Electronic Supplementary Material (ESI) for RSC Advances.

Supporting Information：Structure-Flexible DNA Origami Translocation through a Solid-State Nanopore

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Section S1. Materials and Apparatus

M13mp18 DNA was purchased from NEB (Beijing). All short DNA staple strands were ordered from Sangon Biotech (Shanghai) Co., Ltd.. Streptavtdin was from NEB (Beijing). The nanopore was fabricated on silicon nitride (SiN) wafers (NJRI-001, Nanjing Rhode Nanotech Co. Ltd., China). Transmission electron microscope (FEI Tecnai F30, Nethelands, Philips-FEI) was used to fabricate nanopores on 30 nm thick SiN membrane. The nanopore detection device was an Axopatch 700B .

Section S2. Nanopores Experiments Preparations

S2.1. Silicon Nitride Nanopores Fabrication and Measurement.

To produce a suitable nanopore, a focused electron beam of 300 kV, 70 μA from the TEM was used to form a roughly hourglass-shaped nanopore in the center of the SiN free-standing membrane.The expected nanopore diameter is 20 nm. In fact, the nanopore size ranges from 18 nm to 23 nm.

S2.2. Preparation before the nanopore detection

Before detection, the nanopore chips were firstly soaked in piranha solution (98% H2SO4: 30% H2O2 = 3:1) for 30 minutes. Then, the wafers were rinsed using ultrapure water and preserved in 50% ethanol solution. After assembling the nanopore electric conductivity measurement equipment, the tubings for loading and flowing of the samples were washed with ethanol and then with ultrapure water. To perform the nanopore experiments, the DNA origami samples were diluted into a final buffer solution containing 0.5 ×TBE, 11 mM Mg^{2+} and 1 M KCl. The sample solution was loaded and analyzed using the prepared nanopore chamber.

Samples were added to the cis side, and a positive biased voltage was applied. Under the applied biased voltages, the target origami were driven through the nanopore by electrophoretic force, which resulted in different translocation events. All of the nanopore data were recorded and extracted using Clampfit.

Section S3. Data recording and translocation data analysis

In the experiment, a fixed voltage in the range of 300-600 mV across the membrane was applied via Ag/AgCl electrodes through Teflon chambers. To construct a complete electric current circuit, a positive voltage was applied on the trans side of nanopores and the grounded voltage was applied on the cis side. In the electrical recording step, the experiment was performed in 0.5×TBE buffer pH 7.5, containing 1 M KCl and 11 mM $MgCl_2$, at room temperature by applying a 100 kHz sampling rate and a 10 kHz low-pass Bessel filter. The electrical signals were amplified using an Axopatch 700B patch clamp amplifier (Axon Instruments) and digitized with a Digidata 1550 A/D converter (Axon Instruments). Data were recorded using the Clampex 10.4 software (Molecular Devices) and subsequent analysis was carried out using the Clampfit software (Molecular Devices).

In the experiment, the recorded data was further analyzed by Opennanopore software. The values of current blockage and dwell time from the translocation events were collected to yield statistic results using Matlab.

Section S4. Designs of the DNA origami

In this experiment, three origami were designed by Cadnano. The nanostructures rely on complementary base-pairing of M13 scaffold (7249nt) and different ssDNA staples for assembly. In this design, origin origami was named as origami-1. The entire structure is rigid at both ends and soft in the middle. Deformed structures, origami-2 and origami-3 were obtained by adding several ssDNA oligos. The detailed design of DNA origami are displayed in Fig. S1.

Figure S1. The details of the origami designed by Cadnano. (a) The cross section of origami-1 is on the top. It is easy to see that this structure has 24 double helixes, which

are arranged into a cylindrical. The complementary details between m13mp18 and 145 staples is on the below. (b) Six single-strands newly added are complementary to the middle part of the origami and pull the two ends together to form the origami-3. (c) Two single-strands newly added are complementary to a pair of connectors and form the origami-2. The length of the strands causing the deformations are all 42nt.

Section S5. Preparations of DNA origami

The DNA origami were assembled by hybridization of M13mp18 scaffold and hundreds of staple DNA strands with the concentration ratio of 1:10 (final concentration 20 nM), in 1×TAE, 11 mM Mg^{2+} buffer. The annealing program was carried out from 80℃ to 65℃ at a rate of -1℃/min and then from 65℃ to 25℃ at a rate of -1℃/20 min. After annealing, the origami products were purified using an 1% agarose gel (running buffer: 0.5×TBE, 11 mM Mg^{2+}. 1.5 hour, 70 V, stained with EB and detected under UV) .

The purification process involved extraction of the well-formed DNA origami structure from the gel: 1) the target gel bands were excised from the gel, cut into pieces and frozen under -20℃ for 5 minutes, 2) then the gel blocks were thawed and centrifuged for 4 minutes at 12000 rpm using Freeze Squeeze filters (Bio-Rad). The purified products were collected and the UV absorption at 260 nm was measured to determine the DNA concentration (using the origami extinction coefficient: 1.091×108 M^{-1} cm^{-1}) .

Section S6. Analysis of translocation events

According to the number of events captured in the same time, it was demonstrated that the frequency of events increases, as the voltage increases (Fig. S2).

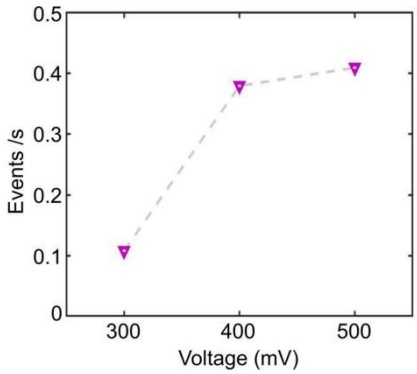

Figure S2. Line diagram of event frequency versus voltage.

Fig. S3 showed representative scatter plots for origami-1 translocations in 1 M KCl buffer through a 20 nm nanopore, recorded at 300, 400 and 500 mV applied across the membrane. For origami-1, the mean blockage currents were about 1431 pA, 1565 pA, 1697 pA, the mean dwell time were about 0.64ms, 0.47ms, 0.46ms for applied biases of 300 mV, 400 mV, and 500 mV, respectively (Fig. S3c). Here, the results indicated that with the increasing applied voltages, the value of the current blockage increased accordingly, but the duration time of translocation events decreased.

