

# RiboVision2: A Web Server for Advanced Visualization of Ribosomal RNAs



ANTON S. PETROV

GEORGIA INSTITUTE OF TECHNOLOGY

Computational Approaches to RNA Structure and Function, Benasque

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# Original RiboVision



Click here for NEW RiboVision2.0!  
Current version of RiboVision is obsolete!

RiboVision Manual

Not secure apollo.chemistry.gatech.edu/RiboVision2/#ECOLI\_LSU&ECOLI\_SSU

1D Panel

2D Panel

3D Panel

The screenshot displays the RiboVision web interface. At the top, there is a navigation bar with a search icon, a star icon, and social media icons. Below the navigation bar, there is a red banner with a warning message: "Click here for NEW RiboVision2.0! Current version of RiboVision is obsolete!". Below the banner, there is a "RiboVision Manual" link. The main interface is divided into three panels: 1D Panel, 2D Panel, and 3D Panel. The 1D Panel shows a "FineOnion" plot with a y-axis labeled "FineOnion" and an x-axis labeled "Nucleotide Number" ranging from 0 to 3,000. The 2D Panel shows two 2D diagrams of the ribosome. The left diagram is labeled "Escherichia coli large subunit ribosomal RNA" and the right diagram is labeled "Escherichia coli small subunit ribosomal RNA". Both diagrams are color-coded and labeled with Roman numerals (I-VI) and nucleotide positions (5', 3', 3'M). The 3D Panel shows a 3D ribbon representation of the ribosome. On the left side, there is a "Select" menu with options: "Species/Subunit", "Select", "Nucleotide Data", "Phylogeny Data", "Protein Contacts", "Import?", "Select proteins", "Protein Contacts", "Inter-Nucleotide Contacts", and "Import". Below the "Select" menu is a "Save" button and a "Save Manager" button. On the right side, there is a "Display" menu with options: "2D Layers", "Edit Layers", "Circles", "Letters", "ContourLine2", "ContourLine", "3D Panel", and "Circles". Below the "Display" menu is a "Save" button and a "Save Manager" button. At the bottom left, there is a logo for the "CENTER FOR THE" and a "Save" button.

