

## **Chiral 3D DNA Origami Structures for Ordered Heterologous Arrays**

Md. Sirajul Islam<sup>1</sup>, Gerrit D. Wilkens<sup>1,2</sup>, Karol Wolski<sup>3</sup>, Szczepan  
Zapotoczny<sup>3</sup>, Jonathan G. Heddle<sup>1\*</sup>

1 Malopolska Centre of Biotechnology, Jagiellonian University,  
Gronostajowa 7A, Kraków 30-387, Poland

2 School of Molecular Medicine, Medical University of  
Warsaw, Warszawa 02-091, Poland

3 Faculty of Chemistry, Jagiellonian University, Gronostajowa 2,  
Kraków 30-387, Poland

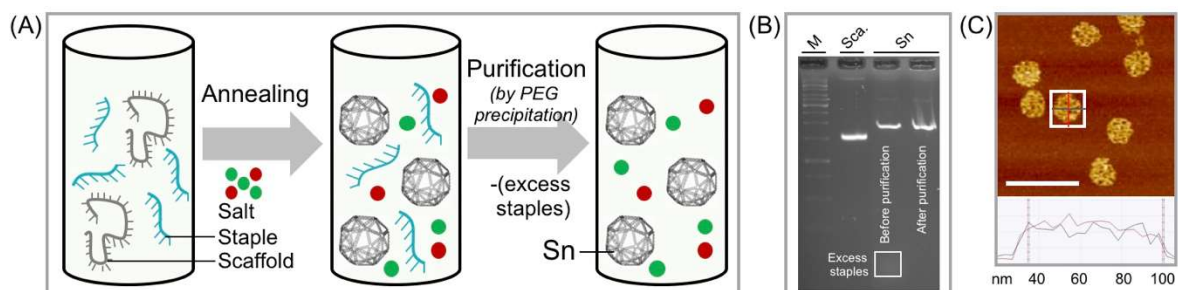
\* Corresponding author email: [jonathan.heddle@uj.edu.pl](mailto:jonathan.heddle@uj.edu.pl)

## INDEX

Production of custom scaffold DNA .....	3
Structure assembly and purification .....	3
Figure S1: Sn origami synthesis and characterization.....	3
Post-design modifications for Snubcube dimer and chain formation.....	3
Figure S2: Post-design modification for staple strands of the SnL and SnR.....	4
Assembly of DNA Snubcube Dimers.....	9
Figure S3: AFM images of SnL-SnL dimer structures assembled at 10 nM conc. and 25 °C. ....	10
Figure S4: AFM images of SnL-SnL dimer structures assembled at 10 nM conc. and 37 °C. ....	11
Figure S5: AFM images of SnL-SnL dimer structures assembled at 10 nM conc. and 45 °C. ....	12
Figure S6: AFM images of SnL-SnL dimer structures assembled at 20 nM conc. and 25 °C. ....	13
Figure S7: AFM images of SnL-SnL dimer structures assembled at 20 nM conc. and 37 °C. ....	14
Figure S8: AFM images of SnL-SnL dimer structures at 20 nM conc. and 45 °C.....	14
Figure S9: AFM images of SnL-SnL dimer structures assembled at 30 nM conc. and 25 °C. ....	15
Figure S10: AFM images of SnL-SnL dimer structures assembled at 30 nM conc. and 37 °C. ...	16
Figure S11: AFM images of SnL-SnL dimer structures assembled at 30 nM conc. and 45 °C. ...	17
Figure S12: AFM images of SnL-SnR dimer structures assembled at 10 nM conc. and 45 °C. ...	18
Figure S13 : AFM images of SnR-SnR dimer structures assembled at 10 nM conc. and 45 °C. ...	19
Table S1: Observed products in SnL-SnL hybridisation.....	20
Table S2: Observed products in SnL-SnR and SnR-SnR hybridisation.....	20
Assembly of Snubcube Chain structures.....	21
Figure S14 : AFM images of 1D chain structure.....	21
Streptavidin labelling of Sn Dimer and Chain structures .....	22
Figure S15: AFM images of SA bound SnL-SnL dimer structures. ....	22
Figure S16: AFM images of SA bound SnL-SnR dimer structures. ....	23
Figure S17: AFM images of SA bound SnR-SnR dimer structures. ....	24
Table S3: Observed attachment of streptavidin to Snubcube dimers.....	25
Figure 18: AFM images of SA bound to 1D chain structure.....	26
Scaffold and unmodified Staple Sequences of SnL and SnR.....	27
Table S4: Sequences of the custom scaffold. ....	27
Table S5: Sequences of the staple strands for SnL without modification .....	28
Table S6: Sequences of the staple strands for SnR without any modification. ....	30
Modified Staple Sequences of SnL and SnR.....	32
Table S7: Sequences of the modified staple strands for SnL for dimer and 1D chain structure. .	32
Table S8: Sequences of the modified staple strands for SnL for 2D structure formation. ....	33
Table S9: Sequences of the modified staple strands for SnR for dimer and 1D chain structure. .	35
Table S10: Sequences of the modified staple strands for SnR for 2D structure formation. ....	36

## 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  $\mu\text{M}$  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/ $\text{Mg}^{2+}$  buffer (5 mM Tris, 1 mM EDTA and 12.5 mM  $\text{MgCl}_2$ , pH 8.0). The annealing was performed in a PCR thermal cycler as follows: 95  $^\circ\text{C}$  for 5 min, 80  $^\circ\text{C}$  to 75  $^\circ\text{C}$  at a rate of -1  $^\circ\text{C}$  per 5 min, 75  $^\circ\text{C}$  to 30  $^\circ\text{C}$  at a rate of -1 $^\circ\text{C}$  per 15 min and 30  $^\circ\text{C}$  to 25  $^\circ\text{C}$  at a rate of -1  $^\circ\text{C}$  per 10 min. -1  $^\circ\text{C}$  per 5 min, 75  $^\circ\text{C}$  to 30  $^\circ\text{C}$  at a rate of -1 $^\circ\text{C}$  per 15 min and 30  $^\circ\text{C}$  to 25  $^\circ\text{C}$  at a rate of -1  $^\circ\text{C}$  per 10 min.

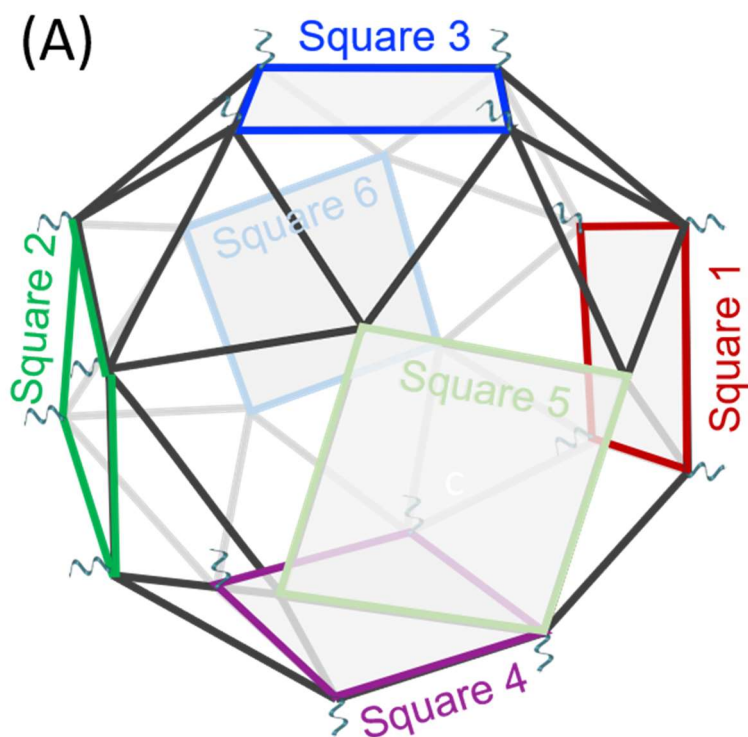


**Figure S1:** Sn origami synthesis and characterization. (A) synthesis of origami structure annealed by mixing scaffold and excess staple strands in the presence of  $\text{MgCl}_2$  followed by PEG precipitation to remove excess staple strands, (B) agarose gel image of the origami structure before and after purification and (C) AFM image of the assembled Sn DNA origami structure. AFM scale bar represents 200 nm.

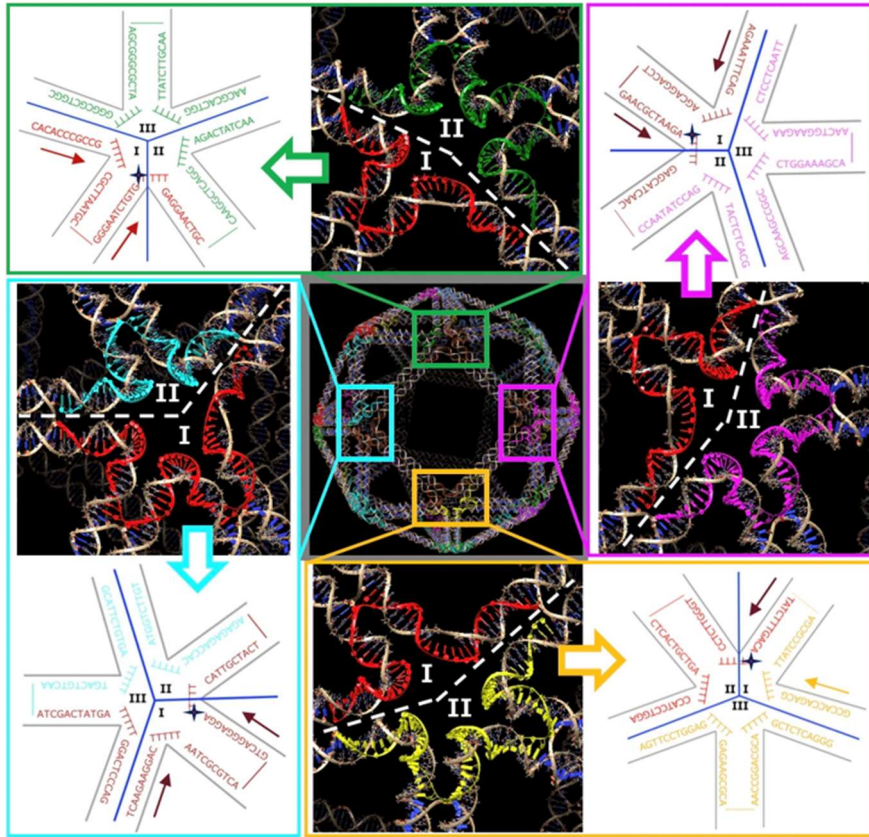
To purify assembled DNA origami structures from excess staple strands, folded structures were mixed with PEG buffer (5 mM Tris, pH 8.0, 15% PEG-8000, 500 mM NaCl, 20 mM  $\text{MgCl}_2$ ) at a ratio of 1:2 and incubated overnight. Then, the mixture was centrifuged at 10000 rpm for 10 min at room temperature. The supernatant was removed, and the pellet was dissolved in 20  $\mu\text{l}$  1x TAE/Mg buffer.

## Post-design modifications for $S_n$ dimer and chain formation

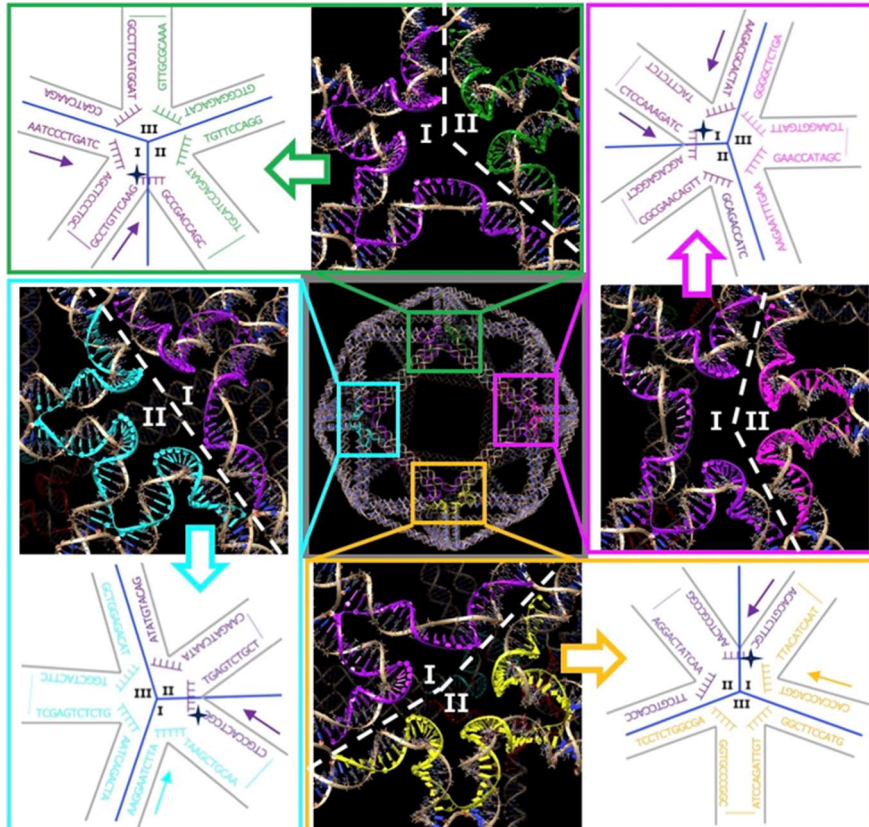
To modify the  $S_n$  structures, the 3D structural model in the PDB file format computed by DAEDALUS was used to identify appropriate staple strands at the corners of each square of the  $S_n$  structure which were extended with strand extensions to form dimeric or chain structures (Fig. S2). A list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



