Supporting Information for

Multiplexed DNA Detection Based on Positional Encoding/Decoding with Self-Assembled DNA Nanostructures

Sha Sun, Huaxin Yao, Feifei Zhang and Jin Zhu*

Department of Polymer Science and Engineering, School of Chemistry and Chemical Engineering, State Key Laboratory of Coordination Chemistry, Nanjing National Laboratory of Microstructures, Nanjing University, Nanjing 210093, China

*Corresponding author. Phone: +86-25-83686291; Fax: +86-25-83317761; Email: jinz@nju.edu.cn
Table of Contents

1. Materials ................................................................................................................. S3
2. Design of Self-Assembled DNA Nanostructures .................................................. S3-S5
3. Experimental Procedures ................................................................................... S5-S6
4. Screening of MgCl₂ Concentration for DNA Hybridization ........................... S6-S8
5. Screening of DNA Hybridization Time ............................................................... S8-S10
6. Single-Target DNA Detection .......................................................................... S10
7. DNA Detection Limit .......................................................................................... S11
8. PCU DNA Detection System ............................................................................. S12
9. Detection of RNA ................................................................................................ S13
10. Two-Target DNA Detection ............................................................................. S14-S18
11. Four-Target DNA Detection ............................................................................. S18-S20
12. Assembly of DCU .............................................................................................. S21
13. Single-Target and Two-Target DNA Detection by DCU Detection System ....... S22-S26
14. DNA Sequence Information ............................................................................. S26-S39
15. References .......................................................................................................... S39
1. Materials

All DNA stands were purchased from Sangon Biotech (Shanghai) Co. Ltd and DL2000 DNA molecular weight marker was from TaKaRa Biotechnology (Dalian) Co. Ltd. Freeze ‘N Squeeze column was purchased from Bio-Rad Laboratories, Inc. and uranyl formate was from Polysciences, Inc. Gel electrophoresis was performed on a Bio-Rad system using 2% agarose gel. UV-vis absorption values were obtained using an Eppendorf Biophotometer Plus facility. Transmission electron microscopy (TEM) imaging was performed using a JEOL JEM-1011 facility.

2. Design of Self-Assembled DNA Nanostructures

DNA sequences for the nanostructures were generated by program Sequin. To reduce undesired interaction patterns, the criton size is set to 7, which means any continuous sequence of 7 or more nucleotides (nt) appears at most once.

DNA nanostructures were designed by following Peng Yin’s LEGO-like model (for all the DNA sequence information, please see Section 14 of the Supporting Information). In our design of the core cuboid part of CU, DNA double helices were arranged as square lattice bundles, as shown in Figure S1. First, we used Sequin to generate sequences for 36 DNA double helices, each of which is 128 BP (base pairs) in length. Then a sequence of 8Ts (eight continuous thymidines) were added to both ends of one strand of each helix (5’-3’ strand for odd helices, 3’-5’ strand for even helices, refer to Figure S1 for the odd and even numbering of helices) to prevent non-specific blunt-end stacking. Second, a nick site was created for each helix every 16 nt. Because of the different numbers of nt for the two strands of each helix, the nick sites are staggered by 8 nt. Third, the nick sites of each odd helix were linked with the corresponding sites of neighboring even helix clockwise. Take H9 (helix 9) as an example, its protruding 8Ts on the 5’ end is linked to the protruding 8Ts on the 3’ end of H14, then the first nick site of H9 should be linked to the first one of H10, the second site of H9 to the second one of H2, the third site of H9 to the third one of H8, and the fourth site of H9 to the fourth one of H14. After the linkage, the remaining 16 nt strands should be merged to 32 nt ones to improve the stability of the nanostructures. The registry marker of CU is direct extension of the 9 helices, each of which is 64 BP in length, at one corner of the core cuboid.
Figure S1. The design of CU viewed from the cross-section of the end of core cuboid opposite to the registry marker. This view gives a top left corner location for the registry marker.

The locations of 14 capture probe strands at the top and bottom surfaces of CU are shown in Figure S2. The locations of 15 detection probe strands of DU are shown in Figure S3 and S4.

Figure S2. The locations of 14 capture probe strands at the top and bottom surfaces of CU, with base numbers and helix numbers specified (circle-marked sites at right: for TT1 and TB1; circle-marked sites at left: for TT2 and TB2).

Figure S3. The locations of 15 detection probe strands at DUT1 (identical for DUT2), with the base number (64 BP) and helix numbers (circle-marked sites) specified.
Figure S4. The locations of 15 detection probe strands at DUB2 (identical for DUB1), with the base number (64 BP) and helix numbers (circle-marked sites) specified.

DCU is assembled by CU and a cuboid. There are 10 linker strands at the 5’ end of CU (linker 1: H0, H2, H4, H8, and H10; linker 2: H24, H26, H28, H32, and H34) and they are complementary to the other 10 strands dangling from the 3’ end of the cuboid (linker 1: H1, H3, H5, H7, and H9; linker 2: H25, H27, H29, H31, and H33). The locations of 10 linker strands are shown in Figures S5 and S6.

