Supporting information

Polymer tube nanoreactors by DNA-origami templated synthesis

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General methods
Materials and instruments

All solvents and reagents were purchased from commercial sources and were used without further purification. DNA staple strands and ATRP initiator modified DNA (DNA-initiator) were either synthesized by 12-Column DNA Synthesizer from POLYGEN GmbH and purified by Agilent 1260 Infinity HPLC system with Agilent Eclipse XDB-C18 column or purchased from Sigma-Aldrich. Agarose gel electrophoresis was performed using Bio-Rad Mini-Sub Cell GT horizontal electrophoresis system. Bio-Rad MyCycler™ Thermal Cycler was used for annealing of MP13mp18
phage DNA and DNA staple strands to form DNA origami. Concentration of DNA origami was determined by Spark ® 20M with Nanoquant plate™.

**Fabrication of DNA tile with multiple DNA handles**

DNA tile with multiple DNA handles was assembled respectively by mixing M13mp18 phage DNA of 7k nt with desired staple strands and modified staple strands in 1 × TAE / Mg buffer (5 mM Tris, 1 mM EDTA, 5 mM NaCl, and 12 mM MgCl₂, pH 8.0) and annealing from 65 °C to 20 °C over 2 h, followed by purification with polyethylene glycol (PEG) precipitation method. Briefly, the DNA tile was treated with 15% PEG(8000) (w/v), 5 mM Tris, 1 mM EDTA, and 505 mM NaCl. The solution was mixed well and centrifuged at 12000 g, at room temperature (RT) for 25 min. The supernatant was removed and the pellet was dissolved in 1 × TAE / Mg buffer. The same procedure was conducted twice to remove all the remaining staple DNA sequences.

**Transformation to DNA tube**

To DNA tile (0.5 pmol) solution was added a set of folding DNA strands (250 pmol each) and the mixture was incubated at 32 degree for overnight. The obtained DNA tube was purified again with PEG precipitation method.

**Synthesis of DNA tube / initiator**

DNA tubes (0.75 pmol in 1 × TAE / Mg buffer) were incubated with DNA-initiator [2] (1 nmol in 0.2 μL aqueous solution) at room temperature for 4 h and they were used as DNA tube / initiator without any purification. 1.5 μL of 20 × TAE / Mg buffer was added to the reaction mixture to keep the constant concentration of Mg²⁺. The excess amount of DNA initiators serves as sacrificial initiator in the ATRP reaction.

**Surface initiated atom transfer radical polymerization**

A catalyst stock solution of CuBr₂ (0.45 mg, 0.002 mmol) and Tris (2-pyridylmethyl) amine (TPMA, 4.64 mg, 0.016 mmol) were prepared in 100 μL of N,N-Dimethylformamide (DMF) and MilliQ water (1 to 1 volume) mixture. The ascorbic acid stock solution, which can generate the active catalyst species, was prepared at 5 mM in 50 mM NaCl, followed by degassing with argon bubbling for 40 mins. To conduct the polymerization reaction, PEGMEMA (Mn = 300l), PEGDMA (Mn = 750), DNA tube / initiator, the catalyst stock solution (1 μL), 20 x TAE buffer (4 μL) were added with the ratio of PEGMEMA: PEGDMA: Initiator = 7200: 800: 1. The reaction solution was degassed with three freeze–pump–thaw cycles and then filled with argon. Ascorbic acid solution (36μL) was feed into the reactor by a syringe pump at the speed of 0.3 μL/min under stirring. The pump was turned off after 2 h and the reactor was incubated for another 4 h. The reaction mixture
after polymerization was purified by 15 % PEG precipitation to obtain the polymer tube.

**Atomic force Microscopy (AFM)**
Imaging was performed with a Bruker Dimension FastScan Bio AFM equipped with the ScanAsyst mode. The sample solution was deposited onto freshly cleaved mica surface, and left for 5 min at room temperature to allow adsorption of the DNA origami structures. After addition of 70 μL of 1 x TAE / Mg buffer, the sample was scanned with the scan rates between 1 and 3 Hz. Several AFM images were acquired at different areas of the mica surface to ensure the reproducibility of the results. All images were analyzed by using the NanoScope Analysis 1.50 and Gwyddion 2.38 software.

**Agarose gel electrophoresis**
5 uL of sample (1.5 nM) was mixed with 1 uL of 6 x loading buffer and run with 0.8 % agarose gel in 0.5 x TBE / Mg for 120 minutes in ice bath. After running, the gel was stained by SYBR Gold for 30 minutes and the image was taken by G: Box Chemi (Syngene).

**Transmission electron microscopy (TEM)**
5 uL of sample (1 nM) was applied on carbon coated copper grid with hydrophilic treatment. After 10 minutes incubation, the remaining solution was removed and the sample grid was stained with 2 % uranyl formate solution for 20 seconds. The stained grid was washed with filtered water for three times and dried in air. Imaging was done with JEOL 1400 instrument and obtained images were analyzed by ImageJ software.