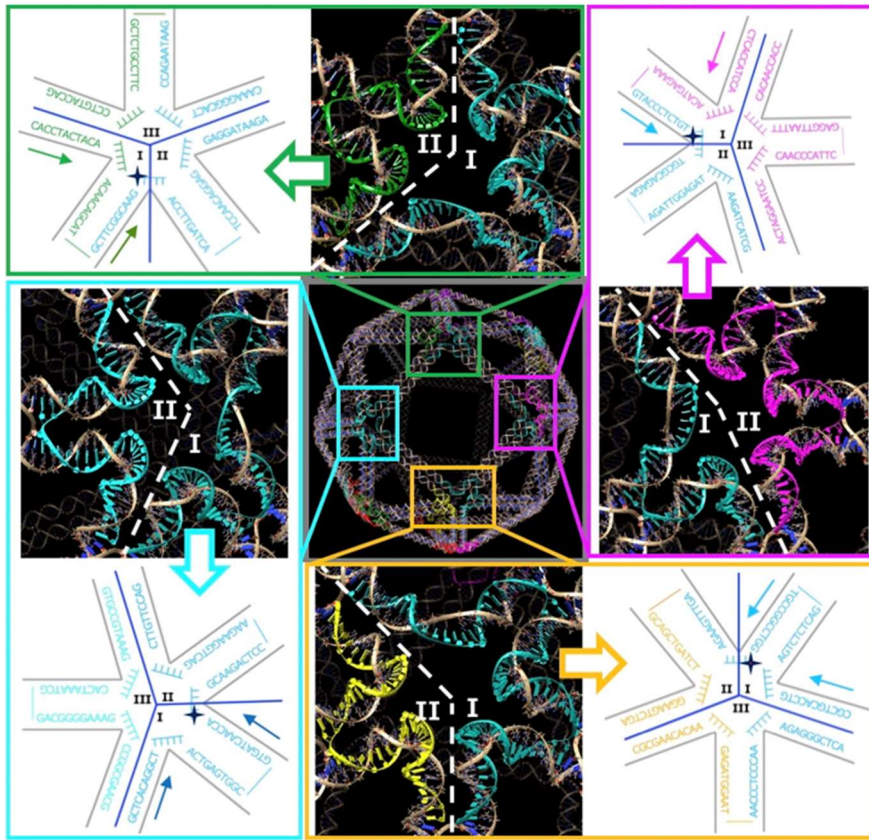
(B) Square 1 of SnL



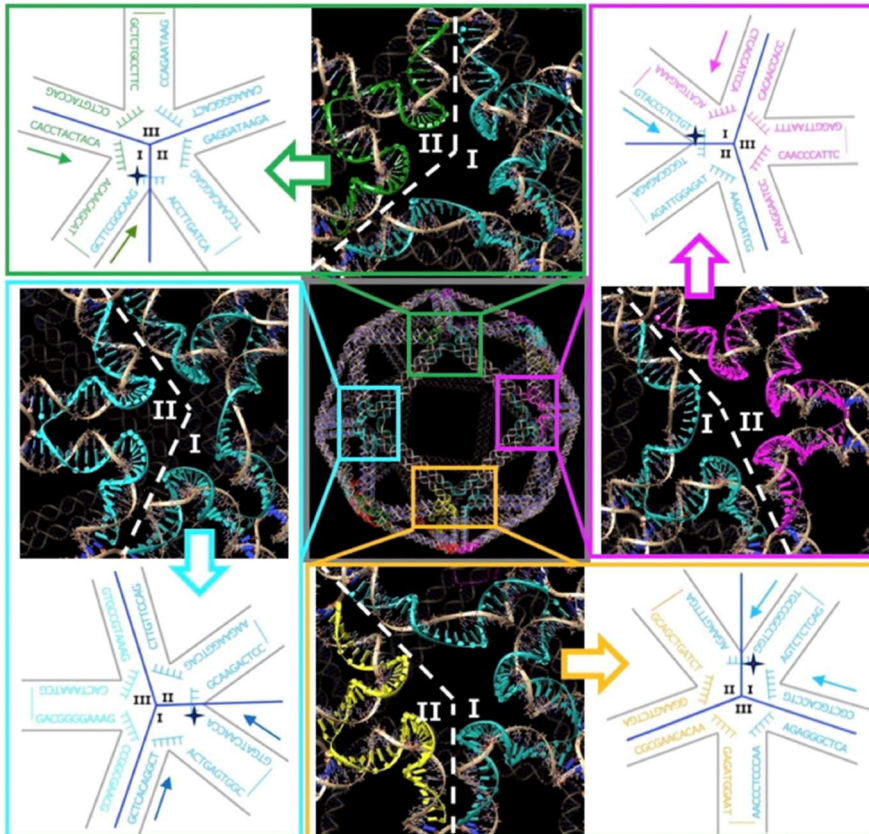
(C) Square 2 of SnL



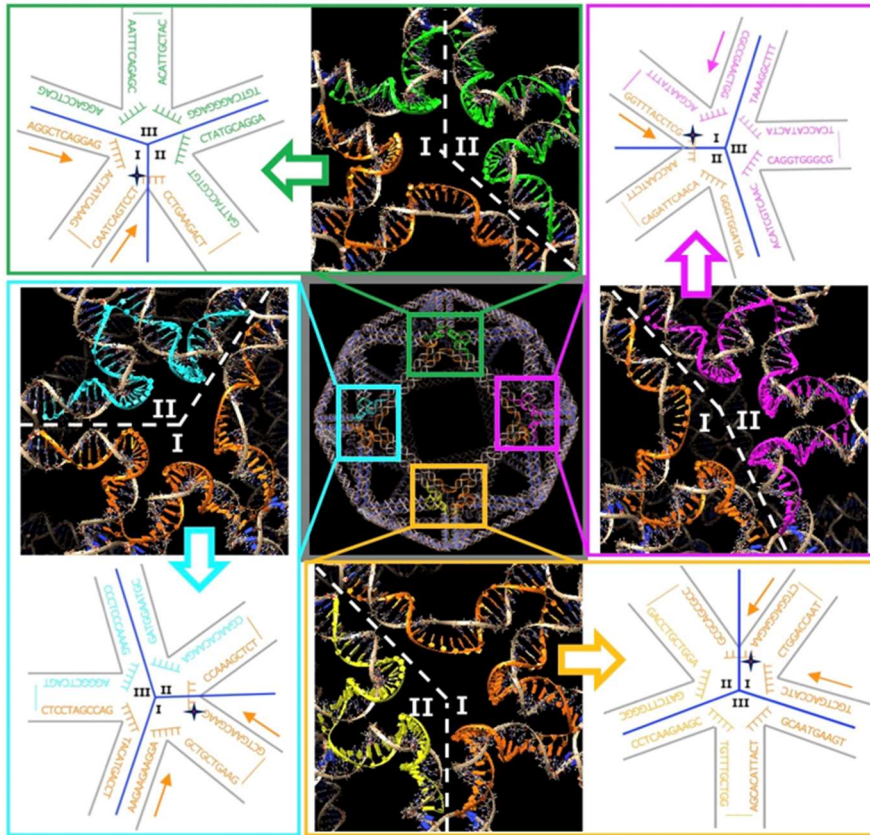
(D) Square 3 of SnL



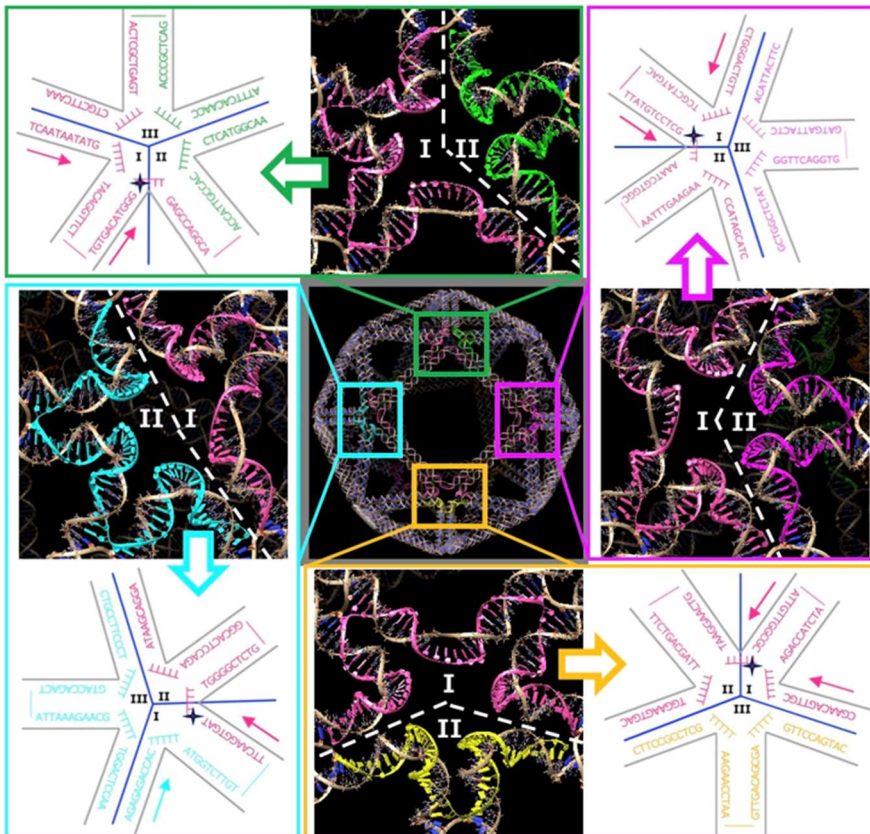
(E) Square 4 of SnL



(F) Square 1 of SnR



(G) Square 2 of SnR





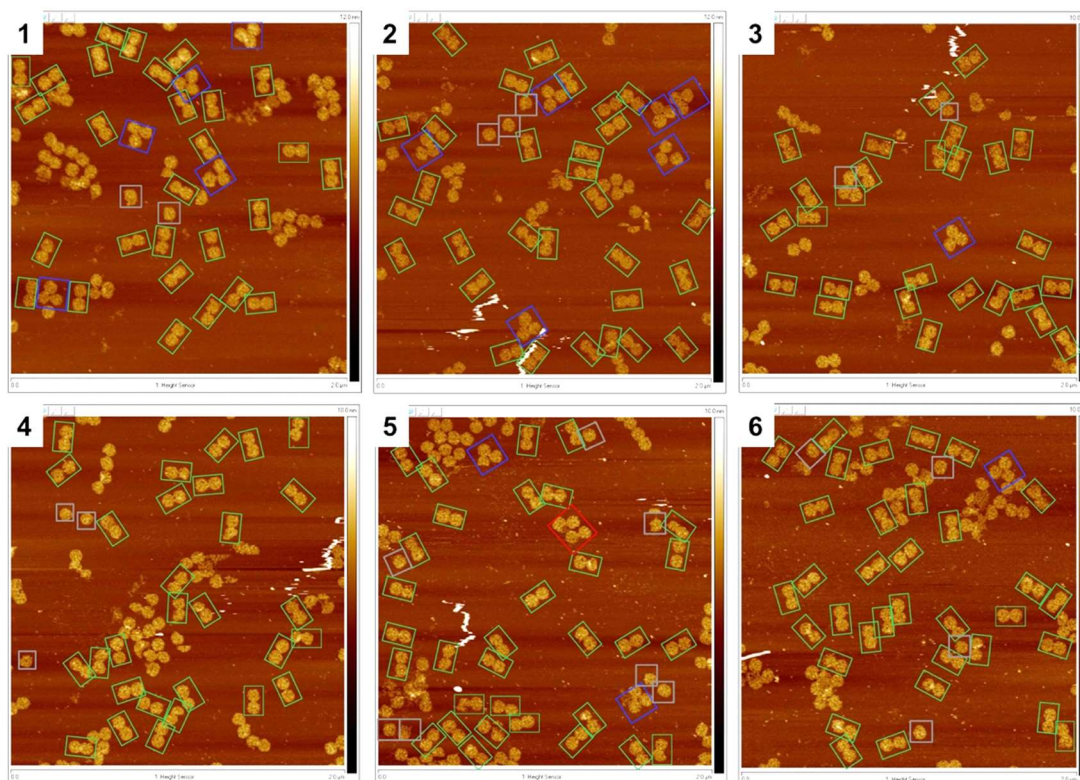


**Figure S2:** Post-design modification for staple strands of the SnL and SnR. (A) 3D model of Sn structure, where squares are labelled as 1-6, details of the staple strand modification scheme for SnL of (B) square 1, (C) square 2, (D) square 3, (E) square 4 and for SnR of (F) square 1, (G) square 2,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

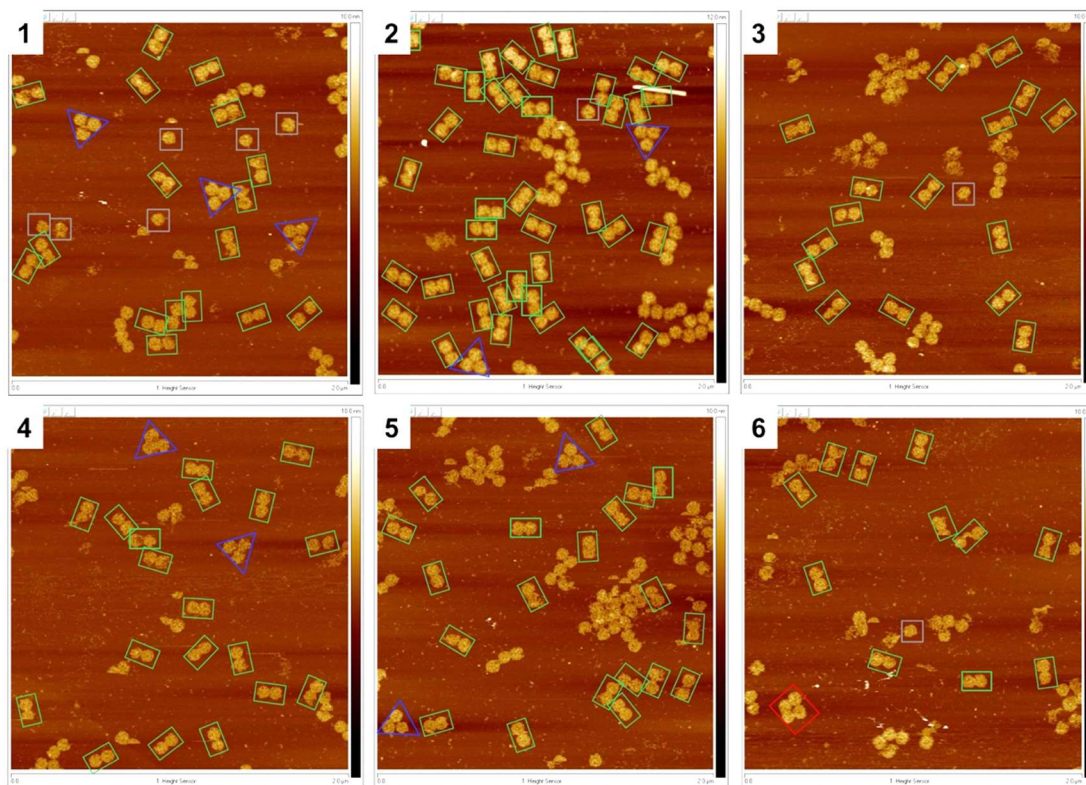
### Assembly of DNA Sn Dimers and Chains

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.

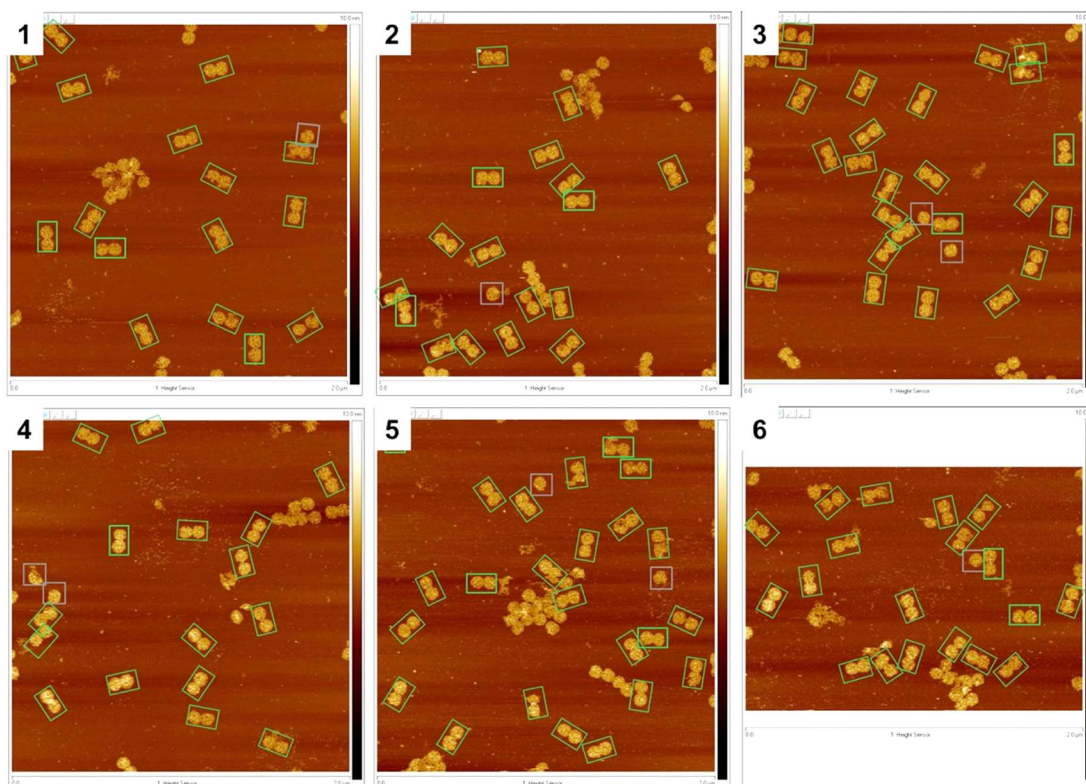
To selectively label Sn dimer and chain structures with streptavidin, a staple strand at the corner of square 5 of SnL (5'-CGA AGC ACT CAT TTT TGG GAA CTG GAG TTA TCC CTA TTT TTT CCT GAA GTA C) was modified with BiotinTEG at its 3' end.



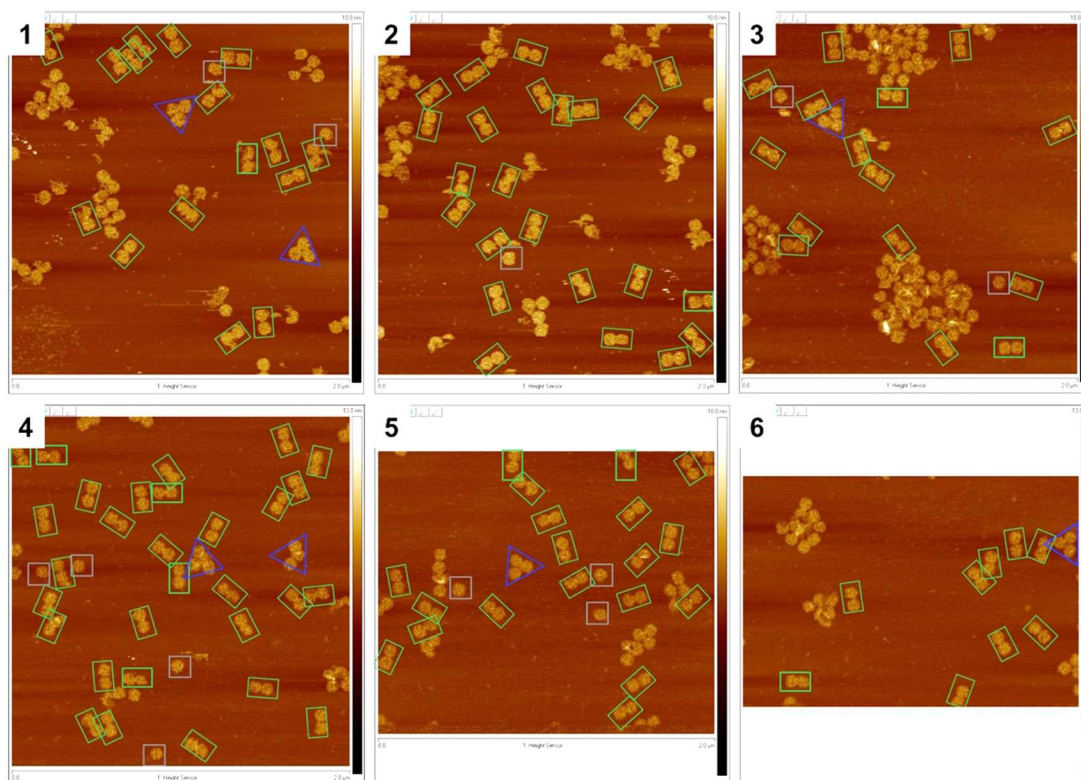
**Figure S3:** AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



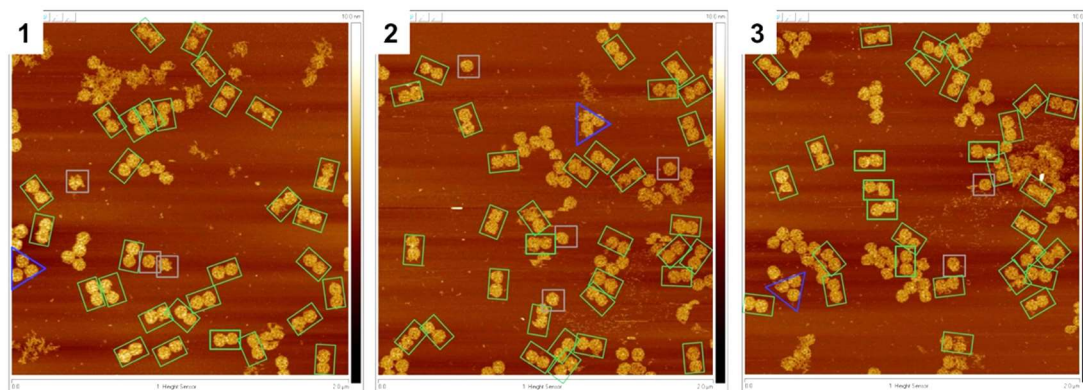
**Figure S4:** AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



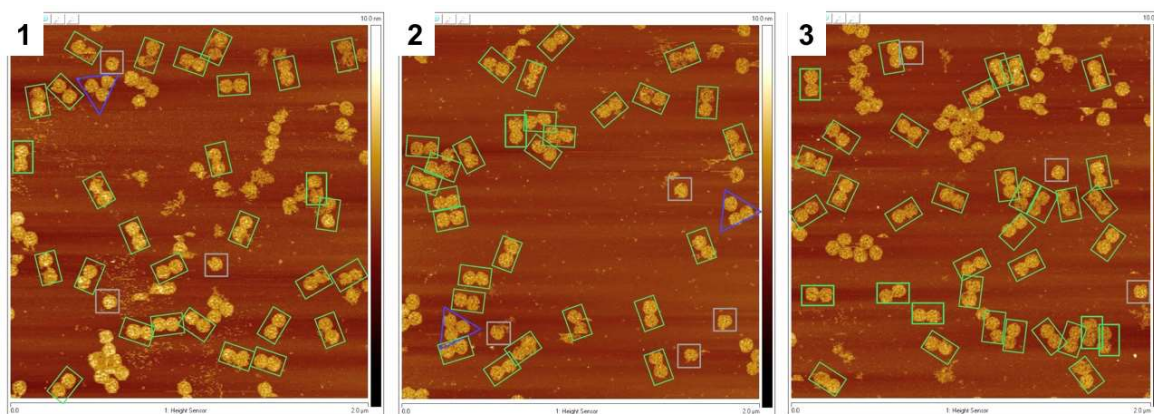
**Figure S5:** AFM images of SnL-SnL dimer structures assembled from 10 nM Sn and incubated at 45 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