Figure S5. The locations of 10 linker strands at CU, with the base number (1 BP) and helix numbers (circle-marked sites) specified.

Figure S6. The locations of 10 linker strands at cuboid, with the base number (128 BP) and helix numbers (circle-marked sites) specified.

3. Experimental Procedures

Preparation of nanostructures: Hundreds of single-strand DNA (ssDNA) were mixed and then freeze-dried. After the dissolution of ssDNA in 0.5×TE buffer (5 mM Tris, 1 mM EDTA, pH=8.0, supplemented with 40 mM MgCl₂) to a final concentration of 200 nM per strand, the solution was annealed from 90 °C to 60 °C at a cooling rate of 5 min/°C and from 60 °C to 24 °C at a rate of 2 h/°C.

S5
Purification of nanostructures: The annealed samples were loaded to a native 2% agarose gel with 0.5 μg/mL ethidium bromide (running buffer: 0.5×TBE buffer, containing 44.5 mM Tris, 44.5 mM boric acid, and 1 mM EDTA, supplemented with 11 mM MgCl₂) and gel electrophoresis was performed at 80 volts for 2 h in an ice bath. Target bands were excised and cut into small pieces. The gel pieces were placed into Freeze ‘N Squeeze columns, frozen at -20 °C for 5 min and then centrifuged at 7000g at 4 °C for 5 min.

Hybridization assay: DNA Nanostructures were quantified by measurements of UV-vis absorption values at 260 nm. Different DNA nanostructures were mixed in a molar ratio of 1:1 and target DNA (3 μL) was then added to the mixture. The solution was diluted with 0.5×TBE buffer to a final volume of 10 μL (5 nM for the final concentration of each nanostructure). The hybridization was allowed to proceed at 30 °C.

TEM imaging: A 2.1 μL of hybridization solution was mixed with 0.3 μL of ssDNA (with a sequence of 5’-GCCTGAAGTCTGGTGCTTAGGCCTTGAAATCA-3’ for the generation of a hydrophilic TEM grid surface) and the whole solution was loaded onto a glass slide. On top of the solution was covered with a carbon-coated TEM grid and the contact between the solution and grid was allowed to proceed for 2 min. The TEM grid was then stained with a 2% uranyl formate aqueous solution (containing 25 mM NaOH) for 2 min followed by twice wash with water. TEM imaging was performed at 100 kV.

4. Screening of MgCl₂ Concentration for DNA Hybridization

![Image of gel electrophoresis bands]

**Figure S7.** Gel electrophoresis bands for purified CU and DUT1. Lane M: DL2000 molecular weight marker (same for all the following gel electrophoresis images); Lane 1: CU; Lane 2: DUT1.
Figure S8. Gel electrophoresis bands for CU, DUT1, and TT1 in the presence of different concentrations of MgCl₂. Lane 1: 11 mM MgCl₂; Lane 2: 20 mM MgCl₂; Lane 3: 30 mM MgCl₂. The concentration of TT1 is 300 nM. The non-penetrating material in the gel is the non-specific aggregation of the hybridization product, which probably appears after storage at 4 °C and could be reduced by pre-heating the sample at 30 °C before gel electrophoresis (same for all the following gel electrophoresis images).
Figure S9. Representative TEM images of CU, DUT1, and TT1 in the presence of different concentrations of MgCl₂. A) and B): 11 mM MgCl₂; C) and D): 20 mM MgCl₂; E) and F): 30 mM MgCl₂. The concentration of TT1 is 300 nM.

5. Screening of DNA Hybridization Time
Figure S10. Representative TEM images of CU, DUT1, and TT1 after hybridization for different durations of time. A) and B): 5 min (hybridization percentage, or HP: 41%); C) and D): 10 min (HP: 63%); E) and F): 20 min (HP: 71%); G) and H): 1 h (HP: 88%); I) and J): 8 h (HP: 91%). HP is defined as the percentage of observed CU-DUT1 over all structurally resolved CU (calculated from ~300 CU). The concentration of TT1 is 300 nM. The small dark square objects in the images are individual DUT1 which prefer head-on settlement on the carbon grid instead of side-on settlement as hybridized DUT1. All kinds of individual DU (DUT1, DUT2, DUB1, DUB2 and DUB3) show head-on settlement in the following TEM images.

6. Single-Target DNA Detection

Figure S11. Representative TEM images of CU and DUT1 in the absence of TT1.

Figure S12. Representative TEM images of CU and DUT1 in the presence of TT1. B) and D) are enlarged view images of A) and C), respectively (rectangles marked in red
serve only as an approximate viewing guide for the enlarged area; same for all the following TEM images if applicable). The concentration of TT1 is 300 nM.

