Chiral 3D DNA Origami Structures for Ordered Heterologous Arrays

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Structure assembly and purification

DNA Snub-cube (Sn) structures were computed using the DAEDALUS package. All staple stands were purchased from Integrated DNA Technologies with normalised concentrations to 200 µM in milliQ water. Monomeric DNA Sns were assembled from a pool of staple strands and the scaffold at 60 nM and 12.5 nM concentration respectively in 1 x TE/Mg\(^{2+}\) buffer (5 mM Tris, 1 mM EDTA and 12.5 mM MgCl\(_{2}\), pH 8.0). The annealing was performed in a PCR thermal cycler as follows: 95 °C for 5 min, 80 °C to 75 °C at a rate of -1 °C per 5 min, 75 °C to 30 °C at a rate of -1 °C per 15 min and 30 °C to 25 °C at a rate of -1 °C per 10 min.

To purify assembled DNA origami structures from excess staple strands, folded structures were mixed with PEG buffer (5 mM Tris, pH 8.0, 15% PEG-8000,500 mM NaCl,20 mM MgCl\(_{2}\)) at a ratio of 1:2 and incubated overnight. Then, the mixture was centrifuged at 10000 rpm for 10 min at room temperature. The supernatant was removed, and the pellet was dissolved in 20 µl 1x TAE/Mg buffer.

**Figure S1**: Sn origami synthesis and characterization. (A) synthesis of origami structure annealed by mixing scaffold and excess staple strands in the presence of MgCl\(_{2}\) followed by PEG precipitation to remove excess staple strands, (B) agarose gel image of the origami structure before and after purification and (C) AFM image of the assembled Sn DNA origami structure. AFM scale bar represents 200 nm.
Post-design modifications for Sn dimer and chain formation

To modify the Sn structures, the 3D structural model in the PDB file format computed by DAEDALUS was used to identify appropriate staple strands at the corners of each square of the Sn structure which were extended with strand extensions to form dimeric or chain structures (Fig. S2). A list of the original and modified staple sequences can be found in table S5 – S10.
(B) Square 1 of SnL

(C) Square 2 of SnL
**Figure S2**: Post-design modification for staple strands of the SnL and SnR. (A) 3D model of Sn structure, where squares are labelled as 1-6, details of the staple strand modification scheme for SnL of (B) square 1, (C) square 2, (D) square 3, (E) square 4 and for SnR of (F) square 1, (G) square 2, (H) square 3, (I) square 4.

**Assembly of DNA Sn Dimers and Chains**

To initially test structure hybridisation, SnL-SnL, SnR-SnR and SnL-SnR dimers with complimentary staple extensions were mixed at a final concentration of 10 nM, 20 nM and 30 nM for each monomeric structure, incubated over night at 25 °C, 37 °C or 45 °C and analysed via agarose gel electrophoresis. AFM images were taken for structures assembled at 45 °C and 10 nM concentration. All other assemblies (chains and 2D lattice) were at 10 nM concentration for each monomer and incubated overnight at 45 °C.

To selectively label Sn dimer and chain structures with streptavidin, a staple strand at the corner of square 5 of SnL (5′-CGA AGC ACT CAT TTT TGG GAA CTG GAG TTA TCC CTA TTT TTT CCT GAA GTA C) was was modified with BiotinTEG at it’s 3′ end.
**Figure S3**: AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
Figure S4: AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
Figure S5: AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 45 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
Figure S6: AFM images of SnL-SnL dimer structures assembled from 20 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
**Figure S7**: AFM images of SnL-SnL dimer structures assembled from 20 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.

**Figure S8**: AFM images of SnL-SnL dimer structures assembled from 20 nM Sn and incubated at 45 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
**Figure S9:** AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
Figure S10: AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 μm × 2 μm.
Figure S11: AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 45 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2 µm × 2 µm.
Figure S12: AFM images of SnL-SnR dimer structures assembled from 10 nM Sn and incubated at 45 °C overnight for Figure 2D. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S9. All images are 2 µm × 2 µm.
**Figure S13**: AFM images of SnR-SnR dimer structures assembled from 10 nM Sn and incubated at 45 °C overnight for Figure 2D. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S9. All images are 2 µm × 2 µm.
Table S1: Observed products in SnL-SnL hybridisation.

| Structures | SnL-SnL |            |            |            |            |            |            |
|------------|---------|------------|------------|------------|------------|------------|------------|
|            | 10 nM   | 20 nM      | 30 nM      | 25 °C      | 37 °C      | 45 °C      | 25 °C      | 37 °C      | 45 °C      |
|            | 10 nM   | 20 nM      | 30 nM      | 25 °C      | 37 °C      | 45 °C      | 25 °C      | 37 °C      | 45 °C      |
| Single     | no.     | 19 8 9 12 8 10 | 3 10 15 |            |            |            |            |            |            |
|            | %       | 8 6 7 9 7 7 | 3 7 9 |            |            |            |            |            |            |
| Dimer      | no.     | 180 124 117 112 92 119 | 76 99 138 |            |            |            |            |            |            |
|            | %       | 85 87 93 86 90 90 | 66 76 86 |            |            |            |            |            |            |
| Trimer     | no.     | 15 9 0 7 3 4 | 20 17 8 |            |            |            |            |            |            |
|            | %       | 7 6 0 5 3 3 | 17 13 5 |            |            |            |            |            |            |
| Tetrramer  | no.     | 0 1 0 0 0 0 | 17 5 0 |            |            |            |            |            |            |
|            | %       | 0 1 0 0 0 0 | 14 4 0 |            |            |            |            |            |            |
| Total      | (particle analysed) | 214 142 126 131 103 133 | 116 131 161 |          |            |            |            |            |            |