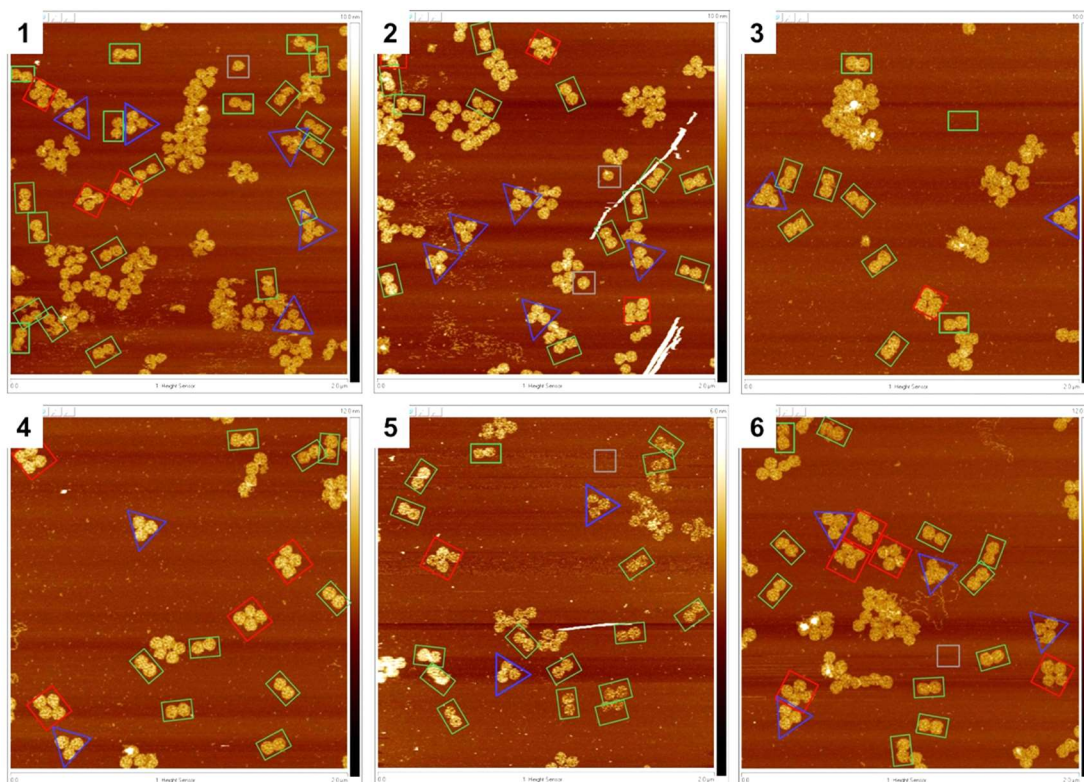
**Figure S6:** AFM images of SnL-SnL dimer structures assembled from 20 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



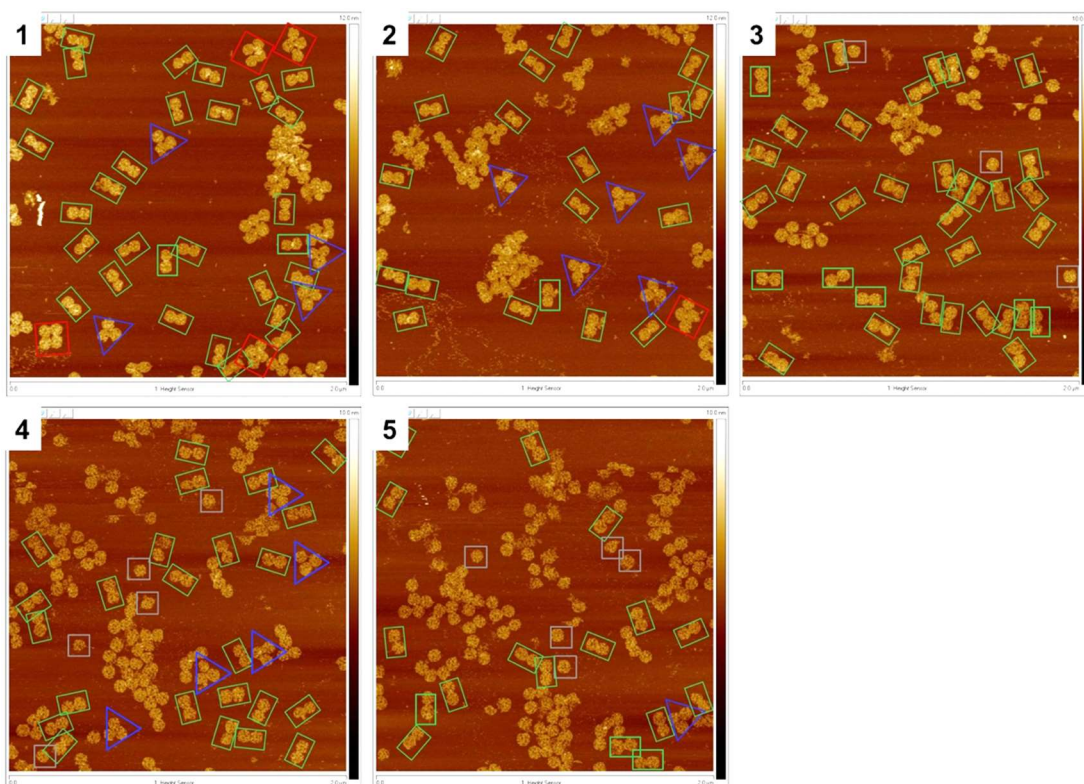
**Figure S7:** AFM images of SnL-SnL dimer structures assembled from 20 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



**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  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .

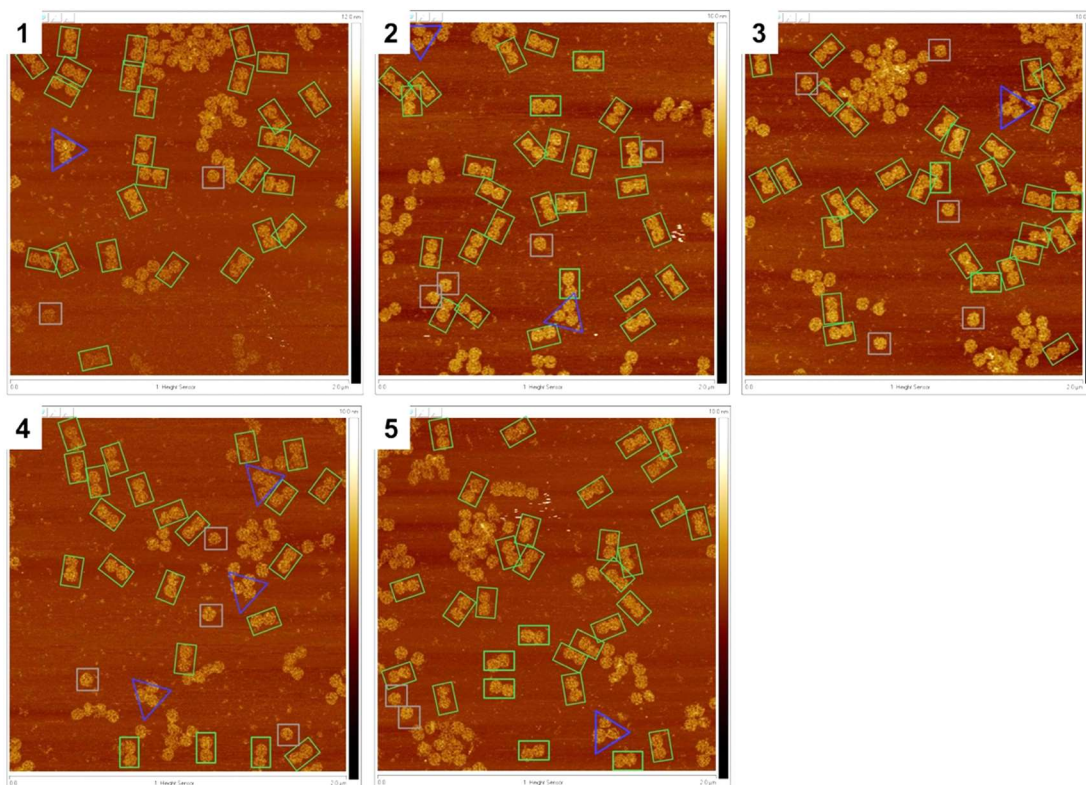


**Figure S9:** AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 25 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .

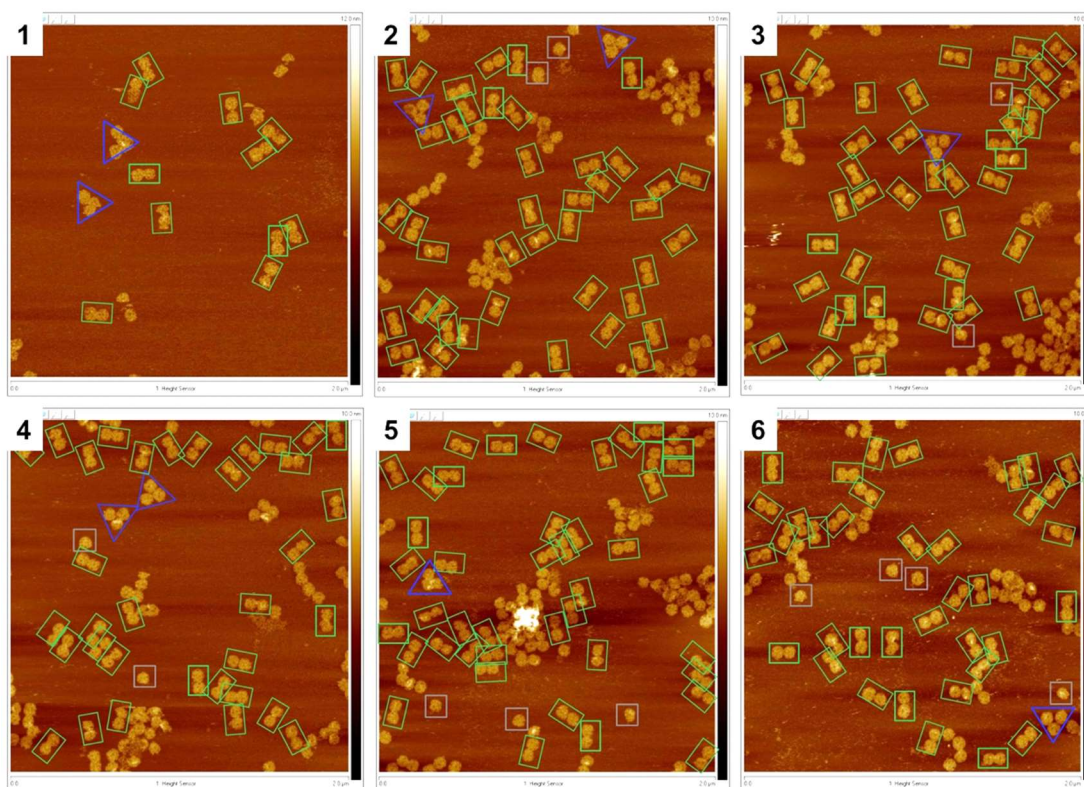


**Figure S10:** AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 37 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .

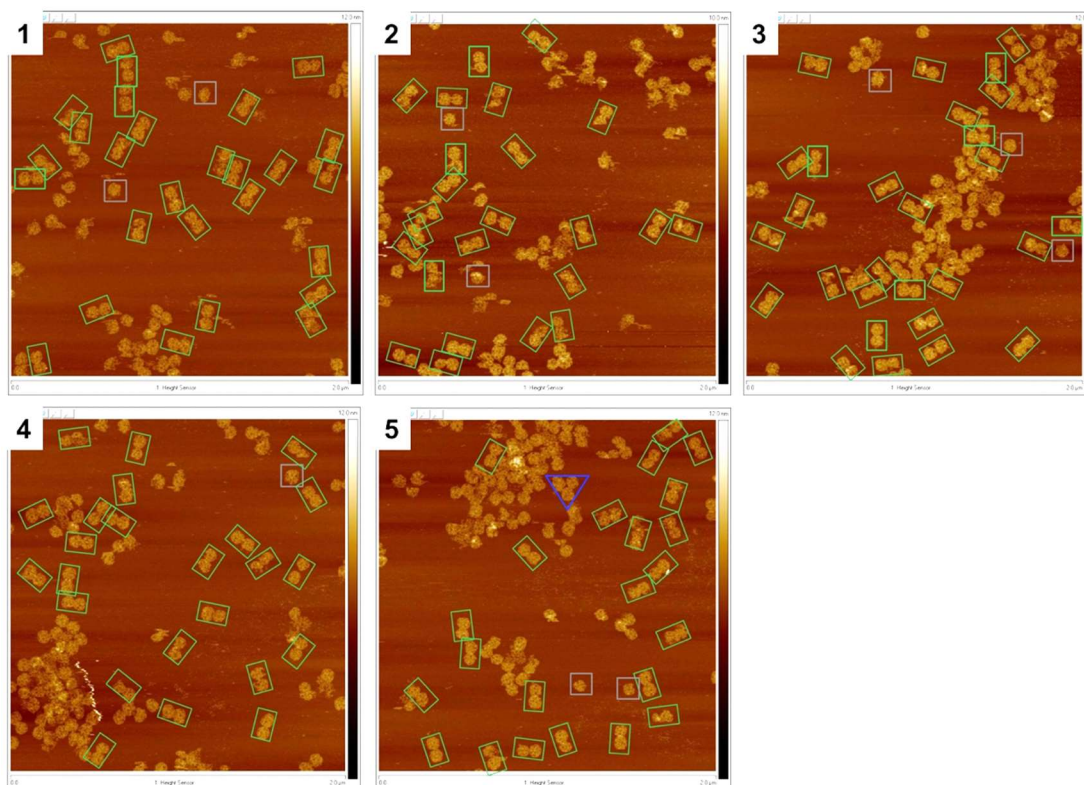




**Figure S11:** AFM images of SnL-SnL dimer structures assembled from 30 nM Sn and incubated at 45 °C overnight for Figure 2B. Structures in single, dimer, trimer and tetramers are indicated with grey, green, blue and red boxes respectively. Structures higher than tetramers are considered as aggregates. Counted numbers of the structures are shown in Supplementary Table S8. All images are 2  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



**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  $\mu\text{m}$   $\times$  2  $\mu\text{m}$ .



**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.

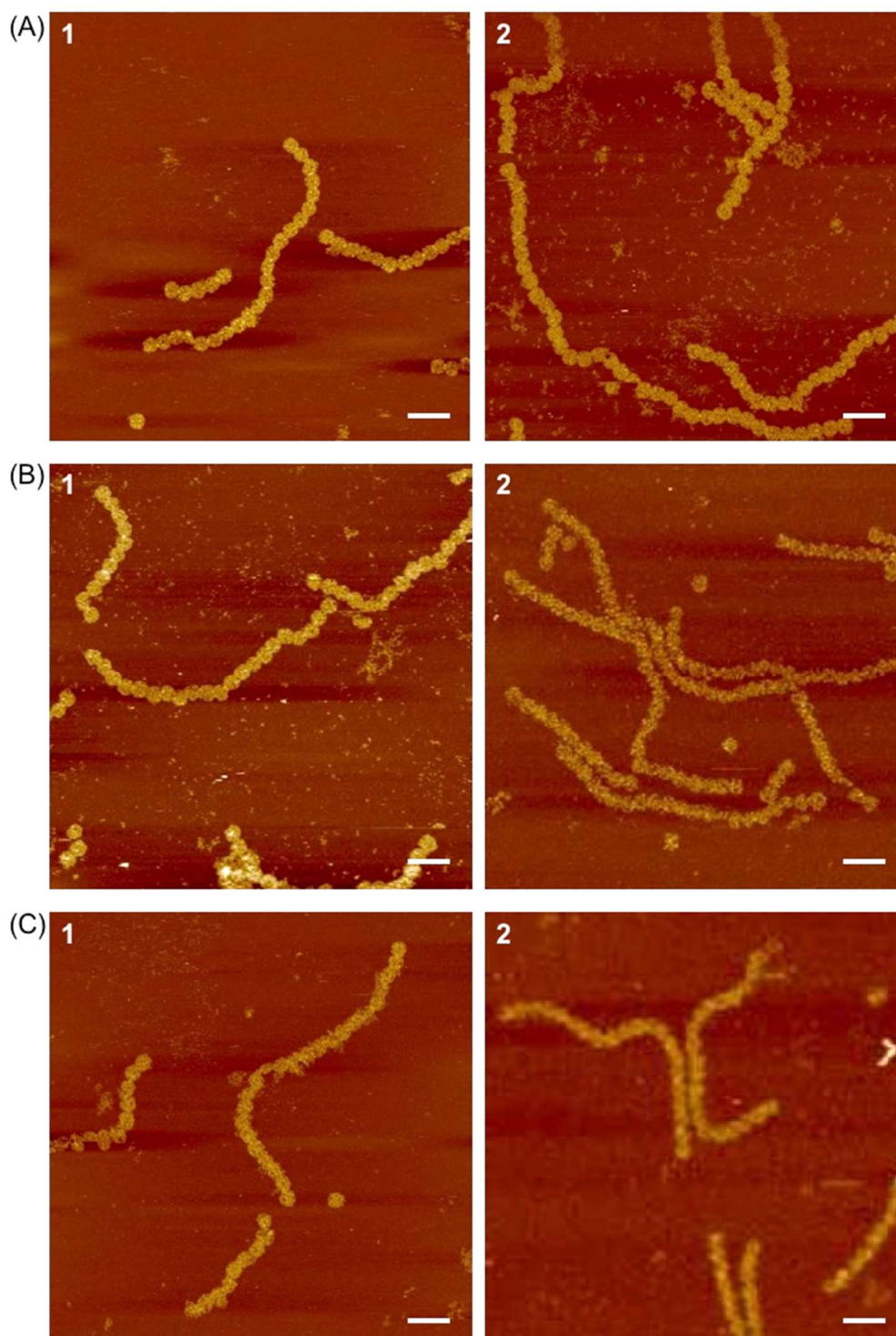
**Table S1: Observed products in SnL-SnL hybridisation.**

Structures		SnL-SnL								
		10 nM			20 nM			30 nM		
		25 °C	37 °C	45 °C	25 °C	37 °C	45 °C	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
Tetramer	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**

