

# The Art of Molecular Programming graphics guidelines

## **Make sure you save an editable version of your figures in case changes need to be made.**

Editors reserve the right to make changes to the figures to ensure graphics consistency.

Editable versions of figures provided in the examples can be found [here](#).

You can request help from our team of graphics adjunct editors in this [spreadsheet](#).

**Figure reproduction** While we encourage you to create new graphics whenever possible, if you would like to reproduce an existing figure, please obtain email permission from the journal/publisher, and save a copy alongside the original versions of the figures.

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## Before you start checklist

The checklist below highlights the most important points from the guidelines to follow. We recommend you go through this list *before* you start making each figure.

- Set canvas width to 4.5 inches.
  - *For example, in Adobe Illustrator, you can change artboard width by clicking “File” → “Document Setup...” → “Edit Artboards” → change the “W” parameter in the “Transform” panel to “4.5 in”*
- For colour images only: set colour format to CMYK (not RGB).
  - *For example, in Adobe Illustrator, click “File” → “Document Color Mode” → “CMYK Color”*
- For non-vector images, make sure your resolution is 300 dpi (600 dpi for line drawings).
- Use 0.5 pt black outlines for figure elements.
- Familiarise yourself with the recommended colour palettes.
- Use Helvetica for labels (or Garamond/Courier *only* as outlined in the font guidelines).
- Use 11 pt font where possible; min 6 pt and max 16 pt.
- What figure elements are you including (arrows, DNA strands, aTAM tiles, structures, etc)? Check the respective guidelines and example graphics for each before proceeding.
- Read the “General guidelines” below to make sure you haven’t missed anything relevant to your figures.
- Save editable versions of your figures!

*For example, in Python’s matplotlib, you can implement many of these guidelines as defaults by running the following at the beginning of your script:*

```
import matplotlib.pyplot as plt

plt.rcParams['figure.figsize'] = [4.5, 3]
plt.rcParams['figure.dpi'] = 300
plt.rcParams['font.sans-serif'] = 'Helvetica'
plt.rcParams['figure.facecolor'] = 'white'
plt.rcParams['axes.labelsize'] = 11
plt.rcParams['legend.fontsize'] = 9
plt.rcParams['axes.linewidth'] = 0.5
plt.rcParams['axes.prop_cycle'] = plt.cycler('color',
['#0d3b66', '#8b2635', '#474747', '#0c7c59', '#ea9c0b', '#30a0dc', '#d88373',
', '#8f8f8f', '#849e57', '#fdc835'])
```

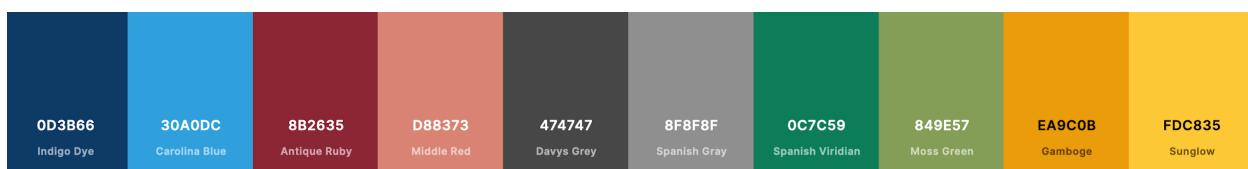
# General guidelines

## Figure size and exporting

- Keep your figures as simple as possible. Use only one idea per figure, hence multi-panel figures are not encouraged. Multiple panels should only be used if the panels all illustrate the same idea. If each panel has its own point, they should be split up.
- Full page figure width: 4.5 inches.
- Where possible, use vector-based formats. Export your figure to *.pdf* and also save the original editable file (e.g. *.ai*, *.eps*, *.ps* or *.svg*).
- If you must use raster graphics (*.bmp*, *.jpeg*, *.png*, *.tiff*), provide graphics at:
  - 600 dpi for line drawings (black and white)
  - 300 dpi for halftones (gray scale – do not convert from colour images)
  - 300 dpi for colour images – must be in CMYK
- Do not use Biorender.

## Colours

- See appendix for copyable versions of the colour palettes.
- As much as possible, incorporate the following colours in your figures, following the sequence below (and black/white). e.g. when making plots, start with blue, then red, etc.
- Avoid combinations of only red/green/orange.
- Hex codes: **0d3b66,30a0dc,8b2635,d88373,474747,8f8f8f,0c7c59,849e57,ea9c0b,fdc835**



- If you need to indicate positive/negative trends, use blue/red instead of green/red.
- Avoid putting type on a dark background, and avoid coloured backgrounds for graphs. Do NOT use a black background in figures.
- For gradient-based images (e.g. AFM), use *Gwyddion* (or reference equidistant hex codes):  
ffffff,fcefd4,f3dcaa,ebc67a,daa45a,bc7748,a64f32,823118,591d0e,2e0d03,000000



- Where possible, export your figures in CMYK (not RGB). Export your figures with a solid background (e.g. white), not transparent.

## Font

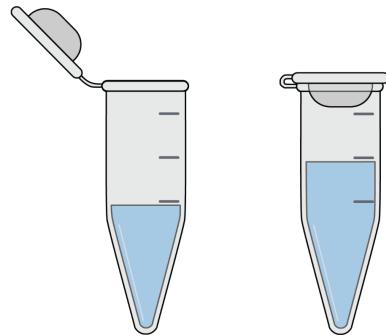
- Use Helvetica for labels and general text.
- Where possible, use black for labels.
- Use Garamond for math, and if a serif font is needed (please check with the editors first).
- If you need a monospaced font (e.g. for DNA sequences or code snippets), use Courier. Code snippets should generally be in pseudocode.
- Recommended font sizes: 11 pt for text, 9 pt for legends with 11 pt for interline spacing. Minimum 6 pt, maximum 16 pt.
- Use *italics* for emphasis and quotes, **bold** for keywords.

## Figure formatting (outlines, plots, arrows)

- For schematics etc, use 0.5 pt black outlines around your graphics elements, and only solid colour fills (no gradients etc.).
- For graphs/plots, use black for axis lines.
- Avoid line weights less than 0.5 point.
- Use filled or unfilled symbols (○, □, △, etc.) but avoid (+, ×, −, \*, etc.). Filled circles are recommended where possible.
- For arrows →, use rounded caps, and a flat arrowhead (for Adobe Illustrator, Arrow 7 at 25% scale – *you can change this by clicking on the word “Stroke” under “Appearance”*).
- For arrows →, 3 pt stroke is recommended.