7. DNA Detection Limit

Figure S13. Representative TEM images of CU and DUT1 in the presence of different concentrations of TT1. A) and B): 5 nM (HP: 10%); C) and D): 10 nM (HP:
37%); E) and F): 20 nM (HP: 65%), G) and H): 30 nM (HP: 88%). HP was determined by calculation from ~250 CU.

8. PCU DNA Detection System

Figure S14. Gel electrophoresis bands for PCU and DUT1 in the absence (lane 1) and presence (lane 2) of TT1. The concentration of TT1 is 300 nM.

Figure S15. Representative TEM images of PCU and DUT1 in the presence of TT1. B) and D) are enlarged view images of A) and C), respectively. The concentration of TT1 is 300 nM.
9. Detection of RNA

Figure S16. Gel electrophoresis bands for CU and DUT1 in the absence (lane 1) and presence (lane 2) of RTT1. The concentration of RTT1 is 300 nM.

Figure S17. Representative TEM images of CU and DUT1 in the presence of RTT1. B) and D) are enlarged view images of A) and C), respectively. The concentration of RTT1 is 300 nM.
10. Two-Target DNA Detection

Figure S18. Gel electrophoresis bands for purified CU, DUT1, and DUB2. Lane 1: CU; Lane 2: DUT1; Lane 3: DUB2.

Figure S19. Representative TEM images of CU and DUB2 in the presence of TB2. B) and D) are enlarged view images of A) and C), respectively. The concentration of TB2 is 300 nM.
Figure S20. Gel electrophoresis bands for two-target detection (separate hybridization). A) CU and DUT1 in the absence (lane 1) and presence (lane 2) of TT1, CU and DUT1 in the presence of TB2 (lane 3), CU and DUT1 in the presence of both TT1 and TB2 (lane 4); B) CU and DUB2 in the absence (lane 1) and presence (lane 2) of TB2, CU and DUB2 in the presence of TT1 (lane 3), CU and DUB2 in the presence of both TT1 and TB2 (lane 4). The concentrations of TT1 and TB2 are 300 nM.
Figure S21. Representative TEM images for two-target detection (in the presence of one target). A) and B) CU and DUT1, CU and DUB2 in the presence of neither TT1 nor TB2; C) and D) CU and DUT1, CU and DUB2 in the presence of TT1 (HP: 50%); E) and F) CU and DUT1, CU and DUB2 in the presence of TB2 (HP: 48%). HP was determined by calculation from ~250 CU. The concentrations of TT1 and TB2 are 300 nM.
Figure S22. Representative TEM images for two-target detection (separate hybridization, in the presence of two targets). CU and DUT1, CU and DUB2 in the presence of both TT1 and TB2 (HP for CU-DUT1: 46%; HP for CU-DUB2: 45%). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~250 CU. The concentrations of TT1 and TB2 are 300 nM.

Figure S23. Gel electrophoresis bands for two-target detection (simultaneous hybridization). Lane 1: CU, DUT1, and DUB2 in the absence of either TT1 or TB2; Lane 2: CU, DUT1, and DUB2 in the presence of TT1; Lane 3: CU, DUT1, and DUB2 in the presence of TB1; Lane 4: CU, DUT1, and DUB2 in the presence of both TT1 and TB2. The concentrations of TT1 and TB2 are 300 nM.
Figure S24. Representative TEM images for two-target detection (simultaneous hybridization). CU, DUT1, and DUB2 in the presence of both TT1 and TB2 (HP for CU-DUT1: 80%; HP for CU-DUB2: 83%; for calculation of HP in the case of simultaneous hybridization, CU-DUT1 and CU-DUB2 are counted for any structure containing CU-DUT1 and CU-DUB2, respectively). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~200 CU. The concentrations of TT1 and TB2 are 300 nM.

11. Four-Target DNA Detection

Figure S25. Gel electrophoresis bands for purified CU, DUT1, DUT2, DUB1, and DUB2. Lane 1: CU; Lane 2: DUT1; Lane 3: DUT2; Lane 4: DUB1; Lane 5: DUB2.
**Figure S26.** Gel electrophoresis bands for four-target (TT1, TT2, TB1, TB2; separate hybridization) detection. Lane 1: CU and DUT1 in the presence of four targets; Lane 2: CU and DUT2 in the presence of four targets; Lane 3: CU and DUB1 in the presence of four targets; Lane 4: CU and DUB2 in the presence of four targets.

**Figure S27.** Representative TEM images for four-target detection (separate hybridization). CU and DUT1, CU and DUT2, CU and DUB1, CU and DUB2 in the presence of four targets (TT1, TT2, TB1, TB2) (HP for CU-DUT1: 22%; HP for CU-DUT2: 23%; HP for CU-DUB1: 25%; HP for CU-DUB2: 24%). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~300 CU. The concentrations of four targets are all 300 nM.
Figure S28. Gel electrophoresis bands for four-target (TT1, TT2, TB1, TB2; simultaneous hybridization) detection. Lane 1: CU, DUT1, DUT2, DUB1, and DUB2 in the presence of four targets.