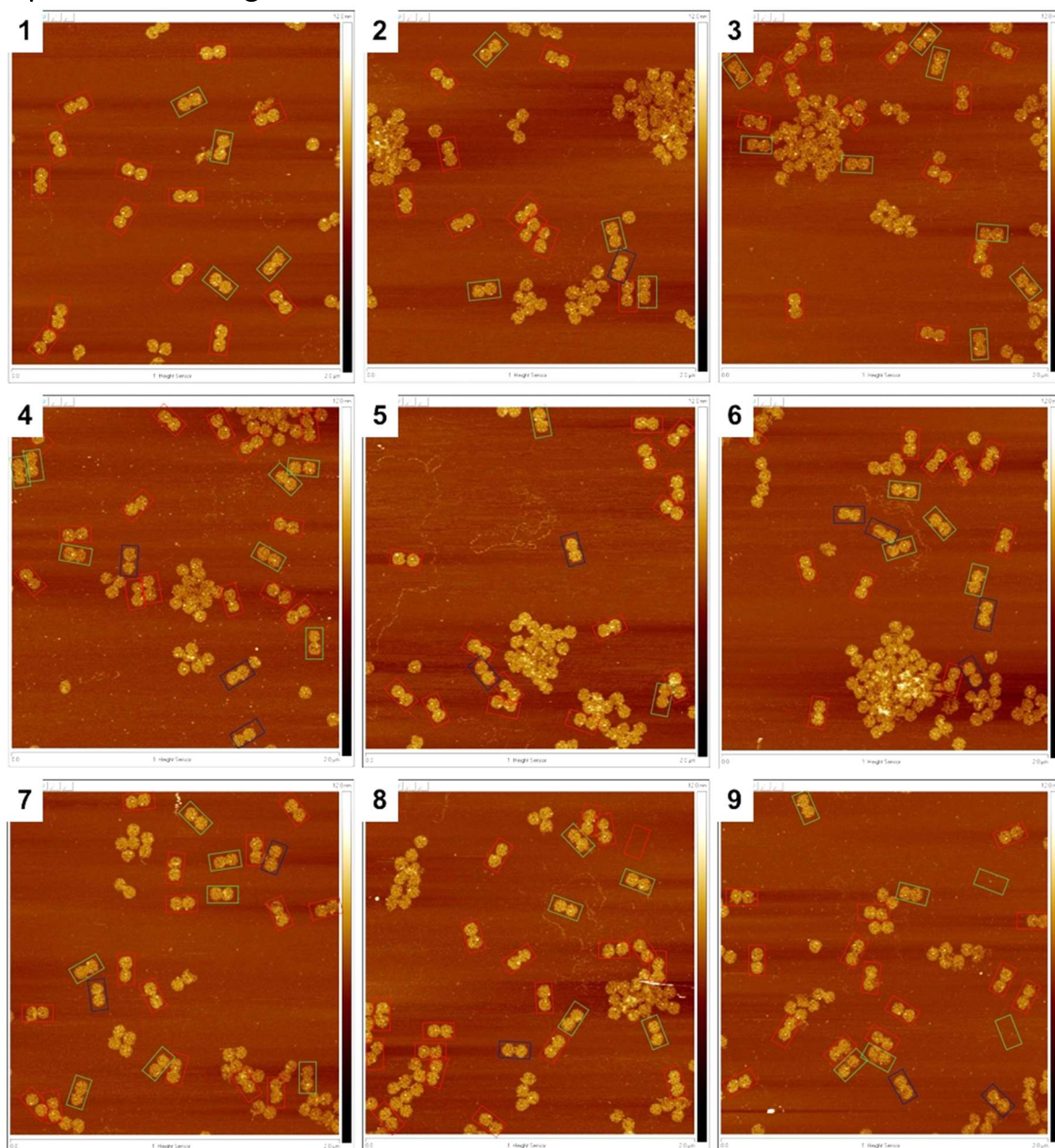
Structures		SnL-SnR (10 nM, 45 °C)	SnR-SnR structures (10 nM, 45 °C)
Single	no.	13	9
	%	6	6
Dimer	no.	205	127
	%	90	92
Trimer	no.	9	2
	%	4	2
Tetramer	no.	0	0
	%	0	0
Total (particle analysed)		227	138

## Assembly of Sn Chain structures

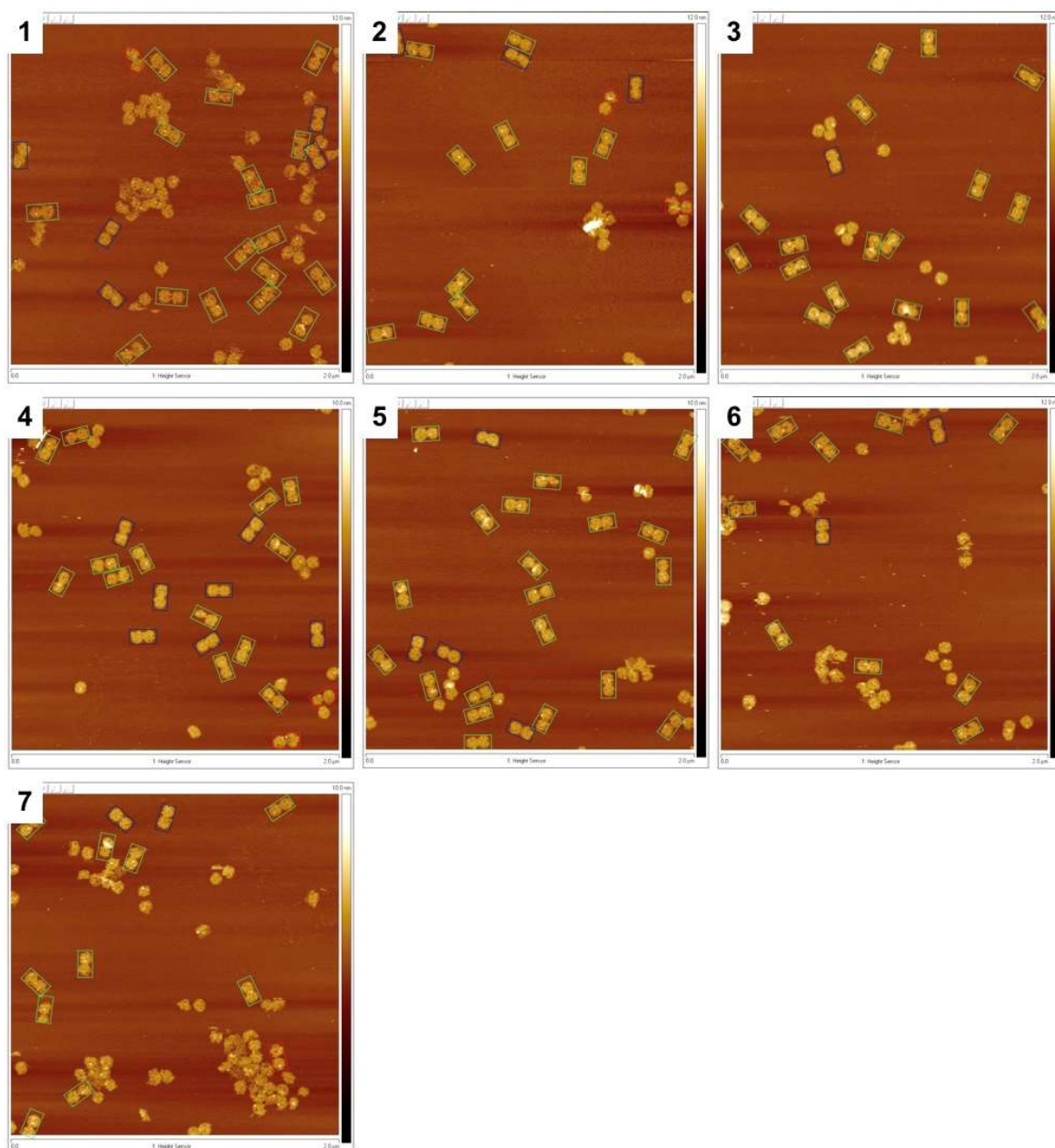


**Figure S14:** AFM images of 1D chain structure of other fields for Figure 4 (upper panel) of (A) SnL-SnL-SnL, (B) SnL-SnR-SnL and (C) SnR-SnR-SnR. AFM scale bars represent 200 nm.

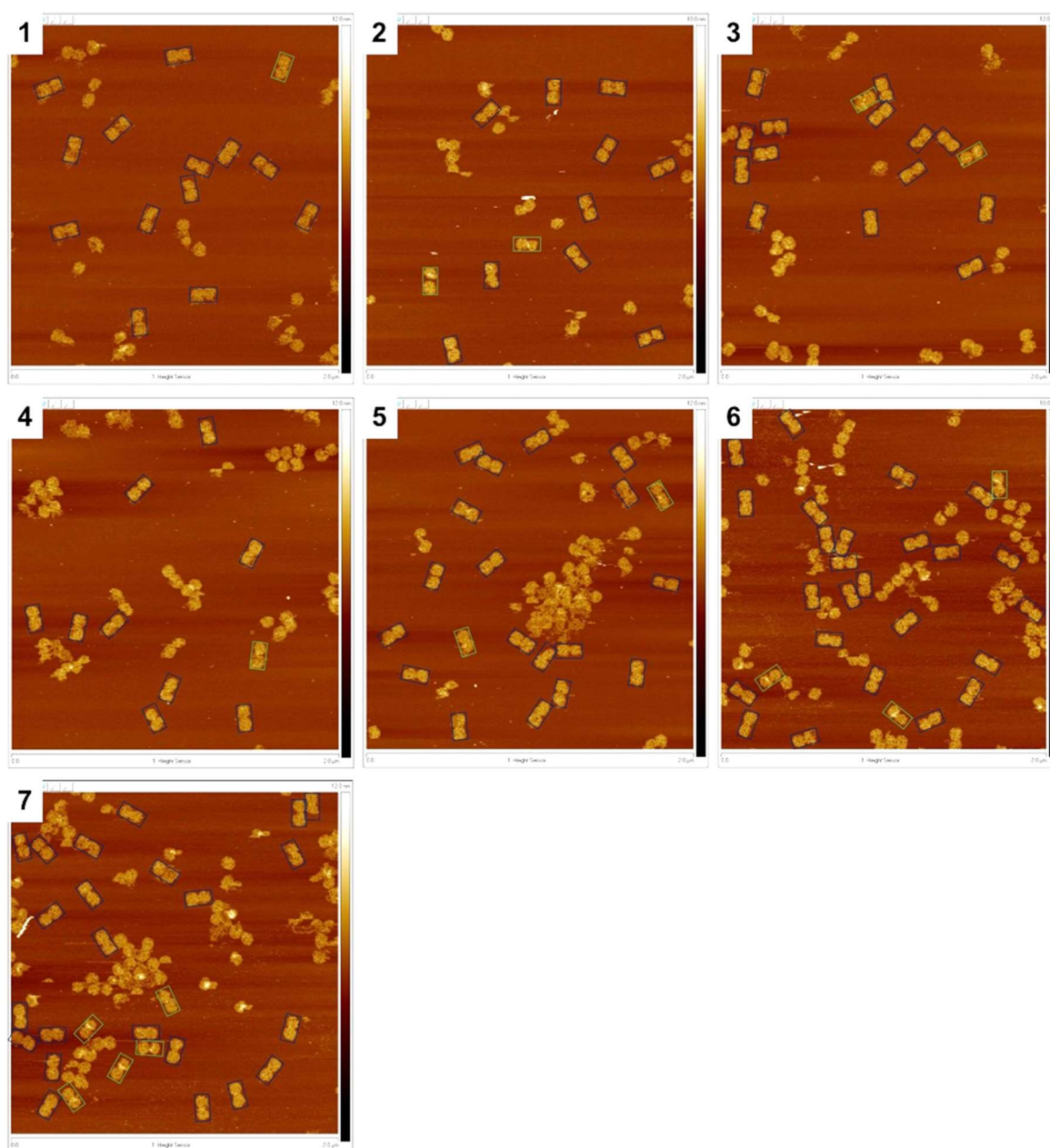
## Streptavidin labelling of Sn Dimer and Chain structures



**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  $2\ \mu\text{m} \times 2\ \mu\text{m}$ .

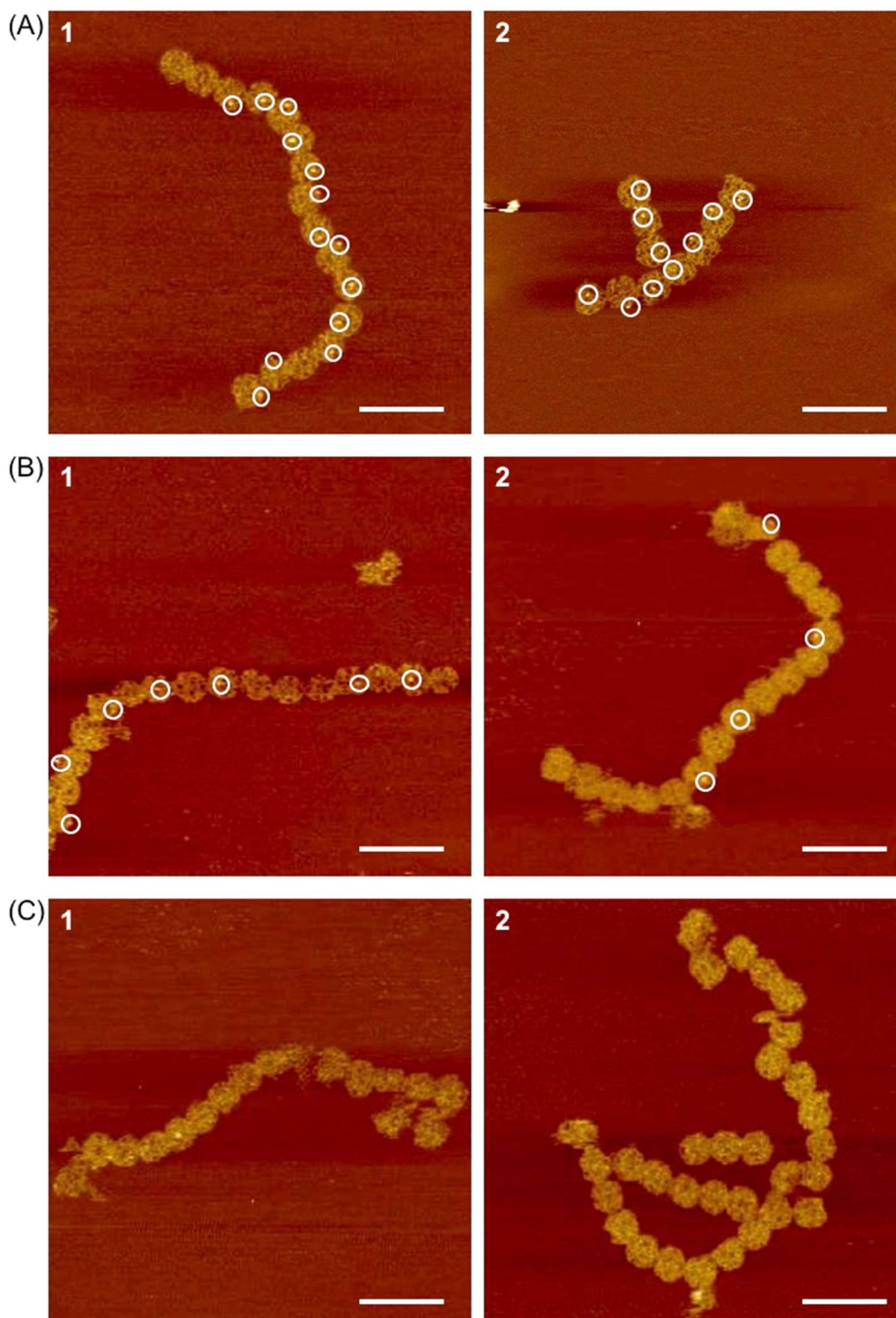


**Figure S17:** AFM images of SA bound SnR-SnR dimer structures for Figure 3C. Dimer structures bound with no, one and two SA are indicated with red, green and blue boxes respectively. Only dimer structures are counted and numbers of the structures are shown in Supplementary Table S10. All images are  $2 \mu\text{m} \times 2 \mu\text{m}$ .



**Table S3:** Observed attachment of streptavidin to Sn dimers

Structures		<b>SnL-SnL</b>	<b>SnL-SnR</b>	<b>SnR-SnR</b>
No SA	no.	19	27	113
	%	9	18	88
Single SA	no.	55	117	16
	%	27	78	12
Double SA	no.	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.