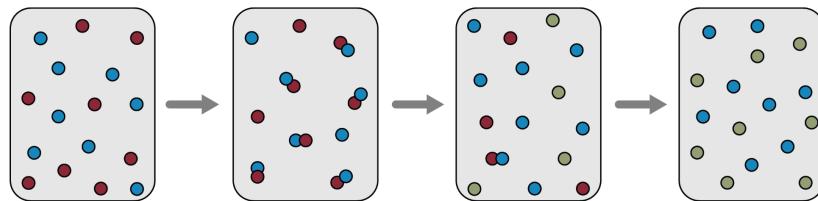
## Example graphic: test tubes

*Guidelines implemented: 4.5 inch figure width (of saved file), CMYK colour mode, solid colour fill, 0.5 pt black outlines, using Carolina Blue from colour palette (in this case with 50% opacity).*



## Example graphic: chemical reaction networks

*Guidelines implemented: 4.5 inch figure width, CMYK colour mode, solid colour fill, 0.5 pt black outlines, colour palette use, arrow guidelines (rounded caps, flat arrowhead, 3 pt stroke).*



# Content-specific guidelines

## Representing DNA

- For strand displacement cascades or similar, represent strands as coloured lines of 2 pt in thickness with arrowheads at the 3' end. Use rounded caps, and flat arrowhead (for Adobe Illustrator, Arrow 7 at 25% scale).
- For dsDNA, use 5 pt spacing between strands, and continuous grey shading (hex code #cccccc) in between strands to represent base pairing.
- These are the *minimum* size requirements – feel free to scale accordingly (e.g. 4 pt strand thickness with 10 pt spacing).
- Where possible, use the lighter hue of the same colour to represent the complementary strand (e.g. indigo dye for forward and carolina blue for reverse). If you need to represent more domains than this colour palette allows, you can use other colours and check with the editors.
- Follow the “Font” guidelines above for domain label formatting.
- Where possible: line length should be roughly proportional to domain length, strands should be straight lines, single-stranded overhangs should be at 30°.
- Where strands overlap, 5' end should be above the 3' end of the previous domain.
- Please check with the editors for representing specifics like mismatches.
- NUPACK exports are acceptable if the identity of nucleotides needs to be specified.
- For DNA origami, avoid simply using cadnano/other software screenshots. For example, export to .svg and remove the grid in the background, adjusting things like line width to make the key features you want to highlight clearer.

## Example graphic: strand displacement

*Guidelines implemented: 4.5 inch figure width, CMYK colour mode, colour palette use, Helvetica font, font size between 6 and 16 pt, recommended font size 11 (right), representing DNA guidelines (minimal size on left, alternative size on right).*

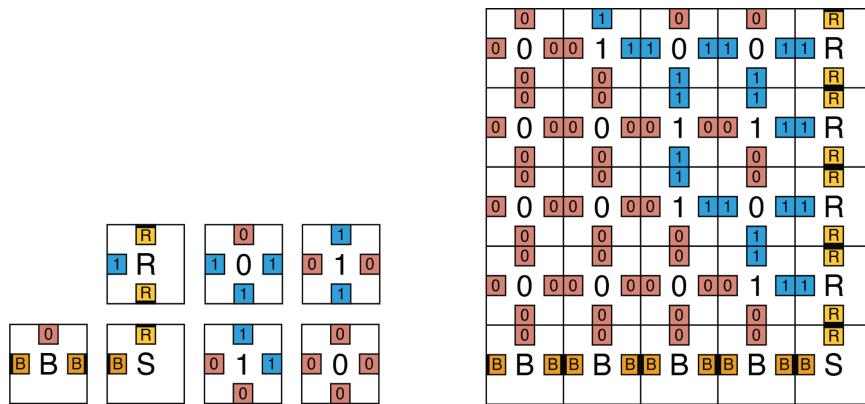


## Tiles in aTAM

- Square tiles should be represented as squares, with glues as little squares within the tile.
  - The colour of the glue should correspond to its value. If you are including a strand representation, use the same colours for the domains. Colouring the glues and/or tiles is optional.
  - Use an additional black 1 pt line at the inner edge of the glue to indicate a strength-2 glue.
  - Labels on the tiles and glues are permitted.

## Example graphic: aTAM binary counter tile set and assembly

*Guidelines implemented: 4.5 inch figure width, solid colour fill, CMYK colour mode, 0.5 pt black outlines, colour palette use, Helvetica font, font size between 6 and 16 pt, recommended font size 11 (tile labels), tiles guidelines.*



## 3D molecular structure guidelines

These guidelines are intended to enable authors to quickly prepare images of 3D molecule structures using either Chimera/Chimera-X or Pymol. A number of different possible presentation styles are provided, to cater for different scenarios. Chimera-X is the recommended program for creating visualizations due to its ease-of-use. Chimera is the progenitor of Chimera-X, and has a similar (but slightly outdated) interface.

The same principles for preparing images from the general graphics guidelines also apply here; images should all have a white background and colours should be based on the provided colour palette.

If you prefer rendering your molecules in another program, it is also possible to prepare your 3D structure in Chimera, then export a 3D file for use in another program (e.g Blender or Autodesk Maya). The video [here](#) gives an example of how this process could be carried out.

Please also provide us with a PDB file for any structures used, to enable us to make any further edits, if required.

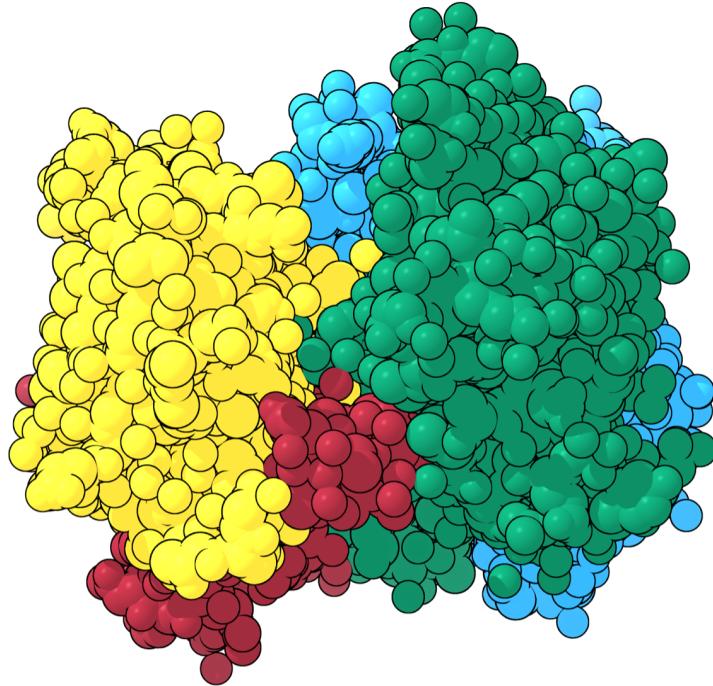
### Proteins/DNA: cartoon 2D-style ([RCSB Molecule of the Month](#))

This cartoon style of representing 3D structures is especially great at highlighting the interactions between molecules, and their overall structure. However, this representation obscures the exact atomic makeup of a structure. The full 3D atomic view (next section) should be used if more detail is required. Guidelines for achieving this effect with Chimera-X/Chimera/Pymol as follows:

#### Chimera-X

- Go to ‘Presets’ at the top menu bar, and set this to ‘Publication’ (sets a white background).
- Load in your structure (typically as a PDB file) and go to ‘Molecule Display’ from the top tab. Here, hide surfaces and cartoons, and show all atoms. Set the style to Sphere:
- Jump to  the ‘graphics’ tab and ensure that lighting is set to ‘flat’ and silhouettes are on. Shadows can be optionally turned on in this same menu, after the lighting is set to flat.
- Adjust the strength of the silhouettes using the following command (command prompt available at the bottom of the program):  
`graphics silhouettes true depthJump 0.002 width 2.5`

- The depthJump and width (silhouette strength) parameters can be adjusted to taste (use the above as starting values), but see the examples for the rough principle of how the resulting images should look like. Further info on these parameters is available [here](#).
- To set colours for different atoms/chains, use the ‘Select’ menu bar to make a selection, then go to ‘Actions’ -> ‘Color’ -> ‘All Options’ -> ‘From Editor’ and enter the appropriate hex code for the desired colour (ideally, colours should follow those presented in the general graphics guidelines). Colour can also be applied to a selected structure through the command: `colour sel #30A0DC` (replace with desired hex code).
- Colours can be set automatically based on the atomic element by selecting ‘Actions’ -> ‘Color’ -> ‘By Element’. The colour codes for elements are selected from this table: <http://rbvi.ucsf.edu/chimerax/docs/user/commands/colortables.html#element>.
- When saving, ensure the background is white (the ‘publication’ preset takes care of this), and use either `.tif` or `.png` (`.png` preferred - much lower file size, with similar quality to `.tif`) image formats, to prevent unwanted reductions in quality. Use defaults for saving image (supersample set to 3), but increase/decrease image resolution if resulting silhouettes don’t match those in the viewfinder. Make sure to use at least 1650/3600 pixels for the image width (600 DPI) for 2.75/6 inch figures respectively.
- Example protein structure (coloured by chain):



Streptavidin (PDB ID 4BX5). Image created with silhouettes depthJump 0.003 and width 2.5, with flat lighting and shadows.