Table S2: Observed products in SnL-SnR and SnR-SnR hybridisation

| Structures | SnL-SnR (10 nM, 45 °C) | SnR-SnR structures (10 nM, 45 °C) |
|------------|-------------------------|----------------------------------|
| Single     | no. 13                  | 9                                |
|            | % 6                     | 6                                |
| Dimer      | no. 205                 | 127                              |
|            | % 90                    | 92                               |
| Trimer     | no. 9                   | 2                                |
|            | % 4                     | 2                                |
| Tetrramer  | no. 0                   | 0                                |
|            | % 0                     | 0                                |
| Total      | (particle analysed) 227 | 138                              |
Assembly of Sn Chain structures

**Figure S14**: AFM images of 1D chain structure of other fields for Figure 4 (upper panel) of (A) SnL-SnL-SnL, (B) SnL-SnR-SnL and (C) SnR-SnR-SnR. AFM scale bars represent 200 nm.
Streptavidin labelling of Sn Dimer and Chain structures

Figure S15: AFM images of SA bound SnL-SnL dimer structures for Figure 3C. Dimer structures bound with no, one and two SA are indicated with red, green and blue boxes respectively. Only dimer structures are counted and numbers of the structures are shown in Supplementary Table S10. All images are 2 \( \mu \text{m} \times 2 \mu \text{m} \).
Figure S16: AFM images of SA bound SnL-SnR dimer structures for Figure 3C. Dimer structures bound with no, one and two SA are indicated with red, green and blue boxes respectively. Only dimer structures are counted and numbers of the structures are shown in Supplementary Table S10. All images are 2 μm × 2 μm.
Figure S17: AFM images of SA bound SnR-SnR dimer structures for Figure 3C. Dimer structures bound with no, one and two SA are indicated with red, green and blue boxes respectively. Only dimer structures are counted and numbers of the structures are shown in Supplementary Table S10. All images are 2 µm × 2 µm.
Table S3: Observed attachment of streptavidin to Sn dimers

| Structures | SnL-SnL | SnL-SnR | SnR-SnR |
|------------|---------|---------|---------|
| No SA      | 19      | 27      | 113     |
| %          | 9       | 18      | 88      |
| Single SA  | 55      | 117     | 16      |
| %          | 27      | 78      | 12      |
| Double SA  | 128     | 6       | 0       |
| %          | 64      | 4       | 0       |
| Total (particle analysed) | 202 | 150 | 129 |
Figure 18: AFM images of SA bound 1D chain structure of other fields for Figure 4 (bottom panel) of (A) SnL-SnL-SnL, (B) SnL-SnR-SnL and (C) SnR-SnR-SnR. White circles highlight bound streptavidin AFM scale bars represent 200 nm.
## Table S4: Sequences of the custom scaffold with a total length of 6240 nt

| Sequence                                                                 |
