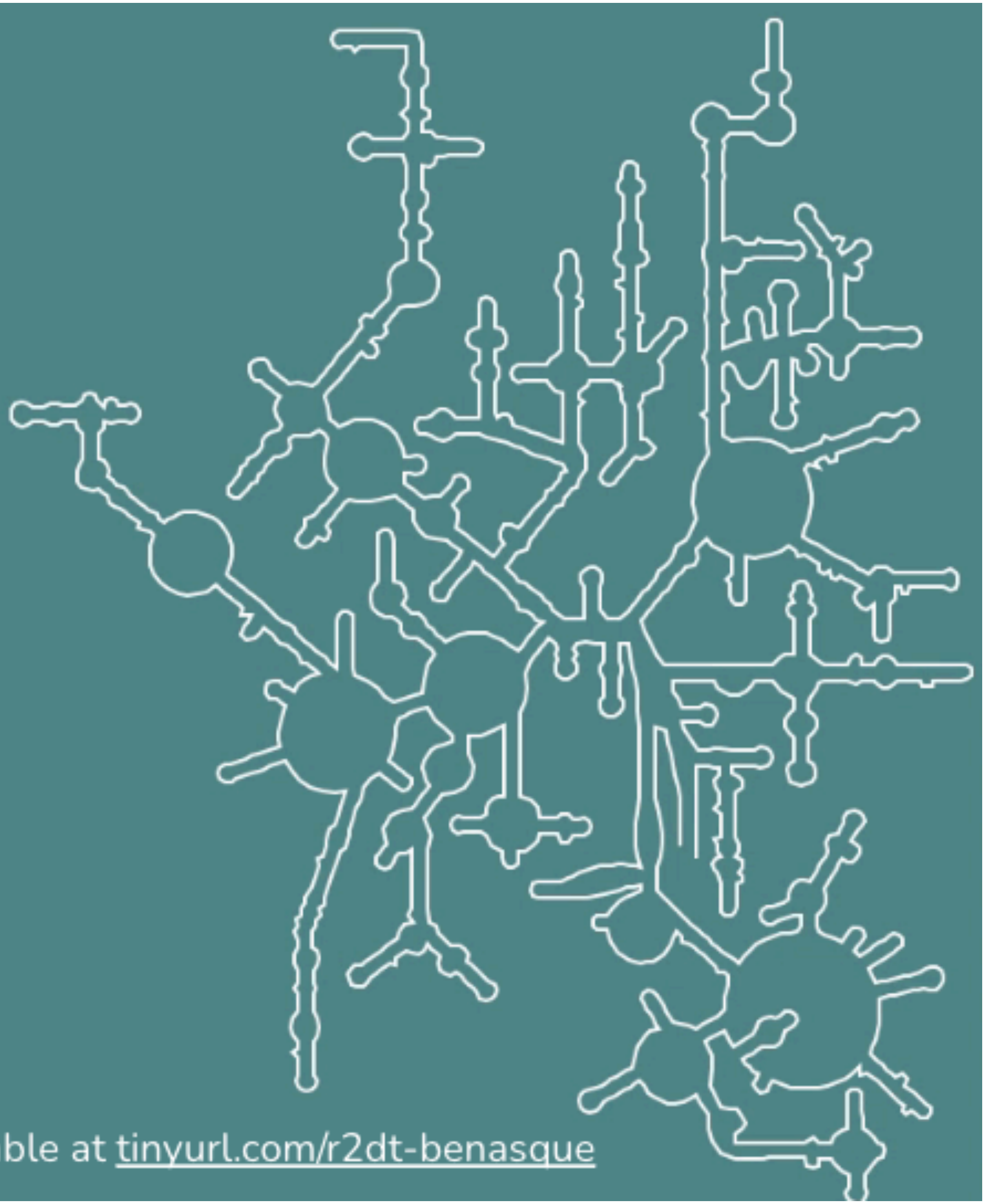
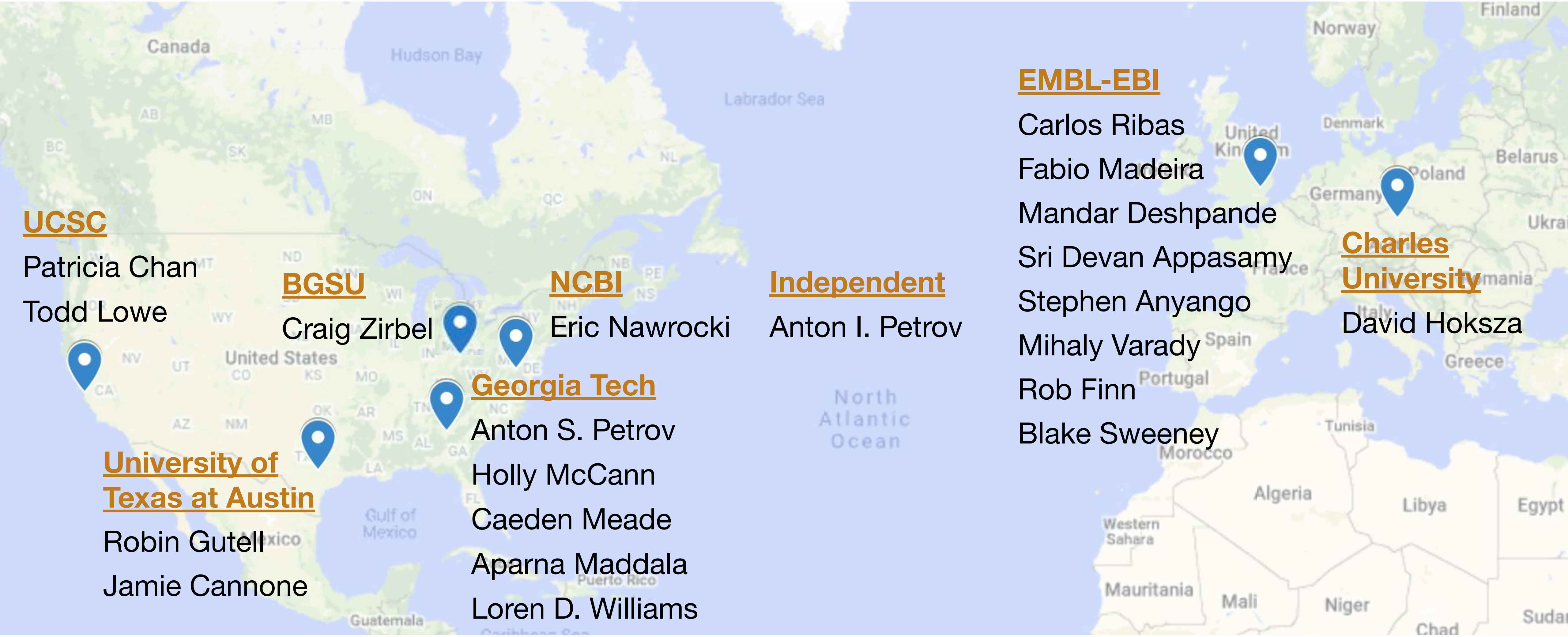
Visualising RNA secondary structure using R2DT