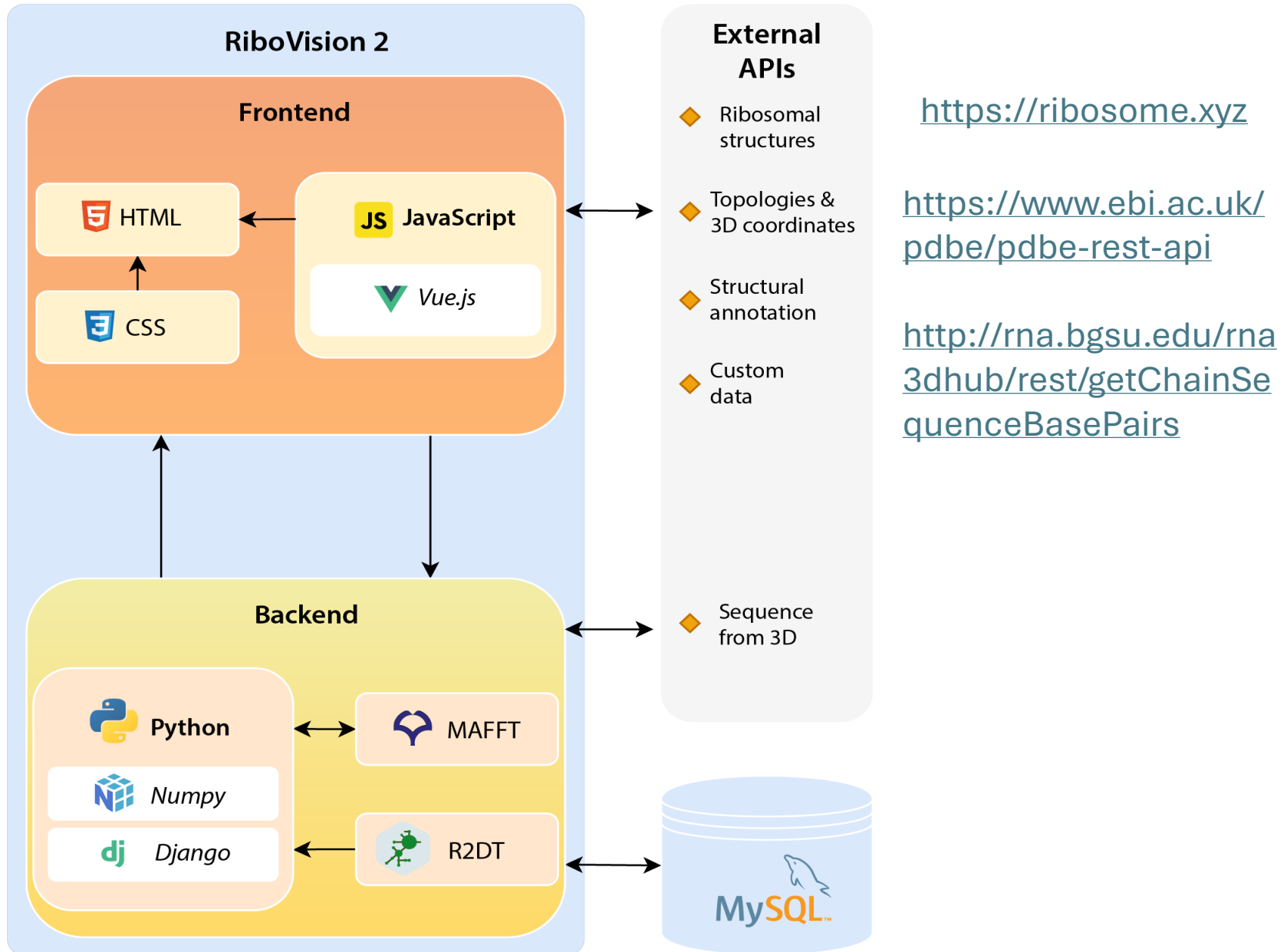
Bernier C. RiboVision suite for visualization and analysis of ribosomes, 2014, Faraday Discussions 169. 195-203.

RiboVision2 a powerful open-source web server that enables:

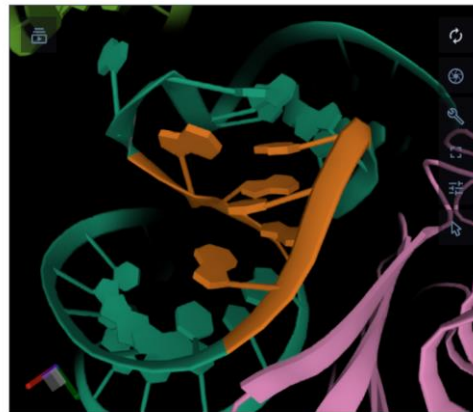
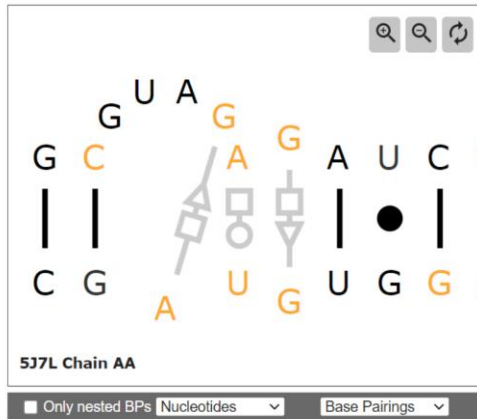
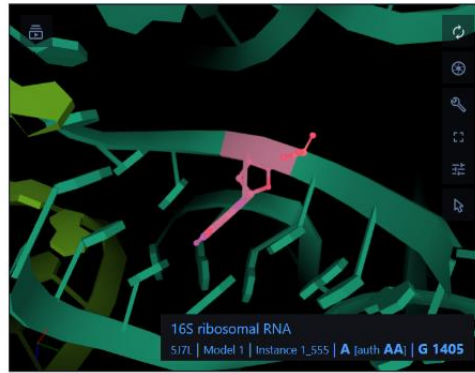
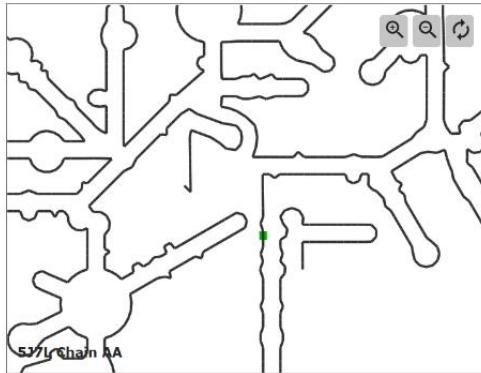
- **Multi-level RNA Structure visualization**, multiple sequence alignment (MSA), secondary, and three-dimensional levels
- Capable of visualizing all ribosomal structures deposited in PDBe
- **Provides and ability to map and visualize user supplied RNA data for simultaneous visualization in 2D and 3D;**
- **Enables exporting results** as publication-ready images
- RiboVision2 is available at <https://ribovision2.chemistry.gatech.edu/>
- The source code is available at [https://github.com/LDWLab/RiboVision\\_2.0\\_GT](https://github.com/LDWLab/RiboVision_2.0_GT)