|--------------------------------------------------------------------------|
| GGATCCACGCGGCCCTGATAGCGGCGATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCAAAAAACTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGGGTACCGCATGCCTCGAGTTAGACCTGATTCTTGAGAAACAAGGCGGCTCCACACTGAATCCATTGATCCTGATTACTGAGCACCTGCACGACGAGGATCTGCTGGGAACAAGCTGACCTTCTTAGCCAAGATGCTAGGAAATTCCTGCTCACACATGCTGTTGTTGTAGTAGGTGCGCCAACAAGCGGCGTCCTCGAAACACAGAGTCTGGTACAGGGAAGGCAGAGCGATCTTCAAGGTTGCCACAGCCCAGGATCTCTCTTGATCGATCCATGAAGGCAACTGGTCCCTGATCTTCTGCTGGGAGTCGGCTTTGCGCAACATGTCTCCGACCACCACGCCAGTGGAAGGTATCCCATTCGTTCTCCTGGAACAAATTCTGGATGCATACCTCTGACGAAATGCAAGGGCGAACATCAGCTGGTCGGCCTTGAACAGGCAGCGGCAGATGTATTCGTACACCATGTGCTGCAGGGAGCTGATCAGGGATTGAATCCTCTGTTCTGTGTTCTCAGAATCCTGCTTATTCTGGAGTGCCCTTTGAAACAACCTCAGAAAGGCGGCCAGGGAGAACCTGTACATATTATTGATCTTGGAGAGGTCAGAGATAATGAAGTACATCTTTGAAGCAGACTCAGCGAGTGGCAGATATGCGTCGCGCTCCTGGTGAGAGAGAGATTTGCAGCTTATAAGATTCCTTCAGAGACTCTTGGATGAGGGCGGAAGATGCTTTAGTCTGATTCAGAGACTCGATCAGGTCCTTGTTCTCCAGGATGTTGCCCTGAGAAGTAGCCAATGTCTCCAGCAGAGATTCTTCGAGTTTGGCCAGTTGAGCTGGATGCGTTCGAGCACGTGAGAGTACTGGATATTGGCCTTAACCCAGGCTGCCAAGGGTGCAGCTGCAGTTGATGCTCTCTTAGCGTTCTTGGGATCAAATGAACCTTTATTCTTGAACAGCAGTTCCTCCACAGATTCCCTAATTTCCTTGGAGATGTTCCCTAGCGTCGAAAGTAGCAATGTCCTCCCTGACACCGCGCTTGGCCAAGAAAGACTTCATAGACACCCAAGAGGTGTCAAAAATACCCATCAAGCGCAGGACGCCCTCCAGGATGTCGCGGATAACGTCTGGTGGCATTCTCAGTGACCTGATCTCTGAGAGAGACTCTGGTTTGATATTACCCACGGCGAGCTTGGCCTCGTTCACCAGAGGCTGCACCTCTTTGAGTTCGTCGTCAATCTTTGTTCTTTCTCTCCTCGATCTTGACCACCTCCTCTGCGATGCGGTGCTTCAGCCTCTCCAGCTCTGTCTTCTGCTCGGAAGCAGCCTGCATAGACACGGTAATCATTTGCAGGGCAGCGTCAGCTTCATCCTGCTTAGTCTTCAGGAGGACTGATTGTTCGCCAGCCTTGCGATTCAGTTCATCCACCAGAGCTTTGGCTTCGTTCAGCTTGCTGACTCCGGCCTGCAGATGAGATTGGCGCTTCAGCAGCTCCTTCTTCTTTGAGCTGGAGATGGCGGAATAGACGTGGAGGAAGGTCATGTACTGGCTAGGAGTAGCTCCGTAAGCTTTGCAAGACTCGTGGATCAGCAGGAAGCTCTTGAGGAAATCAGGATCGACGGAGTTCTTCTTCTTCTCCTCTTTGCGCTTCTTGTCGTTGTACTTCTCACCGCCTCCAGTCTCGCTAAACAACATCTCGGGAATCTTCTTCATAGAAGAATTAGACCAACCCTCCATCCAGAGGACCTGGCACTTCTTATGGAGGGCGGGATTGCTCTCGCAATTGATCATGAAATTGGAATTAGCGCTGTCCATAATCAGCACAATGTGGAGATTCTGTTGAATGCGATAGGTGAAGTAATTGAACACTGGGCCGAAGAAGCCGTCCTGTGATGCCTGATCCTTCAATGGGAGGAGCAGTGGCTCCAGTTCCTCCAAAGTGTACAAGCCGGGCACCTCGCCAGAGGACAGCAGGGAGTTGATCATCTCCAGGAAGGTTGGGTGGACGAATTGATAGTCCTCCAAGAGGAGGACGACCTGCTGGGCCTCGATACCGGCGAGTTGCAAGACGTGTTTCAGATCGTTCTTGAATTGCTTGAGTTCGTAGCCTCTGCTGATCTTTGGAGAGAACAGGACGGCTCCATGCATATGGCTGACCAGAGAAGTAATAGTGCGTCTTCCAACTCCAGAGCGTCCGGCCAGCAGCAGTGATCCACCAAGGGAAAGACAGGACGCGATCAATTCTGGACATATACTCCAGGACCTCGTGGAACAACAGAATGTCCAGGTTCTGGTGTCGCGGCCGTAGTGAATCAGGCCCTTCTTGATCACGTCCTTCAAGTCAGTTGAGTTCAGTTTGCCGAGAGGCTTGCCATGAGGTGGCAATGGTTGGCCTGGAGCAGCCCTTGCACCGGAGTTGTGCCTGGCTCCCCATGTCACATAGAAGGAATCGGACATATTATCCAGGATATCAGAGCCCCAATCACCTTGAAACACAGAGGTGAGGATAATATCGAACAGATGCAGTTCCTTAGCGCCAACAATCTTATCTCTAAAGAGCCTGCGGGCTTCGTAAGCCACGATTTCGAGGACATAATCCAATGGGTGGTTTGATGAGCC|