- To visualize DNA structures in complexes with proteins, commands are available to

make a visual distinction between nucleotides and proteins. To specifically manipulate DNA chains, make sure to select them ('Select' -> 'Chains') before applying any changes. Manual atom selections can also be made by holding the 'ctrl' key and clicking on your target. Pressing the 'up' and 'down' arrow keys with an atom selected will increase/decrease your selection to other atoms/chains connected to the target.

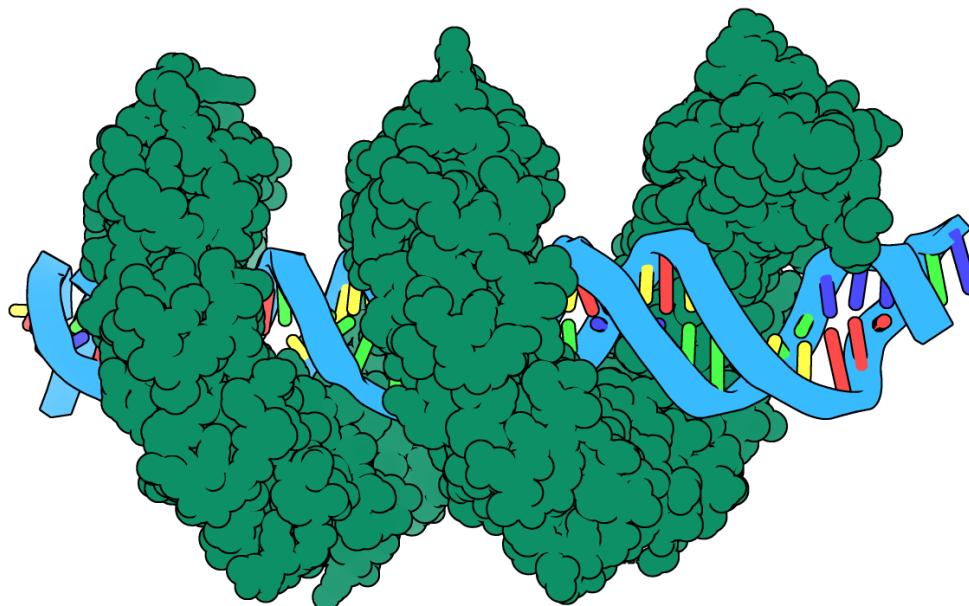
- To represent the DNA backbone as a ribbon, use the command:

```
ribbon style width 4 thickness 2 (both parameters user-adjustable)
```

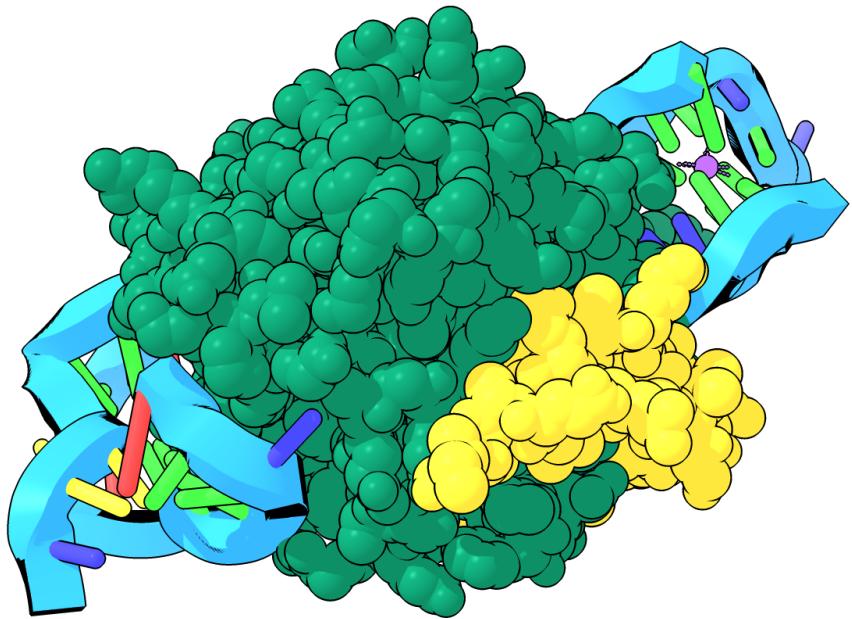
- To adjust base representation, either use the following command or select the desired style in the 'Nucleotides' menu tab:

```
nucleotides ladder radius 0.7 (radius is adjustable)
```

- Some examples using the above commands:



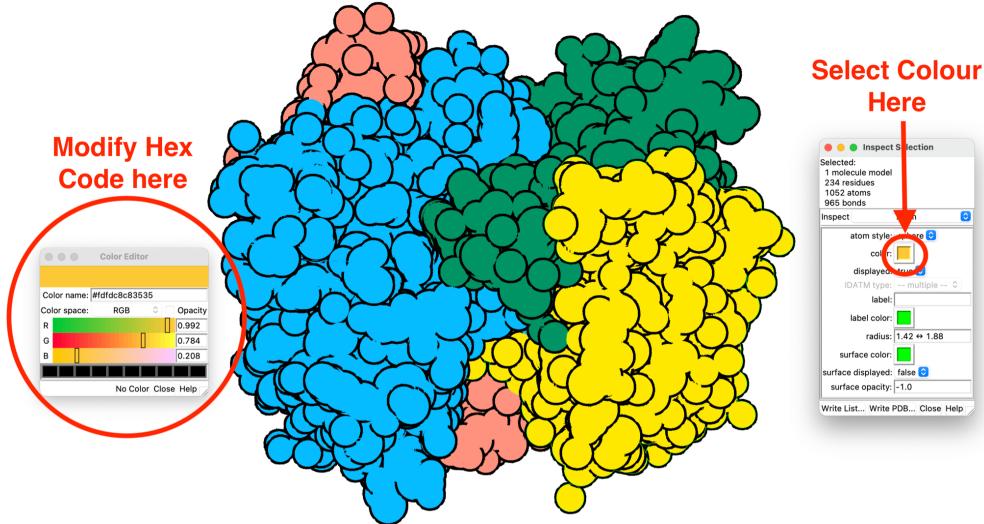
Protein bound to DNA (PDB ID 3UGM). Image created with silhouettes depthJump 0.01 and width 2.5, with flat lighting. DNA settings: ribbon width 4, thickness 2 & ladder radius 0.7. Solvent hidden using hide solvent.