Anton I. Petrov
on behalf of the R2DT team



Aug 19th, 2022 | Benasque These slides are available at tinyurl.com/r2dt-benasque

The R2DT team



UCSC

Patricia Chan

Todd Lowe

University of Texas at Austin

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Carlos Ribas

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Mandar Deshpande

Sri Devan Appasamy

Stephen Anyango

Mihaly Varady

Rob Finn

Blake Sweeney

Charles University

David Hoksza

My slide from 4 years ago

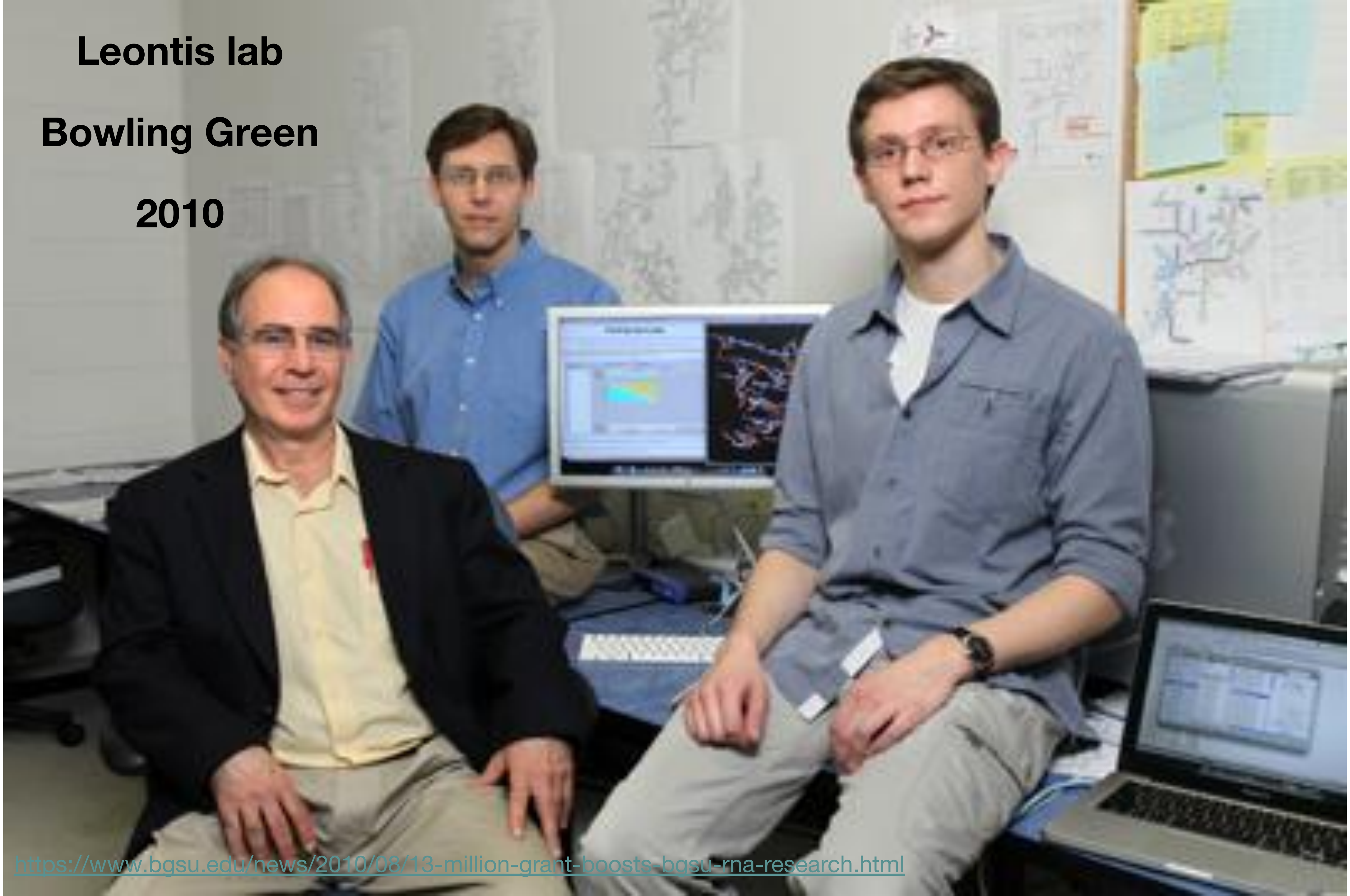
Benasque 2018

top-secret project:

