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Nicolas Levy, Nicolas Schabanel

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Nicolas Levy
École Normale Supérieure de Lyon, LIP (UMR 5668, Équipe MC2), France

Nicolas Schabanel
CNRS, École Normale Supérieure de Lyon, LIP (UMR 5668, Équipe MC2) and IXXI, France

Abstract

Since the 1990s, increasingly complex nanostructures have been reliably obtained out of self-assembled DNA strands: from "simple" 2D shapes to 3D gears and articulated nano-objects, and even computing structures. The success of the assembly of these structures relies on a fine tuning of their structure to match the peculiar geometry of DNA helices. Various softwares have been developed to help the designer. These softwares provide essentially four kind of tools: an abstract representation of DNA helices (e.g. cadnano, scadnano, DNApen, 3DNA, Hex-tiles); a 3D view of the design (e.g., vHelix, Adenita, oxDNAviewer); fully automated design (e.g., BScOR, Daedalus, Perdix, Talos, Athena), generally dedicated to a specific kind of design, such as wireframe origami; and coarse grain or thermodynamical physics simulations (e.g., oxDNA, MrDNA, SNUPI, Nupack, ViennaRNA,...). MagicDNA combines some of these approaches to ease the design of configurable DNA origamis.

We present our first step in the direction of conciliating all these different approaches and purposes into one single reliable GUI solution: the first fully usable version (design from scratch to export) of our general purpose 3D DNA nanostructure design software ENSnano. We believe that its intuitive, swift and yet powerful graphical interface, combining 2D and 3D editable views, allows fast and precise editing of DNA nanostructures. It also handles editing of large 2D/3D structures smoothly, and imports from the most common solutions. Our software extends the concept of *grids* introduced in cadnano. Grids allow to abstract and articulated the different parts of a design. ENSnano also provides new design tools which speeds up considerably the design of complex large 3D structures, most notably: a *2D split view*, which allows to edit intricate 3D structures which cannot easily be mapped in a 2D view, and a *copy, paste & repeat* functionality, which takes advantage of the grids to design swiftly large repetitive chunks of a structure. ENSnano has been validated experimentally, as proven by the AFM images of a DNA origami entirely designed in ENSnano.

ENSnano is a *light-weight ready-to-run independent single-file* app, running seamlessly in most of the operating systems (Windows 10, MacOS 10.13+ and Linux). Precompiled versions for Windows and MacOS are ready to download on ENSnano website. As of writing this paper, our software is being actively developed to extend its capacities in various directions discussed in this article. Still, its 3D and 2D editing interface is already meeting our usability goals. Because of its stability and ease of use, we believe that ENSnano could already be integrated in anyone's design chain, when precise editing of a larger nanostructure is needed.

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1 Introduction

DNA nanostructures design. Since the 1990s, increasingly complex nanostructures have been reliably obtained out of self-assembled DNA strands: from "simple" 2D shapes [5, 28] to 3D gears and articulated nano-objects (e.g. [38, 11]) and even computing structures [29, 30, 35]. The success of the assembly of these structures relies on a fine tuning of their structure to match the peculiar geometry of DNA helices. Various softwares have been developed to help the designer.

A tour of existing softwares. These softwares provides essentially four kind of tools:

- an *abstract representation* of DNA helices, e.g.: cadnano [8], scadnano [7], DNApen [13], 3DNA [14], Hex-tiles [25];
- a *3D representation* of the design, e.g.: vHelix [4], Tiamat [33] Adenita [6], oxDNAviewer [27];
- a *fully automated design*, e.g.: BScOR [4], Daedalus [32], Perdix, Talos, Athena [18, 16, 17]. These are generally dedicated to a specific kind of design, such as wireframe origami;
- *coarse grain* or *thermodynamic physics simulation*, e.g.: oxDNA [9], MrDNA [23], Snupi [20], Nupack [37], ViennaRNA [22],...

Recently, the software MagicDNA [15] proposed to combine some of these approaches to ease the design of configurable DNA origamis. The recent article [12] presents a very detailed survey of all these solutions with their pros and cons. Here is a list of the features of interest found in these softwares:

- *High-level description:* DNA geometry is very peculiar and hard to grasp. The seminal cadnano interface allowed to abstract from it and focus on the relevant aspects of DNA helices: it provides a framework to place DNA helices next to each other, as well as guides to connect them using crossovers, together with an easily-understandable and printable blueprint of the resulting design. In spite of its imperfection in terms of DNA geometry (incorrect turn/bp [34] and absence of roll of helices), cadnano is still the reference for fine tuning a design.
- *Live (editable) 3D view:* With the raise of 3D complex designs involving DNA helices pointing in various directions or even making curves, various softwares proposed 3D rendering of a design. A notable software in this category is Tiamat [33] which introduced a 3D interface capable of fine tuning and editing of the design. Unfortunately, 3D views are not always the best solution to edit a design beyond placing properly DNA helices in space. Indeed, 3D views are often jammed, even for simple design, and the 3D→2D parallax effect makes it hard to evaluate the length of a crossover, especially because its direction, and thus its apparent length, changes when it is moved around.
- *Fine tuning and editing:* As mentioned above, 3D views are not well adapted for editing or fine tuning [12], especially when the 3D view is provided by a "mother" software (Matlab, Maya, or Samson) which was not designed for the specific needs of DNA nanostructures. As it turns out, almost all the softwares, including the all-automated ones, e.g. [15], recommend to export to (s)cadnano for checking and fine tuning their designs. As a matter of fact, the 2D representation of a helix as a double array, initially proposed in cadnano, remains the most practical for editing. Rotating the array representations as in [38, 7] allows an even more convenient rendering of the design. 3D complex designs however cannot be faithfully mapped to 2D, and, no matter what, some helices that are close to each other in 3D, will be mapped at distant locations in a 2D representation. As a result, many crossovers overlay the design and make it confusing to read and edit.

- *Design versatility:* Most softwares focus on a specific class of design: DNA origami, wireframe origami or DNA tiles (SST). Only a few provide an abstraction for dealing with all of them, e.g.: MagicDNA [15] proposes a common framework for classic and wireframe DNA origami. The most versatile remain (s)cadnano(for 2D editing) and Tiamat (for 3D editing). (s)cadnano make it possible to work with any class of designs, but provides almost no specific automation. It should however be noted that Tiamat comes with an integrated sequence generator.
- *Automation:* When designing a DNA origami, many tasks are repetitive and dull, such as "stapling" a rectangle. On the opposite, some tasks require a high technical level, such as routing a scaffold in a wireframe design, or designing 3D staples in a 3D bulk. Both of these types of tasks benefit a lot from automation. Algorithms have been designed to complete these tasks and designers can save a lot of time and avoid mistakes by using them, e.g. [4, 32, 16, 15].
- *Programmable designs:* Many designs gain to be specified as the output of a program: either because they are very big and repetitive (e.g., SST designs); or because they require specific angles and lengths (e.g. quasi-crystals in [38]); or because they sometimes require many trials-and-errors to be properly configured, for instance to match the length of the holy `M13mp18` scaffold strand. To achieve this goal, scadnano [7] and the prototype codenano [10] define a programming framework consisting of various function calls (in python or rust) to describe helices and strands positions. MagicDNA [15] proposes an interesting, user-friendlier, alternative approach, generalizing the wireframe approach, which consists in describing the design as graph embedded in space, whose edges are replaced by configurable chunks of parallel helices, along which the routing of the scaffold and its staples is algorithmically computed.
- *Simulation:* 3D views of a design are only a wishful representation of the design, as strands may not self-assemble as forseen by the designer. If 3D views are essential to choose the right crossovers to bind strands together in order to achieve the desired assembly, they offer no guarantee in the resulting shape. Coarse grained physics simulation [9, 23, 20] and thermodynamic binding estimation [37, 22] softwares allow a much more precise feedback on the feasibility and stability of a design. Their predictions are now considered good enough to demonstrate the validity of a design, e.g. [15]. However, they are computer-intensive and furthermore require a high level of competency to interact with. They can hardly produce a fast-enough feedback to be use during the design process. They are thus usually used at the end of the design chain. Design softwares usually offer to export the design into the sophisticated file format of these simulation softwares for validation.
- *Intuitive fast-responding interface:* Various directions have been explored for designing a adequate graphic user interface for designing DNA nanostructure. As mentioned earlier, 3D views did not improve, and in many cases arguably deteriorated the usability of the interface. This is particularly true when the software is embedded in a mother software in charge of the 3D rendering, which offers, most of the time, only slow or little-to-no editing capacities. As a consequence, (s)cadnano remains the most practical interface so far and this is no wonder it is still intensively used, in spite of its limited ergonomics.
- *Reliability:* Designing complex DNA nanostructures requires focused attention and unfortunate failures or slowness in softwares add considerable stress to the designer. Software reliability can only be ensured by developing them in a *safe* programming language, that is, whose compiler imposes rigorous safeguards to the programmers and checks their code in depth to avoid as much as possible bugs at runtime. Untyped

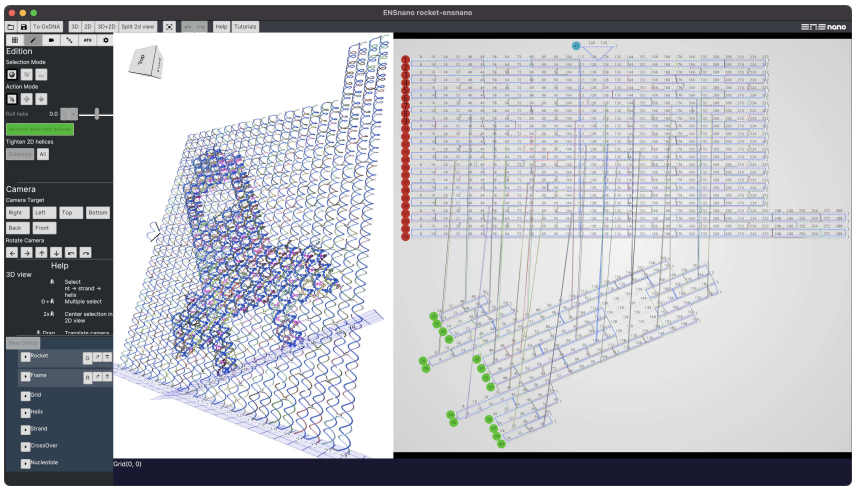


Figure 1 ENSnano interface: the 3D and 2D views of a design

programming languages should thus be ruled out to develop reliable design softwares.

- *Distribution:* The most commonly cited softwares, namely cadnano, oxDNA, oxDNAviewer, MrDNA, Nupack and ViennaRNA, are the easiest to install (they are distributed either as an independent, python packages or web-based app), and are available for the most commonly used operating systems (Windows, MacOS and Linux). We have had varying experience with installing and using softwares embedded into a generic-purpose mother application. Cross-platform distribution, either as an independent or a web-based app, seems thus to be an important usability criteria.

Our contribution. In this paper, we present our software ENSnano which introduces a 3D editable view *working together* with a (s)cadnano-like 2D view. As in cadnano, our helices are attached to *grids* organizing the helices, next to each other, in parallel subsets. We extend this grid concept in three ways:

- first, the grids are now freely and precisely placed and oriented in space in the 3D view;
- second, grids can be any 1D or 2D lattice, for now: the classic square and hexagonal grids, but also circular lattices to design nanotubes;
- third, we take advantage of this lattice structure to introduce a *geometry-aware copy-paste-&-repeat* process.

▶ A 2D and a 3D view working together. 2D and 3D views are illustrated in Fig. 1. The main purpose of the 3D view is to position the grids and helices, from which the coordinates of each nucleotide is deduced. These coordinates are used to suggest crossover positions (see Sec. 3.5). Crossovers can be created indifferently in the 2D or the 3D view. The 3D view provides also indications on the length of the crossovers: crossovers of excessive length are highlighted in black. The 2D view is pretty similar to the standard (s)cadnano view with three important differences:

- the design of the strands in the 2D view has been drastically simplified;
- the 2D view can be freely organized with few mouse clicks (see Sec. 3.3 and Fig.C.6);
- the 2D view can be split into two *interacting* views focusing on different parts of the 2D map of the design, as explained next.

The 2D and 3D views are synchronized: modifications of the designs made in one interface is immediately visible in the other one. Moreover hovering a design element (strand, helix

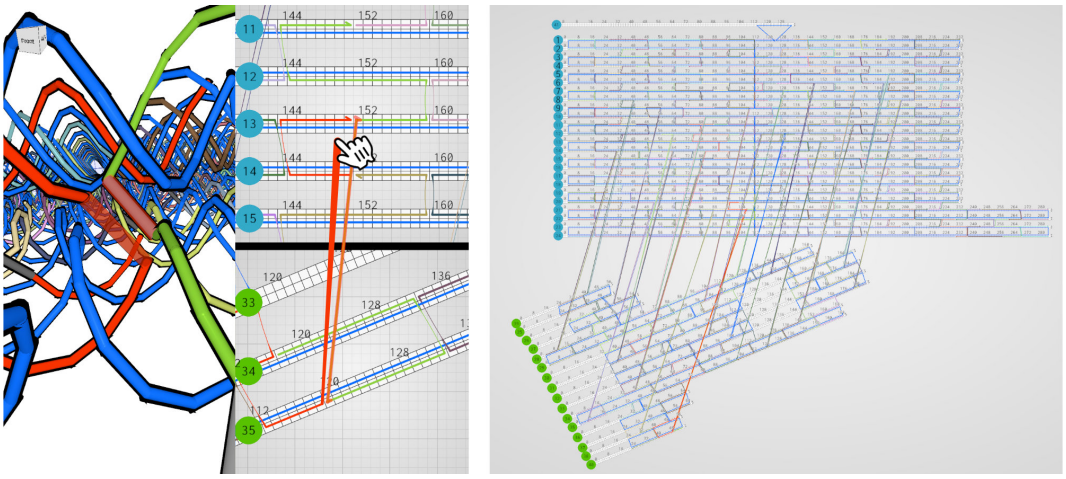


Figure 2 Editing with the 2D split view. (left) Building a crossover between "2D-distant" helices by dragging the mouse from one split view to the other. **(right)** In a single 2D view, the zoom factor required to see both ends of the crossover (highlighted in red) would be so small that precise editing would be impractical.

or nucleotide) with the mouse cursor in one interface will highlight it in both views, which makes the correspondence between the two representations easier to grasp.