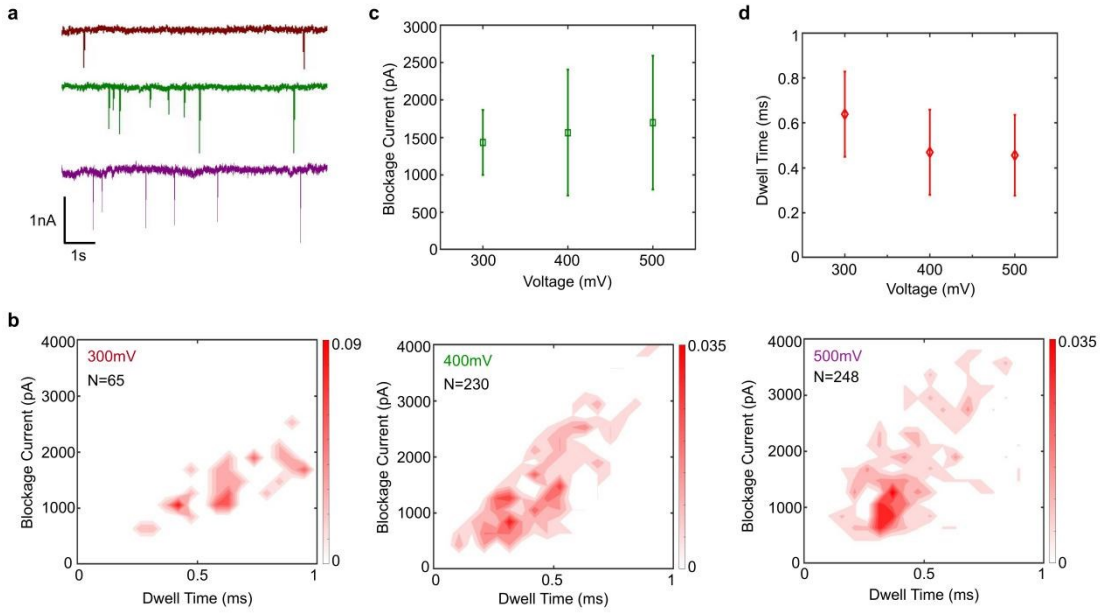

Figure S3. Scatter plots of origami-1 with applied voltage of 300, 400 and 500mV individually. (a) Three current traces in the same time with three applied voltages. (b) Scatter plot of maximum current blockage versus dwell time, histograms of the maximum blockage and dwell time distribution. (c) Mean maximum blockage of DNA

origami as a function of applied voltage. (d) Mean dwell time of DNA origami as a function of applied voltage. All experiments are performed in 1M KCl, pH 8.0.

For the three origami, each origami creates a unique current trace (characteristic signal) as it passes through the nanopore. Fig. S4 showed the characteristic signals of origami-1. It can be seen that a single signal starts from an instantaneous current drop (called the primary-level current) from the standard current level, then the current will rise to a certain level (secondary-level current) for a period of time, and then fall again, and finally rise to the standard current level. We speculate that the primary-level current is generated by the nano-cylinders of origami-1 through nanopore, and the secondary-level current is generated by the single-strands in the middle of origami-1.

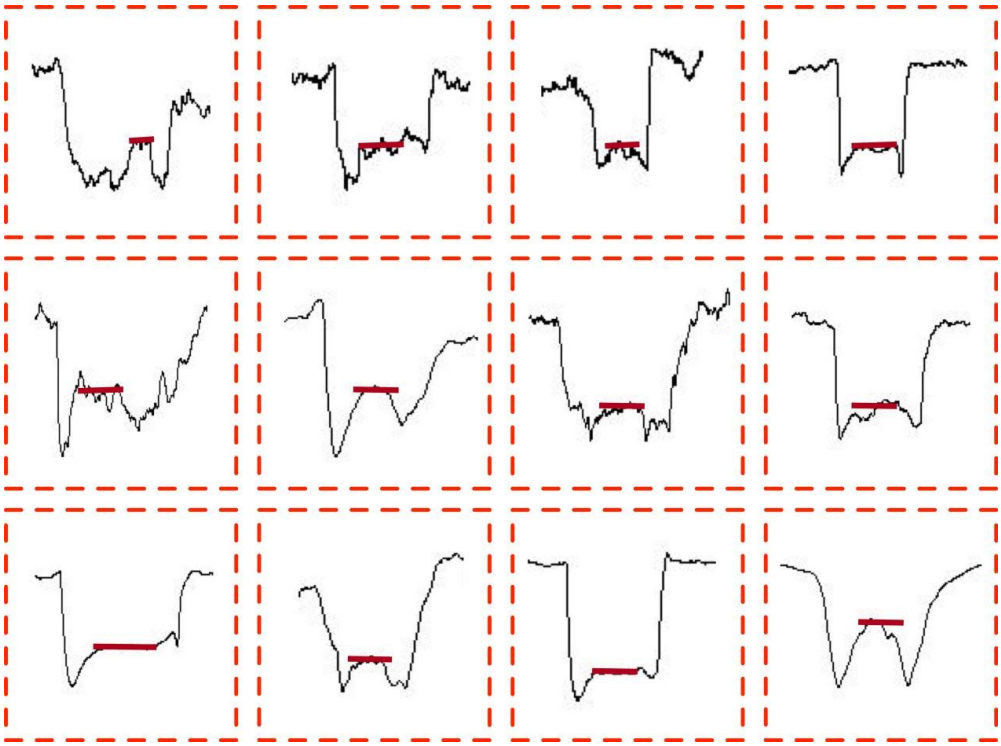

Figure S4. Characteristic signals of origami-1. The red line indicates the duration of the second-level current.

Fig. S5 showed the characteristic signals of origami-2. Origami-2's characteristic signals looks very similar to origami-1's, except that the secondary current duration is shorter. Because origami-2 has almost no distance in the middle.

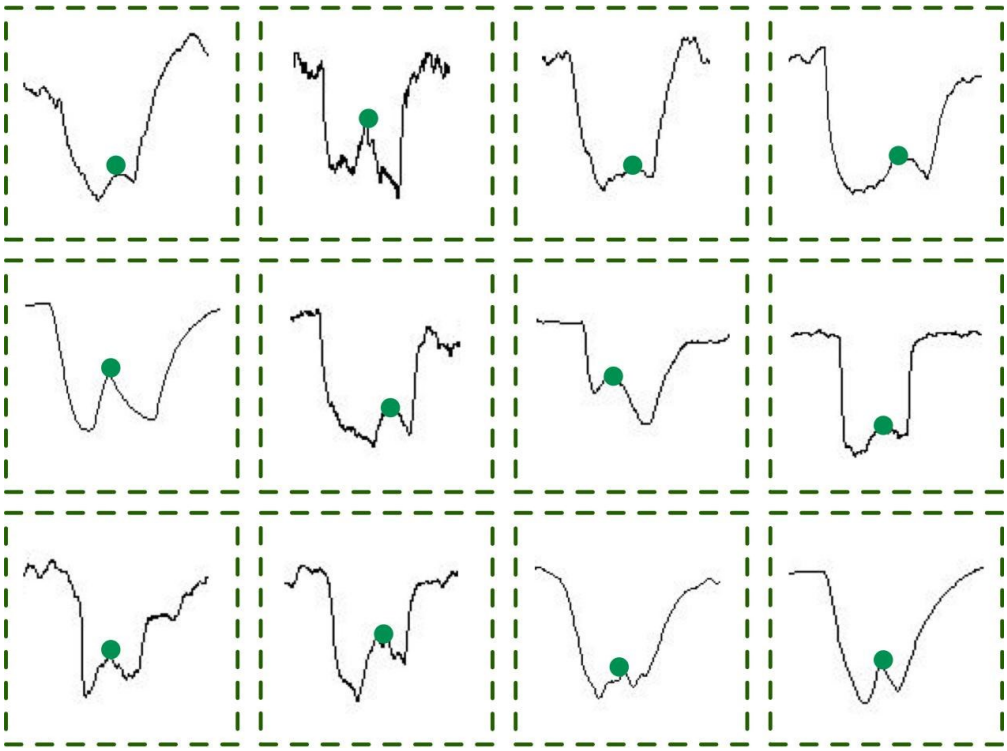

Figure S5. Characteristic signals of origami-1. The green dot indicates the second-level current.

Fig. S6 showed the characteristic signals of origami-3. Origami-3's characteristic signals has no second-level current. Because origami-3 has no distance in the middle.