display 2Ds for **all rRNAs**
in RNAcentral
using **standard layouts**

EMBL-EBI

https://www.benasque.org/general/cgi-bin/pictures.pl#ancor



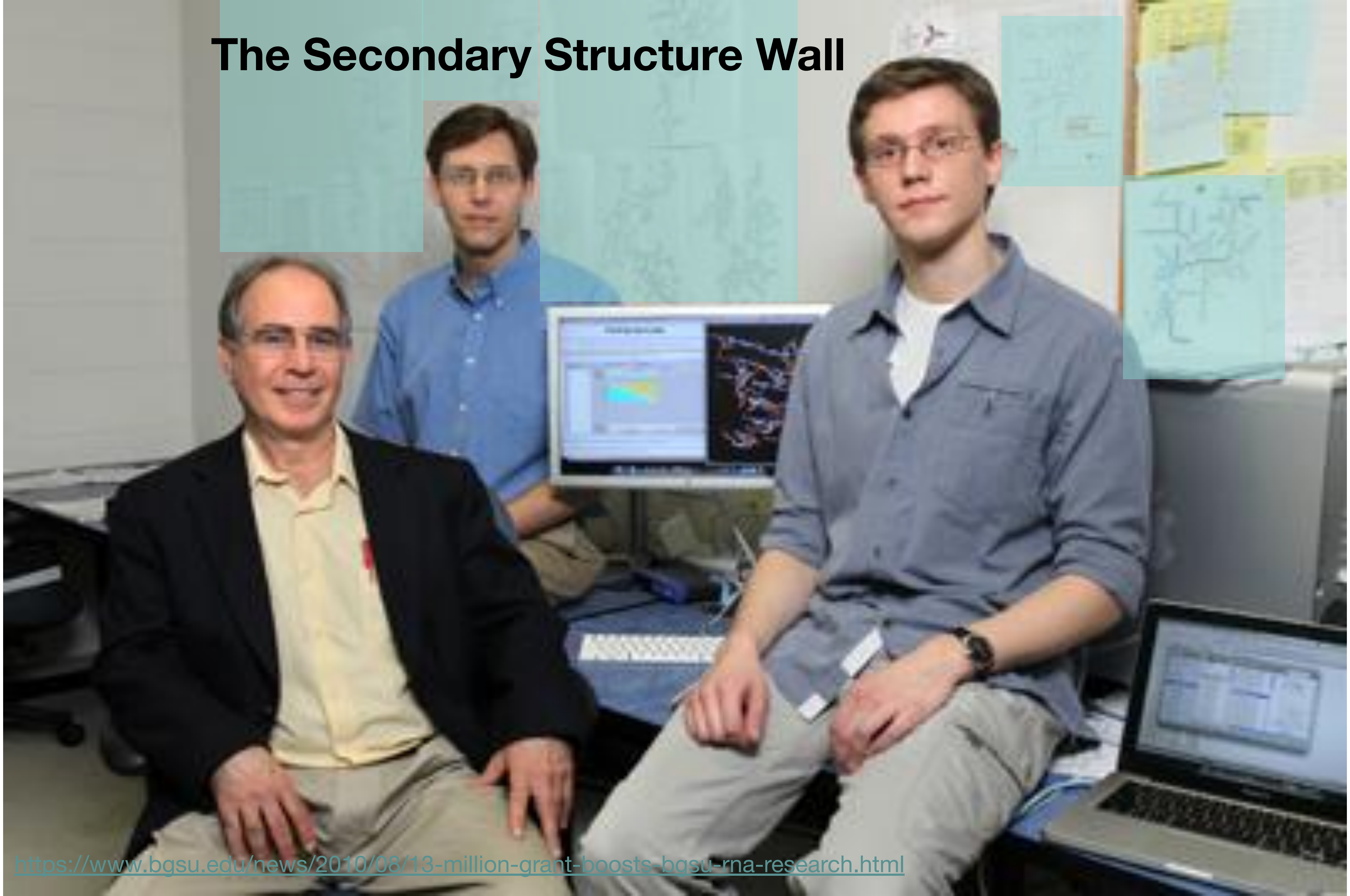
Leontis lab

Bowling Green

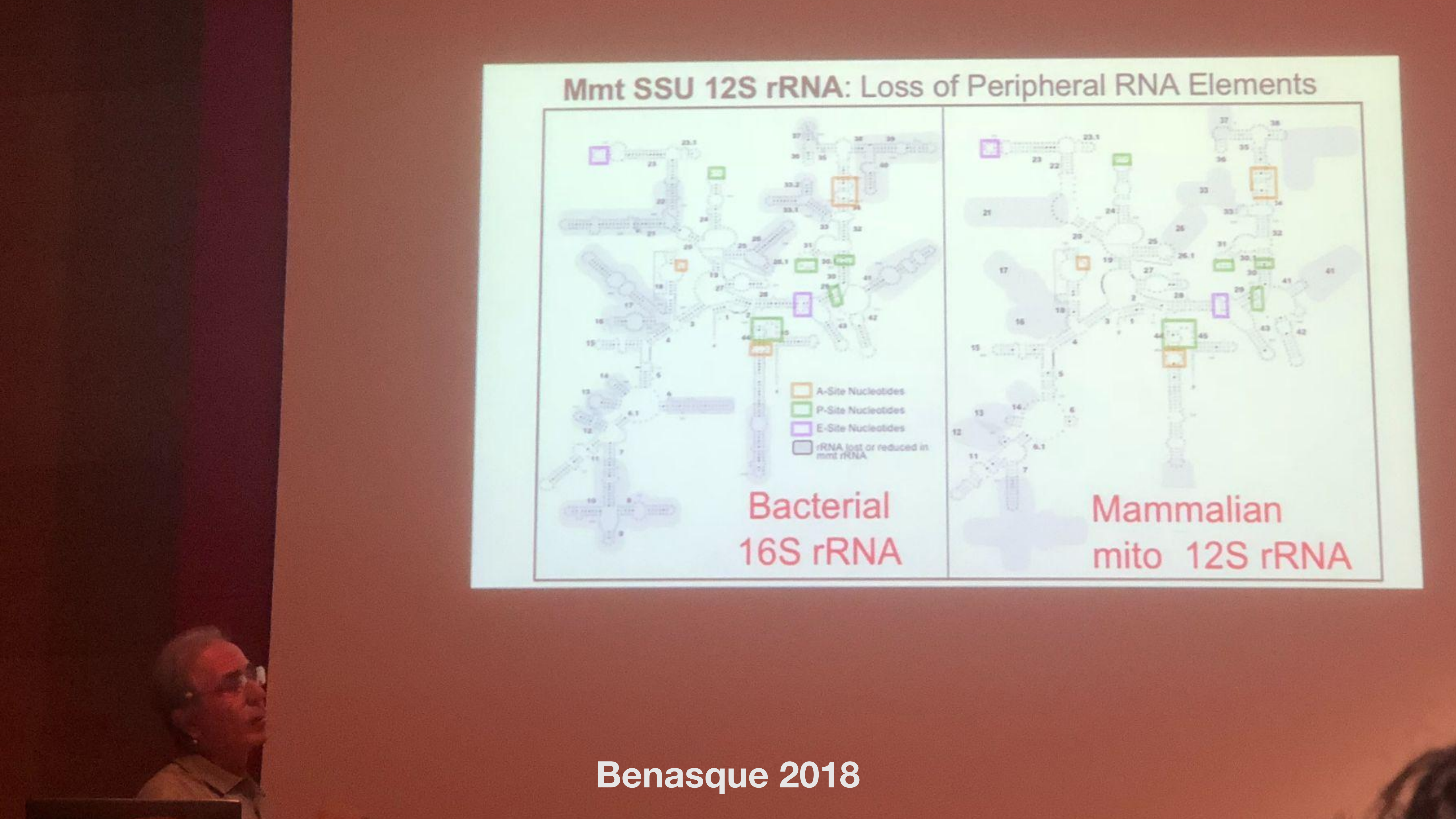
2010

https://www.bgsu.edu/news/2010/08/13-million-grant-boosts-bgsu-rna-research.html