▶ **The 2D split view.** As mentioned above, 3D complex structures cannot be faithfully mapped into 2D: some parts of the design that are close in 3D, will, no matter what, be mapped far apart from each other in the 2D view. The 2D split view of ENSnano allows to edit parts of the design that are mapped far apart from each other in the 2D view, as if they were next to each other, see Fig. 2. This is particularly useful for creating, moving or deleting a crossover between parts that are mapped across the 2D view. Furthermore, the 3D view interacts naturally with this feature by switching automatically to the 2D split view, when we double-left-click on a crossover that binds nucleotides that cannot be shown together in 2D view at its present zoom factor. Double-clicking on an element allows to switch easily back and forth between its locations in the 3D view and 2D view (or the 2D split view, when needed), see Sec. 3.3.

▶ **Natural swift point-and-click editing in the 2D view.** As shown in Fig. 3, the interface of ENSnano is organized so that most of the editing in the design can be made by clicking directly at the wanted location: the action applied is *deduced* from the *natural mouse movement* associated to the desired action together with the local configuration at the click location (see Sec. 3.3).

▶ **Geometry aware copy/pasting** ENSnano introduces a *geometry-aware copy/pasting* of strands and crossovers across the 3D structure, regardless of the actual numbering of the helices and of their arrangement in the 2D view. This allows to build in the blink of a eye a complete set of staples by duplicating repetitively the selected pattern (a subset of strands or crossovers) according to the initial translation, along the helices *and* across the grid lattice, of the firstly pasted copy (see Fig 9 in Section 3.4).

▶ **File format, import and export.** ENSnano file format is pretty similar to scadnano and codenano. It consists in a human readable and editable json file (see Sec. B). Currently, ENSnano imports files from scadnano and cadnano (with similar limitations as scadnano). ENSnano also exports designs to oxDNA for precise physics simulation.

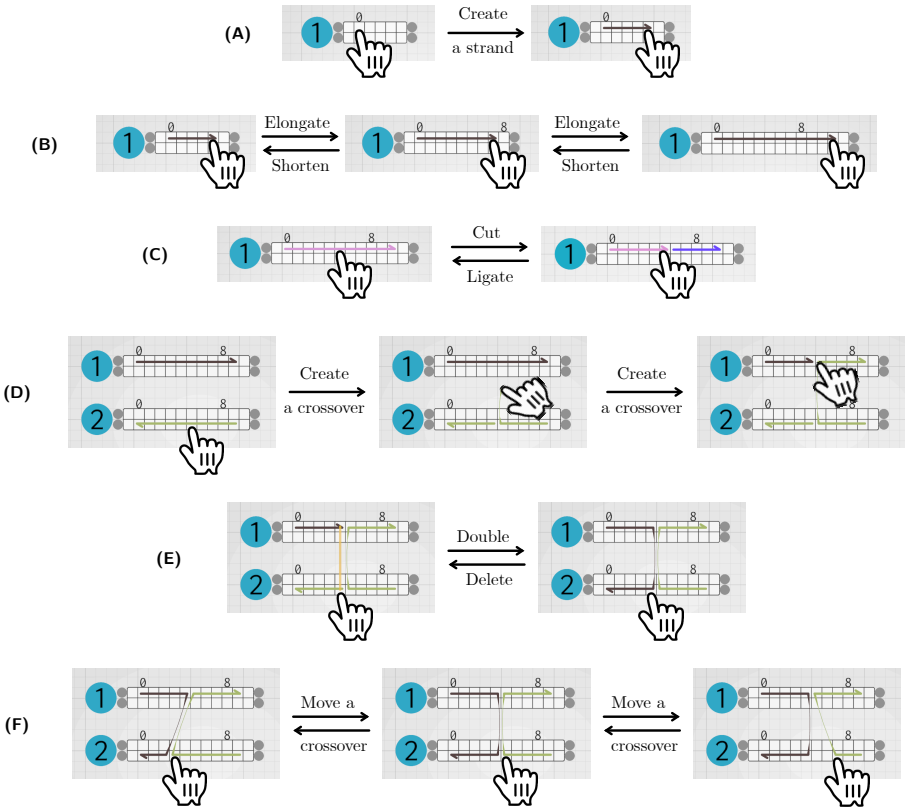


Figure 3 Swift strand editing in the 2D view. (A) Create a strand: Left click on an empty position and drag. **(B) Extend a domain:** Left click on an end of a domain and drag. Note that the helix automatically extends if needed. **(C) Cut & ligate a strand:** A left click in the middle of strand cuts the strands. A left click on the end of a strand next to another ligates them. **(D) Create a crossover:** A left click and drag up-/down-wards on a strand initiates the creation of a crossover that will bind the initial click position to the position where the mouse is dragged to. **(E) Double/Delete a crossover:** A left click on an unconnected end of a strand next to a crossover will double the crossover. A left click on one end of a crossover will break it. **(F) Move a crossover:** A left click-and-drag at one end of a crossover will move this crossover. Note that the possibly neighboring crossover will be pushed and pulled back during the dragging until the final position is set.

We do not provide yet any python framework to generate ENSnano designs. However, ENSnano files can be generated by a python program with moderate efforts. This issue will be resolved in an upcoming version of ENSnano.

▶ **Sequences export.** ENSnano is presently fully functional to design and edit precisely complex DNA origami and to export its staple sequences for ordering.

▶ **DNA parameters.** ENSnano uses the DNA helix physical data collected from [34, 31]. They are presented in appendix in Sec. B.2. They can easily be edited to fit specific needs directly in ENSnano file format (a `json` text file) as explained in Sec. B.

Distribution and Installation ENSnano is developed in the high performance safe programming language Rust [24]. We rely on the cross platform libraries winit, wgpu and iced [2, 3, 1] to produce an *identical and highly responsive* interface across all commonly used operating systems. ENSnano is distributed as a *single-file app* for Windows and MacOS, as well as an open source repository, ready to be cloned and compiled, for Linux and the brave ones. It

can be downloaded directly from ENSnano website [21].

2 ENSnano concepts

2D and 3D editable views. ENSnano combines two graphical interfaces to visualize and edit DNA nanostructures, each of them serving different purposes:

- *the 3D view* helps to visualize and arrange precisely the different elements composing the design in space. It enables to navigate inside the nanostructure, to ensure, for instance, that the crossovers that bind it together, are not too short nor too long. It also allows to arrange complex structures where helices are not parallel. It also provides new 3D tools that helps, for instance, to find suitable positions for crossovers between any kind of helices.
- *the 2D view* presents the blueprint of the design in a streamlined manner, similar to the one initially proposed in cadnano. This linear representation of the helices is easy to read and arguably more ergonomic for most editing task.

As we will see later, both views work together to facilitate the work of the designer. A particular care was given to provide a homogeneous visual experience for both views, with matching color codes between the views, for instance.

Grids. In ENSnano, like in several other nanostructure design softwares, the strands composing a nanostructure are positioned on helices that are assumed to be rigid shapes — currently, rigid cylinders. The 3D shape of the design is greatly influenced by the relative positions and orientations of these helices. In cadnano, the helices are all parallel and their positions are given by a point on a grid. In ENSnano helices are also positioned on a grid, but several grids can coexist in a design, and these grids can have different orientations, which makes it possible to create designs in which all helices point in different directions.

By grouping helices together on a grid, one can organize their design into bulk components made of parallel helices. Each of this component can be thought as a separated cadnano design. As pointed out in the introduction, the 2D view is typically more ergonomic to edit those components. Connecting two non-parallel components in a 2D interface is however a challenging task. This is where the 3D editing of crossovers and the crossover suggestions based on the 3D positions of the nucleotides are useful.

At the moment, ENSnano offers squared and hexagonal grids, as well as nanotubes made of 5 to 60 helices. Grids are internally implemented as a mapping $\mathbb{Z}^2 \mapsto \mathbb{R}^2$. This flexible representation makes it easy to add new grid types in the future, and could be easily extended to arbitrary Cayley graphs.

Group-based organization of the design. Elements of the designs can be grouped in named groups. These groups can be used to quickly select one part of the design, or to adjust altogether the properties of the elements in the set. Groups can for instance be used to quickly set the color of all the helices of a groups for crossover suggestion. They can also be used to hide or show temporarily parts of the design. Groups will have extended capabilities in upcoming versions of our software. Note that the group structure in ENSnano does not requires the groups to be disjoint. This is typically useful in the case where one wants to visualize the interface between two components linked together by a set of crossovers. One can create two groups, each of them containing one of the components and the set of crossovers. Using these groups one can chose to hide everything in the design but one of the components and the crossovers at the interface, as illustrated in Fig A.1.

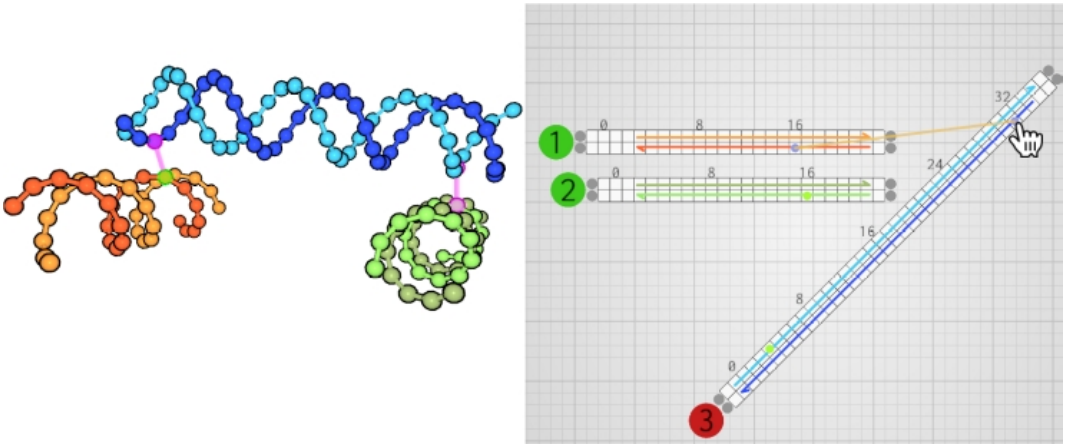


Figure 4 Crossover suggestions. As none of the three helices are parallel, finding crossover positions may be difficult. We thus assign the helices 1 and 2 (the orange and green stranded) to the green family and helix 3 (the blue stranded) to the red (note that the color family is displayed as the background color of their identifier disc in the 2D view). In the 3D view, the suggested crossovers are indicated by a translucent purple connection between two nucleotides. In the 2d view, the nucleotides that could be bound by a crossover are indicated by pairs of dots of matching color.

Design helpers. When designing a DNA nanostructure, special care must be given when choosing the positions of the crossovers. Indeed, the length and orientation of a crossover between two points of two neighboring helices can vary greatly, because of the spiraling nature of DNA helices. For this reason, DNA nanostructure design softwares often offer a feature that suggests positions at which crossovers between two helices are possible.

▶ **Crossover suggestions.** In ENSnano, one can assign to each helix a *color family*: none, red or green. Crossover suggestions will be made between helices of color families red and green: purple translucent clues will show up in the 3D view to indicate possible crossover positions, based on the distance between the nucleotides. Dots of matching colors indicates these same locations in the 2D view. Fig. 4 illustrates this feature.

▶ **Crossover length color shading.** In addition to the suggestion for creating new crossovers, ENSnano also offers visual clues for assessing the length of the existing crossovers. In the 3D interface the crossovers are displayed as cylinders, whose color depends on the distance between their extremities. Short crossovers have the same color as the strand they belong to, while crossover of excessive length are shaded from light grey to dark, where a darker color indicates a longer crossover, see Fig. 5.