**Dynamic and static light scattering (DLS and SLS)**
Light scattering measurements were performed with an ALV/CGS3 compact goniometer system with a He/Ne laser (632.8 nm), ALV/LSE-5004 multiple-tau full-digital correlator and ALV5000 software. For temperature controlled measurements, the light scattering instrument was equipped with a thermostat from Julabo. Measurements were performed at 20 °C at 13 angles ranging from 30° to 150°. All DNA origami solution samples were adjusted to a concentration of 3.5 nM in in TAE / Mg / K (0.3 mM Tris, 0.2 mM acetic acid, 0.06 mM EDTA, 0.6 mM MgCl2, 10 mM KCl, pH 5.3). The solutions were then filtered through Hydrophilic Durapore® filters with a pore size of 0.22 μm (Merck Millipore, Billerica, USA) and transferred into dust-free quartz light scattering cuvettes (Hellma, Müllheim, Germany), which were cleaned before in sagewith acetone in a Thurmont-apparatus. The scattering wave vector q is defined as $q = \frac{4\pi n}{\lambda} \sin \frac{\theta}{2}$ with n=1.333 being the water refractive index. The relaxation function, $C(q,t) = [G(q,t0)-1]^{1/2}$ computed from the
experimental scattering intensity autocorrelation function \( G(q,t) \) was represented either by an inverse Laplace transform (ILT) analysis using the CONTIN algorithm.

In dilute solutions, the relaxation rate \( \Gamma(q) = 1/\tau(q) \) is usually diffusive defining the diffusion coefficient \( D = \Gamma(q)/q^2 \). For species with small size \( R \), \( \Gamma(q) = 1/\tau(q) \) and \( D = D_0 \) are q-independent with \( I ~ cM \) and \( D = D_0 = k_BT/(6\pi\eta_0 R_h) \) where \( c, M, R_h, \eta_0, k_B, \) and \( T \) are the probed species concentration, its molecular weight and hydrodynamic ratio, the solvent viscosity, the Boltzmann constant and the absolute temperature, respectively. For \( qR \sim 1 \), both \( I(q) \) and \( D(q) \) depend on \( q \) defining the probing length \((2\pi/q)\). The former, known as the form factor, yields (at low \( qR_g \)) the radius of gyration \( R_g \),

\[
I(q)^{-1} = I(0)^{-1}(1 + q^2 R_g^2/3)
\]  

whereas the effective \( D \) is given by,

\[
D = D_0(1 + Aq^2)
\]

with \( A \) is a parameter characterizing the shape of the diffusing species.

**Nuclease digestion assay**

DNA tile, DNA tube, and polymer tube were labeled with 0.5 x SYBR-safe solution by during 30 min of incubation. Different amounts (0-50 mU) of nuclease were added to the labeled DNA origami structures and incubated at 37 degree for 30 min. The fluorescence intensity of SYBR-safe was checked by Spark® 20M with Nanoquant plate™ and compared to the sample, to which no nuclease was added.

**ABTS assay**

To 0.3 nM G4-DNA tile, G4-DNA tube, and G4-polymer tube in the buffer composition (97 uL, 20 mM Tris, 1 mM EDTA, 12 mM MgCl₂, pH 5.3 by addition of acetic acid) was added 1 uL of 100 nM hemin. The assay was performed by mixing the hemine added DNA origami solution with 1 uL of freshly prepared 50 mg/ml ABTS solution and 1 uL of 0.1M H₂O₂. Immediately after \( H_2O_2 \) addition, the absorbance spectrum was measured by using a Tecan Spark® 20M plate reader.

**Kinetics of polydopamine formation on G4/hemin DNA nanotile**

G4-DNA tube (3.5 nM) in TAE / Mg / K (0.3 mM Tris, 0.2 mM acetic acid, 0.06 mM EDTA, 0.6 mM MgCl₂, 10 mM KCl, pH 5.3) was mixed with hemin (70 nM) for 30 min at rt. 98 uL of the solution was added to a 384 well UV transparent plate. To G4/hemin DNA nanotile solution was added 1 uL of a freshly prepared 1M dopamine solution and 1 uL of 1M H₂O₂. Immediately after \( H_2O_2 \) addition, the absorbance spectrum was measured every 5 minutes for a duration of 12 hours using a Tecan Spark® 20M plate reader.
Supplementary figures and tables