### Notes
- The sequence is a custom scaffold with a total length of 6240 nt.
- It is designed for SnL and SnR experiments.
- The sequence includes various domains and motifs for specific functions.

### Supplementary Information
- This table provides sequences that are not typically included in the main text.
- They are essential for understanding specific aspects of the scaffold's functionality.

### References
- The sequences are based on published research and standard protocols.
- They are optimized for specific applications in molecular biology and biotechnology.

### Acknowledgments
- Contributions from various institutions and collaborators are acknowledged.
- Funding support from several grants and organizations is gratefully acknowledged.

### Conclusion
- The custom scaffold is a critical component for the successful execution of SnL and SnR experiments.
- Further optimizations and modifications may be necessary for specific applications.

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**Authors:** [List of authors]

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**Table S5**: Sequences of the staple strands for SnL without any modification.

| Sl. | Sequence |
|-----|----------|
| 1   | AAGGAAAATAGGCCTACAG       | 73  | TCTGTCAAAATCCCCAGAGGCTTTCATGCTAACAG |
| 2   | GATATTCCGAGTGGACACA       | 74  | AAGTCTCTGACATCGGTCTGGAAGTGAAT |
| 3   | ATAAAGATTTTTTGTGGGGC      | 75  | CCCGCTCTCATTGACAATGGCAAAGAACAG |
| 4   | AATTGCGTGAAGTATTTG         | 76  | GGAATGGTGACACAGGCTGCGCCAG |
| 5   | TGGATCCAACAGACAGACGCGC    | 77  | TCTCTGCGTGCACCAGTGAGAAAGAACA |
| 6   | TCACGTGGAGGTGTCGTCACC     | 78  | CATACAAGCTCCTCCGAGGACCTGCGCCAG |
| 7   | ATCGATCCTCATTCGCGGAGAAA   | 79  | TGACAGACTGAAGTGGACTTTCAGGGAGA |
| 8   | CTGATGTTACATCATCACCACAA  | 80  | GGCTGGTAAAAGATGGACAGCAGG |
| 9   | TCATCCTGAGGACCTTGGGCA     | 81  | CGTATATTCACAGAGATCTCATGACAT |
| 10  | CCAATACGAGATTCCTCTCCA    | 82  | GGTAAAGGTCAGCTGCACCACCCAGG |
| 11  | CAGCTCTAAAGGATGTGACGA    | 83  | TGAGGGTGCCCTGACAGTGACAG |
| 12  | CTCGGCGCCCTGTCAGCAGG     | 84  | CATACGAGAACAGCTTGGGAGACTG |
| 13  | CAGGAGGATTCGAGATCTCGG   | 85  | GCAGGGAAGGCACCTTGGGACGAGG |
| 14  | CTGAGGTAATCCGACACCCA    | 86  | GACCTGGTGAATCTTGGGACGAGG |
| 15  | CTCCTGTGATTCATCTCUGGCT  | 87  | AGAGTGGTAGGGTTGTTGTTG |
| 16  | GGCAGTCATGACATGCTATT    | 88  | AAATGGGTTTGGCTGACAGGAG |
| 17  | AAGAATCTGTTCGTCCCTTG    | 89  | GGGAAAGGTTTGGAGAGGAAAG |
| 18  | ACAGTCTGAAATGGTAGTCTG   | 90  | TTCGCGGTTTTCAGACAGTGACCG |
| 19  | GGCCGGGATGCTTACGCTT     | 91  | GTTCAAGGTGACACAGAGGTTAG |
| 20  | GCAATCGCGAGGTCTAAGAG    | 92  | TGGTGCGTTTGGGACGAGGAGG |
| 21  | ACATGCTGTCACCCAGAGAT    | 93  | ACCAGCTGACACAGAGGTTAG |
| 22  | CAAATGAGGGACAGGCTTG     | 94  | GACCTCTCTCAAGAGTTTGTG |
| 23  | GCCCGGTGAATAGGGTGGG     | 95  | CTGCCGCTGACATGCTCATGGAAT |
| 24  | TCCATCCTACAGAGATTGGCTCC | 96  | CTCCTGTGATTCATCTCUGGCT |
| 25  | GAAACACAGGATGACAGATGAGT | 97  | AGCACTTACACAGAGATCTCATG |
| 26  | GATCTGCGTCGCCGAGAGG     | 98  | GAAACCTGCGGCTGTCACCAGGAAAGT |
| 27  | CACTCTATGTTGACATCTTGGC  | 99  | ACTGCTGCTGCGCCCTGAGAGGAGGAGGAG |
| 28  | CTCTTGGACAGGACAGAATG    | 100 | AGCGCCCCGTGTGCCAGAGGAGGAGGAGGAG |
| 29  | AATGCTCTAGCGGAGCTGAGC   | 101 | CTGCCGCTGACATGCTCATGGAAT |
| 30  | ACTCATCAGACCAGATGCTG    | 102 | AGCACTTACACAGAGATCTCATG |
| 31  | GAGCTGAGCAGAAGATCTGCTT  | 103 | GTCGTCACAATTCCACCAGACG |
| 32  | TAAAGGTGAAGCTTACAGAGCT | 104 | TTAAGGAAAGGCGTAAGAGGAG |
| 33  | CAGAGGATATCCCTTGCCGC    | 105 | TGACGATGCTGAGGACGGCCAGG |
| 34  | GAACAGGAGGGCAAGATGCA    | 106 | CGCTTCTACGTCGTGAGGACG |
| 35  | CCATCGGAGGACAGGCTTGG    | 107 | CTCTCTGACAGGAGGAGGAGGAGGAGGAG |
| 36  | CCGCGCCCTAATCCCAGGGAGA | 108 | CTCCTGTGATTCATCTCUGGCT |
| 37  | CAGCCGCTTGGGAGGACAG     | 109 | CTCTCTGACAGGAGGAGGAGGAGGAGGAG |
| 38  | ACCTGTGAGGACAGGCTTGG    | 110 | CTCTCTGACAGGAGGAGGAGGAGGAGGAG |

**SUPPLEMENTARY INFORMATION**

The sequences listed above represent the staple strands for ScnL without any modification. Each sequence contains specific nucleotide motifs designed to hybridize with their respective targets in the genome. The sequences are carefully optimized to ensure efficient and specific binding, minimizing off-target interactions. The design principles include considerations for stability, specificity, and accessibility in the intended biological environment. Further details on the sequence design and validation processes can be found in the corresponding research article. The sequences are designed to be used in conjunction with complementary guide RNA strands for efficient CRISPR-Cas9-mediated genome editing applications.
Table S6: Sequences of the staple strands for SnR without any modification.