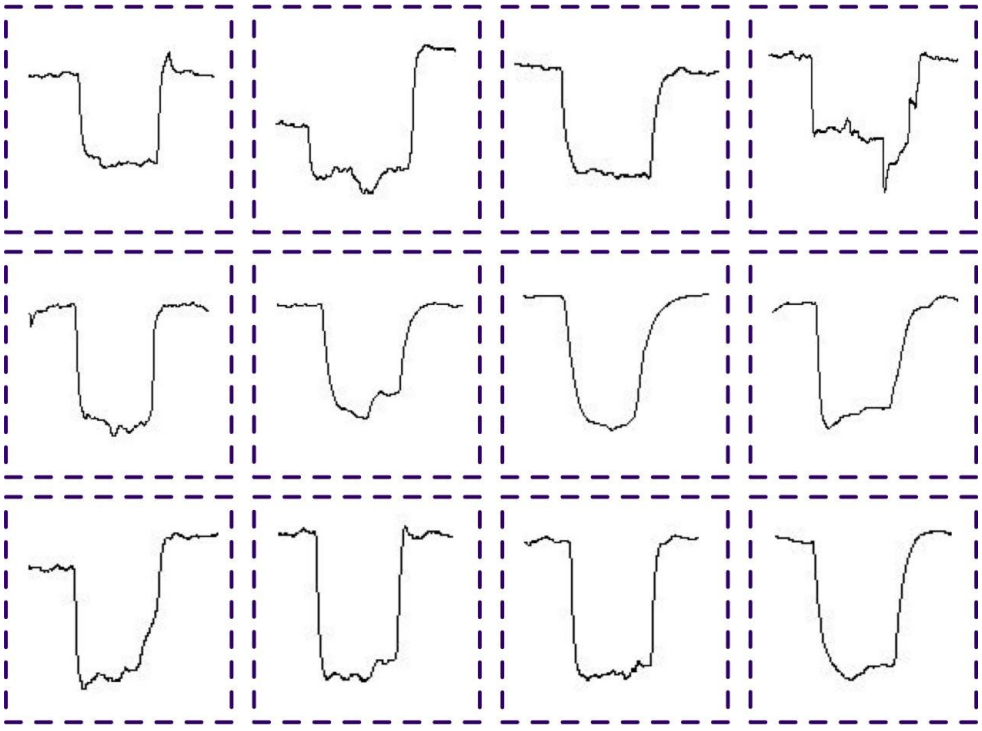

Figure S6. Characteristic signals of origami-3.

Section S7. TEM measurements of DNA origami

Theoretically, the angle range of origami-1,origami-2, origami-3 are 0° to 360°, 0° to 180°, 180° (Fig S7). TEM images of origami-1, origami-2 and origami-3 were shown in Fig. S8, S9, S10. From the statistical results, the actual angles of origami-1 range from 90° to 180°(Fig. S8), the actual angles of origami-2 range from 40° to 180°(Fig. S9), and the actual angles of origami-3 range from 150° to 180°(Fig. S10).

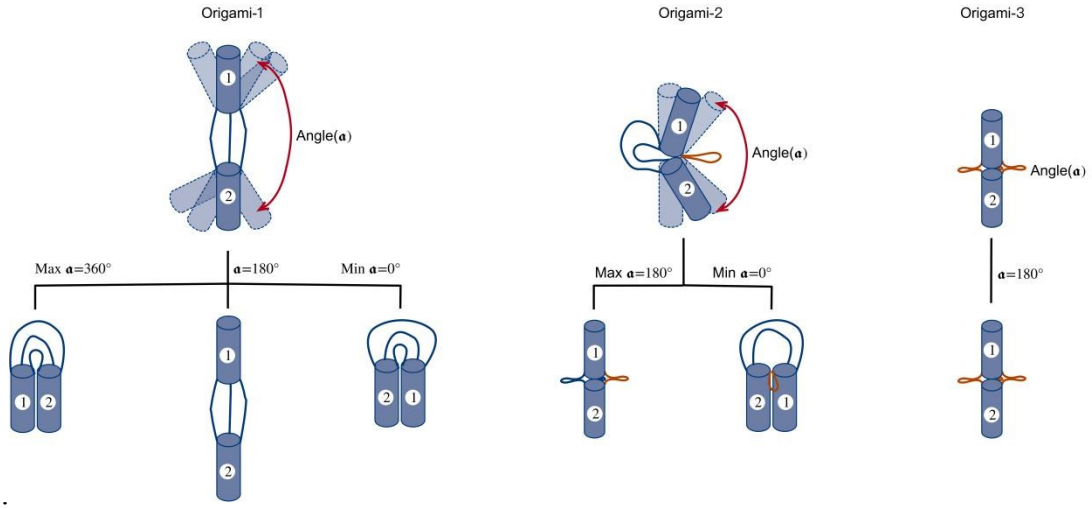

Figure S7. Schematic diagram of angle flexibility of three origami.

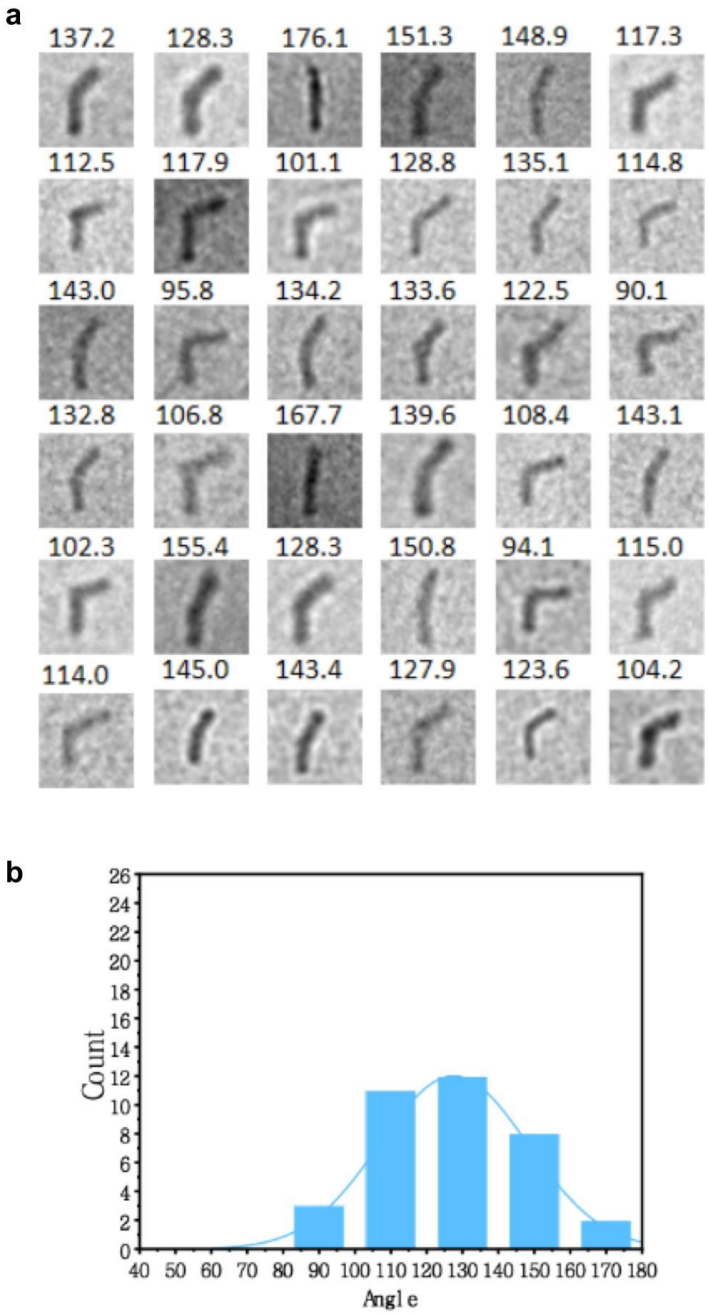

Figure S8. TEM images of the origami-1. (a) The angle array and statistical results of origami-1. The numbers are measured smaller angles. (b) The angle distributions of origami-1.