▶ **Helices (auto)roll.** Rolling a helix around its axis shifts its strands forward or backward and thus has a huge impact on the position of its possible crossovers with neighboring helices. Reciprocally, placing some crossovers will have an impact on its optimal roll which will in turn impact all the crossovers around it. Choosing the roll of the helices gives more freedom in a design, and improves its feasibility. cadnano for instance ignores this factor. ENSnano enables to either input the value of the helix roll or to run a simple physics simulator which will auto-roll the selected helices according to the torsion forces applied by their crossovers, where each crossover is considered as a spring with free length 0.7nm, the expected length of a crossover. This allows a simple and almost instantaneous sanity check of a design as it is being built. Typical use of the auto-roll feature is when we want a specific crossover between a newly created helix and an other one: we first add this crossover regardless of its length and then we auto-roll the newly created helix so that it adjusts its roll to satisfy this desired

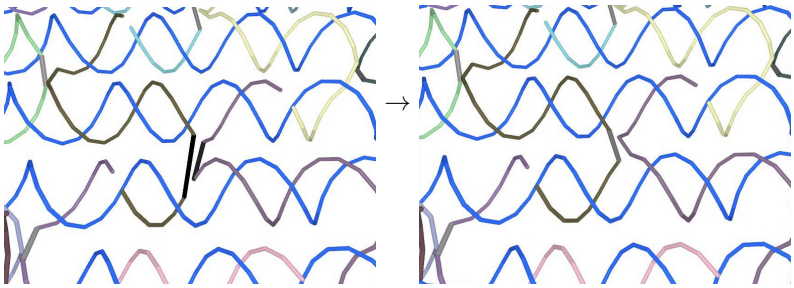


Figure 5 Length color shading of the crossover in the 3D view. (left) In this example, several crossovers of various lengths are visible. Crossovers that are short and don't require the designer's attention are displayed in the same color as their strand. Some crossovers are displayed in light-grey indicating that their moderately excessive length may only represents a minor problem in the design. However, one pair of crossovers is displayed in black. This should catch the designer's eyes and indicates that this pair of crossovers should be rearranged. **(right)** After correcting the two faulty crossovers, they are now shorter and appear in a lighter shade. This indicates that the design on the right panel is more likely to be feasible.

crossover; the crossover suggestion feature will then adapt and indicate where to place the other crossovers according to the initial one.

Basic stability testing. Dependable physics engines such as oxDNA and MrDNA are computer intensive and cannot provide a fast enough feedback for a user in doubt while building up a large design. As pointed out in [12], these softwares tend to be used at the end of the design chain, to validate a complete design, before ordering the corresponding strands. *In ENSnano, we propose to give up on dependable physics simulations of the resulting shape of a design*, but just to focus on its *immediate stability*. Indeed, the commonly accepted *motto* of DNA nanostructures design is that DNA helices can be abstracted as rigid shapes (cylinder or curves) if correctly tied up together. Dependable physics engines are used to check the correctness of this assumption. But, during the whole design process, we take it for granted, because its correctness relies on it. What we need is thus a fast regular feedback on whether the current (assumed to be) rigid helices are "tied up" satisfyingly to keep the desired shape. For this purpose, ENSnano includes a *very basic* rigid body physics simulator in which:

- each crossover is modelled as a spring with free length 0.7nm, the expected length of a covalent bond;
- each contiguous double-stranded part of a helix is modelled as an independent rigid cylinder;
- each single stranded part of an helix is considered as a chain of isolated points connected by crossovers (modelled as spring as above);
- Brownian motion is emulated by jiggling the isolated points (or not), with an adjustable intensity;
- the stiffness of the spring, ambient friction and mass of the nucleotide can be configured live as the simulation runs; we usually recommend to start with a high friction and to lower it slowly as the simulation progresses.

This very basic model has no other ambition than to provide a quick feedback on the stability of the currently developed design and may not always produce correct results. In particular, we need to review in depth the volume exclusion procedure. Some perfectly valid design may converge to a spaghetti mess.

To get a definitive assessment of the physical viability of their design, users are invited to export it to oxDNA.

3 Graphical User Interface and tools

3.1 Getting started

The interface of ENSnano is designed so that every action is only one click away: editing either grids, helices, strands, crossovers, 5' or 3' ends of domains,... do not require any edition mode switching; the intended action is naturally guessed by the program. The interface is divided in four area (see Fig. C.6 page 24):

- the top bar consists of the Open/Save/Export buttons, the view selector (3D and/or (split) 2D), the zoom fitting button, the undo/redo buttons, and the help & tutorials buttons;
- the left bar consists of four panels, from top to bottom: the tool panel, the camera shortcuts, the contextual panel, and the organizer;
- the main view(s) represent(s) the design in 2D and/or 3D;
- and the status bar at the bottom is currently essentially unused.

The camera panel gathers buttons that set the camera in standard positions, which is useful to align the design with the axis. The contextual panel displays and allows to edit information on the current selection. It also displays the help when nothing is selected. The organizer allows to group the design into (non-disjoint) sets as already discussed in Sec. 2.

The tool panel is composed of six tabs (see Fig. C.7):

- the grid tab gathers the tools to create grids and add helices to them;
- the edit tab gathers the tools to edit nucleotides, strands and helices;
- the camera tab presents the visualization parameters;
- the rigid body engine tab presents the (very basic) available physics simulation tools;
- the sequence tab allows to set and export the sequences of the strands;
- and the parameters tab allows to change the font size and the scrolling sensitivity.

What is selected or edited when clicking in the views is determined by the selection mode and by the action mode in the two editing tabs and :

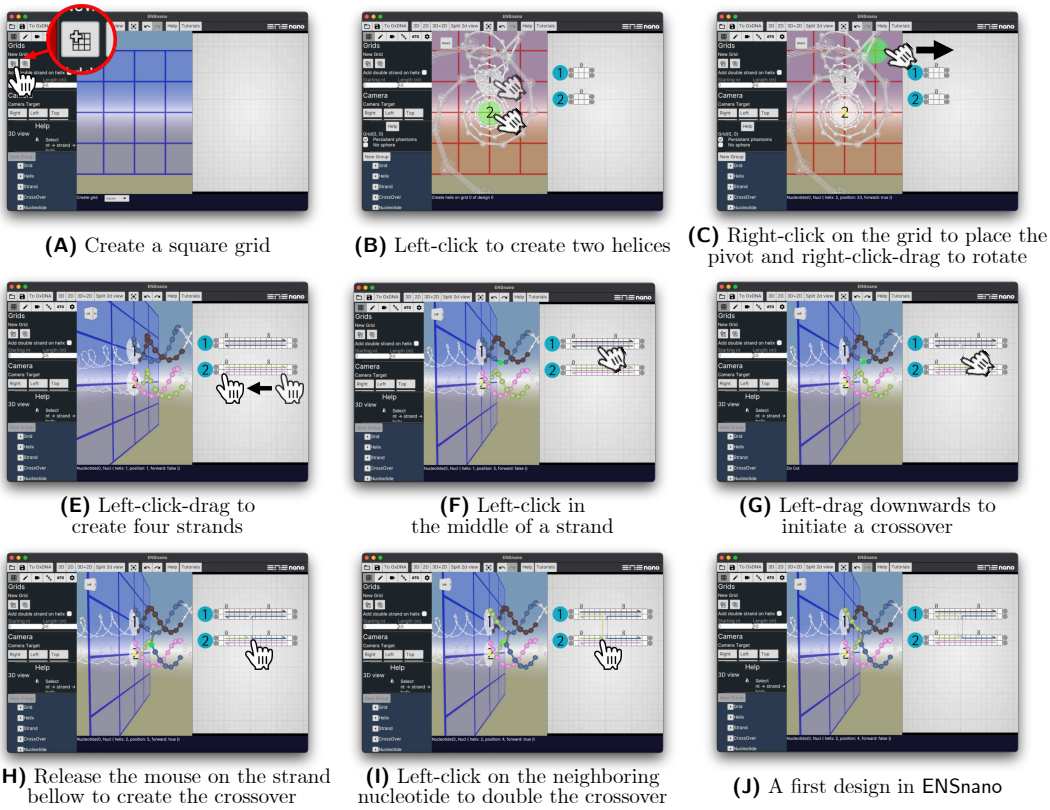
- the selection modes are: for nucleotides and crossovers, for strands, for helices;
- the action modes are: to edit objects, to translate objects, to rotate objects, and to add helices to a grid.

Grids are added to the design using the buttons: for square grid, for hexagonal grid, and for nanotubes. Helices are added to a grid by clicking on the desired position on the grid. One can chose to equip a helix with a double strand at its creation: just set the starting position and length of the strands in the text fields bellow. By default a phantom helix is displayed when an helix is created, this can be switched off in contextual panel after selecting the grid.

Building a first design. Fig. 6 presents step-by-step how to build a very simple design in ENSnano.

3.2 The 3D view

The main purpose of the 3D view is to visualize and organize the components in space.



(A) Create a square grid

(B) Left-click to create two helices

(C) Right-click on the grid to place the pivot and right-click-drag to rotate

(E) Left-click-drag to create four strands

(F) Left-click in the middle of a strand

(G) Left-drag downwards to initiate a crossover

(H) Release the mouse on the strand bellow to create the crossover

(I) Left-click on the neighboring nucleotide to double the crossover

(J) A first design in ENSnano

Figure 6 Step-by-step construction of a first design in ENSnano.

The camera can be: translated (using the mouse left- or middle-click, or the keyboard arrows), rotated freely (using the mouse right-click or Ctrl/⌘+middle-click), and zoomed in and out (using the mouse wheel). Rotations and zooms are performed around the *pivot point* which is highlighted by a yellow ball. The pivot point is set by right-clicking on an element of the design. The button [•] in the top bar allows to auto-adjust the zoom to fit the whole design in the views. *Right-double-clicking* on an element in the 2D view centers this element in the 3D view. *Left-double-clicking* on an element in the 3D view centers this element in the 2D view.

3D arrangement. The grids and helices can be rearranged by selecting them and choosing the action mode ✥ or ⟲. Handles appear to be pulled in the three possible directions. Handles are either aligned with the current orientation of the object, or with canonical axes of the design, see Fig. A.2. The latter choice is preferred to align different components precisely. Clicking again on the action mode ✥ or ⟲ switches from one handles alignment to the other.

Fog. Sometimes, the 3D view can be confusing. The *fog* feature in the tab ■ allows to display only the part of the design within a given radius around the pivot or the camera, fading the rest progressively to invisible, see Fig. 7.

Rendering style. By default, the background of the 3D view is a landscape gradient, which is convenient to keep track of the current camera orientation. It can be replaced by a white

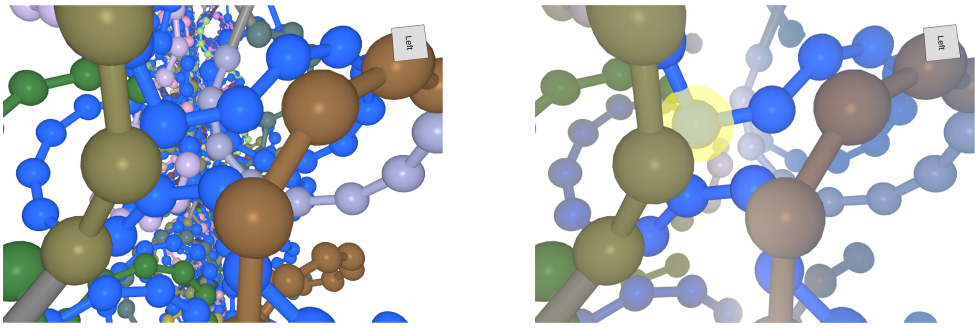


Figure 7 The fog feature. (left) no fog: the background is jammed with strands, and it is hard to focus on the crossovers between the two layers; **(right) with fog:** the background is cleared and the crossover is now clearly visible, ready to be adjusted if needed.

background (e.g., for publication) in the rendering section of the tab 🎥. One can also opt there for a cartoon rendering, where each object is outlined in black (e.g., for printing).

Editing in the 3D view. Sometimes, it is easier to edit directly in the 3D view. Left-click-and-drag on an end of a strand or a crossover allows to translate it along the helix.[1] One can build a crossover by a long-press left-click on a nucleotide (longer than 250ms): a blue ball appears, and dragging to another nucleotide creates the crossover.

3.3 The 2D view

The 2D view is the blueprint of the design. It follows and extends the streamlined interface of cadnano and scadnano by adding a list of features that improves its ergonomics:

- Creation and edition of strands, creation and translation of crossovers, cutting and ligating strands are all done in the same edition mode, using only the mouse *left-click*, as shown in Fig. 3. Note that the *selection in the 2D view* is accomplished by *right-clicking*.
- The 2D and 3D views work together: a translucide green ball indicates in the 3D view which nucleotide is hoverred by the mouse in the 2D view (e.g., see Fig. 3F and 3H). Also, double-right-clicking a nucleotide in the 2D view centers it in the 3D view.
- The helix representations automatically extend when needed, e.g. when elongating a strand. The helix representations can be tighten back using the buttons "All/Selected" under "Tighten 2D helices" in the edition tab ✎, or simply by clicking on their handles.
- Any helix representation can be translated and rotated arbitrarily in the 2D view, to match as closely as possible the 3D arrangement of design, or serve any other purposes, e.g. Fig. A.3 or C.6. Left-clicking on their number will translate the selected helices, while right-clicking will rotate them.
- Moving is the 2D view is done by middle- or Alt/⌥+left-click-and-drag. Zooming in and out is done by scrolling the mouse wheel.

The 2D split view. As mentioned earlier, 3D complex structures cannot be faithfully mapped into 2D, and some parts that are next to each other in space, will inevitably be mapped far apart in any 2D view. This usually makes 2D representation of 3D DNA nanostructures complex to read and even more to edit. For instance, very long crossovers

[1] Cutting and ligating a strand by left-click are disabled in the 3D view because it is too error-prone.