Scaffold and unmodified Staple Sequences of SnL and SnR

**Table S4:** Sequences of the custom scaffold with a total length of 6240 nt

<p>GGATCCACGCGCCCTGTAGCGGCGCATTAAGCGCGGGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCG          CCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTTCTCGCCACGTTTCGCCGGCTTTCCCGTCAAGCTCTAAATCGGG          GGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCAAAAAACTTGATTTGGGTGATGGTTCACGTAGTG          GGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGAGCTTGAGTCCAGCTTCTTTAATAGTGGACTCTGTTCCAAACTG          GAACAACACTCAACCCTATCTCGGGCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCCGGGTACCGCATGCCTCGAG          TTAGACCTGATCTTTGAGAAACAAGGCGGCTCCCACTGAATCCATTGATCCTGATTACTGAGCACCTGCACGACGAGGAT          CTGCTGGAACAAGCTGACCTTCTTAGCCAAGATGCTAGGAAATTCCTGCTCACACATGCTGTTGTTGTTAGTAGGTGCGCCA          CAAAGCGCGCTCCCGAAACACAGAGTCTGGTACAGGGAAGGCAGAGCGATCTTCAAGGTTGCCACAGCCAGGATCTCTC          TTGATCGATCCATGAAGGCAACTGGTCCCTGATCTTCTGCTGGGAGTCGGCTTTGCGCAACATGTCTCCGACCACCAGCC          AGTGAAGGTATCCATTTCGTTCTCTGGAACAATTCGGATGCATACCTCTGACGAAATGCAGGGCGAACATCAGCTGGTC          GGCTTGAACAGGCAGCGGCAGATGTATTTCGTACACCATGTGCTGCAGGGAGCTGATCAGGGATTGAACTCCTCTGTTCTGT          GTTCTCAGAATCCTGCTTATTCTGGAGTGCCCTTTGAAACAACCTCAGAAAGGCGGCCAGGGAGAACCTGTACATATTTATT          GATCTTGGAGAGTTCAGAGATAATGAAGTACATCTTTGAAGCAGACTCAGCGAGTGGCAGATATCGCTCGCGCTCCTGGTC          GAGAGAGATTTGCAGCTTATAAGATTCTTTCAGAGACTCTTGGATGAGGGCGGAAGATGCTTTAGTCTGATTCAGAGATC          GATCAGGTCTTGTCTCCAGGATGTTGCCCTGAGAAGTACCAATGCTCTCCAGCAGAGATTCTTCGAGTTTGGCCAGTTG          GATCTTCTTATCCTCCTCTGTTGGAGCAGCTTAGTCTTCTGTTCTTCCAAATCGGGTTTCTCATGTTGGATGGTGAGGGC          CAGGAGCTGGCCTCTCAGTCTGAGCGGGTGGTTGTGAAATTAACCTCTGTGACGATGCTGGCAGCGTCTGGTGAATGAA          TGGGTTGGGATTCCTAGTGCTCAGGAACAGGCGAACTCCTCGTTATAGTCGATGATCTTATCTCCAATCTGGACCACATA          GCGTGGGCCTTGGGCCACCAATCTCTGCGCAACAGAGGGTACAGAACTGGCTCCACGCCATCCATCTCCTGGATGATCAA          GGCTTGGCGAAGCGGACGGCGAGTTCAGGGCAGTATGAAGTTGGAGTCTTGGTGGTGTATCACTCCAGCCTGGAACT          CTTCAAGTGAGTCTCAGCCACTCAGTAGCCTGTGAGCTGGGATCGATGAGGAAAGGCAACCGCGGATTCGAAGATAAC          CAGTGCGTTCCTCGATTGAGAGGTCACTCGCTGGGCAGACCTTCAGACTTCAGATCAGCTGCTCTGACTCGGTGCAGAGAAA          TCTTCTCAGGTCAAACCTTCTCCAGGCCGCGAGACTTGGTCCACTCCTCCAGACATGTCTTCTGAGAGACTCAGGTGCAGC          GGACAAGTAGGTGATAAAGGCTGCGGCCAACTGAGCCCTCTTTGGGAGGGTTGCCAGTCTCAGTAATCTCGACGACCTG          AGCATTCATCTCTGTGTTCCGGTCCAGCTGATTAATCAACACTTCAGCTGCTTTGATAGTCTCCTGAGCCTTGGACAC          CTCAGCTTCCAACCTAGTCTCTGAGGTCCTGCTGAAATTTCTCCTTCAGTCTGACACCTTCTGACCGACAGAAT          GAGGATTCCTCCAGTTCTCTTCTATCCTCGTCTTCTTCCAGGTTGCTTTCCAGGCGGCTTGTCTCAGCTCCAGAGG          GTGGATGCGTTCGAGCACGTGAGAGTACTGGATATTGGCCTTAACCCAGGCTGCCAAGGGTGCAGCTGCAGTTGATGCTCT          CTTAGCGTTCCTGGGATCAAATGAACCTTTATTCTTGAACAGCAGTTCCTCCACAGATTCCCTAATTTCTTGGAGATGTT          CCTAGCGTCGAAAGTAGCAATGTCTCCCTGACACCGCGCTTGGCCAAAGAAAGACTTCATAGACACCCAAGAGGTGTCAA          GATACCCATCAAGCCGAGGACGCCCTCCAGGATGTCCGGATAACGCTCGGTGGCATTCAGTGACCTGATCTCTGAGAG          AGACTCTGGTTTGATATTACCCACGGCGAGCTTGGCCTCGTTCACCCAGAGGCTGCACCTCTTTGAGTTCGTCGTCATCTT          GTTCTTCTCTCCGATCTTGACCACCTCCTCTGCGATCGGGTGTCTCAGCCTTCCAGCTCTGCTTCTGCTCGGAAGC          ATCCTGCATAGACAGGTAATCATTTCAGGGCAGCGCTCAGCTTCATCTGCTTAGTCTTCCAGGAGGACTGATTTGTCGCC          AGCCTTGGCATTGAGTTCATCCACCAGAGCTTTGGCTTCGTTGAGTTCGCTGACTCCGGCCTGCAGATGAGATTGGCGCTT          CAGCAGCTCCTTCTTCTTTGAGCTGGAGATGGCGGAATAGACGTGGAGGAAGGTGATGACTGGCTAGGAGTAGCTCCGTA          AGCTTTGCAAGACTCGTGGATCAGCAGGAAGCTCTTGAAGAAATCAGGATCGACGGAGTTCCTTCTTCTCCTCTTTGGG          CTTCTTGTGCTTGTACTTCTCACCGCCTCCAGTCTCGCTAAACAACATCTCGGGAATCTTCTTCATAGAAGAATTAGACCA          ACCCTCCATCCAGAGGACCTGGCACTTCTTATGGAGGGCGGGATGCTCTCGCAATTGATCATGAAATTTGAAATTAGCGCT          GTCCATAATCAGCACAATGTGGAGATCTGTTGAAATCGCATAGGTGAGTAAATGAACTGGGCGGAAGAAGCCGCTCCTG          TGATGCTGATCCTTCAATGGGAGGAGCAGTGGCTCAGGTTCTTCCAAAGTGTACAAGCCGGGCGGCTCCAGCAGGACAG          CAGGGAGTTGATCATCTCCAGGAAGGTTGGGTGGACGAATTGATAGTCTTCCAGAGGAGGACGACCTGCTGGGCTCGAT          ACCGGCAGGTTGCAAGACGTGTTTTCAGATCGTCTTGAATTGCTTGGTTCGTTAGTTCGTTAGCTCTGCTGATCTTTGGAGAGACAG          GACGCTCCATGCATATGGCTGACCAGAGAAGTAATAGTGCCTTCCAACTCCAGAGCGTCCGGCCAGCAGCAGTATCC          ACCAGGGAAAGACAGGACGCGATCAATTTCTGGACATATACTCCAGGACCTCGTGGAAACAACAGAATGTCCAGGTTCTGGTT          GTCGCGGCCGTAGTGAATCAGGCCCTTCTTGTACAGTCTTCAAGTCAAGTTCAGTTGAGTTCAGTTTGGCGAGAGGCTTGGCATG          AGGTGGCAATGGTTGGATGTTGAGCAGCCCTTGACCCGAGTGTGCTGGCTCCCATGTCACATAGAAGGAATCGGCAT          ATTTATCCAGGATATCAGAGCCCCAATCACCTTGAACACAGAGGTGAGGATAATATCGAACAGATGCAGTTTCTTAGCGCC          AACAATCTTATCTTAAAGAGCCTGCGGGCTTCGTAAGCCACGATTTTCAGGACATAATCCAATGGGTGGTTTGTAGAGCC          TCCCTCCAGGTCATAGCGAAACAGTCCAGAACCATTTGTGTCAGAAATGCAGGGTGTGAAGAAGTAATGTGAGTAATCATC          GACCGTGAACCTTGGCGCGGACTTGTTCGTACACCTGAACCATAGAGCCAGCCAAGAGGTAGATCTTGTCTGATGAGCCCA          GATGCTATGGTCTTCAAATTTCTTGTGGAGGACAGGTTTCAGGTTAGGGCCATAGATGGTCTGCAACTGTTCCGCGCTCGGG          ATAATCGATTGAGCACAGTCTACAATTTGATGTAACCTGGTGGTGGCTTATGCTTCCCAACTACCGCGGAGAGACAT          GGAAGCCACAATCTTCCGCTGAGCAGCCCTTGACCCGAGTGTGCTGGCTCCCATGTCACATAGAAGGAATCGGCAT          GCTGGACCGTATGGGTTGCCTCCAGGCCATCTTCATAGCCTGTGTCAGGTTAGGTAACACTTGTCTGAGTGGAGTG          TAAACGAGCTTGTGGCATTCTTCTTGGTACTCATAGGTGACTGGAACCTCGCTGTCAACCATCTGAACGCAACAGGTGTGG          TCGACTTCATGTAGAACCCTCAACTGCTTCTTCCAGGCCAATCTTCCGTGGTGTGCACTTGGATTTGGTTTCCAGCTGCTTG          ACCACGTGATGTTATGGATAATGTCGAGAATCAGTGCTTTTCAAGTTTCAGCTCCAGAATACCGGACTCTGTGTTACCTGGG          TCTTCGGAAGATGTGTCATGTTAGTATAGTCTCAATTTGTTCCAGCAGCTGTGCTCAATCTGGTGCAGGAGAGTATCT          TTAATTCGATTCACATCTTCGGTAAACTGTATCTTGGCCAAAGCAGCACAGGATCTGTGATGGGAACAGAGAGAGGTTCC          ACAGCTCCCTGAGAGCTGCGTCCGGTGTGTCAGCACTCCTTTCAGCAGCTGCTCCAGGGTCTTCTTCTCCTCCAGGGCCAGA          TCGTTTCAGCCAGGTTTCGACGTTATTGGACAAGGGCACCTTATTCTTGAATGGCACAACCTTCTCCCTCCAAGGACTTCATT          GCAGTAATGTGCTTAGACTTCTCATCGAACAGACAGAGTTGATACCAGCAACAGCTTCTTGGAGGTGAGACTGAATCAG</p>
---

GATGGATTGGTTGACTGGCCCAAGATCTCCAGCAGGTCATCGTCTCCGATGAAGTAGAAGCGAGGGAAAGCGCTGCGCTTC  
 TCCTCCAGGAACCTCGTTGAGGCTGCGCTGGCATCTCTGCAATTGGTCCAGGATGGTCAGCAGTGAGTTGCGAATGCCTGCG  
 TGGGTAGTCAAGGTTGTGACGCGATTGTCTCTTCTGATATCTGTCAATGATGCTGCGGAAATCTTCATCCACCCTGTTGAAT  
 CTGGTCTGCTCTTTGGCGAGGCTCCGCGACCAAGATTGGTTCAGGTAACCCACTTCTCTGAATATGGTTGAGGTTTC  
 TGCAAATATTCGTTCCAGTTCCGCGAGTTTCTTTCCAGATGCTGACCTTGTCTTCAAAGCCTTTATAGTATGGTGAGTCC  
 TTCAAAGGACTGCAGGAGGCATCTATTGTGCGCCACCTGGTTGACGATGTCCTTCCAATCCTTGATCAGCTTCATGGTGCGG  
 CTCTGGGAGTCCATAGTCGATCAGTGTGAACACAGCACCCACGCCCCAATAATCCAGTTCCTGAGTGCTTCGCGGATG  
 GTCACCTTACCCTGGGCGCGTGTGAGTTCAGATCTTTCAGGTGAGCAGCCTTGGCCACGATGGTATCGGCAACTCTCAGCAGG  
 TCACCGAACAGCAGTTTCTCCAGAGATGTGCCGCGAGGCAGACCCAGCAAGCGGAACAGATCCAGCCAGTGATCGGGTGAC  
 AGGTGTTCTCCGCGGACGTACTTCAGGATAGGGATAACAATCTTATATTTGTCCACCTCAGATTGGAGCTTGACAGTCAATC  
 ACAGAATGCTCCTCCACTTTCCTGAGGCGGTCTGTCGCAATTCATCAGAACTCCTCAAACAAGTAGGTTCTAGTGCGAAAG  
 GTGATCCAATCTTCATTGGCCATTTCTTGAATCCCTGCTGGAACCTTTCGTAGAAGGCCCAAATCTGAGCACAGGACTCA  
 ATATCCTTGCTGATGCTGGAGGCGAGAGAGAAGTTAGGTTCTTCGAGGCGGAAGTGGTGACAGTCAATCGACCAGCTTCTTG  
 CGTGTCACTTCCAAATCGTCAGAACCGGTAATACCAGCAGCAGTAAACAATTTCTAACAGACCATGTGGTCTCTCTTTTCG  
 TTT

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

Sl.	Sequence	Sl.	Sequence
1	AAGGAAATTAGCCGTACAG	73	TCGTCACAATTCACCAGACGCTTCTAAATTC
2	GTATTACCGGATTGCCACGA	74	AGTCTGGAAGCATCTTCCGCCGTGAGCAAT
3	ATATAAGATTTTTGTGGGGC	75	CCCGCCCTCATGATCAATTGGACATCCAAG
4	AAGGATTGGAGATGAAGATT	76	GGACCTGATCAGGGCAACATCTGGGCCAGC
5	TTGATCCCAACAGAAGCAGC	77	TCCTGGCCCGCTCAGGACTGAGAGAGAACAA
6	TCAGCTGGACAGGTGTGCC	78	CATAAGCTTCTGCCGCGGTAGGTCTCACCT
7	ATCGATCCCATGGCAGAAA	79	TGACACAGACTGACAAGTGTACTGGGAAGG
8	CTCAGTAATCCATACCCAA	80	CCCTGCTGCAACCTTCTGGAGATCATTGTG
9	TCATCGGAGACCCTGGAGCA	81	CTGATTATTCAACAGAATCTCCAGATCAACT
10	CCCATCACAGAGTCTCTCTC	82	GGTTAAGGTGCAGCTGCACCCTTGCCTGCGC
11	CAGTCAAAGAGGTGGTCAA	83	TTGATGGGCATCCTGGAGGGCTGCAGCCTG
12	CTCGCCGTCGTGTGAGCAG	84	CTATCAGGCAACGTCAAAGGGCGAAGTTCCA
13	CAGAGGATTCGAGATCTGG	85	GCAGGGATGGCCCTTCTACGAAGAAAACCGT
14	CTGGAGTTGGTATCCTGGAT	86	GAACCTGGGATTCACTACGCCGCTTGGAAC
15	CCTCTGTGTATCTGGGGCT	87	AAGAGTCCGAGTGTGTTCAGTGACAACCA
16	GGCACTGGTAAGCACTGATT	88	AATGGGTTTCTTACACCCTGCATAGCATCT
17	AAGAATCTCTGTCTCCCTG	89	GGGAAAGGTTTGAAGACAAGGTCTCTGACAC
18	ACGATCTGAATGTGAGACTG	90	TTGCCCTTCTACATGAAGTCCGACGCGCCAA
19	GGCCGCGAACTGTACACTT	91	GTTACCCTGTACGAACAAGTCCCACACCTG
20	GCATTGCAAGTCTATGAAG	92	TGTGGTCTTTGGTGGCCAAAGGCGGAGTGG
21	ACTAAGCTGTCCAGGAGAT	93	ACCAAGTCAAAGACATGTCTGGACCACGCTA
22	CAAATTGGAGACGAGTCTTG	94	GACCTCTCTCAAAGATGTACTTCAAATACAT
23	GCCCAGTGTTAAGAAGAAGA	95	CTGCCGTAGCACATGGTGTACGTTATCTCT
24	TCACCCTACGCAAGAAGCTGGTTCGCTGCGC	96	CCTCTTGGTATCGAGGCCAGCAGGAGCGCG
25	GTAACCACAAGTGTAGCGGTCACGATGACTG	97	ACGCATATATCTCTCTCGACCAGGTCGTCT
26	GATCACTGGTCCGCGGAGAACCCGCACTAA	98	GAACATCTCCGGCGCGTGGATCCAAACGAAATTCGAC GCTAG
27	GACCTACTATTGGATCACCTTTCTGTACCC	99	ACTGCTGCTGCCGCTCAGGAAAGTGGAGGATAGAAT TTGTT
28	CCTTGAAGGGGACAATAGATGCCTTGAAGTG	100	AGGTGGACAAGTGGGTGCTGTGTTTCACTGGTCCA ATCTG
29	ACCATCCGCTCACGCGCCAGGGCTGCAGT	101	GAAGCTGATCTCCGAGCATCATGACAGATAAGCCG ACCAT
30	CCTCAACGCCAATTCAGAGATGCGCCCTGC	102	AAAGGTTCAATTAAGTTGGAAGCTGAGGTGTCTGTCA AGAAT
31	CCAAAGAGATCTTTGGTTCGCGGACAGCGCAG	103	TGTTGATTAAGCGATGACCTCTCAATCGAGAGCAGC TGAAG
32	GAGTGGCGCTCAGGTCGTCGAGATGTCAGA	104	CCCTTCTCCTCGGAAGGGAAGAAAGCGAAAGTCCCG GTTT
33	ACTGAAGGCTGTCGGTCAGAAGGTTACTGAG	105	CGTGCAGGTGATCAAGTTTTTGGGGTTCGAGCAGATC CTCGT
34	GGCTGGAATGAAGACTCACTTGAAGTGCACC	106	CGCTTCTACTGCTGTGAAGGAGTGCCTGACGCGCTT CCCT
35	GAGTCAGACCTGAGAAGATTTCTGGATTCCA	107	CTTCTGTGTAGAGATCAGGTCAGTGAAGAATAGCTGTG GACC
36	TAGAGCTTGAACCTTAAAGGGAGCGCATCAG	108	CCGCCATCTCGATCGAGGAGAGAAAGAACAACCAGT CTATT
37	CAAGGATATCTCTCTCGCTCCACCCGATT	109	TGCCCTGGAAGAATTTCTAGCATCTTGGCTAACTTCA TCAC
38	GACTTGAACCTCTCGGAAAAGTGCACATCT	110	GAACACAGAAGCTGTGGCAACCTTGAAGATCCAGGAT TCTGA
39	CTGGAGAAGGGTCTGCTCGCGGACTCAACT		
40	AGATAAGATTACGAAGCCCGCAGGGCTGCTC		
41	CAGGCCAAAATCCGGTGAAGGCTCTTTAG		
42	CCATTGGACTGGAGGAGGCTCATCATCGTG		
43	GCCAAGGCGAGAGTTGCCGATACCAACCAC		
44	GATTTCAGGTCAGGTCACCAACCAATAACCATA		
45	TTCAAGATATTTGCAGAACCCTCCATCCGT		
46	AACGCAATATCAAGTTTACCGAAGCCTGGCT		
47	GAACGATCCCAATAACGTCGAAAATGTGGAG		
48	CAAGCTCGGGTGCAGCCTCTGGTGACCCTCT		
49	GGAGACTGTGCTCGAACGCATCCAACGAGGC		
50	GGAGAGGCTGCTTCCGAGCAGAAGAGGATAG		
51	AAAGAGGAACCTGAAGAAGACCGACAGAGCT		