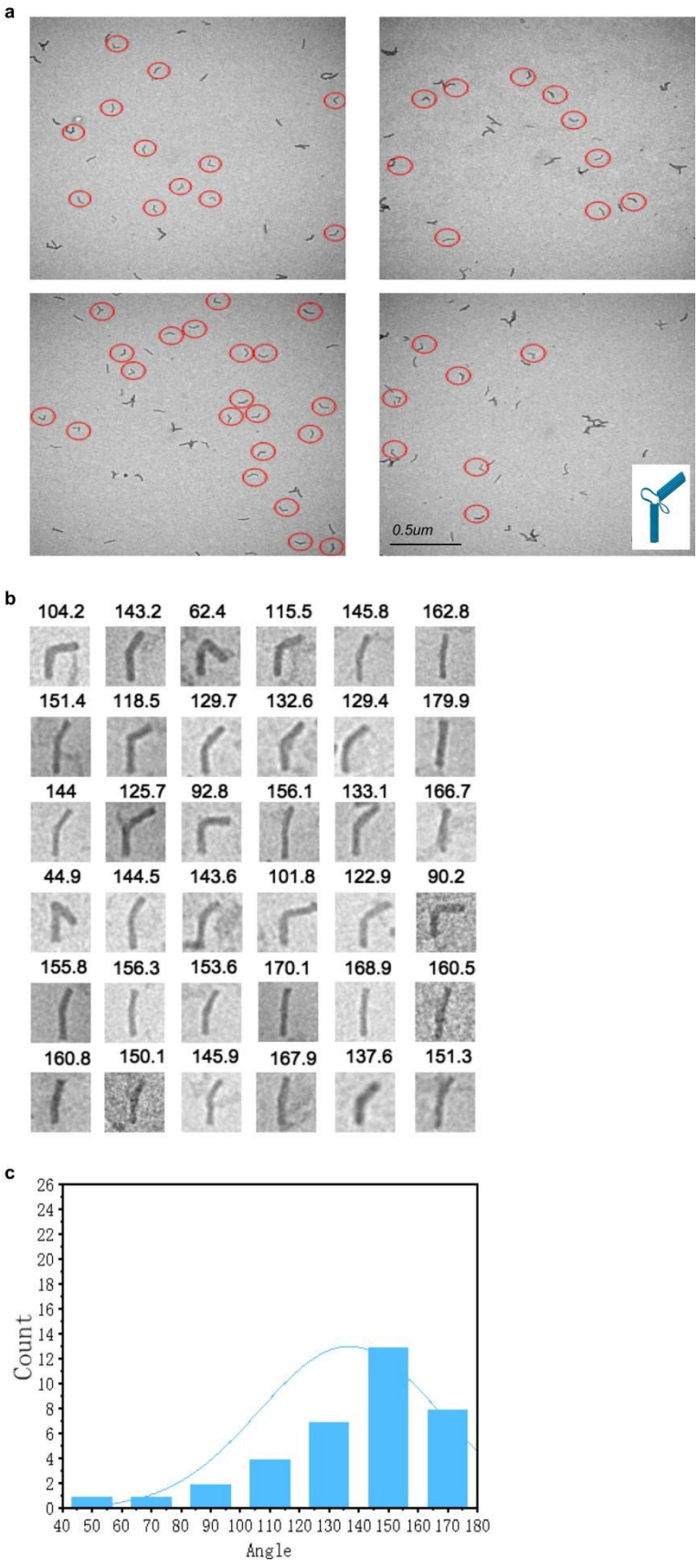

Figure S9. TEM images of the origami-2. (a) The images are under a wide view. The red circles enclosed the structures with clear angles. (b) The angle array and statistical

results of origami-2. The numbers are measured smaller angles. (c) The angle distributions of origami-2.

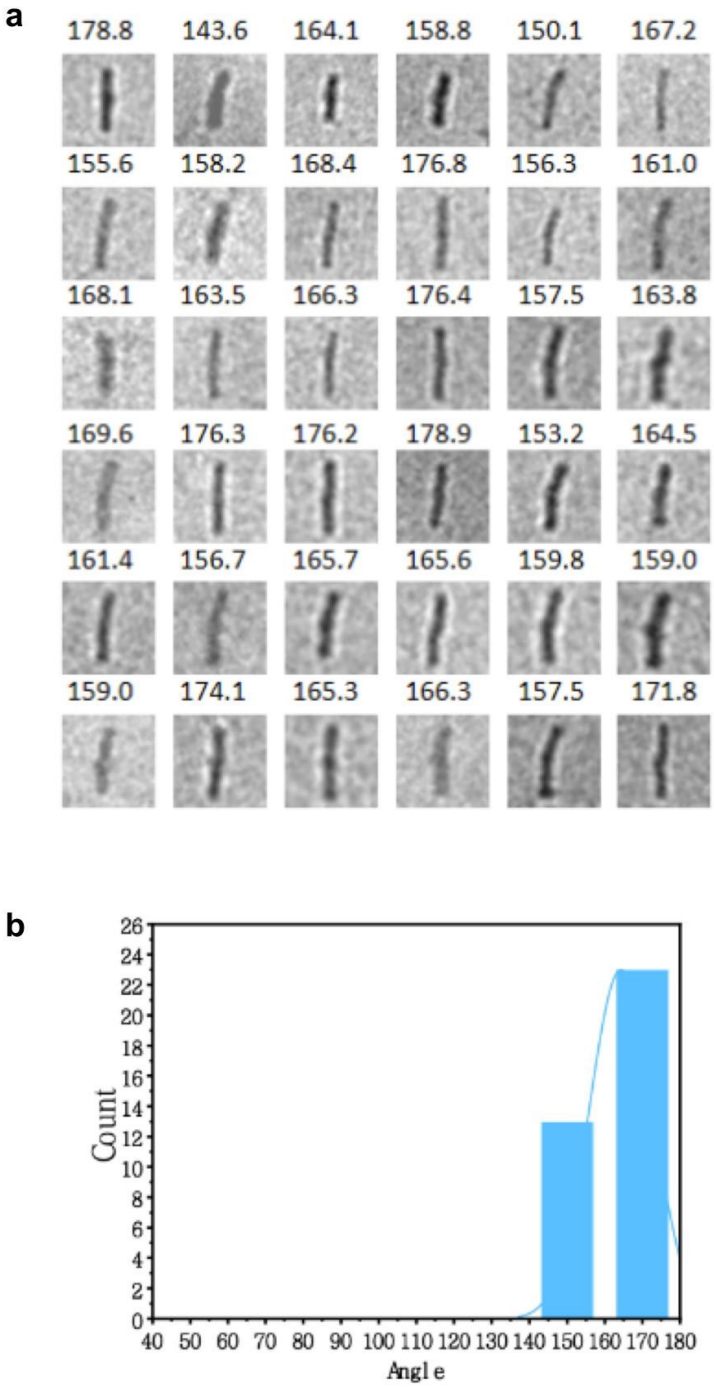

Figure S10. TEM images of the origami-3. (a) The angle array and statistical results of origami-3. The numbers are measured smaller angles. (b) The angle distributions of origami-3.