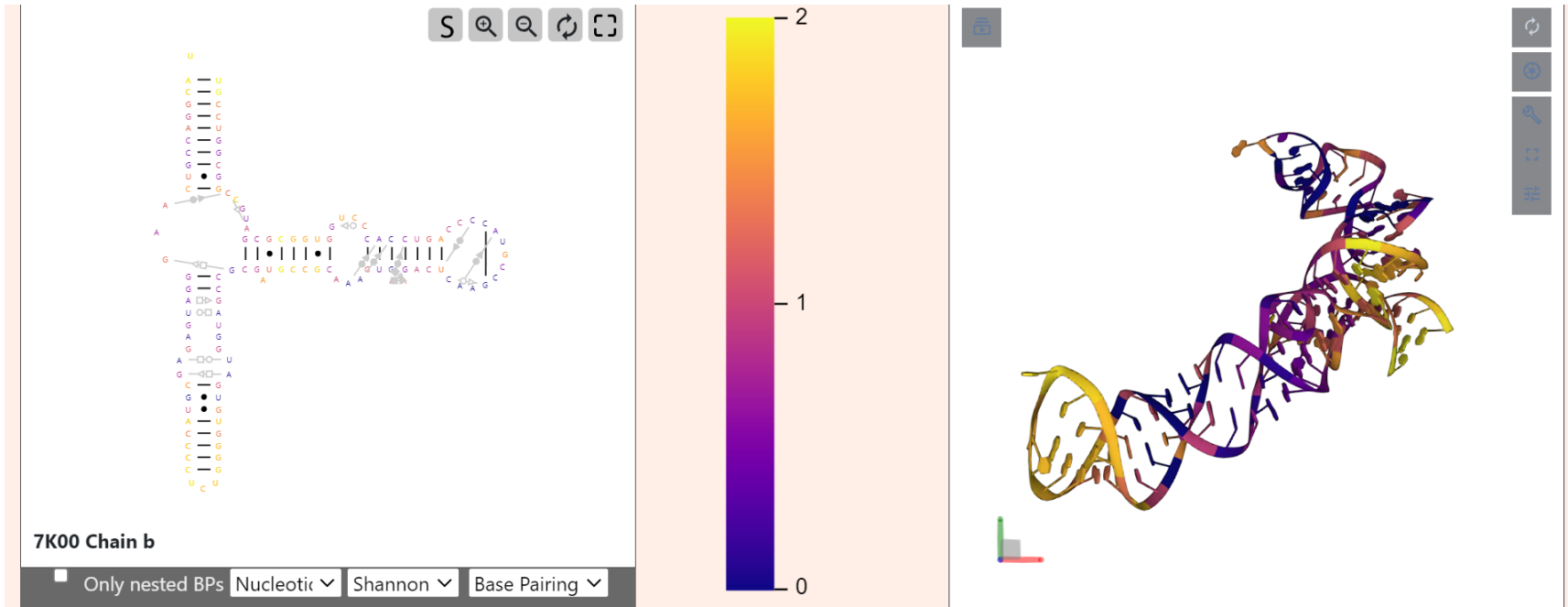
# RiboVision2 Architecture



# Collaboration with PDBe



# Expanding PDBe applet for RiboVision2



Data mapping (evolutionary data, protein contacts, chemical modifications)

Interactivity

Ability to save the visualization as svg image

Integration with Mol\*

# RiboVision mode

- Selection from the provided ribosomal alignments (23S, 28S, 5.8S, 16S/18S, 5S rRNAs); (no mt-rRNA alignments are currently provided).
- Selection of any deposited ribosomal 3D structure containing a matching RNA chain from ribosome.xyz (Kushner et al, NAR, 2023 Jan 6;51(D1):D509-D516. )
- Interactive visualization of RNA base-pairings according to Leontis-Westhof notation (with selectable options).
- Visualization of 2D and 3D from APIs (PDBe) with an attempt to recompute 2D maps with R2DT.
- Computation of some evolutionary data from the selected MSA (conservation and divergence scores )
- Computation of RNA protein interaction for the selected structure on the fly with interactive annotations.
- Visualization of chemical modification from mmCIF annotations (if available).

**RiboVision 2 : Advanced Visualization of RNA molecules** Load session Save session About Help

**RiboVision** User upload

Bacteria ▼

SSU-rRNA ▼

SSU ▼

Select/type PDB entry:   
 7k00

Select the matching RNA chain:   
 16S ribosomal RNA

Download mapped data ▼

Show ribosomal context in 3D

Upload custom mapping data

Select RNA-protein contacts to view in 3D

Select All

SSU protein uS2

SSU protein uS3

Submit Proteins

Select modified residues to highlight

Select All

PSU

G7M

Submit Residues

Download alignment
Download alignment image ▼
Contacts ▼
nucleotide ▼

Structure sequence

4775	4780	4785	4790	4795	4800	4805	4810	4815	4820	4825	4830	4835	4840	4845	4850
G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -	G U C A A G U C A G C - A U G G C C C U U - A U G - A C C U - - - G G G C A C A C A C G U G - - C U A C A A U G G - A C G A A C A A U A G G - A - - -

**MSAViewer**

**2D RNA Viewer**

7K00 Chain A Residue U 1224

Only nested BPs Circle ▼ Select da ▼ Base Pairing ▼

**MOL\* Viewer**

16S rRNA

7K00 | Model 1 | Instance ASM\_1 | A | U 1224

Simultaneous Visualization: All three structural dimensions are displayed together in real-time with options to view them individually if needed for any uploaded RNA

Interactive Mapping: RiboVision2 links all nucleotides in each dimension to one another. If you hover one nucleotide, it highlights that region in all dimensions.