Figure S1 DNA tile. The design of DNA tile\cite{3} and the position of DNA handles to attach ATRP initiator moieties (dark blue circle) chosen from Cadnano software\cite{4}. The details of all staple strand DNA sequences are listed in Table S2.
Figure S2 Relaxation functions $C_{vv}(q,t)$ for the translational diffusion dynamics in aqueous solution of the DNA tile (black filled squares) and DNA tube (red filled circles) at 20°C at a scattering wave vector ($q=0.009 \text{ nm}^{-1}$). Inverse Laplace transformation of experimental data yielded the distribution of one population for both the DNA tile and the DNA tube. Upper inset: The diffusion coefficient $D$ vs $q^2$, $R_h(\text{tile}) = 55 \text{ nm}$ and $R_h(\text{tube}) = 73 \text{ nm}$. Lower inset: Light scattering intensity $1/I(q)$ as a function of $q^2$ for the DNA tile (black squares) and the DNA tube (red circles). $R_g(\text{tile})=54 \text{ nm}$ $R_g(\text{tube}) = 83 \text{ nm}$. 
Figure S3 Normalized field correlation functions $C_{vw}(q,t)$ at a scattering wave vector $q=0.009$ nm$^{-1}$ (black filled squares) and $q=0.024$ nm$^{-1}$ (red filled circles) for the translational diffusion dynamics in aqueous solution of polymer coated DNA tube at 20°C. Inverse Laplace transformation of experimental data yielded to distribution of two populations for both wave vectors. Upper right inset: Double logarithmic plot of the diffusion coefficient $D$, $R_h=122$ nm. Lower right inset: $1/I(q)$ versus $q^2$ for the polymer coated DNA tube (black squares). From equation 1, $R_g$ was calculated. $R_g=108$ nm.
Figure S4 TEM image of stacking polymer tube.
Figure S5 Stability of different DNA origami structures against nuclease digestion. DNA tile, tube, and polymer tube were labeled with SYBR-safe for 30 min. SYBR safe is a cyanine-based organic dye, which shows high fluorescence signal when it is intercalated into dsDNA. Thus, the degradation of DNA origami causes SYBR safe release from DNA origami resulting in decrease of the fluorescence intensity. Different amounts of nuclease (0-50 mU) were added to the labeled DNA origami structures and incubated at 37 degrees for 30 min. The fluorescence intensity of SYBR-safe was recorded and plotted as fluorescence intensity compared to the non-nuclease treated sample (the columns with amount of Dnase “0”). Since both ends of the DNA tubes are open, nucleases could in principle access the tube from both ends, which might explain the 30 % decrease of fluorescence intensity. However, after polymer coating, about 60 % to 70 % emission was observed for the polymer tube, compared to the DNA tube, for which only 20 % to 30 % emission intensity was recorded.
Figure S6 DNAzyme-incorporated DNA tile. (a) 20 DNAzyme moieties are positioned onto the surface opposite to DNA handle-introduced surface (Figure S1). (b) DNA handles are introduced to staple DNA sequence by extending its 3’ that are exposed on to the surface (left). To introduce DNAzyme to the opposite side to DNA handle, DNA handle extended sequences (blue, left) are divided into two sequences; DNA handle-extended part (dashed blue, right) and DNAzyme incorporated part (orange, right).
Table S1 Summary of dimensions of the DNA tile, DNA tube, polymer tube, G4-incorporated DNA tube before / after ATRP (G4-tube / G4-polymer tube) from theoretical, AFM, and DLS.

| Construct       | Theoretical (nm) | AFM (nm)     | DLS, $R_h$ (nm) |
|-----------------|------------------|--------------|-----------------|
| DNA Tile        |                  |              |                 |
| L               | 100              | 99.0 ± 2.2   | 55 ± 3          |
| W               | 70               | 78.0 ± 4.0   |                 |
| H               | 2                | 3.1 ± 0.1    |                 |
| DNA Tube        |                  |              |                 |
| L               | 100              | 97.0 ± 4.9   | 83 ± 2          |
| W               | 22               | 36.0 ± 6.0   |                 |
| H               | 22               | 5.0 ± 0.7    |                 |
| Polymer Tube    | -                | 91.0 ± 6.4   | 122 ± 13        |
|                 |                  | 44.0 ± 6.0   |                 |
|                 |                  | 7.0 ± 0.5    |                 |
| G4-Tube         |                  | 93.3 ± 3.9   |                 |
| L               | 100              |              |                 |
| W               | 22               | 37.0 ± 4.0   |                 |
| H               | 22               | 7.2 ± 1.0    |                 |
| G4-Polymer Tube | -                | 95.7 ± 5.7   |                 |
|                 |                  | 55.0 ± 10    |                 |
|                 |                  | 11.1 ± 1.9   |                 |

Figure S7 ABTS activity of DNAzymes in polymer tubes before / after nuclease addition (50 mU). 80 % of the DNAzyme activity was maintained even in nuclease presence.
Table S2 Detail of staple DNA sequences. Each number corresponds to the position shown in Figure S1. The Sequences extended with sticky DNA handle sequence at 3’ are named as “3stX (X = position number)”. Folding DNA sequences to transform DN tile to DNA tube are named as “FX”. For preparing DNAzyme-introduce DNA tile, the sequences are separated into DNA handle-extended part (3stX half) and DNAzyme-extended part (g4-X half)