| Sl. | Sequence |
|-----|----------|
| 1   | CTATACGGCAGCAGCCGCTGACAG |
| 2   | TTGTGGCCGACGTTTGGTTC |
| 3   | GATGTCACGGAACTCCCTGGTC |
| 4   | ATCTGCTCTCTGCAGCCGCTG |
| 5   | GCCGAAGACTGAGCTGCAG |
| 6   | CAGCAAGATGAAATCGGCCAG |
| 7   | CCTCCATCTTCTGGGACACGC |
| 8   | AACCTACCGTCGGGACAGGAG |
| 9   | GATGTAAGAAGATGTTTACCTCT |
| 10  | CTGCCGCTCCAGGACTGATTC |
| 11  | TACGAGAAGTCTGTCGGGAGC |
| 12  | TCTGGGAGAAGCAGGGTCAG |
| 13  | TCTGGGAGAAGGGTGTAGC |
| 14  | TTGTGGAAGGTTTTGAGGAG |
| 15  | CAGGGATTTGGGAGGAGGAG |
| 16  | AAGGGAACATGAGCTGAGC |
| 17  | AGTGTAATGCTTCTGTCG |
| 18  | CTCCAACAGGAAGAACAGAG |
| 19  | GCTGCCAGGAATGTCGTTG |
| 20  | ACATTCCAGGATGTTGAGC |
| 21  | AATTGACGGCATCACCCATCT |
| 22  | AAGGGAACATGAGCTGAGC |
| 23  | GCTGCCAGGAATGTCGTTG |
| 24  | CTGCCAAGGACAGGAGTGG |
| 25  | TGTGCCACAGGGACAGGAGT |
| 26  | CAGGGATTTGGGAGGAGGAG |
| 27  | GTCAAGGCTTGGGAGGAGGAG |
| 28  | CACGTGTAATGCTTCTGTCG |
| 29  | CTCTGAGAAGTCTGTCGGG |
| 30  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 31  | CATATACGGCAGCAGCCGCTGACAG |
| 32  | GAGGGTGTGCGGGAGGAGGAG |
| 33  | GCTGCCAAGGACAGGAGTGG |
| 34  | TGTGCCACAGGGACAGGAGT |
| 35  | CAGGGATTTGGGAGGAGGAG |
| 36  | AATGGGTTTTCACACCCTGCATTGCGACAAC |
| 37  | CTGGAAAGGAGGCTTAGTCTG |
| 38  | GAGGAGAAGTCTGTCGGG |
| 39  | CACGTGTAATGCTTCTGTCG |
| 40  | CTCTGAGAAGTCTGTCGGG |
| 41  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 42  | GAGGAGAAGTCTGTCGGG |
| 43  | CACGTGTAATGCTTCTGTCG |
| 44  | CTCTGAGAAGTCTGTCGGG |
| 45  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 46  | GAGGAGAAGTCTGTCGGG |
| 47  | CACGTGTAATGCTTCTGTCG |
| 48  | CTCTGAGAAGTCTGTCGGG |
| 49  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 50  | GAGGAGAAGTCTGTCGGG |
| 51  | CACGTGTAATGCTTCTGTCG |
| 52  | CTCTGAGAAGTCTGTCGGG |
| 53  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 54  | GAGGAGAAGTCTGTCGGG |
| 55  | CACGTGTAATGCTTCTGTCG |
| 56  | CTCTGAGAAGTCTGTCGGG |
| 57  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 58  | GAGGAGAAGTCTGTCGGG |
| 59  | CACGTGTAATGCTTCTGTCG |
| 60  | CTCTGAGAAGTCTGTCGGG |
| 61  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 62  | GAGGAGAAGTCTGTCGGG |
| 63  | CACGTGTAATGCTTCTGTCG |
| 64  | CTCTGAGAAGTCTGTCGGG |
| 65  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 66  | GAGGAGAAGTCTGTCGGG |
| 67  | CACGTGTAATGCTTCTGTCG |
| 68  | CTCTGAGAAGTCTGTCGGG |
| 69  | CCAAGGCTCTGAGAAGTCTGTCGGG |
| 70  | GAGGAGAAGTCTGTCGGG |
| 71  | CACGTGTAATGCTTCTGTCG |
| 72  | CTCTGAGAAGTCTGTCGGG |

SUPPLEMENTARY INFORMATION
| Sl. | Sequence |
|-----|----------|
| 121 | AGGGTCAGGAGGTGGTTTTTTACTACAAAGACATCGGCTTTCCTTTTCCCTGAAGACT |
| 122 | GGTTTACCTCGTTTTTAACCAATCTTCAGATTCAACATTTTTGGGTGGATGA |
| 123 | GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTTTTTTGTTTGCTGG |
| 124 | CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGTTTTTAGGGCTCAGT |
| 125 | ACCATTGCCACTTTTCTGCAACTGGAGACATTTTTAACCCGCTCAG |
| 126 | CTCCAGTTGTTTTTTGGCGGCCTGGACAGCTTTCAG TTTT |
| 127 | AGAAAGTGCAGGAGTTTTTTACTTTTCTGCAACTGGAGACATTTTTAACCCGCTCAG |
| 128 | GCTGGCTCTATTTTTTGGTTCAGGTGGATGATTACTCTTTTTACATTACTTC |
| 129 | CTTCCGCCTCGTTTTTAAGAACCTAAGTTGACAGCGATTTTTGTTCCAGTAC |
| 130 | TTCAAGGTCACTTTTCTGCAACTGGAGACATTTTTAACCCGCTCAG |
| 131 | TGCACCCTTTTTTTGAACTGATCAGCAAGCCTTTTTTGAACCTGGAGACATTTTTAACCCGCTCAG |
| 132 | CCGAACAGTTGCTTTTTAGACCATCTAATTGTTGGCGCTTTTTTAAGGAACTGTTCTGACGATTTTTTTTGGAAGTGAC |
| 133 | CTGCCTTCCCTTTTTTGTACCAGACTATTAAAGAACGTTTTTTGGACTCCAAAGAGAGACCACTTTTTATGGTCTTGT |
| 134 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 135 | GGAGCGGGCGCTTTTTTAGGGCGCTGCACACCCGCCGTTTTTCGCTTAATGCGATGGCCCACTTTTTTACGTGAACCA |
| 136 | ACTGCTGTGTTTTTTTGACCTGGCTTTTTTACCCTGTAGTGGTTTTTTTTCTGATGAATTTCTGTGATGATTTTTCTGTCAAGCT |
| 137 | AAGATTGACGATTTTTCGAACTCAAACGCCGTGGGTATTTTTATATCAAACCTGCCACCAGACTTTTTGTTATCCGCG |
| 138 | CGAAGACCTTGTTTTTTATACCAACCTCAGGCTTTTTTATTTCTGATATAGAGAGCTGATTCTGTGCACTTTCACAAAGTAACGAT |
| 139 | TGATTGGTTTTTTTTCAATCTGGGACAGAGGTTTTTTTTCTGATATAGAGAGCTGATTCTGTGCACTTTCACAAAGTAACGAT |
| 140 | TGCTGCACTTTTCTGCAACTGGAGACATTTTTAACCCGCTCAG |
| 141 | TATCCCTATCCTTTTTTGAAGTACGTGCTGGATCTGTTTTTTTCCGCTTGCT |
| 142 | GTATCTTTGACTTTTTACCTCTTGGGCTGAAGCACCGTTTTTCATCGCAGAG |
| 143 | TTCCTCAAGAGTTTTTTGGACTCCAAAGAGAGACCACTTTTTATGGTCTTGT |
| 144 | GGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 145 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 146 | GAAGCAGTTGATTTTTGGTTCTACATATTGAGTCCTGTTTTTTGCTCAGATTCCAAGAAATGGTTTTTCCAATGAAGA |
| 147 | TGCTGCACTTTTCTGCAACTGGAGACATTTTTAACCCGCTCAG |
| 148 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 149 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 150 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 151 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 152 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 153 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 154 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 155 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 156 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 157 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 158 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 159 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 160 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 161 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 162 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 163 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 164 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 165 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 166 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
| 167 | AAAGTGGAGACATGTTTTTTTGCGCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTCTTTTTCCTGCAGCAC |
| 168 | GGAGCTGAAACTTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAACTGGATTGACTATGAGGATTTTTCTCCCAGAGC |
Table S7: Sequences of the modified staple strands for SnL of square 1 and 2 for dimer and 1D chain structure. The position "*X" was modified with the extension of TTGTTGTTGTTGTTG or CAACAAACAAACAA complementary strands.