Figure S29. Representative TEM images for four-target detection (simultaneous hybridization). CU, DUT1, DUT2, DUB1, and DUB2 in the presence of four targets (TT1, TT2, TB1, TB2) (HP for CU-DUT1: 85%; HP for CU-DUT2: 75%; HP for CU-DUB1: 79%; HP for CU-DUB2: 86%). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~200 CU. The concentrations of four targets are all 300 nM.
12. Assembly of DCU

Figure S30. Gel electrophoresis bands for purified CU, a purified cuboid with a size identical to the core cuboid part of CU, and DCU. Lane 1: CU; Lane 2: cuboid; Lane 3: DCU.

Figure S31. Representative TEM images of DCU (HP: 86%). HP is defined as the percentage of observed DCU over all structurally resolved CU (calculated from ~250 CU).
13. Single-Target and Two-Target DNA Detection by DCU Detection System

Figure S32. Gel electrophoresis bands for purified CU, DUT1, cuboid, and DUB3. Lane 1: CU; Lane 2: DUT1; Lane 3: cuboid; Lane 4: DUB3.

Figure S33. Representative TEM images of DCU and DUT1 in the presence of TT1 (HP: 92%). B) and D) are enlarged view images of A) and C), respectively. HP is defined as the percentage of observed DCU-DUT1 over all structurally resolved DCU (calculated from ~200 DCU). The concentration of TT1 is 300 nM.
Figure S34. Representative TEM images of DCU and DUB3 in the presence of TB3 (HP: 93%). B) and D) are enlarged view images of A) and C), respectively. HP is defined as the percentage of observed DCU-DUB3 over all structurally resolved DCU (calculated from ~200 DCU). The concentration of TB3 is 300 nM.

Figure S35. Gel electrophoresis bands for two-target detection. A) DCU and DUT1 in the absence (lane 1) and presence (lane 2) of TT1, DCU and DUT1 in the presence of TB3 (lane 3), DCU and DUT1 in the presence of both TT1 and TB3 (lane 4); B) DCU and DUB3 in the absence (lane 1) and presence (lane 2) of TB3, DCU and DUB3 in the presence of TT1 (lane 3), DCU and DUB3 in the presence of both TT1 and TB3 (lane 4). The concentrations of TT1 and TB3 are 300 nM.
Figure S36. Representative TEM images for two-target detection (in the presence of one target). A) and B) DCU and DUT1, DCU and DUB3 in the presence of neither TT1 nor TB3; C) and D) DCU and DUT1, DCU and DUB3 in the presence of TT1 (HP for DCU-DUT1: 47%); E) and F) DCU and DUT1, DCU and DUB3 in the presence of TB3 (HP for DCU-DUB3: 51%). HP was determined by calculation from ~200 DCU. The concentrations of TT1 and TB3 are 300 nM.
Figure S37. Representative TEM images for two-target detection (separate hybridization, in the presence of two targets). A)-D) DCU and DUT1, DCU and DUB3 in the presence of both TT1 and TB3 (HP for DCU-DUT1: 44%; HP for DCU-DUB3: 48%). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~200 DCU. The concentrations of TT1 and TB3 are 300 nM.
**Figure S38.** Representative TEM images for two-target detection (simultaneous hybridization). DCU, DUT1, and DUB3 in the presence of both TT1 and TB3 (HP for DCU-DUT1-DUB3: 76%). B) and D) are enlarged view images of A) and C), respectively. HP was determined by calculation from ~200 DCU. The concentrations of TT1 and TB3 are 300 nM.

### 14. DNA Sequence Information

| Name          | Sequence (5’-3’)                      | Length |
|---------------|--------------------------------------|--------|
| CU TT1 capture probe | GGCTTCTAAAG                           | 11     |
| CU TT2 capture probe | AACGGCAGGAA                           | 11     |
| CU TB1 capture probe | GAATTATGAGT                           | 11     |
| CU TB2 capture probe | GCAAGGGTCAC                           | 11     |
| DCU TB3 capture probe | CGATGTGTGC                            | 11     |
| DUT1 detection probe | GGTTGTGAGATTTC                           | 15     |
| DUT2 detection probe | GGCTGGCAGGATGCT                       | 15     |
| DUB1 detection probe | GTCCGTACCGGAGC                       | 15     |
| DUB2 detection probe | GACCGAGTTACTGTT                       | 15     |
| DUB3 detection probe | GCAGCTGGTGGACCA                       | 15     |
| DCU linker-1 on CU | TAAGAGCTATGGG                           | 13     |
| DCU linker-2 on CU | CAACAGAGGCAGA                           | 13     |
| DCU linker-1 on cuboid | CCCATAGCTCTTTA                       | 13     |
| DCU linker-2 on cuboid | TCTGCCCTCTGGTT                           | 13     |
| TT1    | CTTTAGAAGCCTGAAATCCAAACAAACC                  | 26     |
Table S2. DNA sequences for the assembly of nanostructures (the sequences used for each nanostructure is marked in the corresponding color: CU, PCU, CU for DCU, cuboid for DCU, DUT1, DUT2, DUB1, DUB2, DUB3)