Section S8. Dispersion analysis of translocation events

From the distribution of the signals, an interesting situation was discovered that origami-1 has the largest dispersion and origami-3 has the smallest. The reason may result from their different flexibility. The dispersion calculation method of signal is to divide the event distribution scatter graph into several rectangular blocks with length of 0.1ms and width of 0.2nA, and the total number is recorded as N, the number of blocks of statistical signal scatter distribution is n, so the dispersion is n/N (Fig. S11a). It can be seen from Fig. S11b that the flexibility of origami mainly affects dwell time of event. Fig. S12 shows the dispersion comparison between origami-1 and origami-2.

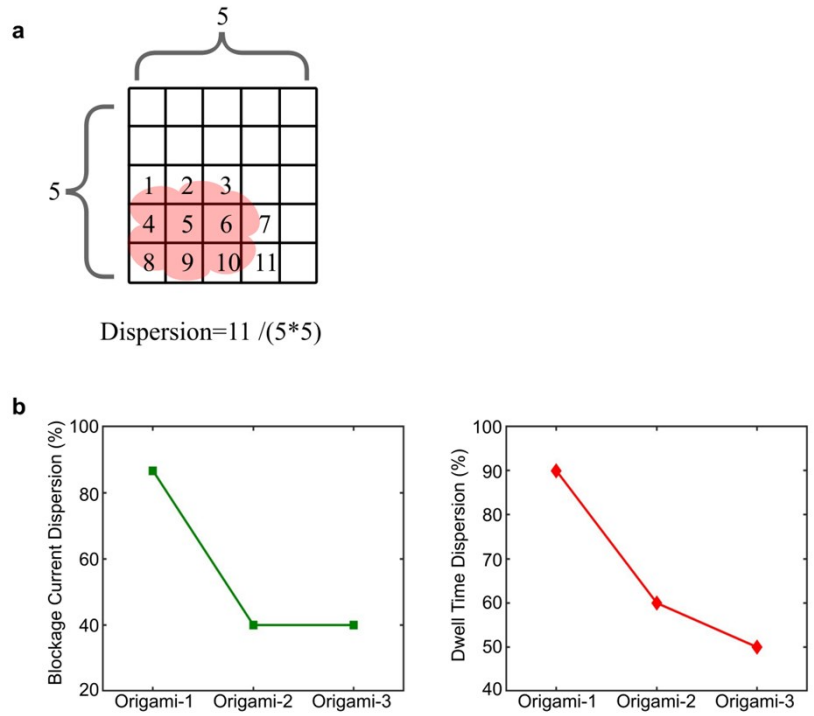

Figure S11. Analysis of the flexibility of origami. (a) Calculation formula of dispersion. (b) Comparison of blockage current and dwell time dispersion in three various origami.

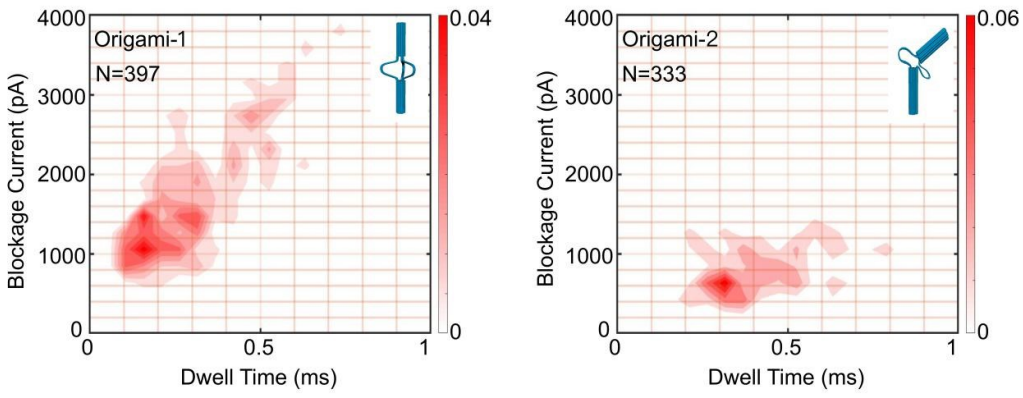

Figure S12. The dispersion comparison between origami-1 and origami-2.

In order to verify whether the variation of signal dispersion is caused by different structural flexibility, 15nm connectors were designed to connect the two cylindrical parts. The new structure was named origami-4. Figure. S13 shows the comparison between origami-4 (75nm) and origami-1 (90nm). As can be seen from the TEM image, the origami-4 is not straight, but it has a large angle, close to 180 degrees. From the experimental result, it is easy to conclude that the flexibility of the structure is an important factor affecting the dispersion.

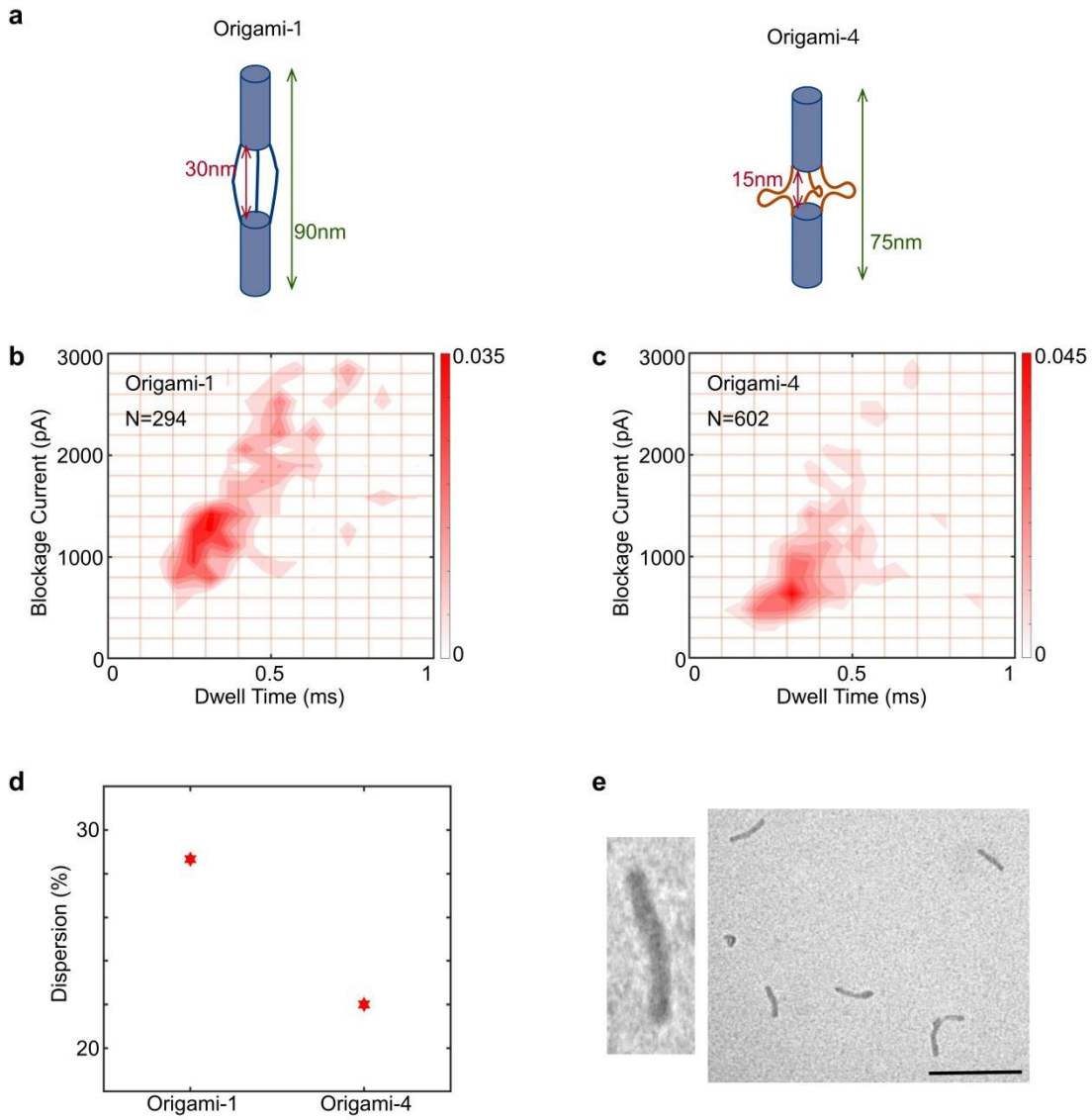

Figure S13. Signal dispersion of structures with different lengths. (a)The diagram of origami with three different length. Scatter plot of maximum current blockage versus

dwell time for origami-1(b) and origami-4(c). (d) Comparison of dispersion between origami-1 and origami-4. (e) The TEM images of origami-4, Scale bar: 200 nm.