| No. | Sequence                                           |
|-----|----------------------------------------------------|
| 1   | CAAGCCCAATAGGAAACCACATGTACAACACAGTT               |
| 3st2| AATGCCCCGTAAACATGGCCGTATCTCCCTCATTTTTTTAGGTGAGGAG |
| 3st3| TGCCTTAGCTGCTATTTTCCGAACAGGAGTGTTTTTAGGTGAGGAG   |
| 3st4| GAGCGGCCACCAGGCAGAAACAGGCAGAGTTTTTTAGGTGAGGAG    |
| 3st5| ACCAGAGACCCCTCCAGAAACCGCCAGGGTGACTTTTTTAGGTGAGGAG |
| 3st6| TATTTTACAGGAAATTTTACATTACAGATTACATATTACACAGGAG    |
| 3st7| CATAAACCAGGGAATAGTAAGAGTTTTTTAGGTGAGGAG          |
| 3st8| ATGGAGGTAAGAGTAAATTATCATATACCCAGGTTTTTTAGGTGAGGAG |
| 3st9| AAAAGTAAATATCTTACCAGAACCCTCTCAGAGTTTTTTAGGTGAGGAG |
| 3st10| CCAATAGCGCAGATGGGAGAGTTTTTTAGGTGAGGAG          |
| 3st11| CCAATTTTACAGGAAGCGGTCTCAATCAATATTTTTTTAGGTGAGGAG |
| 3st12| TCTTACAGGACATTTACAAATAATGAATATTATTTTTAGGTGAGGAG |
| 3st13| ACGGCTGACAGATGGAATACCAAGAATTATTTTTTTAGGTGAGGAG |
| 3st14| CTAATTTATCTTTCTTTACATTACCACTCTAGTTTTTTAGGTGAGGAG |
| 3st15| GGTTATAGAAAAGGAGCGCTTATGGAAAGGAGGCTTTTTTAGGTGAGGAG |
| 3st16| GCTCATTTTACGTTAATTTTTTGAGGTTTTTTAGGTGAGGAG |
| 3st17| AATTACCTAATTTTTTTATTACTGGGCTATATTACACAGGAGTTTTTTAGGTGAGGAG |
| 3st18| TTAAGACGTGAAACATACCGAGTTAAGAATGTTTTTTATTACTGGGCTGAGGAG |
| 3st19| TAGAATGCGAAATTTTTATTACTGGGCTATATTACACAGGAGTTTTTTAGGTGAGGAG |
| 3st20| CTTTACACAGTAGTACATACAGAATATTAAAAATTTTTTTATTACTGGGCTGAGGAG |
| 3st21| TTTAAGGTTTCCGGAAGAAACACAAATATTTCTTTTCTTTTTTTATTACTGGGCTGAGGAG |
| 3st22| CGACAACTAAGTATGACTTTTACAAATACGCTTTTTTATTACTGGGCTGAGGAG |
| 3st23| GGATTAGCGTAATTTAATTTCACTGGGCTATTACATTTCTTTTATTACTGGGCTGAGGAG |
| 3st24| ACGAACAAATACCCCGAGATTTTTTTATTACTGGGCTATTACATTTCTTTTATTACTGGGCTGAGGAG |
| 25  | GAACGGTGGGCAAAAGGAAAAAGGAACAAACTAT               |
| 3st26| TAGCCCTACGCGAAGATATAAAGGAGTTTTTTATTACTGGGCTGAGGAG |
|   |     |
|---|-----|
| 27 | CGGCCTTGCTGGTAATATCCAGAACGAACTGA |
| 28 | CTCAGAGCCACCACCCTCATTTCCTATTATT |
| 3st29 | CTGAAACAGGTAAATAGTTTAAACCCCTCAGATTTTTTTAGTAGGTGTAGAG |
| 3st30 | AGTGTACTTGAAGTTAAGAGGCCGCCACCTTTTTTTATGAGGTGTAGAG |
| 3st31 | GCCACCAGCTCTTTTCTATAATACACCGTACCTTTTTTTATGAGGTGTAGAG |
| 3st32 | GTTTGCACCTCAGAGCCAGCCACCATAGGTGTTTTTTAGTAGGTGTAGAG |
| 3st33 | GACTTGAGAGACAAAAAGGGGCCAAGTTACCTTTTTTAGTAGGTGTAGAG |
| 3st34 | AGCGCCACCATTTGGGAATTATATTTAGCTTTTTTAGTAGGTGTAGAG |
| 3st35 | GAAGGAAAAATAGAGCAAGAAGAAACACGCCATTTTTTTAGTAGGTGTAGAG |
| 3st36 | GCCCAATACCAGGAAACGCCAATAGGTTTACCTTTTTTAGTAGGTGTAGAG |
| 3st37 | ATTTTTAAACCCAGCTCTAATTTCTAAAGACGGTTTTTTTAGTAGGTGTAGAG |
| 3st38 | TTATTTGCTCCCAATCCAAATAAGTGAGTTAATTTTTTAGTAGGTGTAGAG |
| 3st39 | GCTTTACAGCTTTGCTAATTTTTAGTAGGTGTAGAG |
| 3st40 | GAAGGAAAATAAGAGCAAGAAACAACAGCTTTTTTTAGTAGGTGTAGAG |
| 3st41 | GCCCAATACCGAGGAAACCGCAATAGGTTTACCTTTTTTAGTAGGTGTAGAG |
| 3st42 | ATTATTTAACCCAGCTACAATTTTCAAGAACGTTTTTTTAGTAGGTGTAGAG |
| 3st43 | TATTTTGCTCCCAATCCAAATAAGTGAGTTAATTTTTTAGTAGGTGTAGAG |