SUPPLEMENTARY INFORMATION

52	CTGCAATAAGCAGGATGAAGCTGTATCACC
53	TACTTGTCTGTTGGCCGACGCTTACGCTGCC
54	TCCTGAGCACTATAACGAGGAGTTCGCAAGG
55	CTGGCGAAGTGGATGAACTGAAATTCGCCTGT
56	TTGTGGCGACTCTGTGTTTCGAGGTCAAGAA
57	TCAGGTCTGAGCCGCTTGTTCACGCCGCT
58	GACCAGTTGCCGACTCCAGCAGACCTTAT
59	AAATCAAACGAAATCGGCAAAATAGATCAGG
60	GCGTGGTGAGAACGAATGGGATACCCAGAAT
61	TGATCGCGTCTGGAGTATATGTCTTCACTG
62	CCTGTCTGTGTCAGCCATATGCATATTTCTG
63	CAGAGGTATGATGTTCCGCTGCGGAGCCGT
64	ATGCCAGCAGTACACCTATGAGTAGAACCTG
65	TCCTCCACTATGGCGCTACCTCCAAGGAA
66	GATTGGCCAAATCCAAGTGCACATCTGTTT
67	CGATGAGACTGGTATCAACTCTGCCACCGAA
68	GAGTCCGGTCTCCGAGGACCAGGAGAAGT
69	TGTGCCATTGAAGTCTTGAGGGTAAACACA
70	AGTACAACCTAGCAGACTGGAGGCCGGAG
71	TCAGCAAGCAATCTCATCTGCAGCGGTGAGA
72	TTCTATGACTGGATGGAGGGTTGGCCAGCA

111	GCCGGACGCTAATATGTCCGATTCTTCTATCACTGCTGCTG
112	ATTATCTCACATCAAGCAAGATCTACCTCTATCTGTT
113	CGGTCCAGCTCTCGACATTATCCATAACATCGGCAACC
114	GCCAAACTCGGCCGCTTTCTGAGGTTGTTTAGATCCA
115	CAATTCAAGATGCTCAATCGATTATCCCGAGACGAACT
116	CTGGGCAGGCTGGAGGAACTGGAGCCACTGCTCGGAG
117	ACCCACGAGTCTTTCTTGCCAAGCGCGGTCAACCTT
118	AGAACAGAAGGGATGGCGTGGAGCCAGTTCTCCCGAT
119	AGCTGGTGAACAAAGCTTACGGAGCTACTCCGATTGA
120	GGCTTCTCGACTCCGTCGATCCTGATTTCCCATCACA

Sl.	Sequence
121	CACACCCGCGTTTTTCGCTTAATGCGGGAATCTGTGTTTTGAGGAACTGC
122	AGAAATTTAGTTTTTAGCAGGACCTGAACGCTAAGATTTTTGAGCATCAAC
123	TATCTTTGACATTTTCTCTTGGGTCTCACTGCTGATTTTCCATCCTGGA
124	AGAGAGACCCTTTTATGGTCTGTGCATTCTGTGATTTTTGACTGTCAA
125	TGCATCCAGAATTTTTGTTCAGGGTCCGAGACATTTTTGTTCGCGAAA
126	AAGAATTTGAATTTTTGAACCATAGCTCAAGGTGATTTTTTTGGGCTCGA
127	ACACGCTTGGTTTTAACTCGCCGGAGGACTATCAATTTTTTTCGTCACC
128	CTGCCACTCGCTTTTTGAGTCTGCTCAAGATCAATATTTTATATGTACAG
129	GCTCTGCCTTCTTTTCTGTACCAGCACCTACTACATTTTACAACAGCAT
130	GTACCTCTGTTTTTTGCGCAGAGAAGATTGGAGATTTTTAAGATCATCG
131	GCAGCTGATCTTTTTTGGAAAGTCTGACGCGAACACAATTTTGGAGTGGAA
132	GTGCCGTAAGTTTTTCACTAAATCGGACGGGAAAGTTTTTCCGGCGAAGC
133	TGGCTGGCTTTTTATGGTTCAGGTCGATGATTACTTTTTTCACTACT
134	CAGACAGATTTTTTCAACAGGGTGAAGGACATCGTCTTTTTAACCAGTGG
135	TGGCCCTGGAGTTTTTATGAAGAAGACGATGACCTGCTTTTTTGGAGATCTT
136	GACGTGGTCAATTTTGCAGCTGAACCTGGAAAGAAGCTTTTAGTTGAGGTT
137	CGAAGCACTATTTTGGGAACTGGAGTTATCCCTATTTTTCTGAAGTAC
138	CCATTGGCACTTTTTTTCATGGCAAGGGACGTGATCATTTTTGAAGGGCTT
139	ACTATTAAGATTTTTACGTGGACTCGCGATGGCCATTTTTTACGTGAAC
140	TGTTTGGAGGTTTTTTTCTGATGATCTGACGATTTTTTGGAAAGTGAC
141	GATTGACGACTTTTTAACTCAAAGACCGTGGGTAATTTTTTCAAAACCAG
142	CAATCAGTCTTTTTTCTGAAGACTGATACCGTGTTTTTTCTATGCAGGA
143	CCATAAGAAGTTTTTGGCAGGTCTAGAAGATCCCTTTTTGAGATGTTGT
144	TCAAGAGCTTTTTTCTGCTGATCCAGTATACTAATTTTTTTCATGCACACA
145	CAAGGCTCAGTTTTTAGACTATCAAAACGCACTGGTTTTTATCTTGCAAAGCGGGCGCTATTTTTGGGCGCTGGC
146	CCAATATCCAGTTTTTACTCTCAGGCAAGCCGGCTTTTTCTGGAAAGCAAAGTGAAGATTTTTTCTCTCAATT
147	AGTTCTGGAGTTTTTGAAGCGCAAAACCGGACGATTTTTGCTCTCAGGGGCCACAGACGTTTTTTATCCGCGA
148	ATCGACTATGATTTTTGGACTCCAGTCAAGAAGGACTTTTTAATCGCGTCAGTCAGGGAGGATTTTTCATTGCTACT
149	GCCTTCATGGATTTTTCGATCAAGAAATCCCTGATCTTTTAGCTCCCTGCGCTGTTCAAGTTTTTCCGACCAAGC
150	AAGACGCACTATTTTTTACTTCTCTCCTCAAGATTTTTTAGCAGAGGCTCGCGAACAGTTTTTTGCGACCATC
151	TCCTCTGGCGATTTTTGGTGGCCGATCCAGATTTTTTGGCTTCCATGCACCACAGGTTTTTTTACATCAAT
152	GCTGGAGACATTTTTTGGCTACTTCTCGAGTCTGTTTTTAATCAGACTAAAGGAATCTTATTTTTTAAAGCTGCAA
153	GCTTCGGCAAGTTTTTACCTTGATCATCCAACAGGAGTTTTGAGGATAAGACAAAGGGCACTTTTTTCCAGAATAAG
154	ACTAGGAATCCTTTTTCAACCCATTGAGGTTAATTTTTTTCACAACCACCCTCACCATCCATTTTTACATGAGAAA
155	AACCTCCCAATTTTTAGAGGGCTCACGCTGCACCTGTTTTTGTCTCTCAGTGCCGGCTGGTTTTTAGAAGTTTGA
156	GCTCACAGGCTTTTTTACTGAGTGGCGTATCAACATTTTTGCAAGACTCCAAGAAGGTCAGTTTTTCTTGTCCAG
157	CTGGGACTGTTTTTTCGCTATGACTTATGTCCTCGTTTTTAAATCGTGGCTGTTGGCGCTTTTTTAAAGGAACTGC
158	GACTCACCATTTTTTCTATAAAGGCAAACTCGCCGATTTTTACTGGACGAAAAGTGGGTTATTTTTCTCGAACCA
159	CCTACCTCAAGTTTTTAAAGCTGTTGAGTCTAAGCAGTTTTTATTACTGCAATCAAGAATAAGTTTTTGTGCCCTGT
160	AGATGGTGACTTTTTAGCGAGTCCAAGCTCGTTTTTTTTCACTCCACTCGCTATGAAGATTTTTTGGGCGCTGGGA
161	GCTGGATCTGTTTTTCCGCTGTCTACTGCTGTTGTTTTGAGACCTGCTGCTGACCTGATTTTTAAGATCTGAA
162	ACATTCGTGTTTTTCCACGAGGTCCTGTTTTTTTTCTGGTGGATGTGACATGGGGTTTTTAGCCAGGCAC
163	AGGATCAATGGTTTTTATTCAGTGTGAACCTCGAGGCAATTTTTGGTGGTACCCAGAAATAGCCCGTTTTTAGATAGGGTT
164	TCCGCTCGAATTTTTGAACCTAACTTTGAGTCTGTTTTTGTCTCAGATTTTCCAAGAAATGTTTTTGGCAATGAAG
165	ATCCTGTGCTTTTTTGGCCGAACAGTAAAGATCACTTTTTCCCTGCACCATAGCCAGTACATTTTTTACCTTCCT
166	TGAAGCACCGTTTTTATCGCAGAGGAAAGAGGACTTTTTGCTGAAGCGCCTGAACGAAAGCTTTTTTCAAGGCTCTG
167	GACAAGAGGTTTTTCAAAGAGGCAATTAATCTTCTATCCATGCGATGGACAGCGCTATTTTTATTCCAATTT
168	TATTCTGGAGCTTTTTTGAACCTGAAAGACAGAGAGCTTTTTTGTAAAGCACTCTCCATTGTTTTTAAAGATCAGG

**Table S6:** Sequences of the staple strands for SnR without any modification.

Sl.	Sequence	Sl.	Sequence
1	CTATCAGGGCGCCGCTACAG	73	GAGCAGACTGGTCGCGGAGCCCTCAGCCTCA
2	TTGTGGCGCAGTGTGTTC	74	GAGAACGCCTGCCAGCGATGACCAAGCTGA
3	GATTCAATCCATCCTGGGCT	75	GGTGTCAAAGCAGCTAAGTTGGTCTCAATC
4	ATTCCTTCTACCTGGCCGC	76	GCTGGCAATCAGGTCGTCGAGATTACCGAGT
5	GCCAGCAAGCTGAGACTGTG	77	CAGAGCAGAGAAGATTTCTGCACTGAGGA
6	CAGCAAGGATGAAGTCCGAC	78	CCAGTCTATCCTCCACGTCTATTAGGCGGT
7	CCCTCACCATCTCTCGACCA	79	GAGAAGTAGTTTAGCGGAGACTGGCGCCATCT
8	AACTGACTTGCCAGACGCTG	80	CAGTCTCACAGTCAACCAATCCATGTCTAAT
9	GACCTACTGGAGAGTTGCC	81	TCTTCTATCTGGATGGAGGGTTGCCGTGATT
10	CCAAGCGCGGTGCTTCCGAG	82	GTCAGCAACGCCAATCTCATCTGCTTCATCG
11	CTGAAGGAGATTTTCGACGCT	83	GAGACGATTTCCCTCGCTTCTACAGGCCGGA
12	ACTGGAGCCAGCCCAAGGCC	84	ATCAAAAGCGAAATCGGCCAAAATCTTTTTGG
13	CCGGTATTCTCGTCGAAACC	85	GGTCGAGGTCACCCAAATCAAGTCTTATAA
14	CGCAACTCACCTTGGAGGG	86	ACTGAGAAAAGAGTCTCTCTCAGAGTCAAGAA
15	GATTGGAAGGAGATTTCCGC	87	TCAGGTCTGAGCCGCTTGTTCATCAGGTC
16	GTCCGCTTCGGACATGTCTG	88	TCTGAAGGATCTTCCGCCCTCATCGTCAGAG
17	TACGGAGCTATGGCCGACG	89	GTATGCATTTCCGCTGCATTTCCAAGAGTC
18	TTCGGCCAGGGCAAGAAG	90	AAGTGATCCTCACTTGAAGGATTCGAAGGAC
19	GTATTACCGGCATCTGTTTCG	91	CTGATCGACAACATCTGGAGAACAGGCTGG
20	CCTCCACAAGTTACGAAGCC	92	GCCTGGAACAAGTGCACACCACCGCCTTGAC
21	ACCATCCGCGATTTCTCGAC	93	ACAGGCTAACAAAGTGTACCTCAAAGATTGG
22	AATTGATCGACCCAACTT	94	TGCTGATTGCATTCAACAGATCTAGGCTG
23	AGCTGGACCGGGTGGATGAA	95	CCTCCTCTGTATCGAGGCCACGCCACATTG
24	GTAACCACGCAAGTGTAGCGGTACCGATGAC	96	CTGCAAATAAGCAGGATGAAGCTGTATTTCAG
25	TGTCACCAACGCAAGAAGCTGGTGCCTGCCG	97	AGAAAGTGGCAGAACCTCAACCAACGCTGCC
26	CAGGGATTTGGCCCTTCTACGAAGGGGAAGA	98	GAAAAACCTGGCGGTGGATCCAACGAAACGT CAAAGGGC
27	AAGCGAAAGTGGCGAGAAAAGGAAAGTCCAG	99	GGACGCCGCTAGTTTGGAAACAAGAGTCCACTCTGT GTTTCGA
28	GAGGAGCATGGCACGACCGCTCACCCCGAT	100	CAGAACAGAGGTGGCAACCTTGAAGATCGCTTCT GAGAAACA
29	TTAGAGCTAACCCATAAAGGGAGCGGAAAAGTG	101	AATATGTCCGCTTCTGAGGTTGTTTCAAAGATAT CCTGGAT
30	GGTTAAGGTGCAGCTGCACCCCTGAGGTGCT	102	CCAAGGAAATCTCAATCGATTATCCCGAGCGACCT ATGAGTA
31	CAGTAATCAGATCCTCGTCGTGCGCAGCTG	103	CCTCCAGCATCACACCTGTTGCGTTCAGATGCTTCT CTCTCG
32	CAGTTGCCGACTCCAGCAGAAGACTAGCAT	104	CAGCTCCTGGGGAGCGCGACGCATATCTGCCGACT GAGAGGC
33	CTTGGCTAGTGAGCAGGAATTTCTCAGGGAC	105	AACTGAACTCCAGCATCGTCACAGAGGTTAGCCT CTCGGCA
34	AGACTGAGTGTGCAACGCATCCAACCTGGCG	106	TTCGACTAAGATAACCATCGTGGCCAAGGCTTTGG ATACCT
35	TGGTGGTCAATGGGATACCTTCCCTCTGG	107	TCTTTCTTGGCAGAAGACAGAGCTGGAGAGGTGTC TATGAAG
36	CTCCAAGAGATGTACTTCAATATCATCTGCC	108	GGTGTCAAGAAAGGAACATCTCCAAGGAAATTGTC GGTCAGAA
37	GCTGCCTGATGGTGTACGAATACTCTGACCT	109	CTTTGGAGGACACGCTATGTGGTCCAGATTGCGGC TTGTACA
38	CCATTGGACTGGAGGGAGGCTCATGGCTGCT	110	AACACAGAGTTGGCTGAACGATCTGGCCCTGAGG ACCCAGGT
39	CCAGGCCACAACCTCCGGTGCAAGCAAACAC	111	CGCAGGCATTAGAAGTTGTGCCATTCAAGAATTGA CTACCCA
40	CAGAACCTCTGATCACTACGGCCCTGACAC	112	GCTGATCAAGAGCATCATGACAGATATCAAGCGC ACCATGAA
41	AATGGGTTTTCACACCCTGCATTGCGACAAC	113	GGAACCTCGCCGAGGAGTGGACCAAGTCTGCCATC ACTGCCCT
42	GGAGTTGGTCACTGCTGCTGGCCGGCCAAGT	114	TTGCAAAGCTTTTATCACCTACTTGTCCGCATCCA CGAGTC
43	TCACCTCTACGAACAAGTCCGCGACGCTCT	115	GGACGGCTTCAAGAACTCCGTCGATCCTGATCAGG CATCACA
44	TAAGCTCATGCCGGCGGTAGGTTGAAGATCT	116	ACTGCTGCTGATATTATCCTCACCTCTGTGTTAGAA TTTGT
45	ACCTCTGTGGGGCTCATCAAGCGGAAGGCA	117	TCGAACCTGTGCGAGGCTCTTTAGAGATAAGTGGC GCCTACC
46	CCTGTTCTGGTCAAGCATATGCATGGCGGCC	118	GGGTGAAGTGATTATCCATAACATCGACGTGTAC CGCCCA
47	GCGAACATGAGGCTGCTGGCGAGGAGCCGT	119	ATATGTCCAGCCTGGAGATGATCAACTCCCTGGTC CTGGAGT
48	GCAGTATAGACACAGCTGGTGAACCTGGCAC	120	TTGATTAATCCTGAATCGCAAGGCTGGCGAACAGC TGAAGTG
49	TGGTAAGAACCCATACGGTCCAGAAATTGGA		
50	CACTGATCTGTGGGGCGTGGGTGCCACATCT		
51	CTGGAGAAGGGTCTGCTCGCGGTGTGTTCA		
52	TGAAGGACACAATAGATGCCTCTGTACCC		
53	GATCACTGCCGCGGAGAACACCTGCAGTCTCT		
54	GCCAAGCTGAGGTGCAGCCTCTGGCAAATAT		
55	AAGATTGTCCAATCTGAGGTGGATGAACGAG		
56	AGGAAACTGAAGACAAGGTGAGCAGAGGAGA		
57	GAAAGAACGAGGTGGTCAAGATCTCTGGGAA		
58	GATCCCAACTGTTCAAGAATAAAGTCTCTGCG		
59	CTTGATGGACACTCTGGAGGGCGTTCATTT		
60	CAGCTCACCGTTTCCCTTCTCTCGATAGAA		
61	AGAGGAAACTGAAGAAGACCGAGATCGATCC		
62	TGTACCCTAGATGGATGGCGTGGAAAGAATCT		
63	CTGCTGGAACCTGCCAAACTCGAGCCAGTTC		
64	GCACTAGGACGAGGATTTTCGCCTTAAAGCTG		
65	CTCCAACAGGAAGAACAGAAGACGTTCTCTGA		
66	ATTAAGATTTACCGAAGATGTGGTCAAGAA		
67	CGATCTGAACGAACTCAAGCAATAGAACGCA		
68	CCCGCCCTTTCATGATCAATTGCGCCATCAC		
69	AGATCCTGGACCCTTCTCTGTTTCAGAGCAAT		
70	GAAGTCTATATCAACTCTGTCTGTTGCGTGA		
71	CAACCGGACAGCTGCTGAAGGAGTTCGATGA		
72	ACGAGTTCTGCAGAGATGCGCAGCGGCCAAAA		