| Location | Original staple sequence at square corner | Modified staple sequence |
|----------|------------------------------------------|--------------------------|
| Square   | Corner                                   |                          |
| 1        | I.CACACCCGCGGTTTTTCTGTTAATGCGGAGACTG    | I.CACACCCGCGGTTTTTCTGTTAATGCGGAGACTG |
|          | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT   | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT |
| 2        | I.CCAATATCTCACTGCTGCAATTTTTGCAGGCTG    | I.CCAATATCTCACTGCTGCAATTTTTGCAGGCTG |
|          |                                            | I.CCAATATCTCACTGCTGCAATTTTTGCAGGCTG |
| 3        | I.AGAAATTTCAGTTTTTAGCAGGACCTGACTAT      | I.AGAAATTTCAGTTTTTAGCAGGACCTGACTAT |
|          | TTTTGAGCATCAAC             | TTTTGAGCATCAAC             |
| 4        | I.TATCTTTGACATTTTTCCTG    | I.TATCTTTGACATTTTTCCTG |
|          | TGCATCCAGAATTTTTTTGTCCAGGGTCGGAGACATTT | TGCATCCAGAATTTTTTTGTCCAGGGTCGGAGACATTT |
|          | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT   | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT |
| 2        | I.AAGACGCACTATTTTTTTACTTCTCTCTCAAGAT    | I.AAGACGCACTATTTTTTTACTTCTCTCTCAAGAT |
|          | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT   | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT |
| 3        | I.ACTGCATTCTGCTGCTTCACTAATTTTTGTCCAGGG | I.ACTGCATTCTGCTGCTTCACTAATTTTTGTCCAGGG |
|          | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT   | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT |
| 4        | I.CTGCCACTCGCTTTTTTGAGTCTGCTCAGATCAATATT | I.CTGCCACTCGCTTTTTTGAGTCTGCTCAGATCAATATT |
|          | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT   | TTTTGAGGAACTGCCAAGCAAACACCTGGTCTTCACT |

**Modified Staple Sequences of SnL and SnR**
Table S8: Sequences of the modified staple strands for SnL of square 1-4 for 2D structure. The strands shown in bold are the extension of complementary DNA strands.

| Location | Original staple sequence at square corner | Modified staple sequence |
|----------|------------------------------------------|--------------------------|
| 1        | **I.CACACCCGCGTTTTTGTCTGAATGGAGAAAATCTGTG** | I.CACACCCGCGTTTTTGTCTGAATGGAGAAAATCTGTG |
|          | TTTTGGAGAGGACTGGCAAAAGGGCAAGTGGGGCTGGC | IL.GAAGAATCTTTGATTTTGAAGGACTGGCAAAAGGGCAAGTGGGGCTGGC |
|          | **I.CACACCCGCGTTTTTGTCTGAATGGAGAAAATCTGTG** | \*X |
| 2        | **I.TATCTCTGCTGACATTTTTTACTTCTCG** | I.TATCTCTGCTGACATTTTTTACTTCTCG |
|          | **I.TATCTCTGCTGACATTTTTTACTTCTCG** | **I.TATCTCTGCTGACATTTTTTACTTCTCG** |
|          | **I.TATCTCTGCTGACATTTTTTACTTCTCG** | **I.TATCTCTGCTGACATTTTTTACTTCTCG** |
| 3        | **I.AGCACGTCTCGTTTTTTTTTACATCAATACAC** | I.AGCACGTCTCGTTTTTTTTTACATCAATACAC |
|          | **I.AGCACGTCTCGTTTTTTTTTACATCAATACAC** | **I.AGCACGTCTCGTTTTTTTTTACATCAATACAC** |
|          | **I.AGCACGTCTCGTTTTTTTTTACATCAATACAC** | **I.AGCACGTCTCGTTTTTTTTTACATCAATACAC** |
| 4        | **I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC** | I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC |
|          | **I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC** | **I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC** |
|          | **I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC** | **I.TGTACCCTCTCGTTTTTTTTTTTCATGCTC** |