Section S9. Characterization of origami-2 loaded with streptavidin

When the origami-2 loaded with streptavidin in the corner, all the complexes were more likely to form the same angle. TEM images in Fig. S14 confirmed this conclusion. When origami-2 is combined with a single protein, the binding of the protein makes origami-2 to be an unfreely movable state, and the angle of the structure is relatively concentrated, most of which are 130 degrees(Fig. S14b). It can be clearly seen from the statistical graph that the structure with protein is significantly more concentrated and more stable than the structure without protein(Fig. S14c).

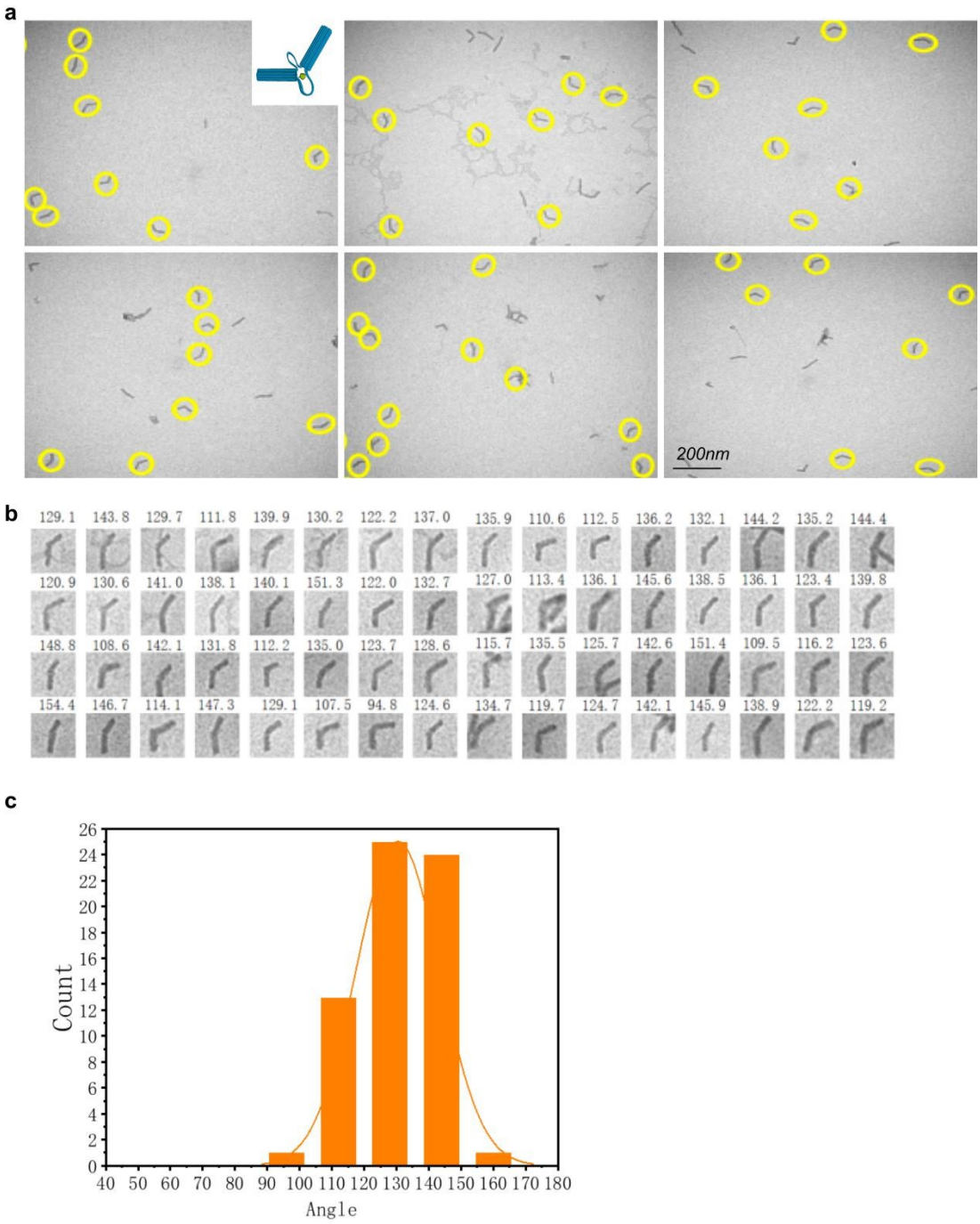

Figure S14. (a)TEM images of the origami-2 with a streptavidin under a wide view. The yellow circles enclosed the structures with clear and almost the same angles. (b)The angle array of origami-2. The numbers are measured in smaller angles. (c) Angle distribution of origami-2 with protein.

Section S10. The DNA sequences used in the experiment

Table S1. List of DNA sequences

ID	Sequences(5’-3’)
bamb-1	CATTTTTGAACGCCATCAAAAGATTGAC
bamb-2	CAAAAGAATACGCCACATAACACTAAAA
bamb-3	CAATAACGGATTCGAGAAAACAGTACAT
bamb-4	CCAAAAAATCAAAAGAATAGCCAAGCGG
bamb-5	ACCTCAAGTGAGGCGGTCAGTAGCCCTA
bamb-6	TGTCTTTGTCCTGAACAAGAAAAAGTAA
bamb-7	AACGCCAAAACAACATGTTCAGCTAATTTTT
bamb-8	TGGTTTTAGGCGAAAATCCTGTTTGATTTTTTT
bamb-9	TTTTTTGCAGAACGCGCTATTAAACCAAGTTTTT
bamb-10	CCTAATTTAAGAGTATTAGCGAGCATGTTACCCAA
bamb-11	AAATCATAGGTCTGTTAATTTACAGGAGGGCTGAG
bamb-12	GCTTCTGTACCTGAGCAAAAGGTTACAATTAGAAT
bamb-13	ACGCTGAGAAGAGTTTTTTAACCAGTAACAGCATT
bamb-14	TGGAAGTTTCATTCCATAAAGGAATATATAACAGT
bamb-15	GAACGAGCCCTCAGGGTGTAGATGGGCGTGCCGGA
bamb-16	CATGTTAATGCGCGGAATACGTGGCACAGAAATGG
bamb-17	CAACTAAGATTAGCATTGAGCGAGAGATAACCCAC
bamb-18	CTTCGCTTCGCACTCCAGCCAAGTTTGAGCAGGGA
bamb-19	AACGATCCCTTCACTGAGAGAGTTGCAGCCGAGAT
bamb-20	GAGCACGAGGAGCGGGCGCTACCGGCGACGCCACC
bamb-21	CCGTTTTAGAACGCGAGGCGTGTTAAAGTTTGAGG
bamb-22	TGCCATCCGGTCATTTGGAACAAGAGTCGAGGTGC
bamb-23	AATCAATGAATCATGAAGGCTTATCCGGATCGTCA
bamb-24	GATTAAGACCTTTTTAACCTCACTTTTTGTTTTAA
bamb-25	CAGCAAATGAAAAAAGCCAGTATAAGGGAACCGGA