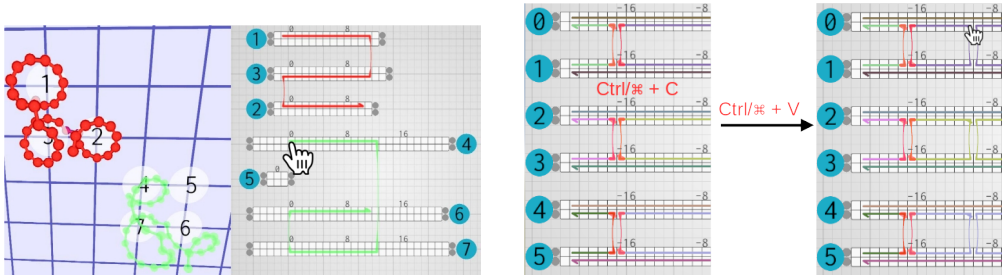


Figure 8 Grid geometry-aware copy and paste of strands and crossovers. (left) Duplication of a strand: the red strand gets duplicated on other helices of the grid. One can check in the 3D interface that the path of the strand is correctly being copied, even if the 2D view could be reorganized to present a clearer representation of the strand. **(right) Duplication of crossovers:** four crossovers are being copied at once on existing strands.

cross each other in every possible direction in the cadnano representation of the double-layer origami in [31], and make it almost impossible to edit. ENSnano's 2D split view solves this issue elegantly by allowing to zoom and to *act seamlessly on two distant parts* of the 2D view, as if they were next to each other. Indeed, one can build a crossover from one split view to the other just as if it was one single 2D view, see Fig. 2. Moreover, crossovers whose ends are in opposite sides of the split view, *are drawn across the views*, making them easy to read and edit.

Note that left double-clicking on a crossover in the 3D view, splits the 2D view as soon as both of its ends do not fit in the 2D view. We thus recommend to 1) create the desired crossover approximately in the 3D view and then 2) to double-click on it, so that it gets focused and drawn across the split view, where the user can then edit it comfortably.

3.4 Grid-aware copy, paste & repeat

Grid geometry-aware copy & paste. Many DNA nanostructure designs consist of repeating the same pattern over and over, e.g.: SST nanotubes [36, 35], rectangular DNA origami [34], or SST 3D assemblies [19, 26]... and many more contains many repeating crossover patterns. A designer can thus save a lot of time by copying and pasting patterns, as proposed for instance in scadnano. ENSnano extends with capacity by using the grid structure to compute the 3D path followed by the pattern copied, to paste the same path at a different location, *regardless of the numbering of the helices and of their relative positions in the 2D view.* Arbitrarily complex strands can thus be copied and pasted across the design, as shown on Fig. 8. For instance, a strand binding two consecutive helices in a nanotube can be copied all around the nanotube: ENSnano will automatically loop the strand around the nanotube from its last to its first helix. In addition to copying strands on empty positions, it is also possible to copy crossovers on existing strands, see Fig. 8. The basic copy and paste functionality if performed by pressing `Ctrl/⌘+C` after selecting the source strands/crossovers and then `Ctrl/⌘+V` and click to place a copy.

Paste & repeat. In addition to the classic copy and paste feature. ENSnano features a geometry-aware *paste and repeat* which remembers as well the translation (in the grid *and* along the helices) between the original and the first pasted pattern, and keeps pasting the pattern with the same translation over and over. This is particularly useful for large repetitive designs such as rectangular part of an origami or SST nanotubes. After copying the strands

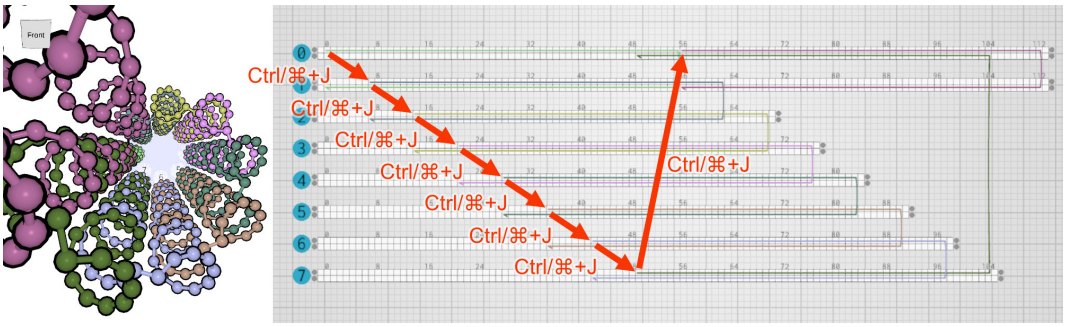


Figure 9 Paste & repeat: Starting from the green strand made of two domains of 56 nucleotides each on helices 0 and 1 of a 8-helices nanotube, this strand is copied with `Ctrl/⌘+C` and pasted with `Ctrl/⌘+J`, one helix below and 7 nucleotides forward. Repeating `Ctrl/⌘+J` compulsively 7 more times creates automatically the other strands, applying repetitively the same translation and thus filling the nanotube with strands in no time. Note that ENSnano is aware of the nanotube-grid geometry and places the 7th pasted olive strand appropriately, binding helices 7 and 0.

or crossover pattern with `Ctrl/⌘+C`, the first duplication is made by pressing `Ctrl/⌘+J`. Once the first copy is positioned, the path from the original to the copy is memorized. Pressing `Ctrl/⌘+J` repetitively, will copy over and over the pattern with the same offset as long as there are helices to support them, as illustrated in Fig. 9.

3.5 Crossover suggestions

Crossover suggestions are currently done by assigning helices to either the green or the red family. Color family are assigned in the organizer, by clicking on the family button which displays either: ∅ for none, R for red, and G for green. The easiest is to create a group for each family of helix and to set the color family for each group at once by clicking on the family button of the group, see Fig. 10. Crossover suggestion is enabled as soon as there are helices of the red and green families. Setting all the families back to ∅ disable the crossover suggestion.

3.6 The basic 3D rigid body physics engine

The tab 🔧 presents the three possible modes of our rigid body physics engine:

- the “Roll” button executes a simple roll of all the helices (see Sec. 2). This is a good way to check the quality of the crossovers. Note that the roll of each helix can be set individually in the tab ✎.
- the “Rigid grid” button runs the physics engine considering that all the helices belonging to the same grid act as one rigid body. This allows to evaluate the interactions between the various components of a design, in particular, the balance of the crossovers between them.
- the “Rigid helices” button runs the physics engine as explained in Sec. 2. In this mode, several parameters can be tuned live: the stiffness of the crossovers, the ambient friction (we recommend to start the simulation with a higher friction and to decrease it with time), and the mass of the nucleotides (beware that tuning this parameter live may explode the design as it will apply some rocket effect). We strongly recommend not to use the volume exclusion option which is inefficient and slow right now. Note that opting for “jiggling

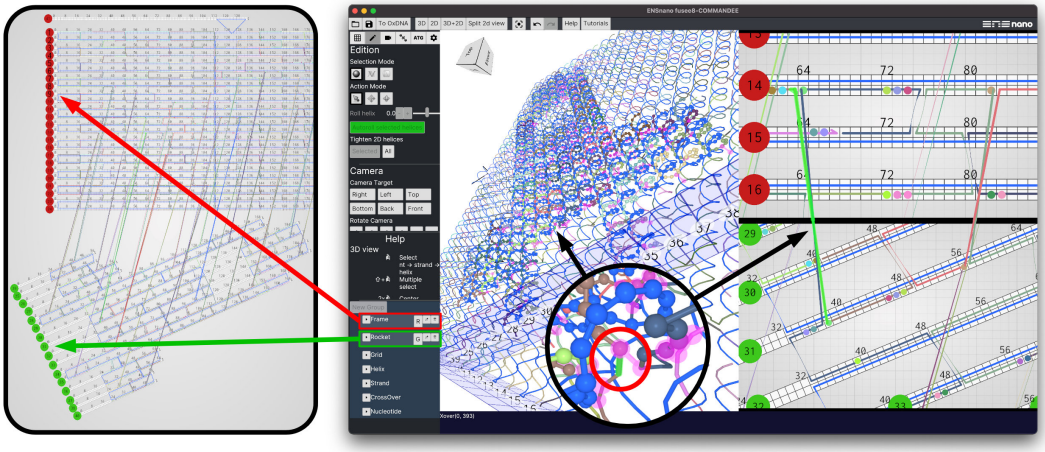


Figure 10 Crossover suggestions between red and green color families. The helices are partitioned into two groups in the organizer: "Frame" and "Rocket" assigned resp. to the red and green families. On can see the pair of matching dots in the split view marking recommended positions for crossovers.

unmatched nucleotides", simulates Brownian motion by adding constantly a random noise to their positions (the rate and amplitude of the noise can be tuned as well).

The two last modes are still at their infancy. The "Rigid grid" mode is useful when combined with the "Guess grid" feature in the tab ⊞, when importing a design from (s)cadnano which has no grid and no 3D embedding. Because the volume exclusion implementation is right now inefficient, the "rigid helices" mode should only be considered as a stability indicator, as it may converge to unrealistic configurations. Note that running the rigid body engine can be undone with `Ctrl/⌘+Z` or the Undo button.

3.7 Sequences export and scaffold sequence optimization

The tab ATG gathers the sequence-related tools. As far as sequences are concerned, ENSnano is, *for now*, "DNA origami-oriented" (this will change in the future). This sequence tab allows to chose the scaffold strand and to assign its sequence. One can load any text file containing a long enough sequence for that purpose. The default scaffold sequence is the `M13mp18`. In ENSnano, the user can either set the starting position of the cyclic scaffold sequence, or let ENSnano *optimize it*. When asked to optimize, ENSnano tries to minimize the risk of error in the strand synthesis, by finding the position that minimizes the number of problematic patterns such as $C^{n\geqslant 4}$, $G^{n\geqslant 4}$ or $(A|T)^{n\geqslant 7}$. The higher the n, the heavier the weight of the problem. Once optimized, ENSnano reports on the number of remaining problematic patterns as shown in Fig. A.4. This position is retained and saved for later reuse. This optimization phase allows usually to avoid any C^{5+} or G^{5+} pattern in no time.

Note that nucleotides that are not matched with the scaffold are given a `?` symbol in the exported excel file.

4 Experimental validation

We have already annealed successfully several DNA origami designed with ENSnano. We present here one of them designed together with the students of the class CR11 on Molecular

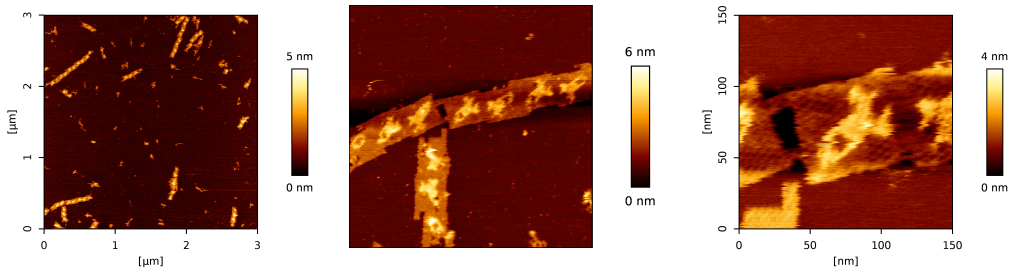


Figure 11 AFM images of our rocket design. These were obtained on a JPK Fastscan Nanoworld 4 equipped with a Nanoworld USC-F0.3-k0.3 tip in tapping mode — 20μL sample of: m13mp18 scaffold at 1nM with staples at 10nM in 1× TAE buffer with 12.5mM magnesium.

computing at the ÉNS de Lyon in December 2020: a rocket DNA origami consisting of two layers made of parallel helices making an odd angle. Please refer to Sec. D in the appendix for the full design and staple sequences. Designing this origami was particularly easy with ENSnano thanks to the crossover recommendation and grid systems. We were able to place the crossovers between the two layers, where the strands of the top and bottom layers were the closest, painlessly, and without any calculation. Splitting the 2D view was of great help as well. The possibility to arrange freely the helices in the 2D view allowed to check readily the design in the 2D view as well as in the 3D view.

The computed strands were annealed at 10nM together with the m13mp18 scaffold at 1nM in 1× TAE buffer with 12.5mM magnesium: starting from 95°C and decreasing to 55°C at −1°C/min and then from 55°C to 45°C at −1°C/15min and then hold at 25°C. AFM images of the resulting DNA origami are presented in Fig. 11.

5 Conclusion and upcoming features

With this first version of ENSnano, its 3D and 2D fast, precise, and versatile editing capacities, and its stability, we have set the basis for an upcoming complete, GUI based, cross-platform, DNA nanostructure design suite. This software will evolve at a fast pace in the upcoming months. Here is a short list of features, we plan to develop next:

- *Versatility:* presently the design is limited to straight DNA helices. We plan to add soon curved double strands and free single strands to the toolbox. We also plan to add soon "decorations" (fluorophores, biotin,...). We also plan to extend our concept of grid to more complex structures (2D as well as 3D).
- *Sequences:* ENSnano is presently limited to DNA origami in terms of sequence export. We are currently working on an interface to set the sequences for the parts of the design which are not matched with a scaffold.
- *Programmability:* ENSnano file format is a standard `json` dictionary, very similar to scadnano file format. Its complete structure is described in appendix B. Even if it is fairly easy to develop a python code to produce ENSnano file, as it was done for the design in Fig. C.6, we plan to propose as soon as possible, a python framework to produce ENSnano design file programmatically.
- *Automation:* Designing the staples is a tedious task. Adding auto-stapling algorithms will be of great help to the designer. Automatic scaffolding will however require a new kind of abstraction of a DNA design.
- *Simulation:* improving the rigid body physics engine will probably require a lot of work. Adding a proper volume exclusion is certainly the most interesting direction to follow.

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A Omitted figures

This section gathers the figures cast away in the appendix due to space constraints.