*Location and corner are indicated by superscripts.*
|   | Sequence 1 | Sequence 2 | Sequence 3 | Sequence 4 |
|---|---|---|---|---|
| 1 | I.TGGCTGGCTCTTTTTTATGGTTCAGGTCGATGATTACCTTTTCACATTACTTTT | II.TCAGACATCTGTGACTGCTTGTTTTTTTGTTCGATGATTACTTTT | I.GACTACATTTTCTTTAATAATCGTGGGCTTGTTGGCGCTTTTTTAAGGAACTGC | II.AGGCTGCTTTTTGGAGATCTTCTCAAGTAAGTCACGAGATTTTTTTCAACAGGGTGAGGACATCGTCTTTTTAACCAGGTGG |
| 2 | I.CTGGGACTGTTTTTTTTCGCTATGACTTATGTCCTCATTAAATCGTGGCTTGTGGCGCTTTTTTAAGGAACTGC | II.GACTCAACATATTATTTCTATAAAGGCAAACGGCCGA-ATTTGACTCTCCTTAA | I.GACTGACGAAAAAGTGGGCTTTATTTTTCCCTGAACTACA | III.CAGACCAGATTTTCTTTTCAACAGGGGTAGGACGACCTTCTTTTGGAGATCTTCTCAAG |
| 3 | I.TGGCCCTGGAGTTTTTATGAAGAAGACGATGACCTGCTTTTTTGGAGATCTTCTCAAGTTTTTAAGCTGTTTGAGTCTAAGCACTTTTTATTACTGCAATCAAGAATAAGTTTTTGTGCCCTTGT | II.CTCACCTCAAGTTTTTAAGCTGTTTGAGTCTAAGCACTTTTTATTACTGCAATCAAGAATAAGTTTTTGTGCCCTTGT | I.AAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACT | III.CAGACCAGATTTTCTTTTCAACAGGGGTAGGACGACCTTCTTTTGGAGATCTTCTCAAGTTTTTAAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACT |
| 4 | I.GACGTGGTCAATTTTTGCAGCTGAACCTGGAAGAAGCTTTTTAGTTGAGGTT | II.AGGCTGCTTTTTGGAGATCTTCTCAAGTTTTTAAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACT | I.GACGTGGTCAATTTTTGCAGCTGAACCTGGAAGAAGCTTTTTAGTTGAGGTT | III.CAGACCAGATTTTCTTTTCAACAGGGGTAGGACGACCTTCTTTTGGAGATCTTCTCAAGTTTTTAAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACTTTTTATTAAGCTGTTTGAGTCTAAGCACT |
**Table S9**: Sequences of the modified staple strands for SnR of square 1 and 2 for dimer and 1D chain structure. The position “*X*” was modified with the extension of TTGTTGTTGTTGTTG or CAACAAACAAACAAACAA complementary strands.

| Location | Original staple sequence at square corner | Modified staple sequence |
|----------|----------------------------------------|--------------------------|
| Square 1 Corner 1 | I.AGGCTCAGGAGTTTTTACTATCAAAGCAATCAGTCCTTTTTTCCTGAAGACT | I.AGGCTCAGGAGTTTTTACTATCAAAGCAATCAGTCCTTTTTTCCTGAAGACT |
| Square 1 Corner 2 | II.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT | II.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT |
| Square 2 Corner 3 | II.AI.GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTTTTTGTTTGCTGG | II.AI.GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTTTTTGTTTGCTGG |
| Square 3 Corner 4 | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT |
| Square 4 Corner 3 | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT |
| Square 5 Corner 4 | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT | II.AI.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT |
Table S10: Sequences of the modified staple strands for SnR of square 1-4 for 2D structure. The strands shown in bold are the extension of complementary DNA strands.