Sl.	Sequence
121	AGGCTCAGGAGTTTTACTATCAAAGCAATCAGTCCTTTTTCTGAAGACT
122	GGTTTACCTCGTTTTTAACCAATCTTCAGATTCAACATTTTTGGGTGGATGA
123	GACCTGCTGGATTTTGTATCTTGGGCCCTCAAGAAGCTTTTTGTGTGCTGG
124	CGAACACAAGATTTTGTATGGAATGCCCTCCCAAAGTTTTAGGGCTCAGT
125	ACCATGGCACTTTTTCTCATGGCAAATTCACAACCTTTTACCCTGCTCAG
126	GCTGGCTCTATTTTTGGTTCAGGTGGATGATTACTCTTTTACATTACTTC
127	CTTCCGCTCGTTTTAAGAACCTAAGTTGACAGCGATTTTGTCCAGTAC
128	TTCAAGGTGATTTTTTGGGGCTCTGGGCACTCCAGATTTTATAAGCAGGA
129	AGAAGGTCAGCTTTTTTGTTCAGCAGGATCAATGGTTTTTATTAGTGTG
130	TGCCGTAAGCTTTTTACTAAATCGGTGACGGGAAATTTTTGCCGGCGAAC
131	TATCCCTATCCTTTTTGAAGTACGTGCTGGATCTGTTTTTCCGCTTGCT
132	GTATCTTGTACTTTTACCTTTGGGCTGAAGCACCCTTTTTCATCGCAGAG
133	TTCTCAAGATTTTTCTTCTGCTGTGCACCTGAGTTTTTCTCTCAGAAA
134	GAAGAAGATTCTTTTCCGAGATGTTCAACGACAAGATTTTATAGCCAAAGA
135	AACACGTCTGTTTTTCAACTCGCCGTGGAGGACTATTTTTCAATTCGTCC
136	GCTGTCCTGTTTTTGCGAGGTGCCGAGATAAGATCTTTTATCGACTATA
137	AGGAAATGTTTTTGGAGGAAGTGAACGCTAAGATTTTGGCATCAAC
138	GGCTGGAGAATTTTTGTGTGACCTGCTGATCTGGAATTTTGTCTGAAGGT
139	GGAGGAGGATTTTTAGAAAGATCCAGACATGGCTATTTTCTCTCAGGG
140	TTCAAGGCGGATTTTCCAGCTGATGCCAGAATTTTCCAGGAGAAC
141	AAGGACAATCGTTTTCTGCACAACCTAAGGTGCCCTTTTTGTCCAATA
142	GCTGACCTGAATTTTTAGATCTGAACGCTCAAGCAGCTTTTTGAACCAAATC
143	TGAAGATGGGCTTTTTCTGGGAGGCACAGAGCGTTTTTAAAGCACTCG
144	GAGATGAAGAATTTTGACCCTGGAGCGCAGCTCTCATTTTTGGGAGCTGTG
145	GATTACCCTGTTTTTCTATGCAGGATGTCAGGGAGTTTTTACATTGCTACAATTCAGAGCTTTTAGGACCTCAG
146	ACATCGTCAACTTTTTAGGTGGCGTCAACACTATTTTTAAAGGCTTCGCCGAAGTGGTTTTACGAATATTT
147	AGCACATTACTTTTTGCAATGAAGTTGCTGACCATCTTTTCTGGACCAATCTGGAGGAGAATTTTGCAGCAGGCC
148	CTCCTAGCCAGTTTTTACATGACCTAAGAAGAAGGATTTTGTGCTGAAGGCTGAACGAAGTTTTTCCAAAGCTCT
149	ACTCGCTGAGTTTTTCTGCTCAAATCAATAATATGTTTTTACAGGTTCTTGTGACATGGGTTTTGAGCCAGGCA
150	CTGGGACTGTTTTTTCGCTATGACTTATGTCCTCGTTTTTAAATCGTGGCAATTTGAAGAATTTTCCATAGCATC
151	CGAACAGTTGCTTTTTAGACCATCTAATTTGTTGGCGCTTTTTAAGGAAGTCTGACGATTTTTTGGAAAGTGAC
152	CTGCCTCCCTTTTTTGTACCAGACTATTAAGAAGCTTTTTGGACTCCAAAGAGAGACCCTTTTATGGTCTTGT
153	AACTCGAGGCATTTTTGCGGTACCCAATAGCCCGAGTTTTATAGGGTTGACCTACTACAATTTTTAACAGCATGT
154	GGAGCGGGCGTTTTTLAGGGCGCTGCACACCCGCCTTTTTTCGCTAATGCGATGGCCACTTTTTACGTGAACCA
155	ACTGCTGTCTTTTTTGTGACCTGCTTTTGGAGGTTTTTTTTCTGATGAATTTCTGTGATGATTTTTCTGTCAAGCT
156	AAGATTGACGATTTTTCGAACTCAAACGCCGTGGGTATTTTTATATCAAACCTGCCACCAGACTTTTGTATCCGCG
157	GCAAGACCTTGTTTTTATCATCCAGGCTGTTGCGCAGTTTTTAGATTGGTGTGCTCCTCCCTTTTTATTGAAGGAT
158	TGTTCAATTACTTTTTTACCTATCATGGACAGCGCTTTTTTAAATCCAATCCATAAGAAGTTTTTGCCAGGTCCT
159	CCAGATTGTGGTTTTTCTTCCATGTCCACCAGGTTTTTTTTACATCAATTTGTCGTTTACACTTTTTTCCACTACTG
160	AATCCAACCCTTTTTATTCATCCAAGGACGTGATTTTTCAAGAAGGGCGGACATCTGTTTTTTGTCCACGA
161	CCAATATCCAGTTTTTACTCTACGCAAGCCGGCCTTTTTGGAAGCAACTGGAAGAATTTTTCTCAATTCT
162	ACTGGTTATTTTTTGCATCCGAGGCTACTGAGTTTTTGGCTGAAGAAACCAGCAAGATTTTCTCCAATTC
163	GTCTCTGAATTTTTTAGACTAAAAGCAATCTATAAGTTTTTCTGCAAATCTCCAACATGAGATTTTAAACCCGATTT
164	GGAGACATGTTTTTGGCCAAAGCCTTCATGGATCGTTTTTATCAAGAGAGCTGATCAGCTTTTTCTGCAGCAC
165	GGAGCTGAAACTTTTTGAAAGCACTAAGCACTCAGGTTTTTGAAGTGGATTGACTATGAGGATTTTTCTCCAGAGC
166	GAAGCAGTTGATTTTTGGTCTACATATTGAGTCTGTTTTTGGCTCAGATTTCAAGAAATGGTTTTTCCAATGAAGA
167	CCAGATTGTGGTTTTTCTCCATGTCCACCAGGTTTTTTACATCAATTTGTCGTTTACACTTTTTTCCACTACTG
168	TGCTTGGCCGATTTTTACAGATCAAGTCACTCCCTGCTTTTTACCAGATTGACTAACATCGACTTTTTACATCTCCG

Modified Staple Sequences of SnL and SnR

**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 CAACAACAACAACAA complementary strands.

Location		Original staple sequence at square corner	Modified staple sequence
Square	Comer		
1	1	I.CACACCCGCCGTTTTTCGCTTAATGCGGGAATCTGTG TTTTTGAGGAACTGC	I.CACACCCGCCGTTTTTCGCTTAATGCGGGA ATCTGTG - *X
		II.CAAGGCTCAGGTTTTTAGACTATCAAAACGCACTGGTT TTTTTATCTTGCAAAGCGGGCGCTATTTTGGGCGCTGGC	II.GAGGAACTGCCAAGGCTCAGGTTTTTAGA CTATCAA
			III.AACGCACTGGTTTTTTTATCTTGCAAAGC GGGCGCTATTTTGGGCGCTGGC
	2	I.AGAAATTCAGTTTTTAGCAGGACCTGAACGCTAAGAT TTTTGAGCATCAAC	I.AGAAATTCAGTTTTTAGCAGGACCTGAAC GCTAAGA - *X
		II.CCAATATCCAGTTTTTACTCTCACGAGCAAGCCGGCT TTTTCTGGAAAGCAAAGTGAAGAAATTTTCTCCTCAATT	II.GAGCATCAACCAATATCCAGTTTTTACT CTCACG
			III.AGCAAGCCGGCTTTTTCTGGAAAGCAAAC TGGAAGAATTTTCTCCTCAATT
	3	I.TATCTTTGACATTTTTCTCTGGGTCTCACTGCTGATTT TTCCATCCTGGA	I.GCCACCAGACGTTTTTTTATCCGCGATATC TTTGACA - *X
		II.AGTTCTGGAGTTTTTGAGAAGCGCAAACCGGACGCA TTTTTGTCTCAGGGGCCACAGACGTTTTTTATCCGCG	II.CCTCTTGGGTCTCACTGCTGATTTTTCCAT CCTGGA
			III.AGTTCTGGAGTTTTTGAGAAGCGCAAAC CGGACGCAATTTTGTCTCAGGG
	4	I.AGAGAGACCACTTTTTATGGTCTTGTCATTCTGTGATT TTTTGACTGTCAA	I.TCAAGAAGGACTTTTTAATCGCGTCAGTCA GGGAGGA - *X
		II.ATCGACTATGATTTTTGGACTCCAGTCAAGAAGGACT TTTTAATCGCGTCACTCAGGGAGGATTTTCATTGCTACT	II.CATTGCTACTAGAGAGACCACTTTTTATGG TCTTGT
			III.GCATTCTGTGATTTTTGACTGTCAAATC GACTATGATTTTGGACTCCAG
2	1	I.TGCATCCAGAATTTTTTGTCCAGGGTCGGAGACATTT TTTGTGCGCAAA	I.AATCCCTGATCTTTTAGCTCCCTGCGCCTG TTCAAG - *X
		II.GCCTTCATGATTTTTTCGATCAAGAAATCCCTGATCT TTTTAGCTCCCTGCGCCTGTTCAAGTTTTTGCCGACCAGC	II.GCCGACCAGCTGCATCCAGAATTTTTTGT TCCAGG
			III.GTCGAGACATTTTTTGTGCGCAAAGCC TTCATGGATTTTTTCGATCAAGA
	2	AAGAATTTGAATTTTTGAACCATAGCTCAAGGTGATTTT TTGGGGCTCTGA	I.AAGACGCACTATTTTTTACTTCTCTCTCCA AAGATC - *X
		AAGACGCACTATTTTTTACTTCTCTCCAAGATCTTT TTAGCAGAGGCTCGCGAACAGTTTTTTGACAGCACATC	II.AGCAGAGGCTCGCGAACAGTTTTTTTGA GACCATC
			III.AAGAATTTGAATTTTTGAACCATAGCTCA AGGTGATTTTTTGGGGCTCTGA
	3	ACACGTCTTGCTTTTAACTCGCCGGAGGACTATCAATTT TTTTCGTCCACC	I.CACCACCAGGTTTTTTTACATCAATACAC GTCTTGC - *X
		TCCTCTGGCGATTTTTGGTGCCCGGCATCCAGATTGTTTT TTGGCTTCCATGCACCACCAGGTTTTTTTACATCAAT	II.AACTCGCCGGAGGACTATCAATTTTTTTCG TCCACC
			III.TCCTCTGGCGATTTTTGGTGCCCGGCATC CAGATTGTTTTTGGCTTCCATG
	4	CTGCCACTCGCTTTTTGAGTCTGCTCAAGATCAATATTT TTATATGTACAG	I.AAGGAATCTTATTTTTAAGCTGCAACTGC CACTCGC - *X
		GCTGGAGACATTTTTTGGCTACTTCTCGAGTCTCTGTT TTAATCAGACTAAAGGAATCTTATTTTTAAGCTGCAA	II.TGAGTCTGCTCAAGATCAATATTTTTATAT GTACAG
			III.GCTGGAGACATTTTTTGGCTACTTCTCG AGTCTCTGTTTTAATCAGACTA



**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
Square	Corner		
1	1	I.CACACCCGCCGTTTTTCGCTTAATGCGGGAATCTGTG TTTTTGAGGAAGTGC	I.CACACCCGCCGTTTTTCGCTTAATGCGGGA ATCTGTG - <b>TTAATCCTCGTCAAT</b>
		II.CAAGGCTCAGGTTTTTAGACTATCAAAACGCACTGGTT TTTTTATCTTGCAAAGCGGGCGCTATTTTTGGGCGCTGGC	II.GAGGAACTGCCAAGGCTCAGGTTTTTAGA CTATCAA
			III.AACGCACTGGTTTTTTTATCTTGCAAAGC GGGCGCTATTTTTGGGCGCTGGC
	2	I.AGAAATTTAGTTTTTAGCAGGACCTGAACGCTAAGAT TTTTGAGCATCAAC	I.AGAAATTTAGTTTTTAGCAGGACCTGAAC GCTAAGA - <b>AATTCAGTCCCTTAA</b>
		II.CCAATATCCAGTTTTTACTCTCACGAGCAAGCCGGCT TTTTCTGGAAAGCAAAGTGAAGATTTTTCTCCTCAATT	II.GAGCATCAACCAATATCCAGTTTTTACT CTCACG
			III.AGCAAGCCGGCTTTTTCTGGAAAGCAAAC TGAAGAATTTTTCTCCTCAATT
	3	I.TATCTTTGACATTTTTCTCTGGGTCTCACTGCTGATTT TTCCATCTGGGA	I.GCCACCAGACGTTTTTTTATCCGCGATATC TTTGACA - <b>AAAGCTTGTAGAGAA</b>
		II.AGTTCTGGAGTTTTTGAAGAAGCGCAAACCCGGACGCA TTTTTCTCAGGGGCCACAGACGTTTTTTTATCCGCG	II.CCTCTTGGGTCTCACTGCTGATTTTTCCAT CCTGGA
			III.AGTTCTGGAGTTTTTGAAGAAGCGCAAAC CGGACGCATTTTTGGTCTCAGGG
	4	I.AGAGAGACCACTTTTTATGGTCTGTGCATTCTGTGATT TTTTGACTGTCAA	I.TCAAGAAGGACTTTTTAATCGCGTCAGTCA GGGAGGA - <b>ACAATGATTCAGGTA</b>
		II.ATCGACTATGATTTTTGGACTCCAGTCAAGAAGGACT TTTTAATCGCGTCAAGTCAAGGATTTTTCTATTGCTACT	II.CATTGCTACTAGAGAGACCACTTTTTATGG TCTTGT
			III.GCATTCTGTGATTTTTGACTGTCAAATC GACTATGATTTTTGGACTCCAG
2	1	I.TGCATCCAGAATTTTTTGTCCAGGGTCGGAGACATTT TTTGTGCGCAAA	I.AATCCTGATCTTTTTAGTCCCTGCGCCTG TTCAAG - <b>TTAATCCTCGTCAAT</b>
		II.GCCTTCATGGATTTTTTCGATCAAGAAATCCCTGATCT TTTTAGTCCCTGCGCCTGTTCAAGTTTTTGGCCAGCAGC	II.GCCGACCAGCTGCATCCAGAATTTTTTGT TCCAGG
			III.GTCGAGACATTTTTTGTGCGCAAAGCC TTCATGGATTTTTTCGATCAAGA
	2	AAGAATTTGAATTTTTGAACCATAGCTCAAGGTGATTTTT TTGGGGCTCTGA	LAAGACGCACTATTTTTTACTTCTCTCTCCA AAGATC - <b>AATTCAGTCCCTTAA</b>
		AAGACGCACTATTTTTTACTTCTCTCTCCAAGATCTTT TTAGCAGAGGCTCGCGAACAGTTTTTTTGCAGACCATC	II.AGCAGAGGCTCGCGAACAGTTTTTTTGA GACCATC
			III.AAGAATTTGAATTTTTGAACCATAGCTCA AGGTGATTTTTTGGGGCTCTGA
	3	ACACGTCTGTCTTTTAACTCGCCGGAGGACTATCAATTT TTTTCGTCCACC	I.CACCACCAGGTTTTTTTACATCAATACAC GTCTTGC - <b>AAAGCTTGTAGAGAA</b>
		TCCTCTGGCGATTTTTGGTGCCTGGCATCCAGATTGTTTT TTGGCTTCCATGCACCACCAGTTTTTTTACATCAAT	II.AACTCGCCGGAGGACTATCAATTTTTTTCG TCCACC
			III.TCCTCTGGCGATTTTTGGTGCCTGGCATC CAGATTGTTTTTGGCTCCATG
	4	CTGCCACTCGCTTTTTGAGTCTGCTCAAGATCAATATTT TTATATGTACAG	I.AAGGAATCTTATTTTTAAGCTGCAACTGC CACTCGC - <b>ACAATGATTCAGGTA</b>
		GCTGGAGACATTTTTTGGCTACTTCTCGAGTCTCTGTTT TTAATCAGACTAAAGGAATCTTATTTTTAAGCTGCAA	II.TGAGTCTGCTCAAGATCAATATTTTTATAT GTACAG
			III.GCTGGAGACATTTTTTGGCTACTTCTCG AGTCTCTGTTTTTAATCAGACTA
3	1	I.GCTCTGCCTTCTTTTTCTGTACCAGCACCTACTACATT TTTACAACAGCAT	I.CACCTACTACATTTTTACAACAGCATGCTT CGGCAAG - <b>TTAATCCTCGTCAAT</b>
		II.GCTTCGGCAAGTTTTTACCTTGATCATCCAACAGGAGT TTTTGAGGATAAGACAAAGGCACTTTTTTCCAGAATAA	II.ACCTTGATCATCCAACAGGAGTTTTTGGAG GATAAGA
			III.CAAAGGGCACTTTTTTCCAGAATAAGGCT CTGCCTCTTTTTCTGTACCAG
	2	I.GTACCCTCTGTTTTTTGCGCAGAGAAGATTGGAGATTT TTTAAGATCATCG	I.CTCACCATCCATTTTTACATGAGAAAGTAC CCTCTGT - <b>AATTCAGTCCCTTAA</b>
		II.ACTAGGAATCCTTTTTCAACCCATTCGAGGTTAATTTTT TTTACAACCACCCTACCATCCATTTTACATGAGAAA	II.TGCGCAGAGAAGATTGGAGATTTTTTAAG ATCATCG
			III.ACTAGGAATCCTTTTTCAACCCATTCGAG GTTAATTTTTTTCACAACCACC
	3	I.GCAGCTGATCTTTTTTGGAAAGTCTGACGCGAACACAAT TTTTGAGATGGAAT	I.CGCTGCACCTGTTTTTAGTCTCTCAGTGCC GGCCTGG - <b>AAAGCTTGTAGAGAA</b>
		II.AACCTCCCAATTTTTAGAGGGCTCACGCTGCACCTGT TTTTAGTCTCTCAGTGCCGCGCTGGTTTTTGAAGTTTGA	II.AGAAGTTGAGCAGCTGATCTTTTTTGA AGTCTGA
			III.CGCGAACACAATTTTTGAGATGGAATAAC CCTCCAATTTTTAGAGGGCTCA
	4	I.GTGCCGTAAGTTTTTCACTAAATCGGACGGGAAAGT TTTTCCGGCGAACC	I.GCTCACAGGCTTTTTACTGAGTGGCGGTGA TCAACCA - <b>*X</b>
		II.GCTCACAGGCTTTTTTACTGAGTGGCGGTGATCAACCAT TTTTGCAAGACTCCAAGAAGTCAAGTTTTTCTTGTCCAG	II.GCAAGACTCCAAGAAGTCAAGTTTTTCTT GTTCCAG
			III.GTGCCGTAAGTTTTTCACTAAATCGGAC GGGAAAGTTTTTCCGGCGAACC