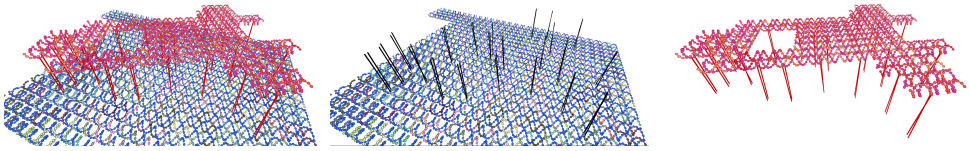
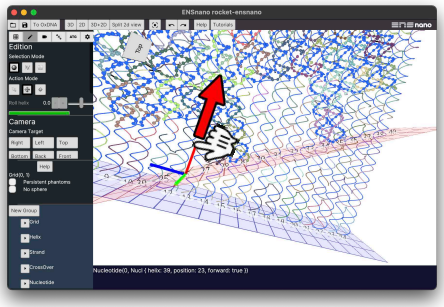
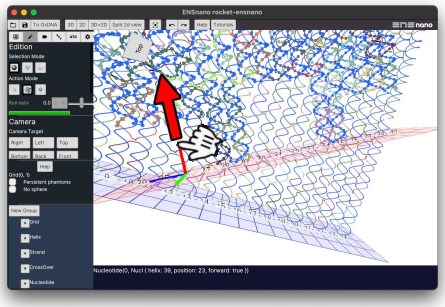


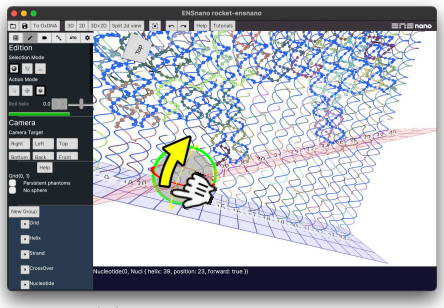
Figure A.1 Using ENSnano's groups to hide elements of the design. **(left)** The two layers of the rocket design which are spread apart to ease the reading of the crossovers in the figures. Two overlapping heterogeneous groups, gathering helices and crossovers, have been created in the organizer, and can be shown or hidden on demand in the 3D view: **(middle)** A first group gathering the helices in the rectangular base, and the crossovers between the two layers; **(right)** A second group gathering the helices of the rocket and the crossovers between the two layers.



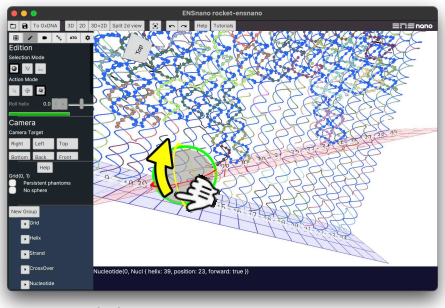
(A) Translation handles aligned with the canonical axes



(B) Translation handles aligned with the object axes



(C) Rotation handles aligned with the canonical axes



(D) Rotation handles aligned with the object axes

Figure A.2 The move and rotate handles to rearrange grids and helices in 3D.

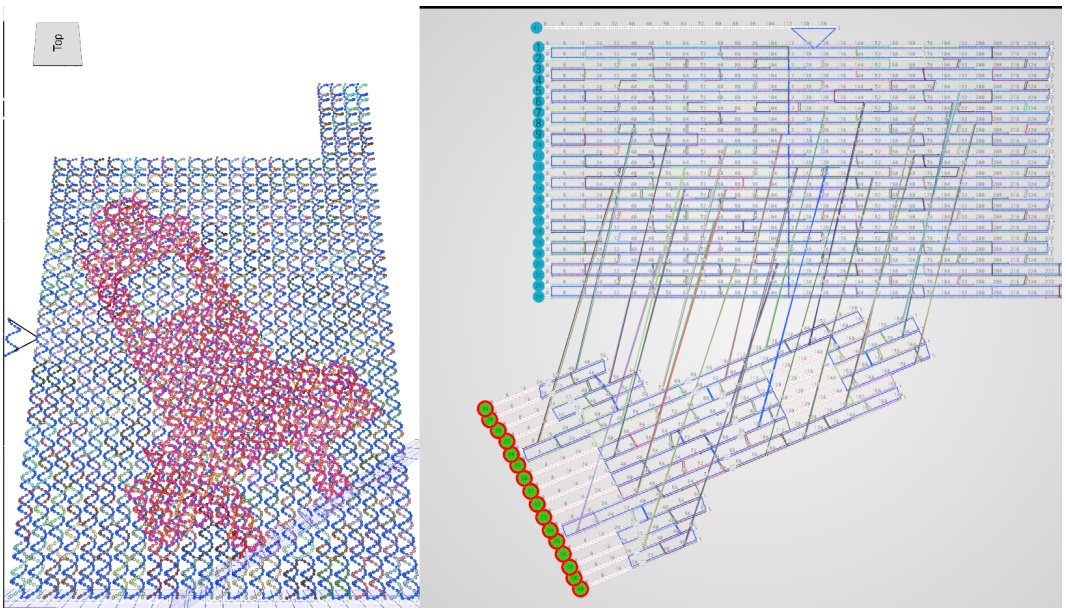


Figure A.3 Comparison between the 2D and 3D interfaces. The 3D interface shows the shape, that we wish that our design will adopt. Since this design is made of two layers making an odd angle. It cannot be faithfully represented in 2D. By separating the helices of the two layers, and adjusting the orientation of the helices composing the rocket layer, one can build a 2D representation of the design that is as close as possible to its intended 3D structure.

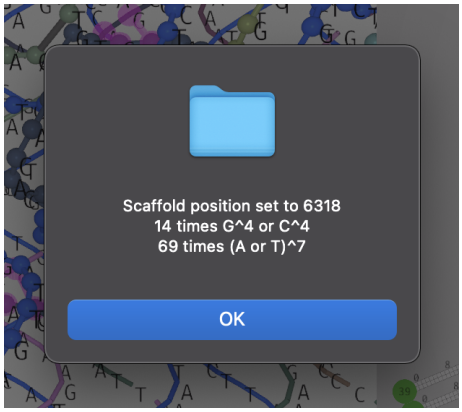


Figure A.4 Report on scaffold sequence position optimization.

B ENSnano File format

B.1 Top-level structure

In ENSnano, designs are loaded from a json file. Here are the top-level element:

- `helices`: a dictionary that maps positive integer to `Helix` object (see the definition of `Helix` object in B.3).
- `strands`: a dictionary that maps positive integer to `Strand` object (see the definition of `Strand` objects in B.4).
- `dna_parameters`: (optional) contains the geometric DNA parameters used for the design. If this field is omitted, default values will be used. The members of this field, and their default values are given in B.2.
- `grids`: an array containing the `GridDescriptor` objects, that represent the grids of the design.
- `scaffold_id`: (optional) the id of the scaffold strand.
- `scaffold_sequence`: (optional) the sequence of the scaffold.
- `scaffold_shift`: (optional) the starting position of the scaffold sequence.
- `groups`: (optional) a dictionary mapping integers (identifier of helices) to a boolean indicating in which group they belong for the cross-over suggestion.
- `small_spheres`: (optional) a set containing identifiers of the grids whose helices do not display their nucleotides as spheres.
- `no_phantoms`: (optional) a set containing identifiers of the grids that do not display phantom helices.

B.2 DNA parameters

The members of the field `dna_parameters` are:

- `z_step`: the distance in nanometers between two consecutive bases along the axis of an helix. The default value is 0.332nm.
- `helix_radius`: the radius of an helix in nanometers. The default value is 1nm.
- `groove_angle`: the small angle between paired nucleotides. The default value is $2\pi \cdot \frac{12}{12+22}$. This values comes from the fact that the width of the major groove is 22 Å and the width of the minor groove is 12 Å.
- `inter_helix_gap`: the distance between two neighbouring helices on a grid. The default value is 0.65nm as suggested in [34, 31].
- `bases_per_turn`: the number of base pairs per full turn of an helix. The default value is 10.44 bases per full turn as suggested in [34].

These parameters are illustrated in figure B.5. The coordinates of a nucleotide at index i on an helix, in the helix referential are:

$$x = i \cdot \texttt{z\_step}, \quad y = \sin(\theta_i), \text{ and } z = \cos(\theta_i)$$

and

$$\theta_i = \rho - i \cdot \frac{2\pi}{\texttt{bases\_per\_turn}} + \frac{\pi}{2} + \begin{cases} \texttt{groove\_angle} & \text{if the nucleotide is on the forward strand} \\ 0 & \text{otherwise} \end{cases}$$

where ρ is the roll of the helix. A shift of $\frac{\pi}{2}$ is added so that the nucleotide at index 0 on the backward strand of an helix is at the top position, following the cadnano convention.

Note that θ_i decreases as index i increases. This is because strands turn clockwise when going from 5' to 3'.

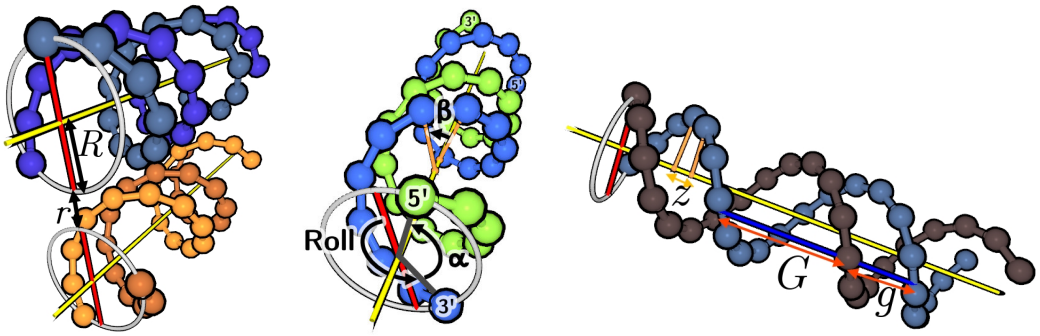


Figure B.5 The configurable DNA geometric parameters: R: the radius of an helix, labelled `helix_radius`; r: the distance between two neighbour helices on a grid, labelled `inter_helix_gap`; α: the minor groove angle, labelled `groove_angle`; β: the angle between two consecutive base-pairs. This angle can be obtained by the formula $\beta = \frac{2\pi}{\texttt{bases\_per\_turn}}$; z: the distance in nanometers between two consecutive bases along the axis, labelled `z_step`; G: the length of the major groove; g: the length of the minor groove; G, g and α are related to each other by the formula $\alpha = 2\pi\frac{g}{G+g}$.

B.3 Helix Object

The field of an helix object are

- `position`: a 3D point giving the origin of the helix.
- `orientation`: a Rotor[2] giving the orientation of the helix. See subsection B.5 to see how to obtain a rotor from a direction vector.
- `roll`: an additional roll performed on the helix.
- `grid_position`: (optional) the position of the helix on the grid it is attached to. This field override the `position` and `orientation` fields.
- `isometry2d`: (optional) an isometry[3] that determines the position and orientation of the helix representation in the 2D view.

B.4 Strand Object

The field of a strand object are:

- `domains`: the (ordered) vector of domains, where each domain is either an insertion or a directed interval of a helix.
- `color`: an integer encoding the color of the strand with the formula $c = 65536 \times R + 256 \times G + B$ where $R, G, B \in \{0, \dots, 255\}$ are its red, green and blue components.
- `junctions`: (optional) an array of objects representing the junctions between the strand's domains.
- `cyclic`: a boolean indicating whether the strand is cyclic or not.

B.5 A word about rotors

In ENSnano's file format, rotations are represented by *rotors*.

A 3-dimensional rotor has a scalar part $s \in \mathbb{R}$ and a bivector part $bv \in \mathbb{R}^3$. A rotor can be obtained by taking the geometric product of two vectors. The geometric product of a and b is defined by $ab = (a \cdot b + a \wedge b)$, i.e. it is a rotor with scalar $s = a \cdot b$ and bivector $bv = a \wedge b$.

[2] https://docs.rs/ultraviolet/0.8.0/ultraviolet/rotor/index.html
[3] `https://docs.rs/ultraviolet/0.8.0/ultraviolet/transform/struct.Isometry2.html`

By properties of the scalar and exterior product of vectors, one can write

$$ab = \cos(\theta) + \Omega \sin(\theta)$$

where $\Omega = \frac{a \wedge b}{\|a \wedge b\|}$ is the axis of the rotation that transforms a in b and θ is the angle between a and b.

Applying the rotor ab to a vector u will rotate the vector u in the oriented plane defined by a and b by twice the angle between a and b.