The Secondary Structure Wall



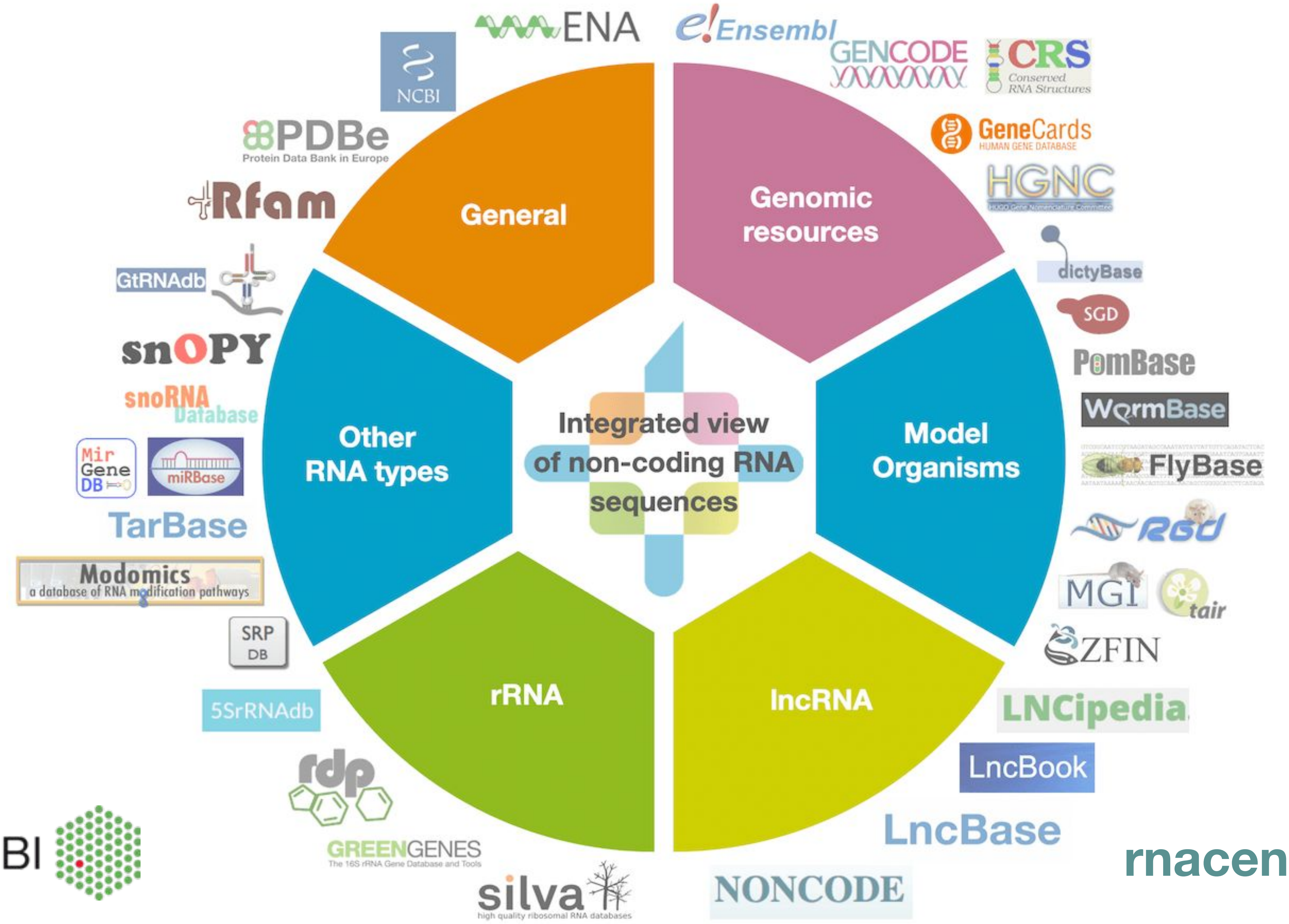
https://www.bgsu.edu/news/2010/08/13-million-grant-boosts-bgsu-rna-research.html



Mmt SSU 12S rRNA: Loss of Peripheral RNA Elements

- 🟧 A-Site Nucleotides
- 🟩 P-Site Nucleotides
- 🟪 E-Site Nucleotides
- ▨ rRNA lost or reduced in mmt rRNA