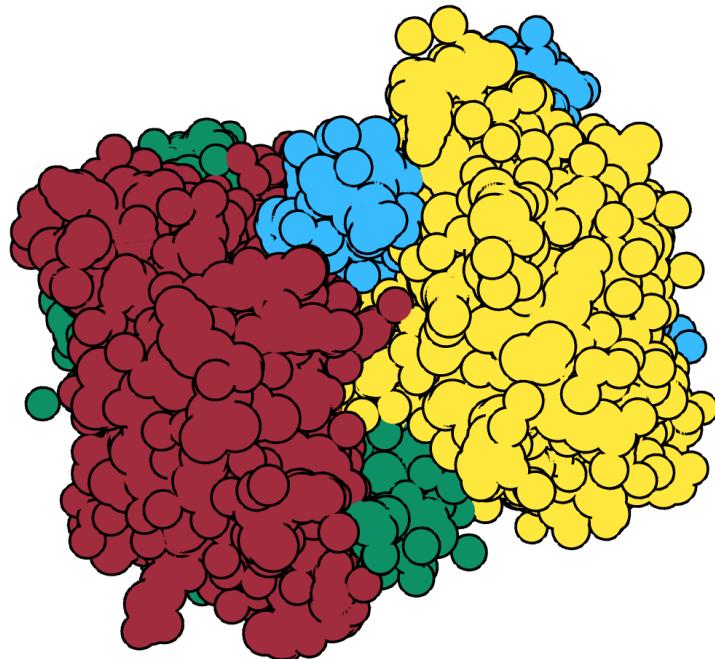
Thrombin in complex with its aptamers (PDB ID 5EW2). Image created with silhouettes depthJump 0.004 and width 2.2, with flat lighting and shadows. DNA settings: ribbon width 4, thickness 3 & ladder radius 0.7.

## Chimera

- As with Chimera-X, set presets to ‘Publication 1’, to immediately set a white background.
- Load in your structure, then go to the ‘Actions’ menu bar, and hide ribbons and surfaces. Set atoms/bonds to ‘show’, and set the style to ‘sphere’ in the same menu.
- Go to the ‘Tools’ menu bar and from the ‘Viewing Controls’ sub-menu, select ‘Lighting’. A new window should pop up, set the mode here to ‘ambient’.
- Jump to the ‘effects’ tab in the same window, and turn on silhouettes. Adjust the ‘width’ parameter to taste (see examples below for typical configurations). It is recommended to also check the ‘multisample’ value under ‘graphics quality’ for improved rendering (but this might be buggy for some setups). Close this window when ready.
- Select different chains/sections of the model using the ‘Select’ menu bar. When a part of the model is selected, it should have a light-green highlight around it.
- To set specific colours, go to the ‘Actions’ menu bar and select ‘Inspect’. Change the colour by selecting the colour box, and entering the desired colour’s hex code in the resulting window:



- When saving (File -> Save Image), it is possible to set the image DPI by checking the 'Use print units' box. Please use a minimum of 600 DPI for images saved (make sure to set the image width to 2.75 inches or 6 inches to avoid massive file sizes). Always save using .png or .tif image formats (.png preferred).
- Example protein structure:



Streptavidin (PDB ID 4BX5). Image created with silhouettes width 7, flat lighting, multisampling and 10 subdivisions (setting under graphics quality).

- Many of the modifications available for DNA in Chimera-X are all available in Chimera in a single tool ('Tools' -> 'Depiction' -> 'Nucleotides'). From here, the procedure is almost identical to that of Chimera-X.
- Adjusting ribbon width/thickness is taken care of in 'Tools' -> 'Depiction' -> 'Ribbon Style Editor' in Chimera. Make sure to change the 'Nucleic' parameters for the changes to have effect on DNA ribbons.
- The command line in Chimera can be accessed via 'Favourites' -> 'Command Line'.

## Pymol

Achieving a cartoony-effect with Pymol is a little more difficult. However, a relatively-simple procedure to obtain a similar result is as follows:

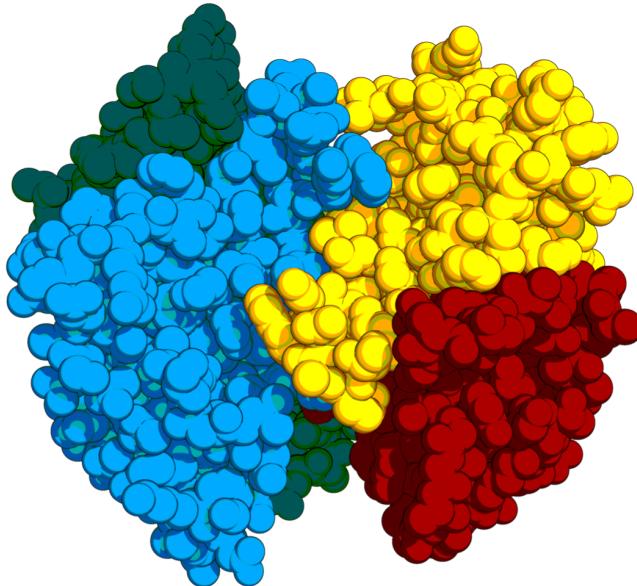
- Load in your PDB file.
- Remove all cartoon and surface representations (select the 'H' on the right next to the name of your PDB file, and hide these representations).
- Show the structure as spheres (select the 'S' on the right, then select 'spheres').
- Solvents can be removed using the command remove solvent (command line at the top of the screen).
- To set specific colours for chains or molecules, change the selection type at the bottom right of the screen (click on the circled area below):



- Then, select your chain/molecule and change colours using the command `color 0x30a0dc, sele` (swap out the hex code for your colour of choice).
- To setup the cartoon style, run the following commands:

```
bg_color white - sets background to white
set specular, 0 - Turns off reflections
set ambient, 0.4 - Increases ambient light
set ray_trace_gain, 0 - Ray tracing settings (for achieving the desired effect)
set ray_trace_mode, 3
set ray_trace_color, black
set ambient_occlusion_mode, 1 - Settings to enhance sense of depth
set ambient_occlusion_scale, 30
```

- To generate an image, click on ‘Draw/Ray’ at the top right, enter the image size (at least 600 DPI) and click on ‘Ray (slow)’ and then ‘Save Image to File’ (ideally .png). Make sure to uncheck the transparent background before rendering.
- An example result:



Streptavidin (PDB ID 4BX5), rendered using the above steps.