| Name | Sequence (5’-3’) | Length |
|------|-----------------|--------|
| 1    | CCGCTCTCTTCTTTTTTTTTTTTTTTTGTGCTTGC | 32     |
| 2    | TGACACCTTTTTTTTTTTTTTTTTGTTTCCGA | 32     |
| 3    | ACGCGGCTTTTTTTTTTTTTTTTGTTGAGGA | 32     |
| 4    | CCGCCTCTTTTTTTTTTTTTTTTTGAGCAAG | 32     |
| 5    | GCCACGACGCAAGCAGTATTATGCGGAAGAT | 32     |
| 6    | GCCTAGCTCCGAACGGAGGCTGATGATAGAA | 32     |
| 7    | CATATCCCTCTCCTACCGGAAAGCGGAGATCGC | 32     |
| 8    | CATCGCTCTTCTTCGGACAGGCGGTCGAGGA | 32     |
| 9    | ATTATCTATGTTCTGCTCCGACGCCGTTATGAG | 32     |
| 10   | TAATATATATCTACCGAGATCGGAGATCGC | 32     |
| 11   | CTCATTTCTTATCATAGGATTCGTTTTTAGG | 32     |
| 12   | GTACCGTCACTCTGCGGCAATTTACCCGGGGA | 32     |
| 13   | AATTATGATCCGGTCTCGGAGGATAATGCGGAT | 32     |
| 14   | TACCTCTCATCTCTCGACCGGATGAGATGAT | 32     |
| 15   | CCACAGATTTACTAACTCGATAGTTAAATGCTAG | 32     |
| 16   | ATCCACGCTCTCGACTGCGGACGCGCGGA | 32     |
| 17   | ATCCCGTTACATGTTCCGTCGCGCCGTTG | 32     |
| 18   | AACCCCTACCCCGGCTACGGGATCTTTGAGT | 32     |
| 19   | TTTATATCTACTTTTATCTCATTGTTGAGGGG | 32     |
| 20   | ATTTCTGTAATATACCTCCTCTGTTGTAAGG | 32     |
| 21   | CCGTGCGGCTCCCTGCTGTGGTGAAGTTGACGC | 32     |
| 22   | AGCCCGTCTTCTGACTCGAATCAGAAGTAAGTCG | 32     |
| 23   | TTCATCTTCTTTTTACTACGGGACGCGGCACAG | 32     |
| 24   | TGGCGCTCACCCTACCATGTCGCAAGGTTGGA | 32     |
| 25   | CGCATCCTACTTCTCGCATATACTTTGAAATTTTCA | 32     |
| 26   | CGTGCTACCCGCTTACGGGATTCCAGGATGAGT | 32     |
| 27   | GAACCTAGCTGCGACCGCAGGAGATGAGTGGTGT | 32     |
| 28   | ATTAACGCTTGACATGTTCCGTCGACAG | 32     |
| 29   | TCCCTGCCCGCTGCCAAGGCTGGAAGTAGAAGA | 32     |
| 30   | GCTGCTACTTACAACCTCAGGTGAGTGTG | 32     |
| 31   | CCTCTACCCTGAAACAAAGAATAGGATATTGG | 32     |
| 32   | CCAGACCTCTGCTTCTTTCTCGGACCGCTGAGTA | 32     |
| 33   | TTACAGCTTCTCGATTAGCTCGCAGGCG | 32     |
|   |   |
|---|---|
| 34 | TCGTGCCTGGTCCCCATAGAGTCACGCCGAAG |
| 35 | CGCTACAACCAACACCGTAGAGGAAGAGAGG |
| 36 | TCAAACATTCTCTATCGGGATAGTAGTATGATTAA |
| 37 | ATATAAATGCTAATCGGTGTAATAATGATG |
| 38 | CGATGACTCCACAGCTGGTGTGACGAGG |
| 39 | CGATCATGCTCGCCGACAGCAGACAGTG |
| 40 | CTCTGTACAGTGCAAGAACCGAATAGCGAGT |
| 41 | AATCGGAATTTGCTATGGGAGGTAATAGC |
| 42 | CATATATTCTTATCTAATCCAGATAATCGG |
| 43 | TACTCCACCTCTCTGTATAATAGGCTAGT |
| 44 | GCACTCGCCCTCTGACATGTTGAGCCGAGC |
| 45 | CAATAGTGATTCGTATATCAGAGGTAACG |
| 46 | GTCGAGACCCGGTTCTTGAGGATACAGG |
| 47 | TCGATCTCTTTTTTTTTTTTTTTTGGGACAA |
| 48 | ATGGTGCTTTTTTTTTTTTTTTTTAGGACAT |
| 49 | CATATAACTTTTTTTTTTTTTTTTTGAGTACAG |
| 50 | GCCCTTCTTTTTTTTTTTTTTTTGGAGACCAAAGATGTTGAGCAGG |
| 51 | ATTTAGCCCGGAGCCCTGTGCTCCTTTTTTTTTTTTTTTTGGTATTGT |
| 52 | TACTGCCCTTTTTTT |
| 53 | CGAAACCCTTTTTTT |
| 54 | TTGGAGCTACCCGACGATTTCTCTTTTTTTTTTGTCCGG |
| 55 | TACTACGTCCTCTCAACCGGCTTAGCGTCGTCGATTAGCAT |