Obtaining a rotor from a direction vector For the reader who would like to write a program to output a design in ENSnano file format, we provide the following procedure that produces a rotor from a direction vector.

```
def to_rotor(v):
    """ Transform a vector v = (x, y, z) to a rotor
    describing the rotation from the x-axis
    to the vector
    """
    x, y, z = v
    norm = (x*x + y * y + z*z)**0.5
    x = x/norm
    y = y/norm
    z = z/norm
    s = 1. + x
    norm_bv = (z * z + y * y)**0.5
    if norm_bv < 1e-5:
        if x > 0:
            return (1., (0., 0., 0.))
        else:
            return(0., (1., 0., 0.))
    norm = (z * z + y * y + s*s)**0.5
    bv = (-y/norm, -z / norm, 0)
    s = s / norm
    return(s, bv)
```

C ENSnano's interface

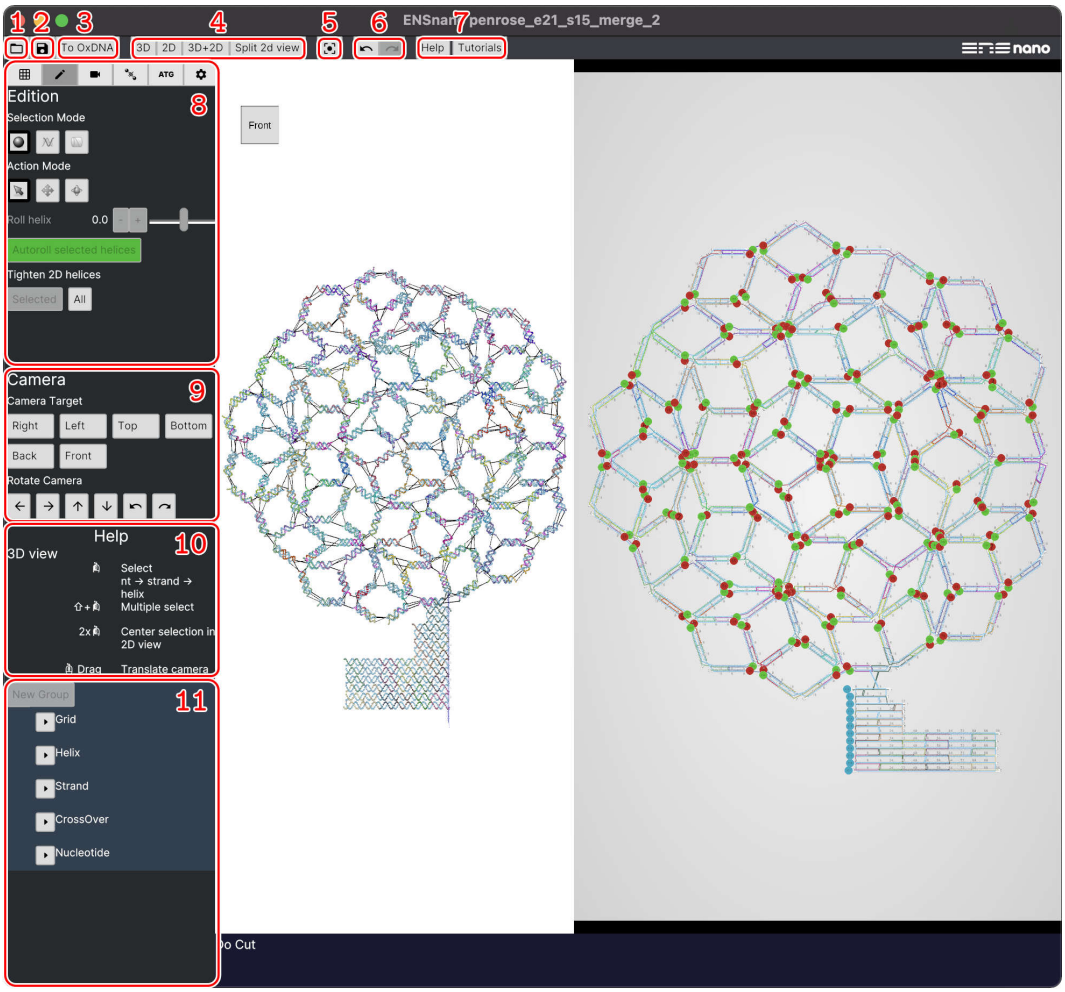
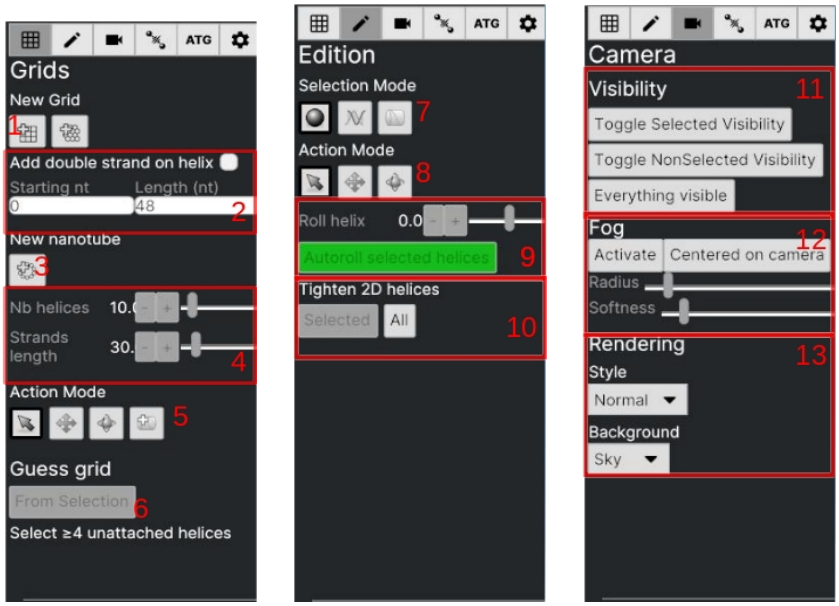


Figure C.6 Overview of ENSnano interface. **(1)** Open a design; **(2)** Save current design; **(3)** Export current design to oxDNA; **(4)** Switch between 2D/3D views and split 2D view; **(5)** Fit the design in the 3D and 2D views; **(6)** Undo/Redo; **(7)** Show Help/Link to tutorials in the contextual panel; **(8)** Tool Panel, organized in tabs (see Figure C.7 for details); **(9)** Camera shortcut panel; **(10)** Contextual panel, containing either information about the currently selected object(s), or a reminder of the mouse and keyboard commands. **(11)** Organizer.
Panels 8–11 have a fixed height, scrolling with the mouse will reveal their possibly hidden contents.



(a) The grid tab. **(b)** The edition tab. **(c)** The camera tab.

(d) The simulation tab. **(e)** The sequences tab. **(f)** The parameters tab.

Figure C.7 The tool panels. (a) Grid: The grid tab contains tool to create grids, nanotubes and helices; it also contains the tools to move and rotate grids and helices; **(1)** Create square and honeycomb grid; **(2)** Adjust the length and position of the strands created whith new helices; **(3)** Create a new nanotube; **(4)** Adjust the length and number of helices composing the nanotube; **(5)** Action mode: Edition/Translation/Rotation/Helix creation; **(6)** Create a grid from a selection of unattached helices — **(b) Edition: (7)**: Change selection mode: Nucleotides/Strands/Helices; **(8)**: Change action mode; **(9)**: Adjust manually or automatically the roll of selected helices; **(10)** Adjust the lengtrh of the helix representation in the 2D view — **(c) Camera: (11)** Make selection or complementary of selection visible/invisible; **(12)** Enable/Disable Fog and adjust fog parameters; **(13)** 3D rendering options — **(d) Simulation: (14)** Start/Stop a simulation — **(e) Sequences: (15)** Show/hide DNA sequences; **(16)** Select/set the scaffold strand; **(17)** Export staples to IDT `.xlsx` format.

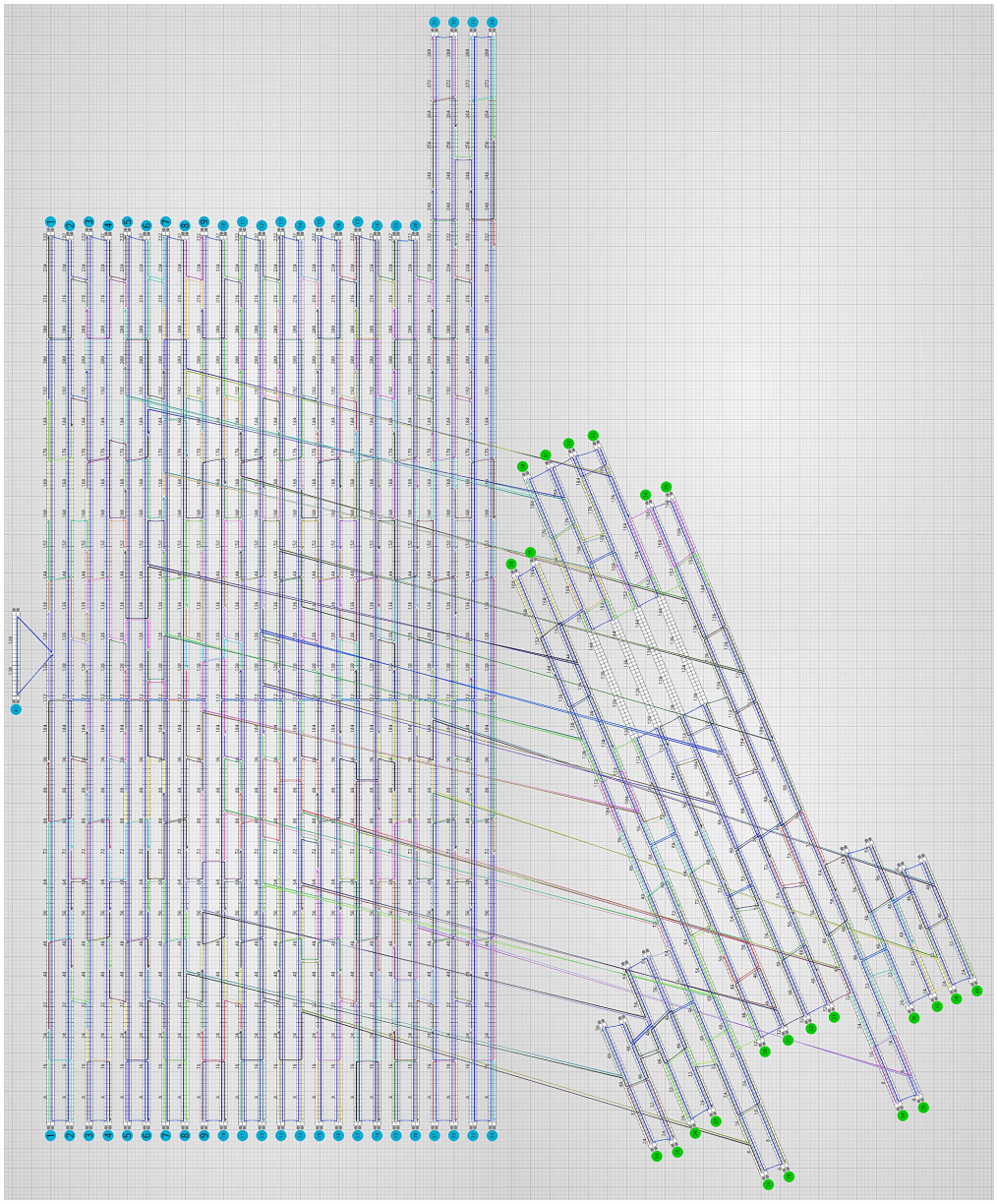


Figure C.8 Our rocket design.

D The rocket design

The ENSnano file for our rocket design, illustrated in Fig. A.3 and imaged in Fig. 11, can be downloaded from ENSnano website:

`http://www.ens-lyon.fr/ensnano#rocket`

Fig. C.8 presents its detailed 2D blueprint of its design.
The table bellow lists all of its staples as computed by ENSnano. For commodity, ENSnano lists the staples in increasing lexicographical order of the 2D coordinates of their 5′-end in the 2D view (i.e., from top to bottom and left to right).