| 3st44 | AGCGCCAACCATTTGGGAATTATATTTAGCTTTTTTAGTAGGTGTAGAG |
| 3st45 | CCTGATTGAAAGAAATTTGGCTAGACCCCAACCAGTTTTTTTAGTAGGTGTAGAG |
| 3st46 | ACAGAAATCTTTGAAATACCAAGTTTCACTTTTTTTAGTAGGTGTAGAG |
| 3st47 | TTATTTATGCGCTAAATGATTAGTTAATTTTTTAGTAGGTGTAGAG |
| 3st48 | AGATTAGATTTAAAGGTTTGAGTACAGTAAATTTTTTAGTAGGTGTAGAG |
| 3st49 | GAATGGCTAGTATTAACACCGCCTCAAATTTTTTAGTAGGTGTAGAG |
| 3st50 | GCCCAAGCCCATTGCAACAGAAATAATTTTT |
| 51 | CCGCCCAGCCATTTGGCAACAGAAATAATTTTT |
| 52 | CCCTCAGAAAGCGCCACCTCAGAAGAGACT |
| 3st53 | CCTCAAGAATACATGGCTTTTGTAGAACCACCTTTTTTAGTAGGTGTAGAG |
| 3st54 | TAACGATGGGACAGTTGGAATTTTAGACCGCTTTTTTTAGTAGGTGTAGAG |
| 3st55 | CACCCAGGTTTGCTATAGGCTGGCCCTCAAATTTTTTAGTAGGTGTAGAG |
| 3st56 | TGCGCATCCGCCAGCATTTAGGTGCAGTTTCTAGTTTTTTAGTAGGTGTAGAG |
| 3st57 | ATCAACCAATAGAAATTTTGGAATTTTAGCTTTTTTAGTAGGTGTAGAG |
| 3st58 | TGACAAACCAAGGCTGCTGGAGATTGATTTTTTAGTAGGTGTAGAG |
| 3st59 | ATACCAAGATAAACCCACAAAGAAATAACAGTTTTTTTAGTAGGTGTAGAG |
| 3st60 | ATCAGAGAAAGAATGCTGGCTATTAGTTTTTTTAGTAGGTGTAGAG |
| 3st61 | TTTTGGTTTAAGCCTTAATCAAGAATCGGAAATTATTTGATAGGTGTTGAGAG |
| 3st62 | AGGTTTGGACGTCAAAATGAAAGCGCTTAATTTTTTTAGTAGGTGTTGAGAG |
| 3st63 | CAAGCAAGACGCGCCTGGTTTATCAAGAATCGGTTTTTTTTAGTAGGTGTTGAGAG |
| 3st64 | AATGCAGACCGTTTTTATTTTCATCTTGCGGGTTTTTTTTAGTAGGTGTTGAGAG |
| 3st65 | CATATTTAGAAATACCGACCGTGTTACCTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st66 | AATGGTTTCAAACGCCAAATGATGTCAGCTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st67 | TAACCTCCATATGTGATAGCTGAAATAAACAATTTTTTTTTAGTAGGTGTTGAGAG |
| 3st68 | AAATCAATGGCTTAGGTTGGGTTACTAAATTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st69 | GCAGCAGAGTATGAAAAATTATGGCACATTATTCTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st70 | AACCTACGCCGAATTATTTCACTTTTCAGTACATTATTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st71 | ATTTTTGCGCTTTTAAAGAGCAGCATAGCAACAGTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st72 | CTTAAATAGAGAAAAAACGCCCAGGTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st73 | GCCACGCTATACGGACAGAACAGCTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st74 | GCCGTAAGAGAGGAGGGAGGAGCTGATTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st75 | GGAAATACCTACATTTTTGACGCTACCTGAAA |
| 3st76 | TATCACGGTACTCAGGAGGTTTGGGGGTTT |
| 3st77 | TGCTCAGTCAGTCTCTGAAATTACAGGAGGTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st78 | GAAAGGGGCAACAGGCGGATAGTAAAGTGGTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st79 | TGAGGCAGGCGTGACCTGAGATAGGCAAGGTGTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st80 | TGCCTTTAGTCAGACGATTGGCTGACGAGTAAATTAGGTGTTGAGAG |