Benasque 2018



Integrated view of non-coding RNA sequences

General

Genomic resources

Model Organisms

lncRNA

rRNA

Other RNA types

NCBI

ENA

Ensembl

GENCODE

CRS Conserved RNA Structures

GeneCards HUMAN GENE DATABASE

HGNC HUGO Gene Nomenclature Committee

dictyBase

SGD

PomBase

WormBase

FlyBase

RGD

MGI

tair

ZFIN

LNCipedia

LncBook

LncBase

NONCODE

silva high quality ribosomal RNA databases

GREENGENES The 16S rRNA Gene Database and Tools

rdp

5SrRNAdb

SRP DB

Modomics a database of RNA modification pathways

TarBase

MirGeneDB

miRBase

snoRNA Database

snOPY

GtRNAdb

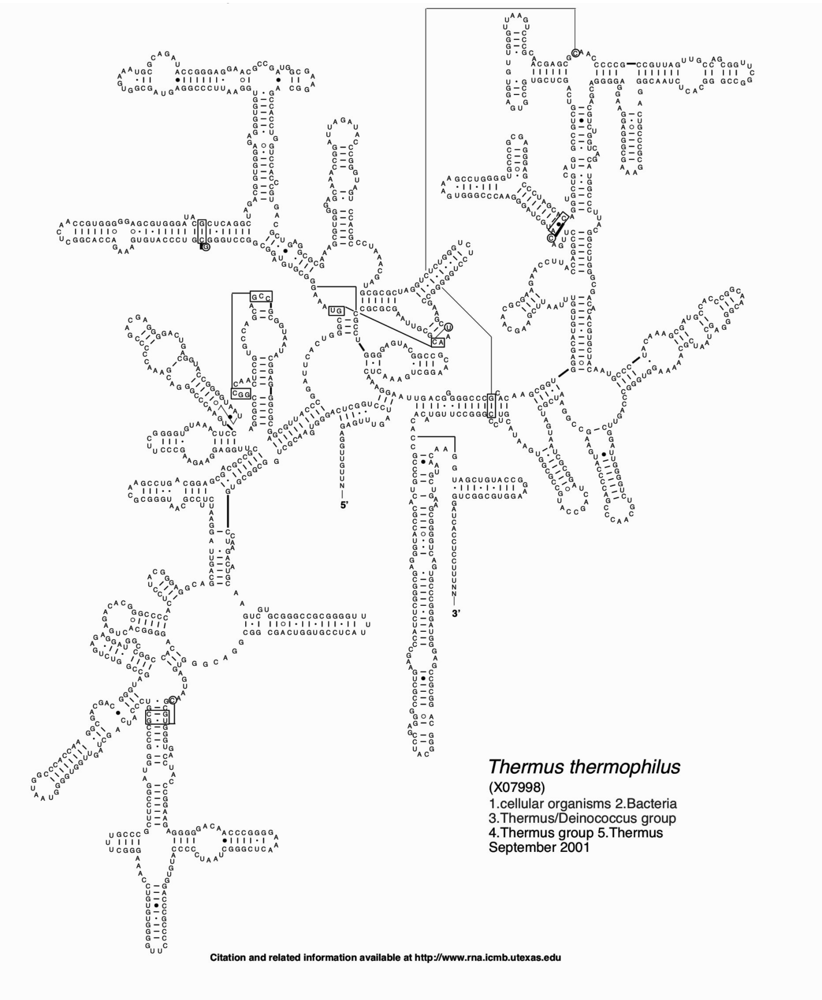
Rfam

PDBe Protein Data Bank in Europe

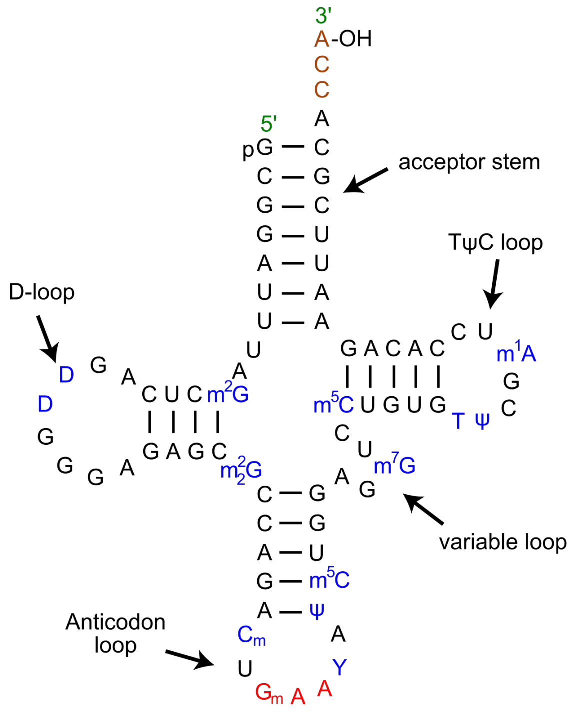
EMBL-EBI