bamb-26	CCACATTTTAATGCGTCAAATCACCATCTCAACGC
bamb-27	GCCTGGGGTGCCTAGAGTCTGGAGTTTCATAGGAA
bamb-28	ATCAACGAATAGTAACTGGATCGTAATGGGATAGG
bamb-29	CTGAATTGTAATAACAAATATTACCCAAAAGAACT
bamb-30	GGATTAGAGGAATTATTTTTTAGGGTTGAGTGTTG
bamb-31	GCGTCTGGCCTTCCTCTCCGTGTCATAAACCATAA
bamb-32	CGAGAAACGGCTTAATAGCGATAGCTTAAAATCAA
bamb-33	TTTTTTGCCTCAGGAAGAATTACGCCAGCTTTTTTT
bamb-34	TTTTTTGAAGCGCATTAGGTTGATATAAGTTTTTTTT
bamb-35	TACCAGAAACCAAAGAAACACTTCGAGCGGCTTAGAG
bamb-36	TTTTTTTTGGGCGCCAGGGTGTATGGGATTTTTTTTTT
bamb-37	TTTTTTGGCGAAAGGGGGGTACCGAGCTCGAATATCCAG
bamb-38	AGTAAAAATGAGTGGGAGAGGCGGTTTGCGTATTTTTTTT
bamb-39	CATCTTCGGAAACGCAATAATCGGAATATATGGTTGAATTAG
bamb-40	TGATAAAAAGTAAGCAGATAGAAGAATTAAAGTCAAAAAATG
bamb-41	CGGTACGTACCTTTTACATCGTTAACAAATTACCTCAATAGT
bamb-42	GGCAAGTGTAGCGGTTTAGAGCCTCAGAAATCAAATGAAAGT
bamb-43	CACCACCAGAGCGTTAGTTAGCCGCCGCGCGTCATTGATGAT
bamb-44	TTGGGTAACGCCAGTGTTGGGACCAACCACGGCTAGTAATCT
bamb-45	GGTCAGGACCTTTAATTGCTCCGGTGTCCAATTCTGGTGGCA
bamb-46	AGTTTATTTTGTCACATATCAGCTAAATCAATAGAAAGAG

	AA
bamb-47	AATTGCGAATGAATCGGCCAAACCAGTGGACGTTACGGAGTG
bamb-48	TACCAGGCCTGAACGAGTTAAGCCCAATTTAAGAATAAGGCG
bamb-49	TTAAGAACTAGACGGGCGCGGCTCATTATGCAGATAAAAGGA
bamb-50	AAAATCACCCGATTAGAAAAGTAGCACCATTACCAAGCCAGC
bamb-51	TTTAGCGCGAGAACAAGCAAGATTCCAAGACCTTCAAGAGGA
bamb-52	TACCGTTTGGAAACAAAATTAATTACATGGAGAAAATTTTAG
bamb-53	GTAAAGAAATGCAATAAAGCTAATTAAGTTAGCTATATTTTC
bamb-54	GAGGCTTTCATAACATCAGTTATTTTTGGGGTGAGAAAGGCC
bamb-55	CCCTCAGAGAACCGTGGTTTGAAGTTACCAGAAGGAAACCGA
bamb-56	TGCGGATTTCAAAGAAGAGGAAGAAAACGAGAATGATATTCA
bamb-57	CAACAGCCTGCATTTTGCGCTCACTGCCCCTGAGAACAGACA
bamb-58	AGCCACCGGAACCTTTCAACCAGGTGGCAACATATGGCATGA
bamb-59	AACTGATATTAACACATCACCTTGCTGAATTTAGGACTTTGA
bamb-60	TGAACGGAGCCCCAAAAACAGTTCGCATAACACTATTGCAAA

bamb-61	CTTATAAAAAGGCTAGCCATAAAAATAGCAGCCTTTGAACAC
bamb-62	ACCCTCAGCCTGTACTTTCCAAGACGGGTCCACGCTGGTTTG
bamb-63	TTATTTATCCCAATAAAATCTAAAGGAATTGTCGTGCATTCC
bamb-64	GCCAAAGACGCAAAGACACCAAACGGAAATTTTAGAGAGACT
bamb-65	GGAACGAGTCAATCAATAAGATACCGACAAAAGGTAAATAAT
bamb-66	AGCCACCTGGCAATCTTCTGAATAATGGTTAACGTTTATAAT
bamb-67	GCGGATTATCAAAAATCAGGTAATACTGTTGCCAGGGCATAG
bamb-68	GCGGAATCGGAACACATTTGAGGATTTATTAAATATCACCGT
bamb-69	ACCCCGGTTGATAAATCAGCTATTACGAAGGGGGTTAACAAA
bamb-70	AGGTGTAAGAATAATACCGAAGCCCTTTAATAAGAAATTAAC
bamb-71	CAGGACGCCTGTAAAAGGATAAAAATTTGGAGACACGGAGAG
bamb-72	TCAGAACACGTGGCCGTGAACCATCACCCCAACGTAGCGTCA
bamb-73	CCGAACAAAATACCAATTCGATTAATTTTAAAAGTCAGATGA
bamb-74	GCGCAACGGTTTTCCCAAGCTTGCATGCCGCTCATCCCCAGC
bamb-75	TACAGAGGTTACAAAATAAACCCAAAAGGTTTCAGGTAA

	ATG
bamb-76	AAAAGAAACAAAAGTCACCGACCAATGAAACCATCGACTGTA
bamb-77	AGATATATACCGCGCCCAATAGCTATTACTGACAAGCAAATC
bamb-78	GCTGGCTGAACGGGCTGTTTATCAACAACGACAATACATGTA
bamb-79	GTACAAAGCCACCGGTAGATTTTCAGGTAAGGGTTTGATTAT
bamb-80	GATAGCAGTGAATTATCACCGGGCGACAATTATTCCGGGGTC
bamb-81	CCCCCGATCACGCTCGCCGCTACAGGGCGGCCGATGGTTGAG
bamb-82	TTTTTTTGTATCATCCGAACGATCTGGCCAACAGAGCAGTAAT
bamb-83	TTTTTTTCGTAACACTTCCATCAAAACAGAAATAAAGCAAAATT
bamb-84	CCTCATATATTTTATTCAAAAAGAGATCTGGAGCAGTATAAGCA
bamb-85	TTTTTTCCATTAAACGGACGGAGAAACAATAAAAAGGGACTTTTT
bamb-86	AACAGAGATATCAAACCCTCAATTTAACACGGTGTACAGATTTTTT
bamb-87	TTTTTCAATAGCTATCTACACCGGGATAATAAAGAAACCATTTTTTTT
bamb-88	ATCAAGACAGAGGCGCCGCTTACCGTGCATCTGCCGCTTTCCATCGGTG
bamb-89	ATTATTCGGAGGGACCCCTGCCTATTTCACCGGAATGCCTTTCAAAGGG