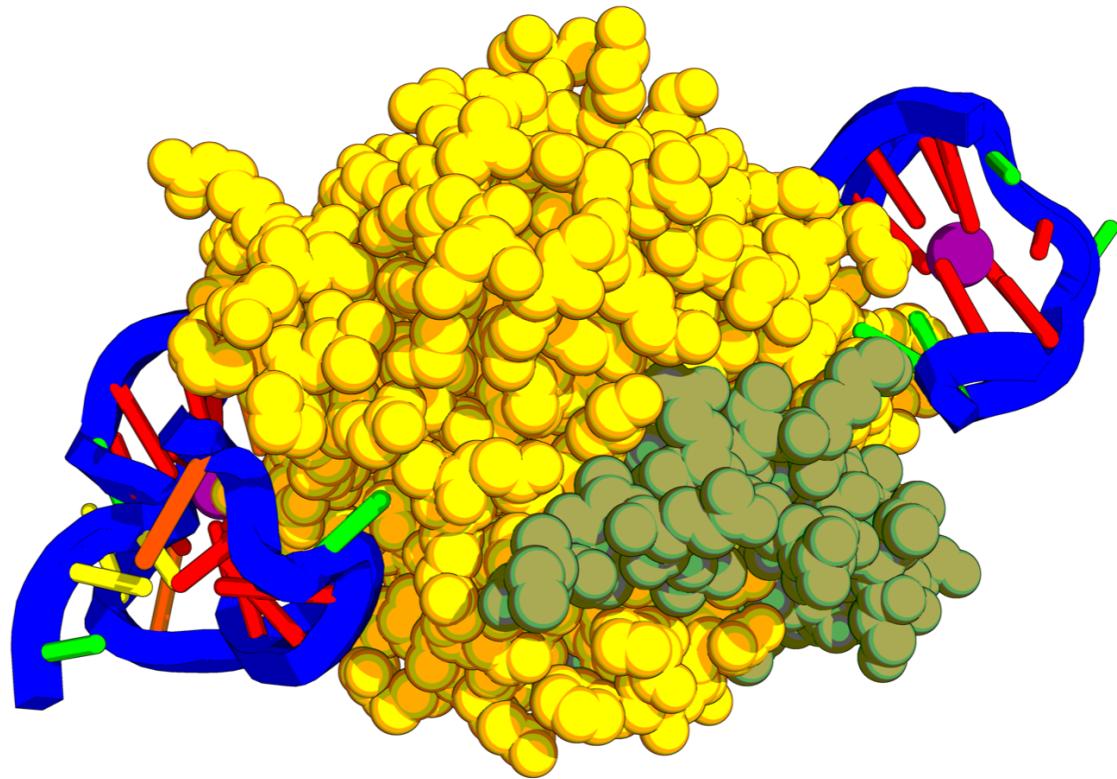
- Some tweaks might be required for different structures, in particular the ‘ambient’ setting. Some other resources for tweaking settings can be found [here](#) & [here](#).
- To obtain an image more closer in style to the Molecule of the Month series, this might be a good starting point: [David Goodsell like images | Getting to know Structural Bioinformatics](#)
- To render DNA in ribbon format alongside a protein, a number of extra commands need to be run:

```

cartoon rect - set DNA backbone as rectangles
set cartoon_rect_width, 1.7 - increase backbone width
set cartoon_ladder_radius, 0.6 - increase DNA ladder radius
set cartoon_nucleic_acid_color, blue - set DNA backbone colour
color orange, resn DA - set specific base colours
color red, resn DG
color green, resn DT
color yellow, resn DC

```

- All above parameters are customizable, but represent a good starting point for rendering DNA chains. An example result is as follows:



Thrombin + aptamers (PDB ID 5EW2), with the same rendering settings as before.

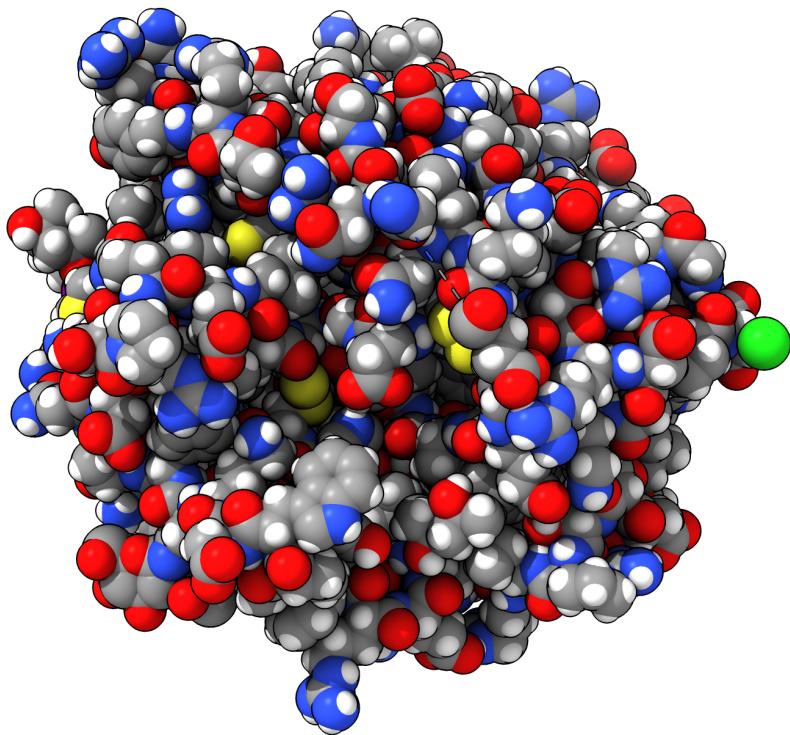
- Make sure that all cartoons are turned off for proteins before running the above steps for the DNA visualization.
- Of course, there are many other visualization options in Pymol, some of which can be found [here](#) & [here](#).

## Proteins: full details

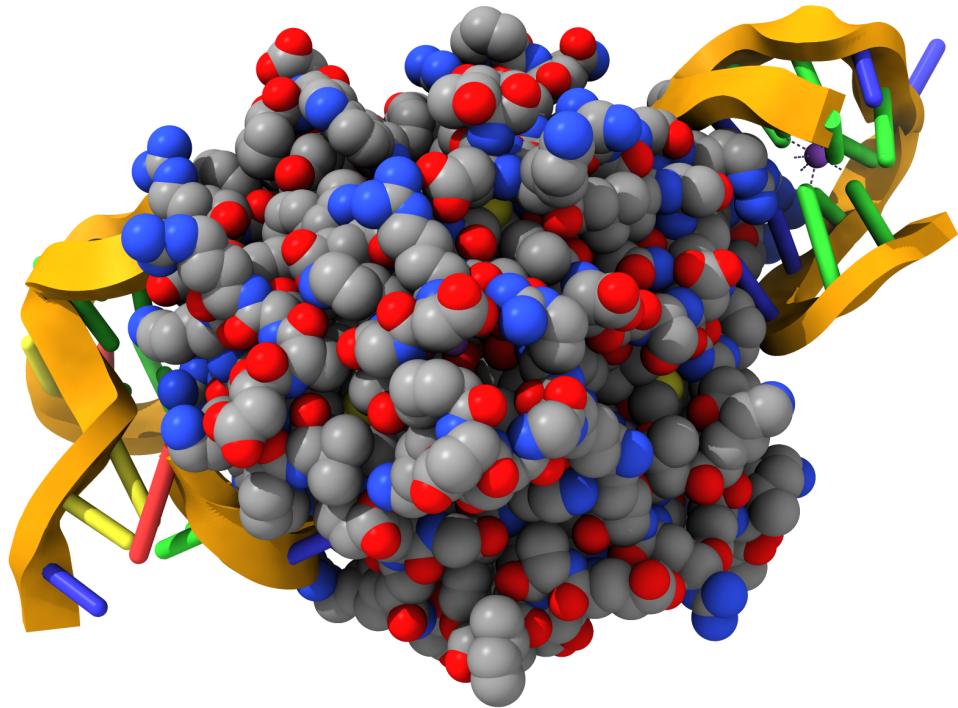
This style presents the full atomic detail of the structure selected. With the increased detail, this format can be overwhelming for larger structures, and should mostly be applied with caution.