| 3st81 | CCGAAACACACCACGGAATAAGTAAGACTCCTTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st82 | ACGCAAGGGTCACCAAATGAACCAACACTCAAGTTTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st83 | TTATACAGGTGCAAGGGTAAATTGAATGACGCTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st84 | TGAAACAACAGTATGTTGACCAAAACTAAAGAATTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st85 | CTTTACAGGTTAGGCAAGCCGACCTCCGAGTGAGAGATTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st86 | GAGGCGTTAGAGAAATAACATAAAAGAACACCTTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st87 | TCATTACCCGACAAATACACATATTTTAGGCTTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st88 | CCAGACGAGCGCCCAATAGCAAGCAAGACGCTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st89 | AGAGGCATAATTCTTCTCAGCTATAACTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st90 | TTTTAGTTTTTCAGCGCAATATAAATTCTGTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st91 | TATGTAACCTTTTTTTTAATGGAAAAATTACCTTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st92 | TTGAATTATGCTGATGCAAATCCACAAATTTTTTTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st93 | GAGCAAAAACTTCTGAAATATGGAAGAGGAGATTTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st94 | TGGATTATGAAGATGGAACAAATATTTTTTTTTTAGTAGGTGTTGAGAG |
| 3st95 | CGGAATTATTGAAAGGAATTGAGGAAAAATTTTTTTTGATTAGGTGTTAGAG |
| 3st96 | ATCAACAGTACATATTTCTCTGATTGATTTGTTTTTTTTAGTGTTAGTGTTAGAG |
| 3st97 | CTAAAGCAAGATAGAACCCTCTTCTGAATCTTTTTTTTAGTGTTAGTGTTAGAG |
| 3st98 | GCGAACAGTCACCTTTGCTGAACCTGTTTGGCAATTTTTTTAGTAGGTGTTAGAG |
| 99 | GAAATGGGATTATTACATTTGCGAGACATCTCT |
| 100 | TTTTATAAGTGATACCCGGCGCTGAG |
| 101 | AGGTTGGATTATTTAATATCTCCTCAATAGATTATTTT |
| 102 | ACAAACAAATTTTATCAATGAGGACAGATCGATAGC |
| 103 | AGCACCCTTTTTAAAAGGTGGCAGCAGATAGTAGAAAA |
| 104 | TACATAACATTTTGACCGGAAATATACACAGGGAA |
| 105 | GCGCATATTATTGTTATACGATTTCTAAATCAGA |
| 106 | TATAGAAGTTTTTGCACAAAAAGGTAAAGTAGAGAATA |
| 107 | TAAAGTACTTTTCCCGGAGAAGAAATTATTTTATGCAAG |
| 108 | ACAAAGAATTTTATAATTACATTTAACAATCAAG |
| 109 | AAAACAAATTTTTCATCATATAATATCTCTATCAGAT |
| 110 | GATGGCAATTATTTATCAATATGTCGTCAGAATAATC |
| 111 | AAAACCTCTTTTACCAGTATAAAAGGGATTCAGATAGCAGTTTT |
| 3st112 | CCGAAATCGGAAATTCTCAGTTGGAACCGGAATTTTTTTTGAGTGGTGTTAGAG |
| 3st113 | CCAGCAGGGGAAATACCCCTTTTATATAGGCCGGCCTTTTTTTAGTAGGGTTAGAG |
| 3st114 | GCATAAAAATTTCCACACAAACACAGAAGGCGCAATTTTTTTAGTAGGGTTAGAG |
| 3st115 | GCTCAACATGTAAGCCTGGGTGTTGCTTCTTTTATTAGTGGTGTTAGAG |
| 3st116 | TTTGCGCACTTTAACTCAGGCAGAAGTACATTTTTTTTTTTAGTAGGGTTAGAG |
| 3st117 | GCTTCTGTGAGGCGGCAACTGTTATTATCCTTTTTTTTAGTAGGGTTAGAG |
| 3st118 | GTAAAAATTTTAAACCAATAGGAACCAGCCACCTTTTTTTAGTAGGGTTAGAG |
| 3st119 | AGACAGTCATTTAAAAAGGTTGAGAAGCTATATTTTTTTTTTAGTAGGGTTAGAG |
| 3st120 | AGTAAAAGAAAATACACCAGTATAATATATTTTTTTTTTAGTAGGGTTAGAG |
| 3st121 | TTTCAATTTGCGTCAATAACCTGTTATATCGCGTTTTTTTTAGTAGGGTTAGAG |
| 3st122 | TCGCAAAATGGGCAGCGAGCAGTGAATAATGTTGTTTTTTTTTAGTAGGGTTAGAG |
| 3st123 | TTTAATTTCGCGCAGAGCTTAAAAACATATTATTTTTTTTAGTAGGGTTAGAG |
| 3st124 | AAGAGGACGAGCTTCAAGAGGCAAGATACATTTTTTTTTAGTAGGGTTAGAG |
| 3st125 | GAAATACACTCTTTTACCAGGGCAAGCAAAAGGTTATTTTTTTTAGTAGGGTTAGAG |