| 56 | CAATCTCTAAATATCCAAATCCACATCCGGGTCGAGCCGACGTG |
| 57 | TGATCCCGTACAAACGCGCTCAGCAATGCGAGTCGAGTGGAT |
| 58 | TCAACACTGAAACCAGCGTACGCTGTTAGGCAAAAAGTCAAG |
| 59 | CACGCTTCTCTGTATAATGCTAAGGGCCTAGAGTCGAGT |
| 60 | TACGCTATTGCAAATGTCAGGGCGGAAATTCGAGACAA |
| 61 | CACCGCGCGCTTTATACACTTTTTTTTTTGTCAACCCGGCTTGGGAC |
| 62 | CCATATTCTTCGCCATCCTGAACCTTTAAATCCGCTGGGAGCAG |
| 63 | AACAATCCTATTGACCGGGAGTACAGGTGGGAGCGCGGGGAGG |
| 64 | TATAACACGTCTTTCTATACATCTCGCGGCTCCGGGTGTCGCCGGGTAGT |
| 65 | TTAATTCCCGTGTCCCGGGGTAATCTCGGCGACACCAGTAGACGAG |
| 66 | ACCCGTGATTACCTCTGTAACCAGTTGTTACCGGGTCTGACAG |
| 67 | CCCGGCCACCCGACCCGCGGCGCGCGGTAGGTAGTG |
| 68 | CTGAAATCCTATTGCCGAGCCCTATTACGTTGGGTCGGCAGGTG |
| 69 | ACGACACCTTTTGCGCGCCGAGATCAAGGGCATAGGGCGACTGGGAGT |
| 70 | CTTAATACCTCTAGACCACCGGCCCCTTTTATAATCCGAGGATGGGTCAGT |
| 71 | TATCACCCTATTCTCTTGCGGAGGATTTTGAGGGTGCGGGTAGTGGT |
| 72 | CACGCCCCGTATCCCGTTACCCGCTCTTGCGCCGAGCAATGGT |
| 73 | GCTATTGCACTCCTGTTGGAATCTCGGAGATCGAGT |
| 74 | TACCCACAGCTTTTACACTAATCTCTGAGTTCCGGCTATAGTGGCAG |
| 75 | TTTTTTTTGTGTTGTA |
| 76 | TTTTTTTTGAAGAACG |
| 77 | TTTTTTTTGGGATACT |
| Position | Sequence                      |
|----------|-------------------------------|
| 78       | ACATTCTTGTTCTCCGGGCAGTATGCAGGAC |
| 79       | TTGCAGCCTACAACCGGAGCACAGGCTCCCG |
| 80       | ACGTCTACGTTTTCGGATATCGGGTATCGG |
| 81       | TTAGCCATCTGACTCCGTAAGCGGTGAGGGA |
| 82       | CTCAGAACCCTGCTAGTATATGTGATTAT |
| 83       | TTCGACTTTTCGCTAGGTCTAACAAAGCCGAA |
| 84       | CCGGACCCCTAAAATCAGCAATGGAGATCGTA |
| 85       | CATCTCACAAATCACGAGATTAGTGTAAAGAC |
| 86       | TATGCTCTATGACCTAGTGTGTTGATGAT |
| 87       | CCAAGTCTTTATGGCGGCTGGAGCCCGG |
| 88       | CAAACGCCTTGTTGATGTTGTTGATGAT |
| 89       | CCCTGGACTTCTTACTGTTTCAGGGAGATG |
| 90       | TACTAATCTACACTCCGAGAACAGGTGATA |
| 91       | CCCCCGCTATGCTAGGTTGAGATGAGAT |
| 92       | TCTGGAACATCTTTAGTTTGTGGTGGAT |
| 93       | ATCCACTAATCTTTGGACAGGGGTGTAGG |
| 94       | CTCTCATCATCCACCCGCTTCAATGAGGTA |
| 95       | TCCAGTCCATGAGCGGCAAGCGGATCGT |
| 96       | TCTGCACTCATGGTCCCTGCTGGGAGATG |
| 97       | CTGCGAGGCTCTGCTGGGAGAGATGAGG |
| 98       | CACACACGCTCCGACCGCAGACAGGAGTTT |
| 99       | TTTTACATCCACACGGGAGGGGAGTGTG |
| 100      | ATATGGGCAGCTCCAAGAGCGGAGATG |
| 101      | CCAAGGCTACACCCGCTTCAATGAGGTA |
| 102      | TTTTGCTTACTCAGGATGACGGGATG |
| 103      | CTGAGGAACATTTCTGCTGGTGGTGGAT |
| 104      | ATACCTAATCTCTAGGCTAGTGTGAG |
| 105      | TCTGTATATCTCAGGCTGGTGGTGGAT |
| 106      | ATACCTATATCAGGCTGGTGGTGGTGGAT |
| 107      | CCAACACCGCAGGCGGCTGAGGAGGAG |
| 108      | TTTTACTGACACCGGAGGGGAGTGTG |
| 109      | CTATATAACCTACAGGAGCGGCGGAGGAG |
| 110      | CCACTGGATCCCAAGGAGGAGGAGGAG |
| 111      | TGAACACACACCTATCCGAGACAGAGGCAGG |
| 112      | TACTGGCTTGCTATGCTGGTGGTGGTGGAT |