Staple 0001; 5':h1:nt2>3':h2:nt2	CAACTTTGAAAGAGGA AGGGAACCGAACTGAC
Staple 0234; 5':h1:nt26>3':h2:nt26	CGGTGTACAGACCAGGCGCATAG TAGCCGGA
Staple 0282; 5':h1:nt96>3':h3:nt96	ATTACCCAAATCAACG ACGGAGATTTGTATC CGCGAAAC
Staple 0301; 5':h1:nt135>3':h3:nt135	AACACCAG GATTTAGGAATACCAC GGAATTAC
Staple 0332; 5':h1:nt159>3':h3:nt159	GGCTTGAGATGGTTT ATTATTACAGGTAGAA CATAACCC
Staple 0344; 5':h1:nt190>3':h3:nt190	ATTGTGAATTACCTTA CTACGTTAATAAAAC ACCAAAAT
Staple 0246; 5':h2:nt41>3':h4:nt41	ACGAGGCG AAACGAAAGAGGCAAA GAGGACTA
Staple 0256; 5':h2:nt56>3':h2:nt56	TGTTACT GCTGGCTGACCTTCATCAAGAGTAATCTTGA TGTCGAAA
Staple 0268; 5':h2:nt72>3':h4:nt72	TCCGCGAC CTCATCTTTGACCCC GAACGAGG
Staple 0345; 5':h2:nt182>3':h1:nt182	GGAACAAC AATTTCAACTTTAATC
Staple 0204; 5':h2:nt231>3':h3:nt231	CCAGTCAGGA GTTTTGCCAGAG
Staple 0005; 5':h3:nt2>3':h4:nt2	TACGTAATGCCACTAC CATTAAACGGGTAAAA
Staple 0235; 5':h3:nt26>3':h1:nt26	CAACCTA CAGACGGTCAATCATA CAGATGAA
Staple 0283; 5':h3:nt88>3':h1:nt88	ATACCAAG ATCGCCTGATAAATTG CAAGAACCGGATATTC
Staple 0291; 5':h3:nt104>3':h5:nt104	AAAGTACA TCGTCACCCTCAGCA GGCCGCTT
Staple 0302; 5':h3:nt120>3':h1:nt120	GCCAAAA ATTCAACTAATGCAGA TAACAAAGCTGCCCCTGACGAGA
Staple 0312; 5':h3:nt135>3':h6:nt135	GAGGCATA ACAGTTCAGAAAACGA CCCTGA GAATATAA
Staple 0321; 5':h3:nt151>3':h1:nt151	AACACTAT AGATTCATCAGTTGA AACGAGTAGTAAATTG
Staple 0333; 5':h3:nt167>3':h5:nt167	TCGTTTA ATATTCATTGAATCCC TGCATCAA
Staple 0355; 5':h3:nt198>3':h30:nt198	AGCGAGAG GATAGCGTCCAATACTGCGGAATCGT GAAGCCCGAAAG AAGGG
Staple 0366; 5':h3:nt214>3':h1:nt214	AAAAGAA CGTTGGGAAGAAAAAT TGCGATTTTAAGAACTGGCTCATTATA
Staple 0247; 5':h4:nt41>3':h6:nt41	AAGACTTT GACAACAACCATCGCC CTTTAATT
Staple 0257; 5':h4:nt56>3':h2:nt56	AGGCTTT AGAATACACTAAAACA CTGCTCCA
Staple 0269; 5':h4:nt72>3':h6:nt72	GTAGCAAC ATTCGGTCGCTGAGG AAATCTCC
Staple 0202; 5':h4:nt231>3':h5:nt231	GGGGTAATAG CAAAGCGAACCA
Staple 0009; 5':h5:nt2>3':h6:nt2	ACAGCTTGATACCGAT GAGGTGAATTTCTTAA
Staple 0236; 5':h5:nt26>3':h3:nt26	CGACAAT TTCATGAGGAAGTTTC GAAGGCAC
Staple 0284; 5':h5:nt88>3':h3:nt88	GAGTTAAA GCGAAAGACAGCATCG CAGCGATT
Staple 0292; 5':h5:nt104>3':h7:nt104	TTGCGGGA GGAATTGCGAATAAT GAAAGGAA
Staple 0303; 5':h5:nt120>3':h3:nt120	GTCTTTA GAATGACCATAAATCA TACATAAC
Staple 0322; 5':h5:nt151>3':h3:nt151	AAGCGGAT CCTCAAATGCTTTAA GTAAGAGC
Staple 0334; 5':h5:nt167>3':h7:nt167	AAAGATT GATAAGAGGTCATTTT CATATA
Staple 0356; 5':h5:nt199>3':h7:nt199	TATCGCG GGATTAGAGAGTACC GAGTAGAT
Staple 0367; 5':h5:nt214>3':h3:nt214	CGAGCTT TAAAATGTTTAGACTG GCTTTTGC
Staple 0248; 5':h6:nt41>3':h39:nt41	GTATCGGT AAATGAATTTTCTGTA CAACGCCTG GAGTGTTGTTCCAG
Staple 0258; 5':h6:nt56>3':h4:nt56	AAGGAGC CACGCATAACCGATAT GGCTACAG
Staple 0270; 5':h6:nt72>3':h8:nt72	AAAAAAAA AACTTTCAACAGTTT TAACACTG
Staple 0313; 5':h6:nt124>3':h29:nt124	TGCTGTAG TTTAAATATGCA GGGGTCGAG GAGCGGGAGCTAAAC

Staple 0346; 5':h6:nt180>3':h2:nt180	CCTTTT AAGAG CATAA CCAGACGACGATAAAA GAACTAAC
Staple 0200; 5':h6:nt231>3':h7:nt231	GACCGGAAGC TCGCAAATGGTC
Staple 0013; 5':h7:nt2>3':h8:nt2	CTAAAGTTTTGTCGTC TAGTTAGCGTAACGAT
Staple 0237; 5':h7:nt26>3':h5:nt26	CGTTAGT TTATCAGCTTGCTTTC AGTTGCGC
Staple 0285; 5':h7:nt88>3':h5:nt88	TGAGAATA AATTTTTTCACGTTGA CTTGCAGG
Staple 0293; 5':h7:nt104>3':h30:nt104	CAACTAAA GATAGCAAGCCCAAT CACCCTCATTTTC ATT CGGTACGCCA
Staple 0323; 5':h7:nt151>3':h28:nt151	TTTCATTC TGCGGATGGCTT TTAGAATCA GTGCCGTAAA
Staple 0335; 5':h7:nt165>3':h30:nt165	ACAGTT TTTGACGA GACGGGGAA
Staple 0357; 5':h7:nt198>3':h33:nt198	TTAGTTTG TTGGGGCG CACCACACCCGC
Staple 0368; 5':h7:nt214>3':h5:nt214	ATACATT AAACTCCAACAGGTCA TTTTAATT
Staple 0259; 5':h8:nt56>3':h6:nt56	CAAACTA TGGGATTTTGCTAAAC GGCTCCAA
Staple 0271; 5':h8:nt72>3':h11:nt72	AGTTTCGT CCACC AAGGA GCCCGTAT
Staple 0304; 5':h8:nt119>3':h5:nt119	TTAGCAAA CATGT CTCAA AAAATCAG
Staple 0314; 5':h8:nt135>3':h10:nt135	CAGGCAAG CTCAGAGCATAAAGCT TATGATAT
Staple 0336; 5':h8:nt174>3':h10:nt174	TCTACTAATAGTAGTA AAACATTATGACCCT GAAAGGC
Staple 0197; 5':h8:nt231>3':h9:nt231	AATAACCTGT TTTTTAGAACCC
Staple 0017; 5':h9:nt2>3':h10:nt2	GTATAGCCCGGAATAG GAGAGGGTTGATATAA
Staple 0238; 5':h9:nt26>3':h7:nt26	CCGTACT CCACAGACAGCCCTCA TTTCCAGA
Staple 0249; 5':h9:nt42>3':h11:nt42	TAGTAC TTTTGCTCAGTACCAG GTTTTAACG
Staple 0286; 5':h9:nt88>3':h7:nt88	AGAGCCAC AGGAACCCATGTACCG CAGCGGAG
Staple 0324; 5':h9:nt151>3':h7:nt151	TGTACCAA GCATTAACATCCAAT TCTGGAAG
Staple 0347; 5':h9:nt182>3':h5:nt182	TTTGCGGG AAAAGG CGAAC TTT AAAGGAG TGGCGAGAAAGG ACTTCAAA
Staple 0358; 5':h9:nt198>3':h11:nt198	TTATTTCA GTAATGTGTAGGTAA GAATCGAT
Staple 0369; 5':h9:nt214>3':h7:nt214	ATAAAAA TTAGCTATATTTTCAT ACCATTAG
Staple 0260; 5':h10:nt56>3':h26:nt56	AGCGGGG CGCCACCCT AAGAGTCCACTATT
Staple 0294; 5':h10:nt102>3':h12:nt102	TGAAAG TTTCGGAACCTATTAT GGCAGGTCA
Staple 0315; 5':h10:nt135>3':h12:nt135	TCAACCGT GCTATTTTTGAGAGAT ATTCGCAT
Staple 0337; 5':h10:nt167>3':h34:nt167	CGGAGACAG GTCATTGCCTG ATTA
Staple 0206; 5':h10:nt231>3':h11:nt231	TCATATATTT TGTCAATCATAT
Staple 0021; 5':h11:nt2>3':h12:nt2	TTTTGATGATACAGGA AAGCGTCATACATGGC
Staple 0239; 5':h11:nt26>3':h9:nt26	GTAATAA GCGGATAAGTGCCGTC GTGTATCA
Staple 0250; 5':h11:nt42>3':h13:nt42	GGGTCAG GAAAGCGCAGTCTCTG GCCACCCTC
Staple 0275; 5':h11:nt73>3':h30:nt73	AAACAGT AAACA ACCACCAGAGCCGCCG TTCATCGG GGTGCCT GCTCACTG
Staple 0287; 5':h11:nt88>3':h29:nt88	CCTGCCTA TATTAAGAGGCTGA TCTATCAG AATCGGCC
Staple 0305; 5':h11:nt120>3':h8:nt120	GAGGGTA TCTAG AAAGC GCAAAGAA
Staple 0325; 5':h11:nt151>3':h9:nt151	GCTATCAG TCAAATCACCATCAA AAATCGGT
Staple 0348; 5':h11:nt182>3':h9:nt182	AAACAAGA AGATTCAAAAGGGTGA GTAATACT
Staple 0359; 5':h11:nt198>3':h13:nt198	GAACGGTA CCCAAAAACAGGAAG ACGCTCAA
Staple 0370; 5':h11:nt214>3':h9:nt214	ACTAGCA TAAATGCAATGCCTGA ACGCAAGG
Staple 0261; 5':h12:nt56>3':h10:nt56	CAGAATG TGCCTTGAGTAACAGT TTAGGATT
Staple 0295; 5':h12:nt102>3':h14:nt102	GACGAT ATTGACAGGAGGTTGA AGCGTCAGA
Staple 0316; 5':h12:nt135>3':h34:nt135	TAAATTAG CAGAACAATATTACCG ACAATATT GCATCGTAACCGTGCATCTG AACCAATA
Staple 0338; 5':h12:nt166>3':h14:nt166	GTAAACGT GAAAAACGCTCATGG TGACCTGA
Staple 0196; 5':h12:nt231>3':h13:nt231	GTACCCCGGT TTGGCAGATTCA
Staple 0115; 5':h13:nt2>3':h14:nt2	CGCCTCCCTCAGAGCC GAGCCACCACCGGAAC
Staple 0240; 5':h13:nt26>3':h11:nt26	CAGAACC AATTTACCGTTCCAGT GTGTACTG
Staple 0251; 5':h13:nt42>3':h16:nt42	AGAGCCA CCATCT GAAAC AAAGGTGAA
Staple 0273; 5':h13:nt66>3':h28:nt66	ACCAGAACC AATAAATCCTCA TATTGGGCG GCAGCAAGCGGAAC

Staple 0306; 5':h13:nt120>3':h31:nt120	TAATATC AACTCAAACTAT ACTTCTTTGATTA ATCAGTGAGGCCACCGAG
Staple 0349; 5':h13:nt182>3':h11:nt182	ACATTTTG ATTGTATAAGCAAATA TCTGGAGC
Staple 0360; 5':h13:nt198>3':h15:nt198	TCGTCTGA GACATTCTGGCCAAC CGGTCAGT
Staple 0371; 5':h13:nt214>3':h11:nt214	ATTTACA TGATAATCAGAAAAGC ATCGTAAA
Staple 0262; 5':h14:nt56>3':h13:nt56	GCGTTTG CCACCCTCAGAGCCGCC
Staple 0296; 5':h14:nt102>3':h16:nt102	CTGTAG AATCAAGTTTGCCTTT CAAAAGGGC
Staple 0176; 5':h14:nt135>3':h16:nt135	TTTGAATG CCTAAAACATCGCCAT AGTTGAAA
Staple 0326; 5':h14:nt150>3':h31:nt150	GGCACAG CCAGCCAT CACGTTGG GTCTG CTTGCC ACATCA GTGTTT
Staple 0339; 5':h14:nt166>3':h16:nt166	AAGCGTAA ACCACCAGCAGAAGA CAATCAAT
Staple 0194; 5':h14:nt231>3':h15:nt231	CCAGTCACAC CACGCTGAGAGC
Staple 0029; 5':h15:nt2>3':h16:nt2	CCAGCAAAATCACCAG CATTTGGGAATTAGAG
Staple 0241; 5':h15:nt26>3':h29:nt26	TTACCATTAGCAAGGCCG TTTCATAATCAAA GCCCTTCA CCAGTGAGACGGGCAAC
Staple 0276; 5':h15:nt68>3':h33:nt68	ATAGCAG GGTCATAGCCCC AACTC TCACAATTCCACACAA GTGAAATT
Staple 0288; 5':h15:nt88>3':h11:nt88	AGCGACAG CGCGTT CCAGC TGGCCTTGATATTCAC TAATGCCC
Staple 0307; 5':h15:nt120>3':h13:nt120	TGATAGC GCTATTAGTCTTTAAT CTTGCTGG
Staple 0350; 5':h15:nt182>3':h13:nt182	AGGTGAGG AGAGATAGAACCCTTC AAATACCT
Staple 0361; 5':h15:nt198>3':h17:nt198	ATTAACAC TCACCTTGCTGAACC TTACAAAC
Staple 0372; 5':h15:nt214>3':h13:nt214	ACAGTGC GACCAGTAATAAAAGG AATGGATT
Staple 0252; 5':h16:nt40>3':h18:nt40	TTATCAC AGAAACGCAAAGACAC CTGGCATGA
Staple 0263; 5':h16:nt56>3':h15:nt56	ATTCATT GTCACCAATGAAACCATCG
Staple 0277; 5':h16:nt72>3':h35:nt72	AATATTGA TTTGTCACAATCA TGCAGGTCG TCAGGAA
Staple 0297; 5':h16:nt102>3':h18:nt102	GACATT TTACCAGCGCCAAAGA GCCGAACAA
Staple 0317; 5':h16:nt135>3':h18:nt135	GGAATTGA TAACAACTAATAGATT TTATCAGA
Staple 0327; 5':h16:nt150>3':h14:nt150	AATCAAC TAAAAATACCGAACGA GAATACGT
Staple 0340; 5':h16:nt166>3':h18:nt166	ATCTGGTC AATACATTTGAGGAT AGAAGGAG
Staple 0191; 5':h16:nt231>3':h17:nt231	CAGCAGCAAA CTTTGCCCGAAC
Staple 0033; 5':h17:nt2>3':h18:nt2	AAATACATACATAAAG TGTTAGCAAACGTAGA
Staple 0242; 5':h17:nt26>3':h15:nt26	ATATAAA CGTCACCGACTTGAGC TAGCACCA
Staple 0308; 5':h17:nt120>3':h15:nt120	GGAGCAC GGAAGGTTATCTAAAA GCGCGAAC
Staple 0351; 5':h17:nt182>3':h15:nt182	ATTAGACT TCAAATATCAAACCCT TAAAACAG
Staple 0362; 5':h17:nt198>3':h19:nt198	AATTCGAC CATTATCATTTTGCG AATAAAGA
Staple 0373; 5':h17:nt214>3':h15:nt214	TTAAATC TGAAAAATCTAAAGCA CGCCTGCA
Staple 0253; 5':h18:nt40>3':h21:nt40	TTAAGAC GCCCAA ACCCT ATTTGCCAG
Staple 0264; 5':h18:nt56>3':h16:nt56	AAAAGAA CACGGAATAAGTTTAT CGGAAATT
Staple 0278; 5':h18:nt82>3':h20:nt82	GGAAACGCAATAATAACG GCAATAGCTATCTTA ATAAAAAC
Staple 0298; 5':h18:nt102>3':h20:nt102	AGTTAC GAAAAGTAAGCAGATA TGAAAATAG
Staple 0318; 5':h18:nt135>3':h20:nt135	TGATGGCA ATACTTCTGAATAATG GGCGAATT
Staple 0328; 5':h18:nt150>3':h16:nt150	TTCCTGA AGAGCCGTCAATAGAT AGTTGGCA
Staple 0341; 5':h18:nt166>3':h20:nt166	CGGAATTA CCATATCAAAATTAT CTTTGAAT
Staple 0190; 5':h18:nt231>3':h19:nt231	GTTATTAATT ACGTCAGATGA
Staple 0037; 5':h19:nt2>3':h20:nt2	TCAGAGAGATAACCCA TAATTGAGCGCTAATA
Staple 0243; 5':h19:nt26>3':h17:nt26	GAGTTAA TCCTTATTACGCAGTA GTGGCAAC
Staple 0265; 5':h19:nt48>3':h18:nt48	CAAGAAACAATGAAATA GAATACCC
Staple 0289; 5':h19:nt88>3':h15:nt88	CTTTTTAA CAGAAG ATGGT CAACCGATTGAGGGAG TAATCAGT
Staple 0309; 5':h19:nt120>3':h17:nt120	TTGGATT ATTCATCAATATAATC TATCTTTA
Staple 0352; 5':h19:nt182>3':h17:nt182	AAAACAGA GAACAAAGAAACCACC TTAGAAGT
Staple 0363; 5':h19:nt198>3':h21:nt198	AATTGCGT CGGGAGAAACAATAA AAACAGTA
Staple 0374; 5':h19:nt214>3':h17:nt214	AGGTTTA TTAAAAGTTTGAGTAA AACTCGTA