SUPPLEMENTARY INFORMATION

4	1	I.TGGCTGGCTCTTTTTTATGGTTCAGGTCGATGATTACTT TTTTACATACT	I.TGGCTGGCTCTTTTTTATGGTTCAGGTCGAT GATTAC- <b>TTAATCCTCGTCAAT</b>
		II.CTGGGACTGTTTTTTTCGCTATGACTTATGTCCTCGTT TTTAAATCGTGGCTTGTGGCGCTTTTTTAAGGAAGTGC	II.TCACATTACTCTGGGACTGTTTTTTTCGC TATGAC
			III.TTATGTCTCGTTTTTAAATCGTGGCTTGT TGGCGCTTTTTTAAGGAAGTGC
	2	I.CAGACCAGATTTTTTCAACAGGGTGAGGACATCGTCT TTTTAACAGGTGG	I.GACTCACCATATTTTTCTATAAAGGCAAAC TCGCCGA- <b>AATTCAGTCCCTTAA</b>
		II.GACTCACCATATTTTTCTATAAAGGCAAACCTGCCGAT TTTTACTGGACGAAAAGTGGGTTATTTTTCTCGAACCA	II.ACTGGACGAAAAGTGGGTTATTTTTCTC GAACCA
			III.CAGACCAGATTTTTTCAACAGGGTGAGG ACATCGTCTTTTTAACAGGTGG
	3	I.TGGCCCTGGAGTTTTTATGAAGAAGACGATGACCTGCT TTTTTGAGATCTT	I.CGATGACCTGCTTTTTGGAGATCTTCTCA CCTCAAG- <b>AAAGCTTGAGAGAA</b>
		II.CTCACTCAAGTTTTTAAGCTGTTGAGTCTAAGCACT TTTTATTACTGCAATCAAGAATAAGTTTTGTGCCCTGT	II.AAGCTGTTGAGTCTAAGCACTTTTTATTA CTGCAA
			III.TCAAGAATAAGTTTTGTGCCCTGTTGG CCCTGGAGTTTTTATGAAGAAGA
	4	GACGTGGTCAATTTTTGCAGCTGAACCTGGAAGAAGCTT TTTAGTTGAGGTT	I.GACGTGGTCAATTTTTGCAGCTGAACCTGG AAGAAGC- <b>ACAATGATTCAGGTA</b>
		AGATGGTTGACTTTTTAGCGAGTTCCAAGCTCGTTATTT TTCACCTCACTCGCTATGAAGATTTTTTGGGCCTGGGA	II.AGTTGAGTTAGATGGTTGACTTTTTAGCG AGTTCC
			III.AAGCTCGTTATTTTTCACTCCACTCGCTA TGAAGATTTTTTGGGCCTGGGA

**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 CAACAACAACAACA complementary strands.

Location		Original staple sequence at square corner	Modified staple sequence
Square	Corner		
1	1	I.AGGCTCAGGAGTTTTTACTATCAAAGCAATCAGTCCTTT TTTCCTGAAGACT	I.AGGCTCAGGAGTTTTTACTATCAAAGCAAT CAGTCCT - *X
		II.GATTACCGTGTTTTTCTATGCAGGATGTCAGGGAGGT TTTTACATTGCTACAATTCAGAGCTTTTTAGGACCTCAG	II.CCTGAAGACTGATTACCGTGTTTTTCTAT GCAGGA
			III.TGTCAGGGAGGTTTTTACATTGCTACAAT TTCAGAGCTTTTTAGGACCTCAG
	2	I.GGTTTACCTCGTTTTTAAACCAATCTTCAGATTCAACATT TTTGGGTGGATGA	I.CGCCGAAGCTGGTTTTTACGAATATTTGGTT TACCTCG - *X
		II.ACATCGTCAACTTTTTCAGGTGGGCGTCAACATACTAT TTTTTAAAGGCTTTCGCCGAAGTGGTTTTTACGAATATTT	II.AACCAATCTTCAGATTCAACATTTTTGGGT GGATGA
			III.ACATCGTCAACTTTTTCAGGTGGGCGTCA CCATACTATTTTTTAAAGGCTTT
	3	I.GACCTGCTGGATTTTTGATCTTGGGCCCTCAAGAAGCTT TTTTGTTGCTGG	I.TGCTGACCATCTTTTTCTGGACCAATCTGG AGGAGAA - *X
		II.AGCACATTACTTTTTGCAATGAAGTTGCTGACCATCT TTTTCTGGACCAATCTGGAG	II.GCGCAGCGCCGACCTGCTGGATTTTTGAT CTTGGGC
			III.CCTCAAGAAGCTTTTTTGTGTTGCTGGAGC ACATTACTTTTTTGAATGAAGT
	4	I.CGAAACACAAGATTTTTGATGGAATGCCCTCCCAAAGT TTTTAGGGCTCAGT	I.AAGAAGAAGGATTTTTGCTGCTGAAGGCT GAACGAAG - *X
		II.CTCTAGCCAGTTTTTACATGACCTAAGAAGAAGGAT TTTTGCTGCTGAAGGCTGAACGAAGTTTTTCCAAAGCTCT	II.CCAAAGCTCTCGAACACAAGATTTTTGAT GGAATGC
			III.CCCTCCCAAAGTTTTTATGGGCTCAGTCTC CTAGCCAGTTTTTACATGACCT
2	1	I.ACCATTGCCACTTTTTCTCATGGCAAATTCACAACCTT TTTACCCGCTCAG	I.TCAATAATATGTTTTTTACAGGTTCTTGTGA CATGGG - *X
		II.ACTCGCTGAGTTTTTCTGCTTCAAATCAATAATATGTT TTTTACAGGTTCTTGACATGGGTTTTTGAGCCAGGCA	II.GAGCCAGGCAACCATTGCCACTTTTTCTCA TGGCAA
			III.ATTTCAACAACCTTTTTACCCGCTCAGACT CGCTGAGTTTTTCTGCTTCAAA
	2	I.GCTGGCTCTATTTTTTGGTTCAGGTGGATGATTACTCTT TTTACATTACTTC	I.CTGGGACTGTTTTTTTTCGCTATGACTTATG TCCTCG - *X
		II.CTGGGACTGTTTTTTTTCGCTATGACTTATGCTCTCGTT TTTAAATCGTGGCAATTTG	II.AAATCGTGGCAATTTGAAGAATTTTTCCAT AGCATC
			III.GCTGGCTCTATTTTTTGGTTCAGGTGGAT GATTACTCTTTTTACATTACTTC
	3	I.CTTCCGCCTCGTTTTTAAAGAACCTAAGTTGACAGCGATT TTTGTCCAGTAC	I.CGAAACAGTTGCTTTTTAGACCATCTAATTG TTGGCGC - *X
		II.CGAAACAGTTGCTTTTTAGACCATCTAATTGTTGGCGCT TTTTTAAAGAACTGTTCTGACGATTTTTTTGGAAGTGAC	II.TAAGGAAGTCTGACGATTTTTTTTTGGA AGTGAC
			III.CTTCCGCCTCGTTTTTAAAGAACCTAAGTT GACAGCGATTTTTGTTCCAGTAC
	4	I.TTCAAGGTGATTTTTTGGGGCTCTGGGCACTCCAGATT TTTATAAGCAGGA	I.AGAGAGACCACTTTTTATGGTCTTGTTTCA AGGTGAT - *X
		II.CTGCCTTCCCTTTTTGTACCAGACTATTAAGAAGCGTT TTTTGGACTCCAAAGAGAGACCACTTTTTATGGTCTTGT	II.TGGGGCTCTGGGCACTCCAGATTTTTATAA GCAGGA
			III.CTGCCTTCCCTTTTTGTACCAGACTATTA AAGAAGCTTTTTGGACTCCAA
		III.GTATCTTTGACTTTTTACCTCTTGGGCTGA AGCACCGTTTTTCATCGCAGAG	

**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.AGGCTCAGGAGTTTTTACTATCAAAGCAATCAGTCCTTT TTTCCTGAAGACT	I.AGGCTCAGGAGTTTTTACTATCAAAGCAAT CAGTCCT - <b>ATTGACGAGGATTAA</b>
		II.GATTACCGTGTTTTTTCTATGCAGGATGTCAGGGAGGT TTTTACATTGCTACAATTTTCAGAGCTTTTTAGGACCTCAG	II.CCTGAAGACTGATTACCGTGTTTTTTCTAT GCAGGA
			III.TGTCAGGGAGGTTTTTACATTGCTACAAT TTCAGAGCTTTTTAGGACCTCAG
	2	I.GGTTTACCTCGTTTTTAAACCAATCTTCAGATTCAACATT TTTGGGTGGATGA	I.CGCCGAAGTGGTTTTTACGAATATTTGGTT TACCTCG - <b>TACCTGAATCATTGT</b>
		II.ACATCGTCAACTTTTTTCAGGTGGGCGTCACCATACTAT TTTTTAAAGGCTTTCGCCGAAGTGGTTTTACGAATATT	II.AACCAATCTTCAGATTCAACATTTTTGGGT GGATGA
			III.ACATCGTCAACTTTTTTCAGGTGGGCGTCA CCATACTATTTTTTAAAGGCTTT
	3	I.GACCTGCTGGATTTTGTATCTTGGGCCCTCAAGAAGCTT TTTTGTTGCTGG	I.TGCTGACCATCTTTTTCTGGACCAATCTGG AGGAGAA - <b>TTCTCTACAAGCTTT</b>
		II.AGCACATTACTTTTTTGAATGAAGTTGCTGACCATCT TTTTCTGGACCAATCTGGAG	II.GCGCAGCGCCGACCTGCTGGATTTTTGAT CTTGGGC
			III.CCTCAAGAAGCTTTTTTGTGTTGCTGGAGC ACATTACTTTTTTGAATGAAGT
	4	I.CGAACACAAGATTTTTGATGGAATGCCCTCCCAAAGT TTTTAGGGCTCAGT	I.AAGAAGAAGGATTTTTGCTGCTGAAGGCT GAACGAAG - <b>TTAAGGGACTGAATT</b>
		II.CTCCTAGCCAGTTTTTACATGACCTAAGAAGAAGGAT TTTTGTGCTGAAGGCTGAACGAAGTTTTTCCAAAGCTCT	II.CCAAAGCTCTCGAACACAAGATTTTTGAT GGAATGC
			III.CCCTCCCAAAGTTTTTGGGGCTCAGTCTC CTAGCCAGTTTTTACATGACCT
2	1	I.ACCATTGCCACTTTTTCTCATGGCAAATTTACAACCTT TTTACCCGCTCAG	I.TCAATAATATGTTTTTACAGGTTCTTGTGA CATGGG - <b>ATTGACGAGGATTAA</b>
		II.ACTCGCTGAGTTTTTCTGCTTCAAATCAATAATATGTT TTTTACAGGTTCTTGTGACATGGGTTTTTGAGCCAGGCA	II.GAGCCAGGCAACCATTGCCACTTTTTCTCA TGGCAA
			III.ATTTACAACCTTTTTACCCGCTCAGACT CGCTGAGTTTTTCTGCTTCAA
	2	I.GCTGGCTCTATTTTTTGGTTCAGGTGGATGATTACTCTT TTTACATTACTTC	I.CTGGGACTGTTTTTTTCGCTATGACTTATGCTCTGTT TCCTCG - <b>TACCTGAATCATTGT</b>
		II.CTGGGACTGTTTTTTTCGCTATGACTTATGCTCTGTT TTTTAAATCGTGGCAATTTG	II.AAATCGTGGCAATTTGAAGAATTTTTCCAT AGCATC
			III.GCTGGCTCTATTTTTTGGTTCAGGTGGAT GATTACTTTTTTACATTACTTC
	3	I.CTTCCGCCTCGTTTTTAAAGAACCTAAGTTGACAGCGATT TTTGTCCAGTAC	I.CGAACAGTTGCTTTTTAGACCATCTAATTGTTGGCGCT TTGGCGC - <b>TTCTCTACAAGCTTT</b>
		II.CGAACAGTTGCTTTTTAGACCATCTAATTGTTGGCGCT TTTTTAAAGAACTGTTCTGACGATTTTTTTGGAAGTGAC	II.TAAGGAAGTCTGACGATTTTTTTTGGAA AGTGAC
			III.CTTCCGCCTCGTTTTTAAAGAACCTAAGTT GACAGCGATTTTTGTTCCAGTAC
	4	I.TTCAAGGTGATTTTTTGGGGCTCTGGGCACTCCAGATT TTTATAAGCAGGA	I.AGAGAGACCCTTTTTATGGTCTTGTGTTTCA AGGTGAT - <b>TTAAGGGACTGAATT</b>
		II.CTGCCTTCCCTTTTTTGTACCAGACTATTAAGAAGCGTT TTTTGGACTCCAAAGAGAGACCCTTTTTATGGTCTTGT	II.TGGGGCTCTGGGCACTCCAGATTTTTTATAA GCAGGA
			III.CTGCCTTCCCTTTTTTGTACCAGACTATTA AAGAAGCTTTTTTGGACTCCAA
3	1	I.AGAAGGTCAGCTTTTTTGTCCAGCAGGATCAATGGTT TTTATTCAAGTGTG	I.AGGATCAATGGTTTTTATTCAAGTGTGAAGT CGAGGCA - <b>ATTGACGAGGATTAA</b>
		II.AACTCGAGGCATTTTTTGCAGTACCAATAGCCCGAGT TTTTATAGGGTTGACCTACTACAACTTTTTAAACAGCATGT	II.TGCGGTACCAATAGCCCGAGTTTTTATA GGGTTGA
			III.CCTACTACAACCTTTTTAACAGCATGTAGA AGGTCAGCTTTTTTGTCCAGC
	2	I.TGCCGTAAAGCTTTTTACTAAATCGGTGACGGGGAAAT TTTTGCCGCGAAC	I.GATGGCCACTTTTTTACGTGAACCATGCC GTAAAGC - <b>TACCTGAATCATTGT</b>
		II.GGAGCGGGCGCTTTTTAGGGCGCTGCACACCCGCCGT TTTTCGTTAATGCGATGGCCACTTTTTTACGTGAACCA	II.ACTAAATCGGTGACGGGGAAATTTTTGCC GGCGAAC
			III.GGAGCGGGCGCTTTTTAGGGCGCTGCAC ACCCGCCGTTTTTTCGCTTAATGC
	3	I.TATCCCTATCCTTTTTGAAGTACGTGCTGGATCTGTTT TTTTCCGCTTGT	I.TTTGAGGAGTTTTTTTTCTGATGAATTTCTG TGATGA - <b>TTCTCTACAAGCTTT</b>
		II.ACTGCTGTTGTTTTTGTGACCTGCTTTTGTAGGAGTTTT TTTTCTGATGAATTTCTGTGATGATTTTTCTGTCAAGCT	II.CTGTCAAGCTTATCCCTATCCTTTTTTGA GTACGT
			III.GCTGATCTGTTTTTTCGCTTGTACTG CTGTTCTGTTTTTGTGACCTGCT
	4	I.GTATCTTGACTTTTTACCTCTTGGGCTGAAGCACCCTT TTTCATCGCAGAG	I.AAGATTGACGATTTTTTGAACCTCAAACGCC GTGGGTA - <b>TTAAGGGACTGAATT</b>
		II.AAGATTGACGATTTTTTGAACCTCAAACGCCCTGGGTAT TTTTATATCAAACCTGCCACCAGACTTTTTGTTATCCGCG	II.ATATCAAACCTGCCACCAGACTTTTTGTTA TCCGCG
			III.GTATCTTGACTTTTTACCTCTTGGGCTGA AGCACCCTTTTTTATCGCAGAG

SUPPLEMENTARY INFORMATION

4	1	I.TTCCTCAAGAGTTTTTCTCCTGCTGTGCACCTGAGTTT TTTCTCTCAGAAA	I.CTGTTGCGCAGTTTTTAGATTTGGTGCTGCT CCTCCC - <b>ATTGACGAGGATTAA</b>
		II.GCAAGACCTTGTTTTATCATCCAGGCTGTTGCGCAGT TTTTAGATTTGGTGCTGCTCCTCCCTTTTATTGAAGGAT	II.ATTGAAGGATTTCTCAAGAGTTTTTCTTC CTGCTG
			III.TGCACCTGAGTTTTTCTCTCAGAAAGCA AGACCTTGTTTTATCATCCAGG
	2	I.GAAGAAGATTCTTTTTCCGAGATGTTCAACGACAAGAT TTTTAGCGCAAAGA	I.CAACGACAAGATTTTTAGCGCAAAGATGTT CAATTAC - <b>TACCTGAATCATTGT</b>
		II.TGTTCAATTACTTTTTTACCTATCATGGACAGCGCTT TTTTAATCCAATCCATAAGAAGTTTTTGCCAGGTCCT	II.TTCACCTATCATGGACAGCGCTTTTTTAAT TCCAAT
			III.CCATAAGAAGTTTTTGGCCAGGTCCTGAA GAAGATTCTTTTTCCGAGATGTT
	3	I.AACACGTCTTGTTTTCAACTCGCCGTGGAGGACTATTT TTTCAATTCGTCC	I.AACACGTCTTGTTTTCAACTCGCCGTGGA GGACTAT - <b>TTCTCTACAAGCTTT</b>
		II.CCAGATTGTGGTTTTTCTTCCATGTCCCACCAGGTTTTT TTTACATCAATTGTCGTTTACACTTTTTTCCACTCACTG	II.CAATTCGTCCGCTCTGTCTTTTTTTCCCTG GTGGA
			III.AAGACGCACTATTTTTTACTTCTCTCTCC AAAGATCTTTTTAGCAGAGGCT
	4	I.GCTGTCCTCTGTTTTGCGAGGTGCCGAGATAAGATCTT TTTATCGACTATA	I.GGACATTCTGTTTTTGTTCACAGAGCTGT CCTCTG - <b>TTAAGGGACTGAATT</b>
		II.AATCCAACCTTTTTATTTCATTCCAAGGACGTGATT TTTTCAAGAAGGGCGGACATTCTGTTTTTTGTTCCACGA	II.GCGAGGTGCCGAGATAAGATCTTTTTATC GACTATA
			III.AATCCAACCTTTTTATTTCATTCCAAG GACGTGATTTTTCAAGAAGGGC