| 113      | CGATTCGCTCCGCTCGGAGGGTGGATG |
| 114      | ATACCTATATGCTGCTGGTGGTGGTGGAT |
| 115      | TCGGATCCGACCGCCAGGAGGAGGAGGAG |
| 116      | TACTGGCTTGCTATGCTGGTGGTGGTGGAT |
| 117      | CCATCCATCCGCTGCTGGTGGTGGTGGAT |
| 118      | ATACCTATATGCTGCTGGTGGTGGTGGAT |
| 119      | GCGGCTGCGGCTGCTGGTGGTGGTGGAT |
| 120      | CCACTGGATCCCAAGGAGGAGGAGGAG |
| 121      | TGCACCTGTGCTCTAGGCAATCCGGGAGGCTAA |
166  GGCTCTCCTGTCCTCCGTAAGGTAGGTG
167  CACGAAACCGTGTTGGAATATGGGATGT
168  CTGTTCAACCCGAGGCTGTCGGTCGC
169  AGTTCCTGGCTCTTGATGACACAGGAGGCTG
170  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
171  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
172  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
173  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
174  TATCCACTACCCCTGAGGCGAGTGCGGTTCGCG
175  AGTTGCTCCGCTCTTGTTGGACACAGGAGGTCG
176  TTTTTTTTGGCTTAATAGCCAGCAGGCTGGAAGCTGTTAG
177  GTATTGTCTCGGCGCCGCGCGCGGTGTTGACACCAGGACTAAAG
178  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
179  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
180  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
181  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
182  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
183  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
184  TATCCACTACCCCTGAGGCGAGTGCGGTTCGCG
185  AGTTGCTCCGCTCTTGTTGGACACAGGAGGTCG
186  TTTTTTTTGGCTTAATAGCCAGCAGGCTGGAAGCTGTTAG
187  GTATTGTCTCGGCGCCGCGCGCGGTGTTGACACCAGGACTAAAG
188  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
189  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
190  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
191  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
192  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
193  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
194  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
195  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
196  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
197  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
198  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
199  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
200  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
201  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
202  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
203  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
204  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
205  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA
206  CACAAGCCACATGACTTCTGTCAAACGTCACAAGAGACGGTGGGTGGT
207  GTATCTCAAAACACTATATTGCTCATCGCGTCGGGGGTATTAGGGGAT
208  GTCCCTTCTAGCCTTCACTAATGTATATGTTGTGCGGCGTAATATGCT
209  CGCGCCTCGTATCACGATCGATGATCTGTAGAACAATGACATGGATCA