| 3st126 | GAATAAGAACGCAAGAAGCTGCTCTAAAGACATTATTTTTTTTAGTAGGGTTAGAG |
| 3st127 | CCAGGATCCTTTGCGAGGAAATAGGTTTTTTTTTTTAGTAGGGTTAGAG |
| 3st128 | CTGACTTCTGAGGCAAAGAATACAGTGGAATTTTTTTTTAGTAGGGTTAGAG |
| 3st163 | GTTTGAGGGAAAGGGGATGTGCTAGAGGATCTTTTTTAGTAGGTTGAGG |
| 3st164 | CTTTCACTCCCAAAAAACAGGAGACCCGAGAGTTTTTTTAGTGAGGGTGTAGG |
| 3st165 | AGAAAAAGCACATTAAATGAGCAGTCTGAGGAGTTTTTTTAGTGAGGGTGTAGG |
| 3st166 | GTTAGCTAGGATAAATTTTTGATTTAATCTTTTTTTAGTTAGGTGTTAGG |
| 3st167 | CAACGCCAATTTTTGAGAGATCTTCTGATAATTTTTTTAGTAGGTGTAGG |
| 3st168 | CAATAAAATAGTTGATTTCCAATTTAGAGAGTTTTTTTAGTAGGTGTAGG |
| 3st169 | TCCATATACATAACGAAAGGCAACTTTATTATTTTTTTTAGTAGGTGTAGG |
| 3st170 | TACCTTTTAAGGTCTTTACCCTGACAAAGGAAATTTTTTTAGTAGGTGTAGG |
| 3st171 | CAAAAATCATTTGCTCTTTTTGATAAGTTTTTCTTTTTTTAGTAGGTGTAGG |
| 3st172 | TTGGCCAGACTCAGTGTAGATTTGTTGTTAATTCTTTTTTAGTAGGTGTAGG |
| 3st173 | AAGAGTTCACTGGGGGTAAATGCTCAAACATTTTTTTATTAGTTAGGTGTAGG |
| 3st174 | TTTCAACTATAGCGCTCGACTCTGATACCTTTTTTTAGTAGGTGTAGG |
| 3st175 | CCAGCGCTTTAATCTTTGCTATCAGGTTACAGGATTTTTTTTAGTAGGTGTAGG |
| 3st176 | CGGCTATGCAAAGTTTTTTTACCTTTATTTTTTTTATTAGTTAGGTGTAGG |
| 3st177 | TTTTCTGAAAAAGGCTGAAATCTCTACAGGTTTTTTTTAGTAGGTGTAGG |
| 3st178 | ATATATTCTTTTTTCAGCTGAAAAATGGATTTTTTTTAGTAGGTGTAGG |
| 3st179 | AATAAATAGGTCAGTGGGGAGGTGTATGTTATTTTTTTTAGTAGGTGTAGG |
| 180 | CGTAACGATCTAAGGTTTTGTCGTAAGG |
| 181 | ACCCAAAATCAAGGTTTTTGGGTGTAAGG |
| 3st182 | TGGACCTCTTTTCACCGTGAACCTTGCTGTTTTTTTTTAGTAGGTGTAGG |
| 3st183 | TGGTTTATACGTCACGTTGAGAGTCTCTCCTTTTTTTTAGTAGGTGTAGG |
| 3st184 | GGCCAGCTGCGCTGAGGTGCTTAGCTGCAAGGTTTTTTTTAGTAGGTGTAGG |
| 3st185 | TCTTGCGATAGCAATTTGAATGCGCGCTGCGAGTTTTTTTTAGTAGGTGTAGG |
| 3st186 | ATTAAGTTTGTAGCAGAACCTGCGAGTAAACATCTTTTTTTAGTAGGTGTAGG |
| 3st187 | TAGATGGGGGTAAACGCAAGGCTGTGCACTTTTTTTTAGTAGGTGTAGG |
| 3st188 | ACCCGGTGCTGCTATAGTGACCCTCCTGTTTTTTTTAGTAGGTGTAGG |
| 3st189 | CATGTCAAGATTCTCCGTTGAAAGCAGTTGTTTTTTTTAGTAGGTGTAGG |
| 3st190 | TCAGGTTCACTTTTCGCGGAAGGACAATGAGGTTTTTTTTAGTAGGTGTAGG |
| 3st191 | CTGTAAATATGCTGAGGCTGCTGCTGCTGCTGCTGGAAACTGTTTTTTTTAGTAGGTGTAGG |
| 3st192 | CAAAATTAAAGTACGTTGCTGAGGAAGGCTGATTCTTTTTTTTAGTAGGTGTAGG |
| 3st193 | TGGAACTAAAGCATCCACTTTGCTGAGGCTAGCTTTTTTTTAGTAGGTGTAGG |
| 3st194 | TTTTTTGCGCAGAAAACACGAAATGAAAGTTTTTTTAGTAGGTGTAGG |
| 3st195 | AAAAAAGTTGAGGTTACTAGGCTTATTTTTTATTAGTAGGTGTAGG |
| 3st196 | ACTGGATAACCGAAACACATTTATGACTTTTTTTTAGTAGGTGTAGG |
| 3st197 | ACGAACTAGCGTCAATAACTGCGGAATGGTTTTTTTTTTAAGTTAGGGGTAGAG |
| 3st198 | CGATTTTAGAGGAGGATGGAAACGGACCCGCTGGAATGGAGGGTGGAGAG |
| 3st199 | CTTTGAAAGAAGACTGCTATTATTTAAATAATAATTTTTTATAGGTTGAGAG |
| 3st200 | GCTGCACTAGAGGCTTGGAGAATGAGGGTTTTTTTTTTGTTAGGGGTAGAG |
| 3st201 | ACGGCTACTATCTATGCGCGGAAACGTGGAACCACATTTTTTTATAGGGGTAGAG |
| 3st202 | AAAGGCCAAGGAAAGGAACCTAAGCTTTTCCAGTTTTTTATAGGTTGAGAG |
| 3st203 | GAGAATAGCTTTTTGGGGGATCGCGGTCAGCATTTTTTTATAGGGGTAGAG |