bamb-90	TTTTTTTATAGCCCGGAATCCCATGTAGAAGGAATTTGCACGTTTTTTT
bamb-91	TTAGCAAGGCCGGAGCATTTTTTTTCATGCCGCCAGACAGGATAAAGGG
bamb-92	GAACCAGCTCAGAGAGACGATGGAGCTAGCTTTGAATACCAAAAGATGA
bamb-93	GTGCCGTTTCAACAGAGCCTTAATCGGCAAAATCCCCCCAGCTCTTTTC
bamb-94	ATTTTCGTCTAAAGCCGCCTGCAACAGTGTCTTTACTTAGCCCACTCAT
bamb-95	TGACCTAAATTTAACCACCCTCAGCTTTACATGGAACCGCCAGCCCTCA
bamb-96	CAAAGAATTAGCAAAAATCGGAATAAAAAAGATTCCCTCGTTATATTTT
bamb-97	TACTTTTTAACATCTCAATTCTACTAATAGGCCAGTGAGATAGTAGCAT
bamb-98	TTAGAACAAAAACAGGCAAGGGCGCGAGCTGAAAAGCGAACGTGTGAAT
bamb-99	CCAGAACAAGGGAGCGTAAAGCACTAAATCGGCCCCGCCTGGAACCCTA
bamb-100	GGGCGCTATGGTTGCTTTGACCAGAGCGTGGCCTTCCAGAATAGTGCCT
bamb-101	CCTACATGCCAGTGCCAGTCACGACGTTGTTATGTAATCAAAAACGACG
bamb-102	CGGATAAACTCAGGGGATAGCATATTCCAGAACCTACCATATAAATTGC
bamb-103	AAAGAGGTCAGGCTAACCAGGCAAAGCGCCAATAGTAACCATTCGCCAT
bamb-104	AGCGTCCCTTTACCTAGTCAGAAGCAAATCCAACAGCTGC

	TCTACCTTA
bamb-105	CCAATCGACTATATTCCCTTAGAATCCTTAACCTTATTAA AGGATATTC
bamb-106	TTTTTCACCAGCAGAAGATAAAAAATACGCCTGATAAGTA CAGTAAAAT
bamb-107	TACAAAGAGGTAGACGAACTAGAGATGGAGATACAGTAG CTCAACATGT
bamb-108	TGAAACAATCACCGGCGCGTTAAAGAACGTGGACTCAAA TCAGGGAAAG
bamb-109	TTCCAGTAGCCCCCTTTAATAGCGAAATTAGCGTTACTCC TCAAATTCA
bamb-110	TTTGACGCTAACCGTATTCCAATCGTCTGACAATAGCTAT TAGCCACGC
bamb-111	GGTAGCATAAAACGCTTTGACGGAAATAATTATTTACATT GGAGCGTAA
bamb-112	TTACCGCTCCCCGGATGTGCTGCAAGGCCGGGCCTACGTA ATACTAAAG
bamb-113	GAGTGAATGAAAACGGTTGGGTTATATACAAGACATGAG TAACAGTGCC
bamb-114	CCTGCTCCTGACCACAGAGGCTTCTGTCCAGACGATAGAT AACCTTATC
bamb-115	GCAGTCTGCAGGTCCCACCACCTTGACGAGTTTTTTGGGG TCCACTATT
bamb-116	AGTGTTTCAGATGAATATACAGATTATATCATCAAAACGT TACAACTCG
bamb-117	TCCGCGAGATTATACGAAGGCAAGGGCGGGCACCGCTTC TGGCATCGTA
bamb-118	AAGAACGTTAAGACTCCTTATTACATAAGATTGAGATTAA AGGCACCGT

bamb-119	GATTAAGTCGACTCTAGAGGACAGCCATCGAAACAAAATTGTCAGATGA
bamb-120	GAAGTATACATTATCATTTTGTATCATCAAGCCCAGTCACCAAATTTTC
bamb-121	GCATCAAAAAGATTCGAACCAGCTTGCCTCAACTTCTACGTTTTGTACC
bamb-122	TTGAGTATAGACTTTACAAACGACCGTGGTACCGCTGCTCAGAGAATAG
bamb-123	TTCATCGAACGTCACTTGAGCCATTTGGTACCAGCATTAAGATGTACTG
bamb-124	TTGCGGGTATTCTATATTTTCATCGTAGAATCGGCTGACAAGAACCGAA
bamb-125	CTTAATGGCGCGTAACCACCACAGGGAACAGTCCCCGCCGCGACAGGAA
bamb-126	GCGGGAGAAGAATGTTTTTGCCTTTATTAATATGATTCTAGCGCATGTC
bamb-127	ATTCAGTAGAAGTTCGGAATCGGGAACAAACGGCGATAATTCTTGTTAA
bamb-128	CGCGCGGAGCTAACTCACATTCAGTGAGCTACAACTTTTCAGAGGTTTA
bamb-129	GAAAAATTAATCATAGTAGATATGCAACTAAAGTACTTTTGAAGCAAAC
bamb-130	GGAAAGCTATATGTTGAAACAAACATCACCTGATTAACAGGAGCGTACT
bamb-131	TGTAGCCGTTAAAAGAAGATTAACAAGAGAATCGAGGTAGCTGAGATTT
bamb-132	CAATAAATCATACATTATGACTTGGGAAAGGAATATAAGAGCTAAATTT
bamb-133	GCCACTACCAAGCGTGCAACAACCAGTCACACGACATAG

	AACGCCATTA
bamb-134	GTAACAGCCAGAATCGCTTTCACCTGTCGTGCCAGTGATTGCTAAAGTT
bamb-135	GACCATTTTTAATTCTGACGAATAGCGATTGAATCACAACCCGTCGGAT
bamb-136	CACGTTGCCAAATATTTTGTTTAACGTCGAGGGTAGGGGTTTCACCCTC
bamb-137	GTCGAAAAAACATCCCTTCTGACCTGAACAGATTCGGAAAAACTGCAGG
bamb-138	GAATAAGGACCGGATAAGAGGTCATTTTTTTAAATTTAGTTTATTTGGG
bamb-139	TTTTTTACCGCACTCATAACCTCCCGACTTGGGTCGCTCATGAGGAAGTTTTTTT
bamb-140	TATTAAATCTATCAGAATTCTTTGCCCGTATAATCCTTTTGATTTCAGATTGTTTG
bamb-141	TCACGTTCAGCGAAAGTTTAGAAATGACAGCATCGTATTCATAGAAACCATCCCAT
bamb-142	TCAGAAATAATCGTAAAACTATGATAAACAACTAATACCAGTTGCGATTTGATTCC
bamb-143	TTTTTTTTGCTAAACAACTCGAGAGGACGGGAGGCAAGAAACAATGAAATAGTTTTT
bamb-144	TTTTTTCCAGGCGCATAGACTTTTTGAGGCTTGGGGACGACGACAGTATCGTTTTTT
bamb-145	TTTTTTTTGGTGGTTCCGATAATTGTTTTGCCAAGAATAACATAAAAACAGGTTTTTT
H1	CGCCCACGCATAACCGATATACAGCTTGCTTTCGAGGTGAAT
H2	CAACGCTAACGAGCGTCTTTCGAGGTTTTGAAGCCTTAAATC

H3	GTAGGGCTTAATTGAGAATCGCATAATTACTAGAAAAAG CCT
H4	ACTAATAGATTAGAGCCGTCAATATCTGGTCAGTTGGCAA AT
H5	CAAACTATCGGCCTTGCTGGCAAATTAACCGTTGTAGCAA TA
H6	CGAGCCGGAAGCATAAAGTGTAGTAATCATGGTCATAGC TGT
bamb-33-bio	biotin-TTTTTTGCCTCAGGAAGAATTACGCCAGCTTTTTTT
bamb-8-bio	biotin-TGGTTTTAGGCGAAAATCCTGTTTGATTTTTTT