S31
DUT1-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT1-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT2-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT2-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT3-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT3-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT4-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT4-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT5-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT5-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT6-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT6-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT7-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT7-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT8-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT8-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT9-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT9-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT

DUT10-1 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-2 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-3 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-4 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-5 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-6 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-7 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-8 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-9 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
DUT10-10 TTTTTTTTTCGCGCCGAGGAGACTCATTTT
| Sequence | Details |
|----------|---------|
| DUT1-1  | TTTTTTTTGGCAACCTGTGGGCGTGTTTTTTTTGGTTGTTGGATTTCA |
| DUT1-2  | TTTTTTTTTACCGGATGCGCGGATTTTTTTTTGGTTGTTGGATTTCA |
| DUT1-3  | TTTTTTTTACTTCGTAACATATTGTTTTTTTTGGTTGTTGGATTTCA |
| DUT1-4  | TTTTTTTTTCAATACAGTCTGAACTTTTTTTTGGTTGTTGGATTTCA |
| DUT1-5  | TTTTTTTTACCCGACGTGTGGTTATTTTTTTTGGTTGTTGGATTTCA |
| DUT2-1  | TTTTTTTTTTCGCAGGTGGAGTTTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-2  | TTTTTTTTTGTCTCCGTGGAAGTATTTTTTTTGGCTGGCAGGATGCT |
| DUT2-3  | TTTTTTTTAACCCGAGGCGAGTGCTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-4  | TTTTTTTTGACATCGCGCCAAGACTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-5  | TTTTTTTTACCGTTGGGATAAATGTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-6  | TTTTTTTTGTCTCTGTTGGACACATTTTTTTTGGCTGGCAGGATGCT |
| DUT2-7  | TTTTTTTTTCGTTCACGAGACATATTTTTTTTGGCTGGCAGGATGCT |
| DUT2-8  | TTTTTTTTCGTTGCCTGAACTTGGTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-9  | TTTTTTTTTCCGTCACGTTTAAGGTTTTTTTTGGCTGGCAGGATGCT |
| DUT2-10 | TTTTTTTTTACGCTACCGAGGTACTTTTTTTTGGCTGGCAGGATGCT |
| DUB1-1  | GTCGGTTCACGGAGCTTTTTTTTTTCGCAGGTGGAGTTTTTTTTTT |
| DUB1-2  | GTCGGTTCACGGAGCTTTTTTTTTGTCTCCGTGGAAGTATTTTTTTT |
| DUB1-3  | GTCGGTTCACGGAGCTTTTTTTTTAACCCGAGGCGAGTGCTTTTTTTT |
| DUB1-4  | GTCGGTTCACGGAGCTTTTTTTTTGACATCGCGCCAAGACTTTTTTTT |
| DUB1-5  | GTCGGTTCACGGAGCTTTTTTTTTACCGTTGGGATAAATGTTTTTTTT |
| DUB1-6  | GTCGGTTCACGGAGCTTTTTTTTTGCCTCTGTGGACACATTTTTTTT |
| DUB1-7  | GTCGGTTCACGGAGCTTTTTTTTTGCTCTGGACACATTTTTTTT |
| DUB1-8  | GTCGGTTCACGGAGCTTTTTTTTTTCGTTCACGAGACATATTTTTTTT |
| DUB1-9  | GTCGGTTCACGGAGCTTTTTTTTTTCGTTGCCTGAACTTGGTTTTTTTT |
| DUB1-10 | GTCGGTTCACGGAGCTTTTTTTTTTCCGTCACGTTTAAGGTTTTTTTT |
| DUB1-11 | GTCGGTTCACGGAGCTTTTTTTTTACCGATCCGAGACTTTTTTTT |
| DUB1-12 | GTCGGTTCACGGAGCTTTTTTTTTTGGCTGGCAGGATGCT |
| DUB1-13 | GTCGGTTCACGGAGCTTTTTTTTTACTCTGTAACATATGTTTTTTTT |
| DUB1-14 | GTCGGTTCACGGAGCTTTTTTTTTCAATACAGTCTGAACTTTTTTTT |
| DUB1-15 | GTCGGTTCACGGAGCTTTTTTTTTACCGATCCGAGACTTTTTTTT |
| DUB2-1  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-2  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-3  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-4  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-5  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-6  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-7  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-8  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-9  | GACCAGATCTGTGTTTTTTTTCCGAGAGTTGGAGTTTTTTTTTTTT |
| DUB2-10 | GACCGAGTTACGTTTTTTTTTCAACGCTACCAGGGTACTTTTTTTT | 47 |
| DUB2-11 | GACCGAGTTACGTTTTTTTTTGAACGCTACCGAGGTACTTTTTTTT | 47 |
| DUB2-12 | GACCGAGTTACGTTTTTTTTTACCAGCAGGAGCATACGCTTTTTTTTT | 47 |
| DUB2-13 | GACCGAGTTACGTTTTTTTTTACCACGCGGTATTCACTTTTTTTT | 47 |
| DUB2-14 | GACCGAGTTACGTTTTTTTTTACCACGCGGTATTCACTTTTTTTT | 47 |
| DUB2-15 | GACCGAGTTACGTTTTTTTTTACCACGCGGTATTCACTTTTTTTT | 47 |
| DUB3-1   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-2   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-3   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-4   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-5   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-6   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-7   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-8   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-9   | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-10  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-11  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-12  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-13  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-14  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |
| DUB3-15  | GCAGCTCGTGACCCATTTTTTTTTAAGCACTACCCGACTTTTTTTT | 47 |

15. References

S1  N. C. Seeman, *J. Biomol. Struct. Dyn.*, 1990, 8, 573-581.
S2  B. Wei, M. Dai and P. Yin, *Nature*, 2012, 485, 623-627.
S3  Y. Ke, L. L. Ong, W. M. Shih and P. Yin, *Science*, 2012, 338, 1177-1183.