rnacentral.org

Some RNAs need to be visualised in standard orientations

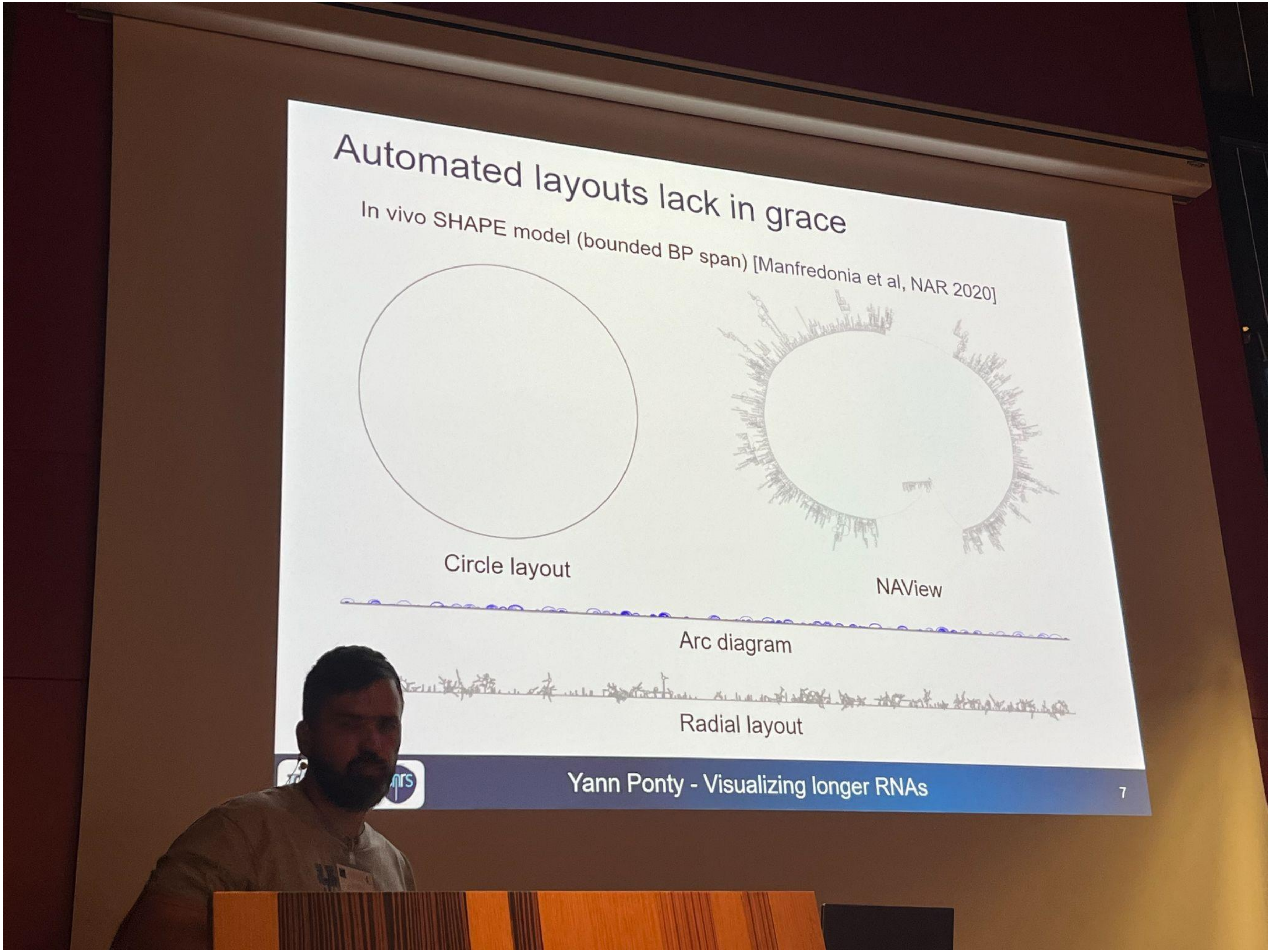


Ribosomal RNA (rRNA)



Transfer RNA (tRNA)

The majority of RNAcentral sequences are rRNAs and tRNAs



Automated layouts lack in grace

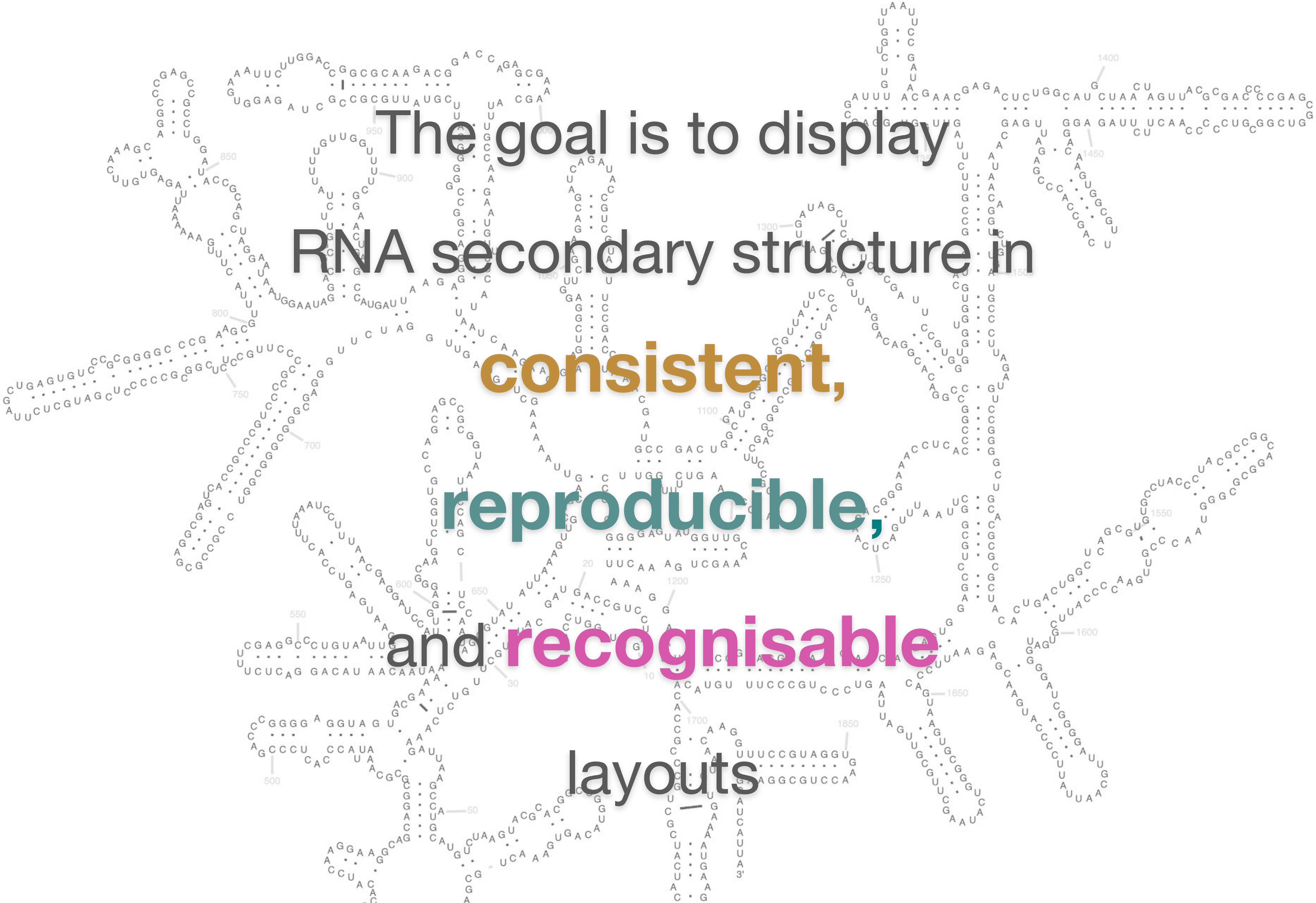
In vivo SHAPE model (bounded BP span) [Manfredonia et al, NAR 2020]