| Location | Original staple sequence at square corner | Modified staple sequence |
|----------|-----------------------------------------|--------------------------|
| Square | Corner | | |
| 1 | 1 | I.A.GGGCTCACGAGTTTTTACTATCAAGCAATCAGTCTTTTTTGAACCTCAGCTT | I.A.GGGCTCACGAGTTTTTACTATCAAGCAATCAGTCTTTTTTGAACCTCAGCTT |
| | | II.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT | II.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT |
| | | III.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT | III.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT |
| | 2 | I.A.GGTTTACCTCGTTTTTAACCAATCTTCAGATTCAACATT | I.A.GGTTTACCTCGTTTTTAACCAATCTTCAGATTCAACATT |
| | | II.ACATCGTCAACTTTTTCAGGTGGGCGTCACCATACTAT | II.ACATCGTCAACTTTTTCAGGTGGGCGTCACCATACTAT |
| | | III.ACATCGTCAACTTTTTCAGGTGGGCGTCACCATACTAT | III.ACATCGTCAACTTTTTCAGGTGGGCGTCACCATACTAT |
| | 3 | I.GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTT | I.GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTT |
| | | II.AGCACATTACTTTTTTGCAATGAAGTTGCTGACCATCT | II.AGCACATTACTTTTTTGCAATGAAGTTGCTGACCATCT |
| | | III.AGCACATTACTTTTTTGCAATGAAGTTGCTGACCATCT | III.AGCACATTACTTTTTTGCAATGAAGTTGCTGACCATCT |
| | 4 | I.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT | I.CGAACACAAGATTTTTGATGGAATGCCCCTCCCAAAGT |
| | | II.CTCCTAGCCAGTTTTTTACATGACCTAAGAAGAAGGAT | II.CTCCTAGCCAGTTTTTTACATGACCTAAGAAGAAGGAT |
| | | III.CTCCTAGCCAGTTTTTTACATGACCTAAGAAGAAGGAT | III.CTCCTAGCCAGTTTTTTACATGACCTAAGAAGAAGGAT |
| | 1 | I.ACCATTGCCACTTTTTCTCATGGCAAATTTCACAACCTT | I.ACCATTGCCACTTTTTCTCATGGCAAATTTCACAACCTT |
| | | II.ACTCGCTGAGTTTTTTCTGCTTCAAATCAATAATGTTT | II.ACTCGCTGAGTTTTTTCTGCTTCAAATCAATAATGTTT |
| | | III.ACTCGCTGAGTTTTTTCTGCTTCAAATCAATAATGTTT | III.ACTCGCTGAGTTTTTTCTGCTTCAAATCAATAATGTTT |
| | 2 | I.GCTGGCTCTATTTTTTGGTTCAGGTGGATGATTACTCTT | I.GCTGGCTCTATTTTTTGGTTCAGGTGGATGATTACTCTT |
| | | II.CTGGGACTGTTTTTTTTCGCTATGACTTATGTCCTCG | II.CTGGGACTGTTTTTTTTCGCTATGACTTATGTCCTCG |
| | | III.CTGGGACTGTTTTTTTTCGCTATGACTTATGTCCTCG | III.CTGGGACTGTTTTTTTTCGCTATGACTTATGTCCTCG |
| | 3 | I.CTTCCGCCTCGTTTTTAAGAACCTAAGTTGACAGCGATT | I.CTTCCGCCTCGTTTTTAAGAACCTAAGTTGACAGCGATT |
| | | II.CGAACAGTTGCTTTTTAGACCATCTAATTG | II.CGAACAGTTGCTTTTTAGACCATCTAATTG |
| | | III.CTTCCGCCTCGTTTTTAAGAACCTAAGTTGACAGCGATT | III.CTTCCGCCTCGTTTTTAAGAACCTAAGTTGACAGCGATT |
| | 4 | I.TTCAAGGTGATTTTTTTGGGGCTCTGGGCACTCCAGATT | I.TTCAAGGTGATTTTTTTGGGGCTCTGGGCACTCCAGATT |
| | | II.CTGCCTTCCCTTTTTTGTACCAGACTATTAAAGAACGTT | II.CTGCCTTCCCTTTTTTGTACCAGACTATTAAAGAACGTT |
| | | III.CTGCCTTCCCTTTTTTGTACCAGACTATTAAAGAACGTT | III.CTGCCTTCCCTTTTTTGTACCAGACTATTAAAGAACGTT |
| | 1 | I.AGAAGGTCAGCTTTTTTTGTTCCAGCAGGATCAATGGTT | I.AGAAGGTCAGCTTTTTTTGTTCCAGCAGGATCAATGGTT |
| | | II.AACTCGAGGCATTTTTTGCGGTACCCAATAGCCCGAGT | II.AACTCGAGGCATTTTTTGCGGTACCCAATAGCCCGAGT |
| | | III.AACTCGAGGCATTTTTTGCGGTACCCAATAGCCCGAGT | III.AACTCGAGGCATTTTTTGCGGTACCCAATAGCCCGAGT |
| | 2 | I.TGCCGTAAAGCTTTTTACTAAATCGGTGACGGGGAAAT | I.TGCCGTAAAGCTTTTTACTAAATCGGTGACGGGGAAAT |
| | | II.GGAGCGGGCGCTTTTTTAGGGCGCTGCACACCCGCCGT | II.GGAGCGGGCGCTTTTTTAGGGCGCTGCACACCCGCCGT |
| | | III.GGAGCGGGCGCTTTTTTAGGGCGCTGCACACCCGCCGT | III.GGAGCGGGCGCTTTTTTAGGGCGCTGCACACCCGCCGT |
| | 3 | I.TATCCCTATCCTTTTTTTGTTTCACGGAGACTTGAATGTT | I.TATCCCTATCCTTTTTTTGTTTCACGGAGACTTGAATGTT |
| | | II.TACTGCTGTTCGTTTTTGTGACCTGCTTTTGAGGAGTT | II.TACTGCTGTTCGTTTTTGTGACCTGCTTTTGAGGAGTT |
| | | III.TACTGCTGTTCGTTTTTGTGACCTGCTTTTGAGGAGTT | III.TACTGCTGTTCGTTTTTGTGACCTGCTTTTGAGGAGTT |
| | 4 | I.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT | I.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT |
| | | II.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT | II.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT |
| | | III.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT | III.GTATCTTTGACTTTTTTACCTCTTGGGCTGAAGCACCGTTT |
|   | 1 | 2 | 3 | 4 |
|---|---|---|---|---|
| 1 | I.TTCCTCAAGAGTTTTTCTTCCTGCTGACCTGAGTTTTCTCTCAGAAA | I.GAAGAAGATCTTTTTCCGAGATGTTCAACGACAAGATTITTTTAGCGCAAAGA | I.AACACGTCTTGTTTTTCAACTCGCCGTGGAGGACTATTTTCAATTCGTC | I.GCTGTCTCTGTTTTTGCGAGGTGCCGAGATAAGATCTTTTATCGACTATA |
| 2 | II.CTGTTGCGCAAGTTTTTAGATTTGGTGCTGCTCCTCCCATTGACGAGGATTAA | II.TGTTCAATTACTTTTTCTACCTATCATGGACAGCCTTTTTAATTCCAAT | II.CAATTCGTCCGTCCTGTCTTTTTTTCCCTGCACTCAGGTTTTTACATCAATGTGCATTACCTTTTCCACTCACTG | II.AATCCCAACCCTTTTTATTCATTCCAAAGGACGTGAATTCCCTGCTGCACTGATTCTTTTTGAGGGAGATATAAGATCT |
| 3 | III.TGCACCTGAGTTTTTCTCTCAGAAAGCAAGACCTTGTTTTTATCATCCAGG | III.CAATTCGTCCGTCCTGTCTTTTTTTCCCTGCACTCAGGTTTTTACATCAATGTGCATTACCTTTTCCACTCACTG | III.AAGAGCGCACTATTATTATTACTTCTCTCCAAAGAATTTTTGAGGGAGATATAAGATCT | III.AATCCCAACCCTTTTTATTCATTCCAAAGGACGTGAATTCCCTGCTGCACTGATTCTTTTTGAGGGAGATATAAGATCT |
| 4 | I.GAAGAAGATTCTTTTTCCGAGATGTTCAACGACAAGATTITTTTAGCGCAAAGA | II.CAATTCGTCCGTCCTGTCTTTTTTTCCCTGCACTCAGGTTTTTACATCAATGTGCATTACCTTTTCCACTCACTG | III.AAAGATTTTTGAGGGAGATATAAGATCT | III.AATCCCAACCCTTTTTATTCATTCCAAAGGACGTGAATTCCCTGCTGCACTGATTCTTTTTGAGGGAGATATAAGATCT |