### Chimera-X

- To achieve this effect in Chimera-X, follow the guidelines from the cartoon section, but replace the flat lighting with ‘full lighting’ from the ‘Graphics’ tab. Silhouettes are best left unmodified or off in this mode.
- Examples:



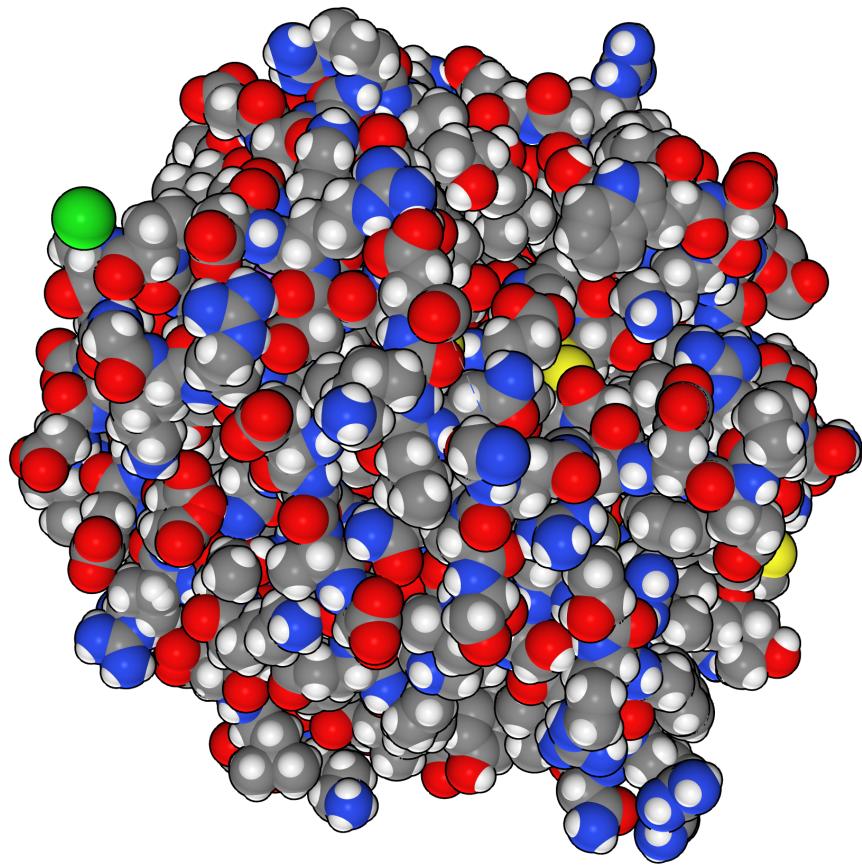
Thrombin (PDB ID 3U69). Image created with full lighting, standard silhouettes and shadows. Solvent was hidden, and atoms were coloured by element.



Thrombin in complex with its aptamers (PDB ID 5EW2). Image created with silhouettes off, full lighting and shadows on. DNA settings: ribbon width 4, thickness 2 & ladder radius 0.7. Thrombin atoms were coloured by element.

## Chimera

- To achieve the same effect in Chimera, the user needs to adjust the parameters in the ‘Viewing Controls’ menu (see the example below). In particular, it is beneficial to set the reflectivity parameter in the shininess menu (in Viewing Controls) to a low value (e.g. 0.2) to reduce distracting reflections on the structure of interest.
- Example:

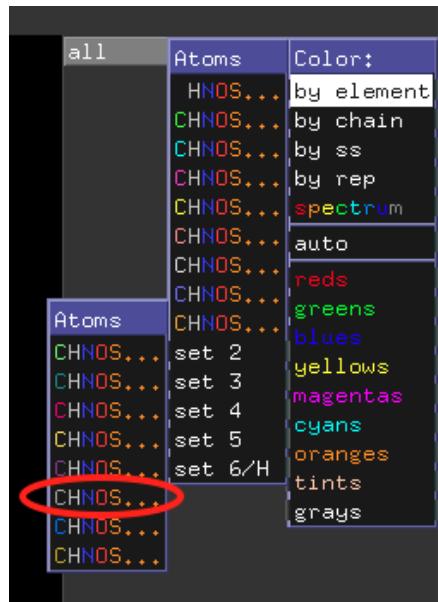


Thrombin (PDB ID 3U69). Image created with three-point lighting, 0.2 reflectivity, sharpness 128 and silhouettes with width 3.0. Graphics quality subdivisions were set to 10, with multisampling enabled.

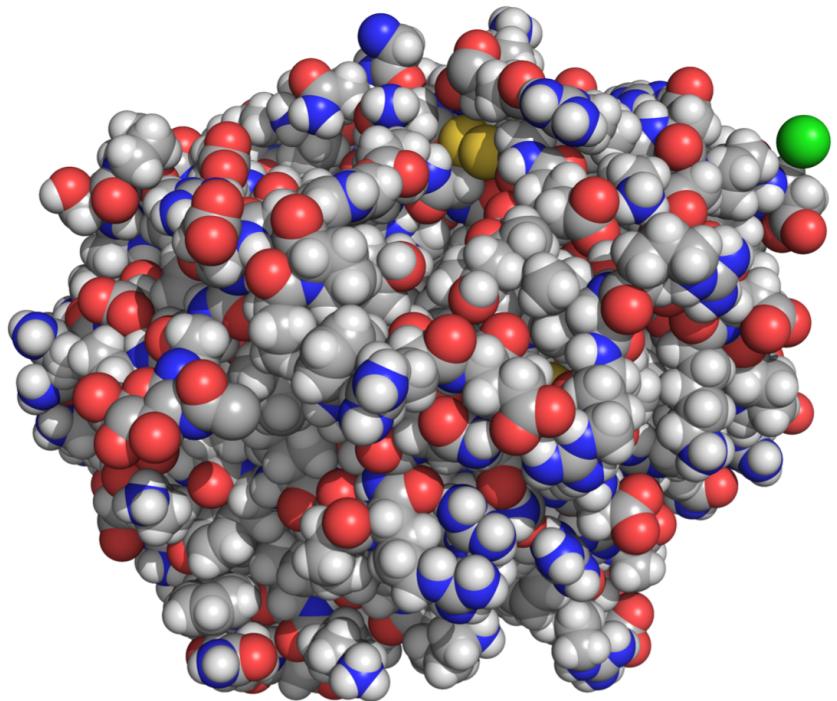
## Pymol

- Creating a photo-realistic 3D image of a detailed atomic view in Pymol takes very little configuration:

```
bg_color white
set ray_trace_mode, 0 (removes molecule outlines)
set shininess, 80
set ambient_occlusion_mode, 1
set ambient_occlusion_scale, 30
```
- Make sure to hide any solvents (command: `remove solvent`) which can obscure the structure of the target molecule. The colour by element command which best matches that of Chimera is set 2, variant 6:



- Generate the ray-traced image using the method presented in the previous Pymol cartoon-view guidelines.
- Example:



Thrombin (PDB ID 3U69), rendered using ray\_trace\_mode 0. Colours generated using colour by element, set 2 variant 6.

## Large DNA nanostructures

Presenting large DNA nanostructures (such as DNA origami) with the previous methods can prove to be too overwhelming, given the large size of these structures. It is preferable to omit some of the details of these structures using the technique in this section, in order to allow the general shape of the structure to be clearly visible. If designing DNA origami in Cadnano, .json design files can be easily converted into PDB structures (producing idealized representations) using the converter [here](#).