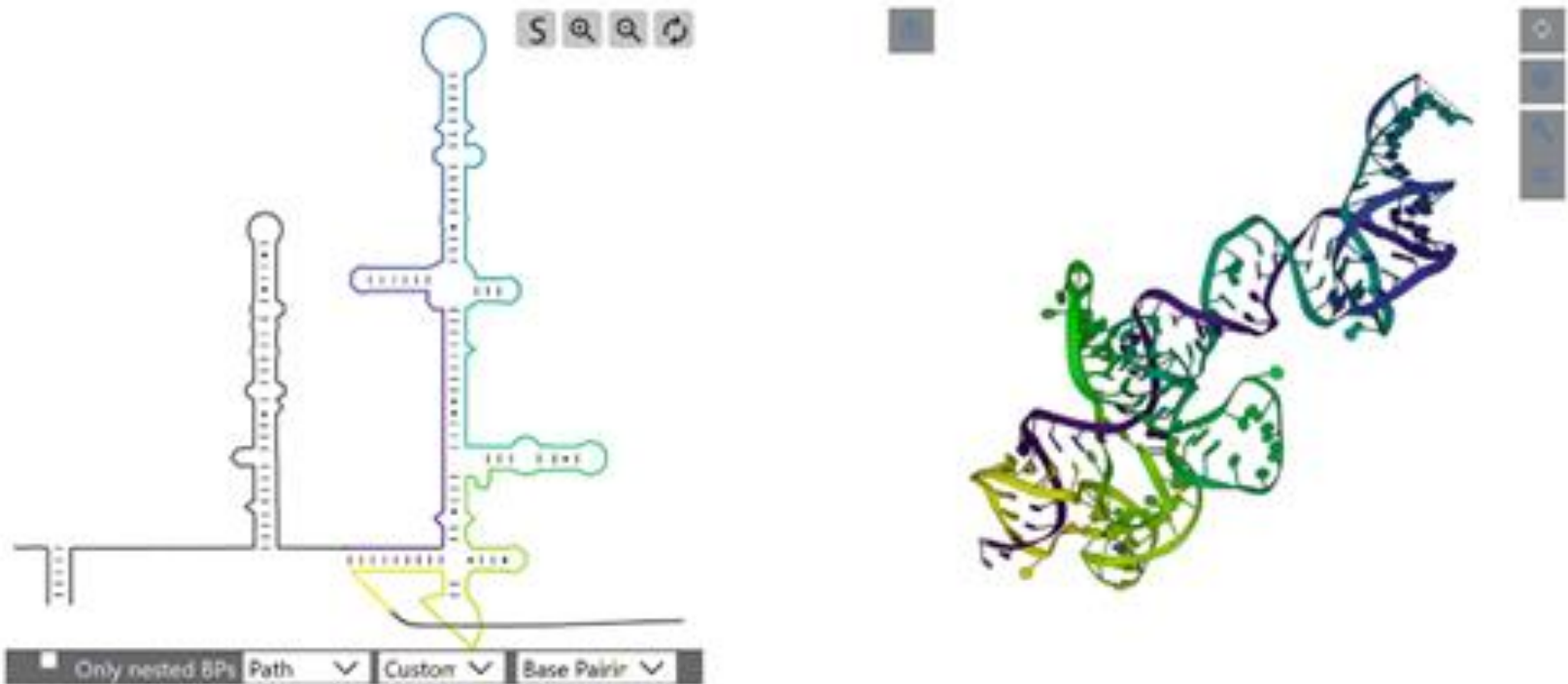
# Additional features

- Full screen options for 2D and 3D panels
- Ability to supply and map user supplied data onto 1D, 2D and 3D representations (limited availability of coloring schemas)
- Saving visualizations as 2D and 3D images.
- Saving 2D as svg
- Saving work in 3D as PyMOL scripts.

# Custom Mode

- Expands an ability to visualize any RNA molecule in 1D, 2D, and 3D
- Users are expected to supply a single sequence or an MSA in fasta format and a 3D structure in the mmCIF or PDB formats.
- For the CIF format, several dictionaries are required.
- For PDB format, a full RNA sequence is also required.
- Custom mode uses R2DT to generate a 2D layout and merges an MSA with 3D derived sequence to integrate the representations

# Custom Mode Example



User-uploaded HCV-IRES RNA, 6IP8, Chain zz with mapped custom data (indices)

# Limitations

- No available templates for mt-Ribosomes (yet!)
- Limited availability of color pallets for Data mapping
- Slow handling of CIF files in the custom mode
- Chemical modifications are extracted from mmCIFs
- Limited error notifications.