| 204 | ACGTTAGTAAATGAAATTTCTGTAAGCGGAG |
| 205 | TTTTCGATGCCCACCTACGTAAACCGTC |
| 206 | TATCAGGTTTTTGCTGGATTGGGAAACGGCG |
| 207 | GGGAGAGGTTTTTGTAAAGCTAGGAGGCCAATTCCAG |
| 208 | CAACGACGTTTTTGTAAATGGGATAGGGTAATAACGGG |
| 209 | GATTGACCTTTTTAGTAAAGCTGGTTGAAACAGCAAAAC |
| 210 | AGAGAATCTTTTTGTCTTACAAAAAACAAGCATAAA |
| 211 | GCTAAATCTTTTCTGTAGCTACATGTATTGCTGA |
| 212 | ATATAATTTTTCTATGGAATCCCCCCTCCCCTAAAAGTCA |
| 213 | TAAATATTTTTGGTAAAGAAAAATCTACGACCAGTCA |
| 214 | GACGTTTTTTTTTTTATAAGGGAAAGGCGGCGAG |
| 215 | ACGTCAATTTTTGAGCAGCTCGGAACGAACCCTCA |
| 216 | CACGCCAAGTTTTCTTTTCAAGCTTTTTGTTTGCCATTTTTT |
| 217 | AACATCACTTGCGTCTAGTAAAGGAGT |
| 218 | TGTAACATTTCTGTGATAGTAAT |
| 219 | AGTCTGTCCATCGGAAATTTAAGCCT |
| 220 | ATATAGTGGATGACACCGGTAAAGG |
| 221 | AGCCGAAATCTGAGATAAGGTGTGTTTTT |
| 222 | TAAAGGGGTAAATGAGCAAGGACG |
| 223 | AGAGCCGGAGCTAACCAGGAGGCCG |
| 224 | TATAACGTGGTTTTCTGGTTGAATC |
| 225 | GACTATGTTGGTTTCGACGAGCAG |
| 226 | GCGCTAATGCGCGCTCACGGCG |
| F1 | ATATAATAATACGTAGCCGGAATAGGAGGACCATGTCAGAAGCTTT |
| F25 | ATATAATAATACGTAGCCGGAATAGGAGGACCATGTCAGAAGCTTT |
| F27 | CAAGGCCCAGTGGTAATACCTCAGAAGCGAAGT |
| F28 | CGGCCGACCACCCTGATTTTTCTATTAT
| F51 | CTCAGAGCCATTGCAACAGGAAAAATATTTTT |
| F52 | GGAATACACCGCCACCCTCAGAAGTQAGACT |
| F75 | CTCCTAGACTACATTTTGACGTCACCTGAAA |
| F76 | GAAATGGATACCGGGTATGCTAGCAGGTTT |
| F99 | TATCACCGTTATTTACATTGGCAGATTTCTG |
| F132 | GAACGTGGGTCACCAGTACAAAACCTTAATTGTA |
| F133 | TGTAAGCATTAGAGGCCTCGACGGGAATCTCAAA |
| F156 | CCCCGATTTCCACAGCAGCCCTACATCTTCGAA |
| F157 | CGTAACGACTAAATCGGACCCCTAGTTGTTCC |
| F180 | GAAAGCATCTAAAGTTTTGTGGAATTGCAAGT |
| F181 | ACCTGGCTGCAGCATGTTTGGGTAGGGCGGGTTGG |
| g4-6half | TTATTCTACGAAGAGGGTTTGGGTCAGGTTGG |
| 3st6half | TAAATATTCATTCAGTTTTTTTAGTGAGGTGAG |
| g4-13half | ATCGGCTGAGCATGTTTGGGTCAGGTTGG |
| 3st13half | TAGAAACCTACATCATTTTTTTAGTGAGGTGAG |
| g4-18half | TTAAGACGTTGAAAATTTTTTTTAGTGAGGTGAG |
| 3st18half | ATAGCGATAACAGTACTTTTTTTAGTGAGGTGAG |
| g4-36half | GCCCAATACCGAGGAACTTTTTTTAGTGAGGTGAG |
| 3st36half | ACGCAATACGGTACCTTTTTTAGTGAGGTGAG |
| g4-37half | GATATTTAACCCAGCTTTTTTTAGTGAGGTGAG |
| 3st37half | ACAAATTTCAGAGAGGTTTTTTTAGTGAGGTGAG |
| g4-63half | CAAGCAAGACCGCGCTTTTTTTAGTGAGGTGAG |
| 3st63half | GTTTATCAGAATAAGGTTTTTTTAGTGAGGTGAG |
| g4-67half | TAACTCCCATATGTATTGGGTCAGGCGGGTTGG |
| 3st67half | GTGAAATAAAGGAAACTTTTTTTAGTGAGGTGAG |
| g4-84half | TGAACCAAAAAGGTATTGGGTCAGGCGGGTTGG |
| 3st84half | TACAAACTAAAGGAACTTTTTTTAGTGAGGTGAG |
| g4-85half | CTTTGAGTTCGCAAATTTTTTATTGGTGGGTCAGGCGGGTTGG |
| 3st85half | CCTCCCGACGTAGGAAATTTTTTATTGGTGGGTCAGGCGGGTTGG |
| g4-90half | TTTTAGTTTTTGAGCTTTTTTTATTGGTGGGTCAGGCGGGTTGG |
| 3st90half | CAGTAAATTCTCATTTTTTATTGGTGGGTCAGGCGGGTTGG |
| g4-94half | TGGATTATGAAAGTGAATTTTTTTATTGGTGGGTCAGGCGGGTTGG |
| 3st94half | TGAACCAAAAATTTTTATTGTTTTTATTGGTGGGTCAGGCGGGTTGG |
| g4-121half | TTTCATTGGTCAATAAATTTTTTTATTGGTGGGTCAGGCGGGTTGG |
| 3st121half | ACCTTTTATATGCCTTTTTTAGTAGGTGGTAGAG |
| g4-141half | GCAAATATCGCTGTGTTTTTGTAGTAGGTGGAG |
| 3st141half | GCCCTCTGCTGCCTCATTTTATGAGGTGGTAGAG |
| g4-142half | ACCGTCTTAATGCAA TTTTGGTAGGGCCGGTGGG |
| 3st142half | TGCTTQAGAGGTGCA TTTTTTAGTAGGTGGTAGAG |
| g4-168half | CAATAATACAGTGT AGTTTTGATTGAGGTGTTAGAG |
| 3st168half | TTCCCAATTTTAGAGAG TTTTTTTAGTAGGTGGTAGAG |
| g4-172half | TTTGCCAGATCGTTG TTTTGGTAGGGCAGGGTGGG |
| 3st172half | AGATTAGGTTTAAA TTTTTTAGTAGGTGGTAGAG |
| g4-189half | CATGTCAGAgATCTCC TTTTGGTAGGGCCGGTGGG |
| 3st189half | GGGGAAACCTGTTGTTG TTTTTTTAGTAGGTGGTAGAG |
| g4-190half | TCAAGTCACTTTTGGCG TTTTGGTAGGGCCGGTGGG |
| 3st190half | GGGAGGCAAGCAGAT TAGTTTTAGTAGGTGGTAGAG |
| g4-195half | ACAAAGTGGATGCTT TTTTGGTAGGGCCGGTGGG |
| 3st195half | AGAGGTATTTAAATA TTTTTTTAGTAGGTGGTAGAG |
| g4-199half | CTTGAAAAGAACCTGG TTTTGGTAGGGCCGGTGGG |
| 3st199half | CTCTTTATTAAATA TTTTTTTAGTAGGTGGTAGAG |

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