ERRATUM TO

3D DNA Nanostructure: Methods and Protocols

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The original version of this chapter was inadvertently published with a missing reference. The reference is listed below and it is updated. It is also cited in the page number 44, 45 and 46.

“Douglas SM, Marblestone AH, Teerapittayanon S et al (2009) Rapid prototyping of 3D DNA-origami shapes with caDNAno. *Nucleic Acids Res* 37:5001–5006.”

The original version of this chapter was inadvertently published with an incomplete name (Luvena Ong) of the author. Here is the complete name and it is updated throughout the book.

Luvena L. Ong.

The updated online version of the original book can be found at
DOI [10.1007/978-1-4939-6454-3](https://doi.org/10.1007/978-1-4939-6454-3)

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Chapter 5 in: Steffen L. Sparvath, Cody W. Geary, and Ebbe S. Andersen, Computer-Aided Design of RNA Origami Structures, Methods and Protocols, Methods in Molecular Biology, vol. 1500, DOI [10.1007/978-1-4939-6454-3_5](https://doi.org/10.1007/978-1-4939-6454-3_5).

The original version of this chapter was inadvertently published with wrong figures (Figure 3, 4, 8 and 10). Correct figures have been updated.

A. Create a 3D model

1. Find 3D motifs
2. Align the motifs
3. Ligate the PDB file
4. Refine the structure

B. Write the 2D structure

1. Write the secondary structure
2. Incorporate sequence restrictions
3. Trace the structure
4. Output a NUPACK code

C. Design the sequence

1. Design sequences
2. Evaluate the folding
3. Design primers
4. Order template and primers

```

CGUCGGCGUCUGAAGCCUGACGGACGCUGACACGCGCU
CGCUUACGGCUGAAAGGCUCACGGCCUGGAGCCUGGCGC
GCCGAGGCUGGUAACGGCCUCUGGGAGCCUUAUGCGAG
ACGCCGACCGGGAGCUGGUACUGCGUAGCAGUGCCAGG
UUAGGCGUGAGCGAUCACGCUAUAGAGCCACAAUUCUUC
UGAACUGUGACGGUCUACGAUUCUGCGGGAUCUGUAA
CGGACUCUGCCUUGCAUUGAUUGCGGAUUAUCAGUG
CCUCGCUUUAUGGGAUUAACUAGAGCCGUAUGUGC
GGUGAAGAGCCUACGCCAGCGUGGAGCCGUCUGGUGAAG
  
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Fig. 3 Workflow for RNA origami design. The design process can be divided into 3 tasks: (1) creating a 3D model, (2) converting the 3D model to a secondary structure (3) designing the sequence. This tutorial describes the modeling, data editing and calculation steps that are required to complete each of these tasks

Fig. 4 The final 3D model and 2D blueprint of the 2H-AE RNA origami structure. Side view of the 3D model (**a**) and 2D blueprint (**b**) of the 2H-AE RNA origami with the sequence and structural elements of the A-form RNA double helices (grey), immobilized crossovers (magenta), kissing-loop (blue), UUCG tetra-loops (orange), G–U wobble pairs (green), and the T7 RNA polymerase promoter sequence (red)

Fig. 8 Creating the 2D blueprint. *Assemble2* shows the secondary structure (**a**) of the 3D model. The secondary structure is copied to a text file (**b**) by typing it using the characters in (**d**). After the sequence constraints, e.g., immobile crossovers (**e**), have been added the *trace.pl* Perl script can output a blueprint with a refined secondary structure (**c**)

#2:2@P is fitted to #0:43.B@P

match #2:2-3,9-10@P #0:43-44.B,2-3.A@P

Fig. 10 Syntax of the command line in Chimera. The command *match* in *Chimera* aligns a tetra-loop (model #2) onto the end of a double helix (model #0) by aligning the first atom specified in the first model (#2:2@P) to the first atom in the second model (#0:43.B@P), which is the static model