### Chimera-X

- Large DNA structures should only have their DNA backbone rendered, in ribbon format. To set this up, load in the structure, and hide all atoms and surfaces. Set cartoons to ‘show’ (as in previous guidelines) and adjust ribbon thickness using the following command (or similar):

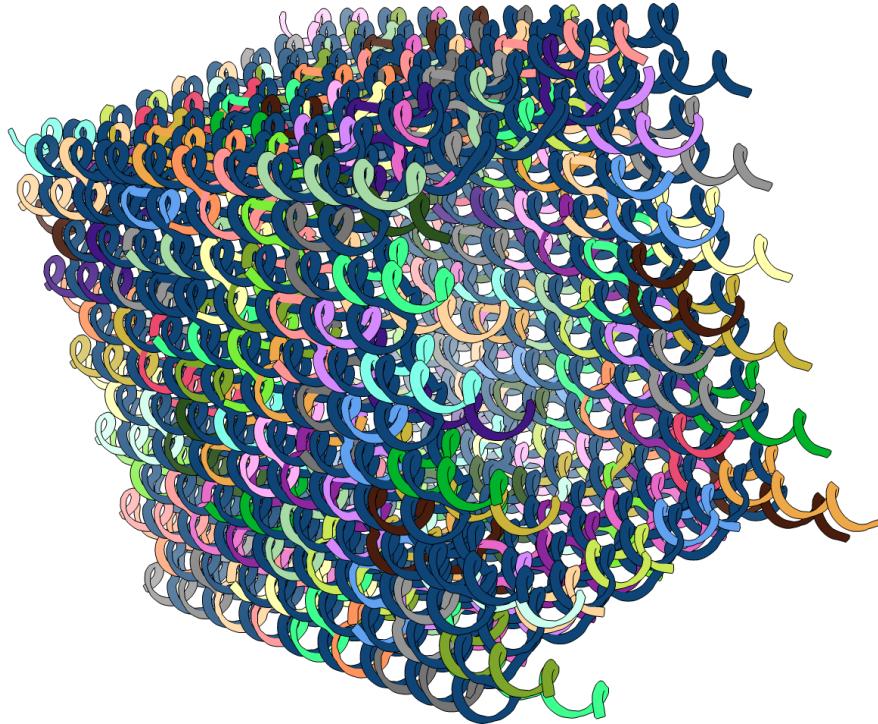
```
ribbon style width 4 thickness 2 (both parameters user-adjustable)
```

- Make sure to colour the structure by chain i.e. have the scaffold in one colour, and assign the rest of the staples a random colour (can be done automatically via ‘Actions’ -> ‘Color’ -> ‘All Options...’ -> Color by chain). Please ensure that the scaffold colour is set to the [Indigo Dye \(#0d3b66\)](#) colour from the general graphics guidelines.
- Lighting can be set to flat or full according to preference (however, flat lighting produces better quality results). Examples of both are provided:

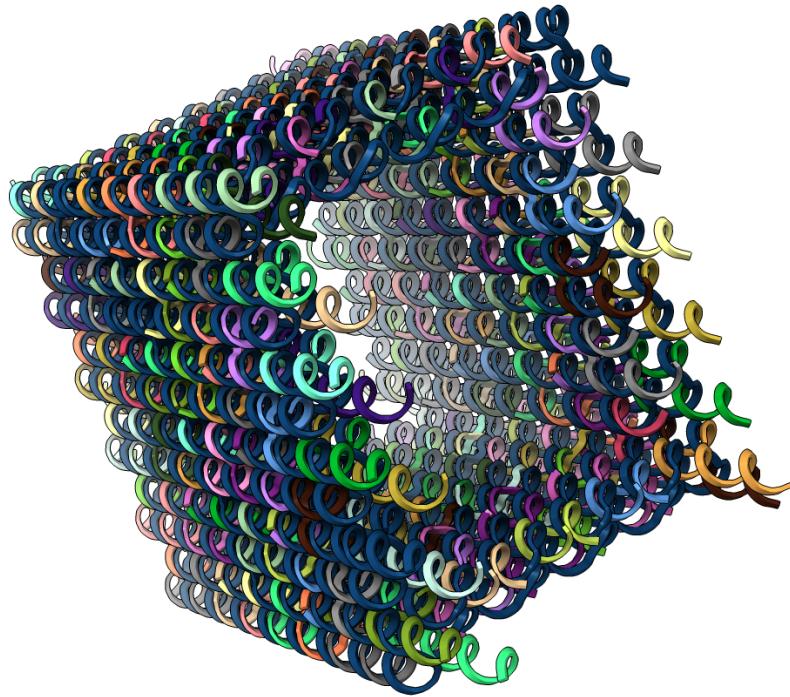


DNA Origami barrel available [here](#). Image produced using flat lighting, with ribbons width 4 &

thickness 2.



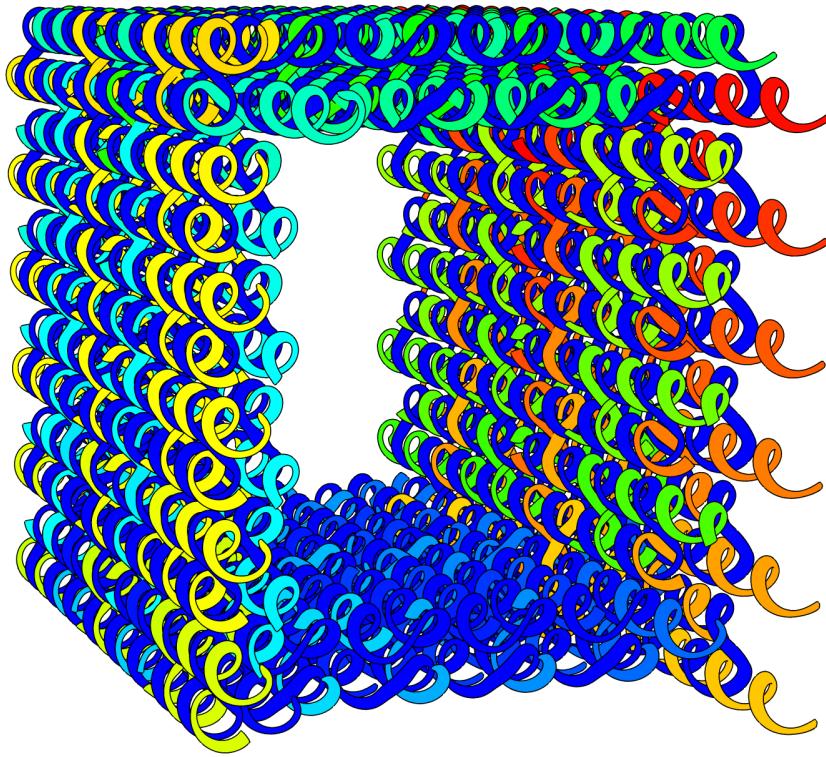
DNA Origami barrel available [here](#). Image produced using flat lighting, with ribbons width 4 & thickness 2.



DNA Origami barrel available [here](#). Image produced using full lighting, with ribbons width 4 & thickness 2.

## Chimera

- As with Chimera X, hide all atoms/bonds and only display ribbons/cartoons for large DNA structures. Ribbon width/thickness can be modified via the Ribbon Style Editor (see previous notes for Chimera).
- Coloring by chain is less straightforward in Chimera. The easiest option is to run the command rainbow chain, which colours each chain according to a set range (modifiable in ‘Tools’ -> ‘Depictions’ -> ‘Rainbow’). The resulting colours are less easy to distinguish, however, which might make this difficult for viewing. It is potentially possible to set specific colours via scripting (but this has not yet been tested).
- An example is provided below:



DNA Origami barrel available [here](#). Image produced using ambient lighting, with silhouettes width 2.0, and ribbons with width 3 & height 1.

