTAAGCCGGCGAACGTGG ATCACTTGAATACTTCTTTGATTAGTTGTTCC CGGCCTTGGTCTGTCCATCACGCATTGACGAGCACGTATA CCGCCAGCTTTTATAATCAGTGAGAGAATCAGAGCGGGAG TATCAGGGCGAAAATCCTGTTTGACGGGCAAC TGGACTCCGGCAAAATCCCTTATACGCCAGGG AGTTTGGACGAGATAGGGTTGAGTGTAATAAC GTTGTAGCCCTGAGTAGAAGAACTACATTCTG GTAAAAGACTGGTAATATCCAGAAATTCACCA AGAAGTGTCATTGCAACAGGAAAAAATCGTCT CTAAATCGGAACCCTAAAACCGTC TAGAGCTTGACGGGGAAAAGAACG CGAGAAAGGAAGGGAATGCGCCGCTACAGGGC GCGTACTATGGTTGCTAATTAACC ACGTGCTTTCCTCGTTGCCACCGA CTAAACAGGAGGCCGAGAATCCTG

## 3D DNA origami

## 3D Origami annealing and assembly protocol

Monomers of the three-dimensional DNA origami cylinder were annealed following the method from Douglas et al<sup>38</sup>.. The 8064-nt scaffold (10 nM) was mixed with unpurified staple strands (100 nM) in 5 mM Tris, 1 mM EDTA, pH 8.0 with MgCl<sub>2</sub> (10 mM), and annealed (Ramp: 80 to 65 °C over 15 min. and 65 to 20 °C over 18 hours.). After annealing, monomers were purified by agarose gel electrophoresis. Trimers were assembled by combining monomers in equimolar ratio in TAE buffer (1x) with MgCl<sub>2</sub> (20 mM), and annealing from 40 to 20 °C over 12 hours. 3D DNA Origami cylinder with helical path:





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Supplementary Fig. 24. Schematic illustration of the cylindrical DNA origami structure with the

connector strands between the individual origami rings shown in yellow and the handle strands for DNA-PAINT in red. The design and sequence routing of the three cylinders is shown in the lower four panels. The details of the design and the sequences will be published separately.

## Legends for supplementary videos

Supplementary Movie 1 Origami. Animated 3D DNA-PAINT super-resolution images of a single

DNA structure (color indicates height). Localizations are shown along with a helical fit (red line).

Supplementary Movie 2 Polymer. Animated 3D DNA-PAINT super-resolution images of a single

polymer bound to a DNA structure (color indicates height). Localizations are shown along with a

helical fit (red line).

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