Staple 0279; 5':h20:nt72>3':h22:nt72	AGGGAAGC TTTATCCCAATCCAA GACTTGCG
Staple 0299; 5':h20:nt102>3':h38:nt102	CAGCCT TGTTTAACGTC ATTCGCCAT TGCGGGCCTCTCAGGCA
Staple 0319; 5':h20:nt135>3':h22:nt135	ATTCATTT AAACATCAAGAAAACA CAAAGAACGC
Staple 0329; 5':h20:nt150>3':h18:nt150	GCGCAGA GAAGGGTTAGAACCTA TCATCATA
Staple 0342; 5':h20:nt166>3':h22:nt166	ACCAAGTT ACAATTTCATTTGAA TGTAAATG
Staple 0406; 5':h20:nt231>3':h22:nt231	ATATACAGTA ATAACCTTGCTTCTGT AAATCAT
Staple 0041; 5':h21:nt2>3':h22:nt2	CCAACGCTAACGAGCG TTTATCCTGAATCTTA
Staple 0244; 5':h21:nt26>3':h19:nt26	GAGCCTA GAACAAAGTCAGAGGG CAAGAATT
Staple 0254; 5':h21:nt42>3':h23:nt42	TTACAAA AGATTAGTTGCTATTT CCGTTTTT
Staple 0266; 5':h21:nt58>3':h35:nt58	CATATTA GCATTAGACGGG TCACG
Staple 0310; 5':h21:nt120>3':h19:nt120	ATGAAAC CAATTACCTGAGCAAA CTGATTGT
Staple 0353; 5':h21:nt182>3':h19:nt182	TTTAATGG CGGATTCGCCTGATTG TTGCACGT
Staple 0364; 5':h21:nt198>3':h23:nt198	CATAAATC CCTCCGGCTTAGGTT ATAAACAC
Staple 0375; 5':h21:nt214>3':h19:nt214	TGAGTGA ACAGTACCTTTTACAT AGATTTTC
Staple 0420; 5':h21:nt245>3':h22:nt245	GCTATTAATTAATTTTCCCTTAG GACGCTGA
Staple 0280; 5':h22:nt72>3':h24:nt72	GGAGGTTT GCGCCCAATAGCAAG CCCATCCTA
Staple 0320; 5':h22:nt133>3':h23:nt133	GAGAAA CTTCTGACCTAAATTT CAGCTAATGCAGAACGCGCCTGTTTATCAACA TTTAGT
Staple 0330; 5':h22:nt150>3':h20:nt150	CGCAAGA AAATTAATTACATTTA ACAAAATC
Staple 0343; 5':h22:nt166>3':h24:nt166	CTGATGCA GACCGTGTGATAAAT CTGTCCAGACGACGAC
Staple 0407; 5':h22:nt229>3':h24:nt229	AGGTCTGA GCCTGTTTAGTATCAT GCAGAGG
Staple 0422; 5':h22:nt260>3':h24:nt260	GAAGAGTC CTTACCAGTATAAAG GCCATATTTAA
Staple 0417; 5':h22:nt284>3':h21:nt284	CGATAGCTTAGATTAA AATCCTTGAAAACATAG
Staple 0045; 5':h23:nt2>3':h24:nt2	CCAAGTACCGCACTCA AAGAACGGGTATTAAA
Staple 0245; 5':h23:nt26>3':h21:nt26	AAGCAAG TGCACCCAGCTACAAT TCTTTCCA
Staple 0255; 5':h23:nt41>3':h23:nt41	ATTTTCAT ATCAATAATCGGCTGTCTTTCCTTATCATTCC TCGAGAAC
Staple 0267; 5':h23:nt58>3':h21:nt58	CATTACC TGAAGCCTTAAATCA ATAAACAGC
Staple 0290; 5':h23:nt88>3':h40:nt88	ATATAGAA TTTTAGCGAACCTCCC ATAAGAAA GCGATCGG TCAGGCTGCGCAACTGT
Staple 0300; 5':h23:nt103>3':h23:nt103	CCGGTATTC ATAGATAAGTCCTGAACAAGAAAAATAATAT CAAATCAG
Staple 0311; 5':h23:nt118>3':h21:nt118	TAATTTCAT ACTTTTTCAAATATAT AGAAGATG
Staple 0354; 5':h23:nt182>3':h21:nt182	AAATAAGA GGGTTATATAACTATA TTACCTTT
Staple 0365; 5':h23:nt198>3':h23:nt198	CGGAATCA ATATAAAGTACCGACAAAAGGTAAAGTAATT AAGGCGTT
Staple 0376; 5':h23:nt214>3':h21:nt214	AGAAAAA GAGACTACCTTTTTAA AATATATG
Staple 0421; 5':h23:nt245>3':h21:nt245	TACAAATT AATAGTGAATTTATCA AAATCGTC
Staple 0281; 5':h24:nt71>3':h23:nt71	ATTTACGAGCATGTAGAAACCA CGTAGGAAT
Staple 0331; 5':h24:nt158>3':h22:nt158	AATAAACAACATGTT AATGGTTTGAAATACC AATCCAAT
Staple 0408; 5':h24:nt229>3':h23:nt229	CATTTTCGAGCCAGTAATAAGAGA TAATTACT
Staple 0423; 5':h24:nt257>3':h23:nt257	CAACGCCAACATGTAATTTAG ATGCGTTA
Staple 0419; 5':h24:nt284>3':h23:nt284	GGCTTAATTGAGAATC CCAACGCTCAACAGTAG
Staple 0217; 5':h25:nt54>3':h9:nt54	TTTGGATCGG TCCGAA CTCCACGCTGG TGGT CAAAAT GTT TAGCATT CAGGAGGTT
Staple 0233; 5':h26:nt23>3':h30:nt23	AAATCCTGTTTGATGG TTTGC AGAGTT CCAGGG ACATTAAT
Staple 0086; 5':h28:nt2>3':h13:nt2	AGCTGATT ATCACCGGAACCA GCCACCCT
Staple 0378; 5':h28:nt53>3':h8:nt53	GTCAAAGGGCGA AAAGAACGTGGACTC AAC CAGAACCG CACCAGTA
Staple 0208; 5':h28:nt65>3':h9:nt65	AAAACCG GACTCCTCAAGAG CTCAGAACCGCCACCCTC
Staple 0388; 5':h28:nt98>3':h10:nt98	GAACCATCACCCAA CCGATTAAAGGG AGGATTAAGCAAT CTGATAAATTATCTGAAACA
Staple 0397; 5':h28:nt143>3':h5:nt143	GCACTAAATC GTGCTTTCCTCG AGAGCTTAATTGCT CTATTATAGTCAGAAGCA
Staple 0210; 5':h29:nt32>3':h27:nt32	TGGTTTTTCTTTTCA CCGCCTGGCCCTGAG CCCAGCAGGCGA
Staple 0387; 5':h29:nt72>3':h31:nt72	AACGCGCG CCAGTCGGGAAACCT TCTGTCC
Staple 0377; 5':h30:nt41>3':h14:nt41	TGCGTTGC AATGAGTGAGCT CTTATTA

Staple 0379; 5':h30:nt57>3':h12:nt57	CCCGCTTT GGGAGAGGCGGTTTGCG TTAAAGC
Staple 0230; 5':h30:nt106>3':h33:nt106	GAATCC TTATA GTAATA TGAGTAGA
Staple 0393; 5':h30:nt112>3':h8:nt112	TGAGAA AGGAGG ATCAAGTTTTTT ACTAAAGTACGGTG AAATCATA
Staple 0083; 5':h30:nt148>3':h35:nt148	ATAAC GCACGT GGCGC CTACAG AATGT GAACAAACGG
Staple 0396; 5':h30:nt162>3':h28:nt162	AGCCGGCG CCCCGATTTAGAGCTT GGAACCCTAAAGGGAGC
Staple 0214; 5':h30:nt170>3':h9:nt170	AACG CGGGC GGCAAGTGTAGCGGTC AAC CGAGCTG AGAAGCCT
Staple 0386; 5':h31:nt73>3':h33:nt73	ATCAGTGT CATAAACGCAAATTAA ATTCGTA
Staple 0389; 5':h31:nt88>3':h28:nt88	TAAAAGAG GTCGTGCCAGCAGGAA TTAGACTGCATTAATG GGCGATGGCCCACTACGT
Staple 0395; 5':h32:nt161>3':h8:nt161	GTTGCGCT GCTAGGGC GATTCCCAATTCTG TGGCATCAAT
Staple 0380; 5':h33:nt41>3':h18:nt41	GTTATCCGC GCATGCC ATAGAAAATTCAT GAAACCGA
Staple 0384; 5':h33:nt57>3':h16:nt57	TTTCCTGT CATACGAGCCGGAAG AAAGCCTGG CATTTTC CACCG GGAAGGTA
Staple 0385; 5':h33:nt73>3':h35:nt73	ATCATGGT CGGGTACCGAGCTCGA CCAGTTTGAGGGGAC
Staple 0390; 5':h33:nt103>3':h35:nt103	TTTGTTA ATCAAAAATAATTCGC TGTAGATGGGC
Staple 0079; 5':h33:nt189>3':h6:nt189	CGCGT ACGCTG AAGAAAGCG AATTGCT
Staple 0067; 5':h34:nt2>3':h19:nt2	ACGTTGTAAAACGACG GGGTTTTCCCAG AGAATTAACTGAAC TAATAAGAG
Staple 0391; 5':h34:nt88>3':h11:nt88	GGAACGCC AATCAGCTCATTTTTT CCGTTGTAGCAAT CGGC ATGCCGGA
Staple 0064; 5':h34:nt117>3':h11:nt117	GCCTTCCTGTAGCCAG TAATGGGATAGGT TGCAACAG TAATATTTTGTTAAA CTACAAAG
Staple 0381; 5':h35:nt42>3':h37:nt42	GATCCGATT GCAAGGGCACTCCAGC CTCGCTATTACGC
Staple 0383; 5':h35:nt57>3':h33:nt57	TATCGGCC ACTCTAGAGGATCCC CATAGCTG
Staple 0394; 5':h35:nt143>3':h12:nt143	CGGATTGACCG CTTTCATCAAC AGAG TTTAAATT
Staple 0215; 5':h35:nt168>3':h32:nt168	TCGGATTCTCCGTGG GAGCGAGTAACAACCCG CGCGCTTAATGCGCCG GTACTATG
Staple 0071; 5':h36:nt23>3':h34:nt23	GGGATGTGCT AAGTTGGGTAACGCCA GCCAGTGCCAAGCTT
Staple 0382; 5':h37:nt36>3':h19:nt36	CAGCTGGCGAAAGG TGGGAAGG CGATTTTT TTACAGAGAGAATAAC CCGAAGCC
Staple 0072; 5':h37:nt64>3':h35:nt64	TTCTGGTGCCGGAAA CAGCTTTCCGGCACCGC GACGACAG
Staple 0219; 5':h39:nt23>3':h25:nt23	AATAGCCCGAGATAGG CCCTTATAAATCAAAAG
Staple 0090; 5':h40:nt54>3':h23:nt54	AAGCGCC AAAAA TAAGAACGCGAGGCG GGCTTAT