### Pymol

Pymol is not recommended for viewing large DNA structures as crossovers are not properly visualized.

# Appendix

## Main AoMP colour palette copyable code

```
/* CSV */
0d3b66,30a0dc,8b2635,d88373,474747,8f8f8f,0c7c59,849e57,ea9c0b,fdc835

/* Hex array */
[#0d3b66,"#30a0dc","#8b2635","#d88373","#474747","#8f8f8f","#0c7c59",
 "#849e57","#ea9c0b","#fdc835"]

/* RGB tuples (divide by 255 to get 0-1 scale) */
[(13,59,102),(48,160,220),(139,38,53),(216,131,115),(71,71,71),(143,1
43,143),(12,124,89),(132,158,87),(234,156,11),(253,200,53)]

/* Object */
{"Indigo": "0d3b66", "Carolina": "30a0dc", "Blue": "30a0dc", "Antique": "30a0dc", "Ruby": "8b2635", "Middle Red": "d88373", "Davys": "474747", "Grey": "474747", "Spanish": "8f8f8f", "Gray": "8f8f8f", "Viridian": "0c7c59", "Moss": "0c7c59", "Green": "849e57", "Gamboge": "ea9c0b", "Sunglow": "fdc835"}

/* Extended Array */
[{"name": "Indigo", "Dye": "0d3b66", "hex": "0d3b66", "rgb": [13, 59, 102], "cmyk": [87, 42, 0, 60], "hsb": [209, 87, 40], "hsl": [209, 77, 23], "lab": [24, 2, -30]}, {"name": "Carolina", "Blue": "30a0dc", "hex": "30a0dc", "rgb": [48, 160, 220], "cmyk": [78, 27, 0, 14], "hsb": [201, 78, 86], "hsl": [201, 71, 53], "lab": [62, -11, -39]}, {"name": "Antique", "Ruby": "8b2635", "hex": "8b2635", "rgb": [139, 38, 53], "cmyk": [0, 73, 62, 45], "hsb": [351, 73, 55], "hsl": [351, 57, 35], "lab": [32, 43, 16]}, {"name": "Middle", "Red": "d88373", "hex": "d88373", "rgb": [216, 131, 115], "cmyk": [0, 39, 47, 15], "hsb": [104, 47, 85], "hsl": [10, 56, 65], "lab": [63, 31, 23]}, {"name": "Davys", "Grey": "474747", "hex": "474747", "rgb": [71, 71, 71], "cmyk": [0, 0, 0, 72], "hsb": [0, 0, 28], "hsl": [0, 0, 28], "lab": [30, 0, 0]}, {"name": "Spanish", "Gray": "8f8f8f", "hex": "8f8f8f", "rgb": [143, 143, 143], "cmyk": [0, 0, 0, 44], "hsb": [0, 0, 56], "hsl": [0, 0, 56], "lab": [59, 0, 0]}, {"name": "Spanish", "Viridian": "0c7c59", "hex": "0c7c59", "rgb": [12, 124, 89], "cmyk": [90, 0, 28, 51], "hsb": [161, 90, 49], "hsl": [161, 82, 27], "lab": [46, -38, 11]}, {"name": "Moss", "Green": "849e57", "hex": "849e57", "rgb": [132, 158, 87], "cmyk": [16, 0, 45, 38], "hsb": [82, 45, 62], "hsl": [82, 29, 48], "lab": [62, -21, 34]}, {"name": "Gamboge", "hex": "ea9c0b", "rgb": [234, 156, 11], "cmyk": [0, 33, 95, 8], "hsb": [39, 95, 92], "hsl": [39, 91, 48], "lab": [70, 20, 73]}, {"name": "Sunglow", "hex": "fdc835", "rgb": [253, 200, 53], "cmyk": [0, 21, 79, 1], "hsb": [44, 79, 99], "hsl": [44, 98, 60], "lab": [83, 6, 75}]]
```

## Gwyddion-inspired colour palette copyable code

```
/* CSV */
ffffff,fcefd4,f3dcaa,ebc67a,daa45a,bc7748,a64f32,823118,591d0e,2e0d03
,000000

/* Hex array */
["#ffffff","#fcefd4","#f3dcaa","#ebc67a","#daa45a","#bc7748","#a64f32"
,"#823118","#591d0e","#2e0d03","#000000"]

/* RGB tuples (divide by 255 to get 0-1 scale) */
[(255,255,255),(252,239,212),(243,220,170),(235,198,122),(218,164,90)
,(188,119,72),(166,79,50),(130,49,24),(89,29,14),(46,13,3),(0,0,0)]

/* Object */
{"White":"ffffff","Papaya Whip":"fcefd4","Wheat":"f3dcaa","Gold Crayola":"ebc67a","Earth Yellow":"daa45a","Copper":"bc7748","Chinese Red":"a64f32","Kobe":"823118","Seal Brown":"591d0e","Dark Sienna":"2e0d03","Black":"000000"}

/* Extended Array */
[{"name":"White","hex":"ffffff","rgb":[255,255,255],"cmyk":[0,0,0,0],
"hsb":[0,0,100],"hsl":[0,0,100],"lab":[100,0,0]}, {"name":"Papaya Whip",
"hex":"fcefd4","rgb":[252,239,212],"cmyk":[0,5,16,1],"hsb":[40,
16,99],"hsl":[40,87,91],"lab":[95,0,15]}, {"name":"Wheat","hex":"f3dca
a","rgb":[243,220,170],"cmyk":[0,9,30,5],"hsb":[41,30,95],"hsl":[41,
75,81],"lab":[89,1,27]}, {"name":"Gold Crayola","hex":"ebc67a","rgb":[235,198,122],"cmyk": [0,16,48,8],"hsb": [40,48,92],"hsl": [40,74,70],"lab": [82,4,43]}, {"name":"Earth Yellow","hex":"daa45a","rgb": [218,164,90],"cmyk": [0,25,59,15],"hsb": [35,59,85],"hsl": [35,63,60],"lab": [71,12,46]}, {"name":"Copper","hex":"bc7748","rgb": [188,119,72],"cmyk": [0,37,62,26],"hsb": [24,62,74],"hsl": [24,46,51],"lab": [56,22,37]}, {"name":"Chinese Red","hex":"a64f32","rgb": [166,79,50],"cmyk": [0,52,70,35],"hsb": [15,70,65],"hsl": [15,54,42],"lab": [44,34,34]}, {"name":"Kobe","hex":"823118","rgb": [130,49,24],"cmyk": [0,62,82,49],"hsb": [14,82,51],"hsl": [14,69,30],"lab": [32,34,33]}, {"name":"Seal Brown","hex":"591d0e","rgb": [89,29,14],"cmyk": [0,67,84,65],"hsb": [12,84,35],"hsl": [12,73,20],"lab": [20,27,24]}, {"name":"Dark Sienna","hex":"2e0d03","rgb": [46,13,3],"cmyk": [0,72,93,82],"hsb": [14,93,18],"hsl": [14,88,10],"lab": [8,16,11]}, {"name":"Black","hex":"000000","rgb": [0,0,0],"cmyk": [0,0,0,100],"hsb": [0,0,0],"hsl": [0,0,0],"lab": [0,0,0]}]
```