Circle layout

NAView

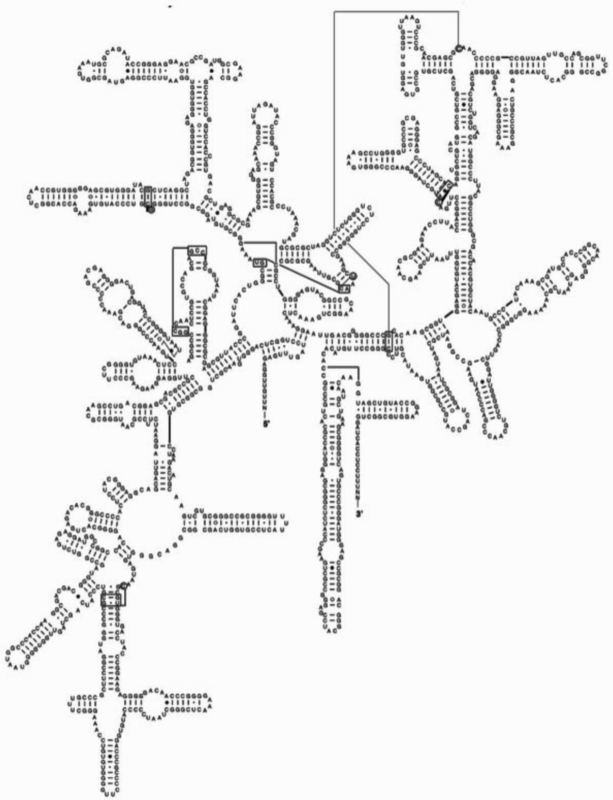
Arc diagram

Radial layout

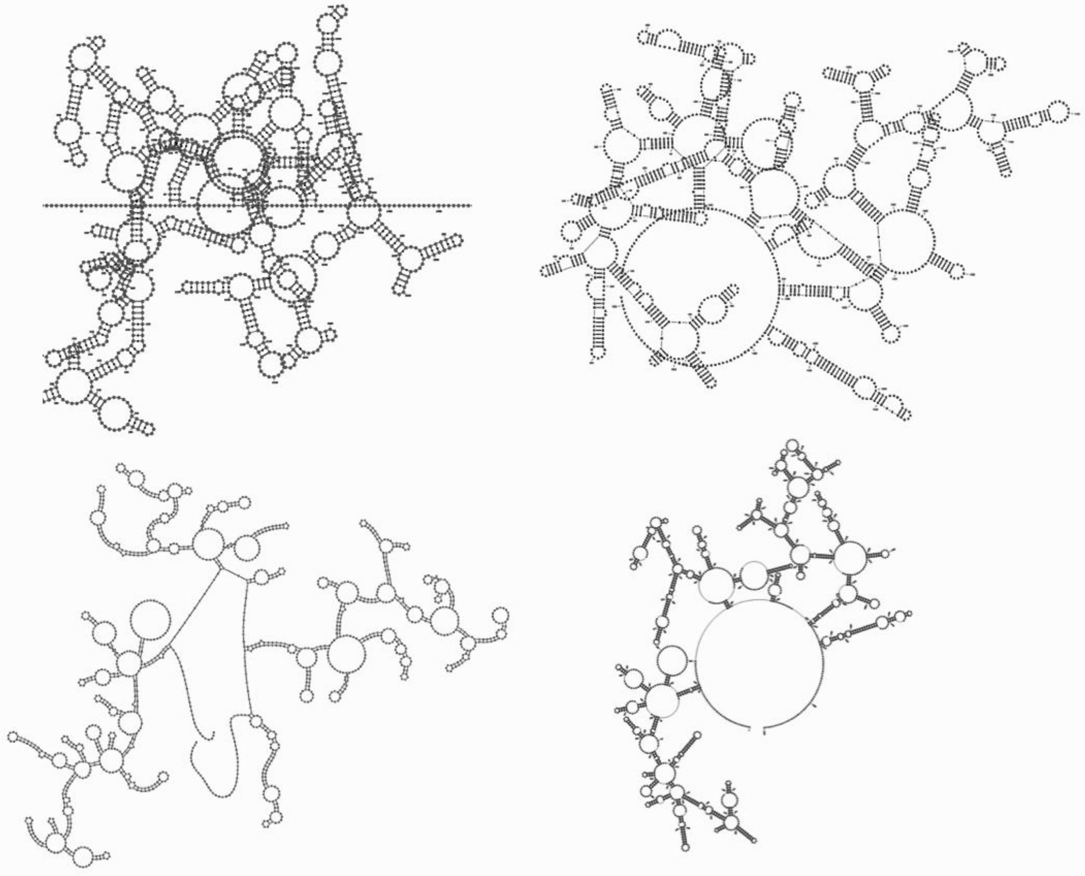


The goal is to display
RNA secondary structure in
consistent,
reproducible,
and **recognisable**
layouts

But automatically generated diagrams are not always useful

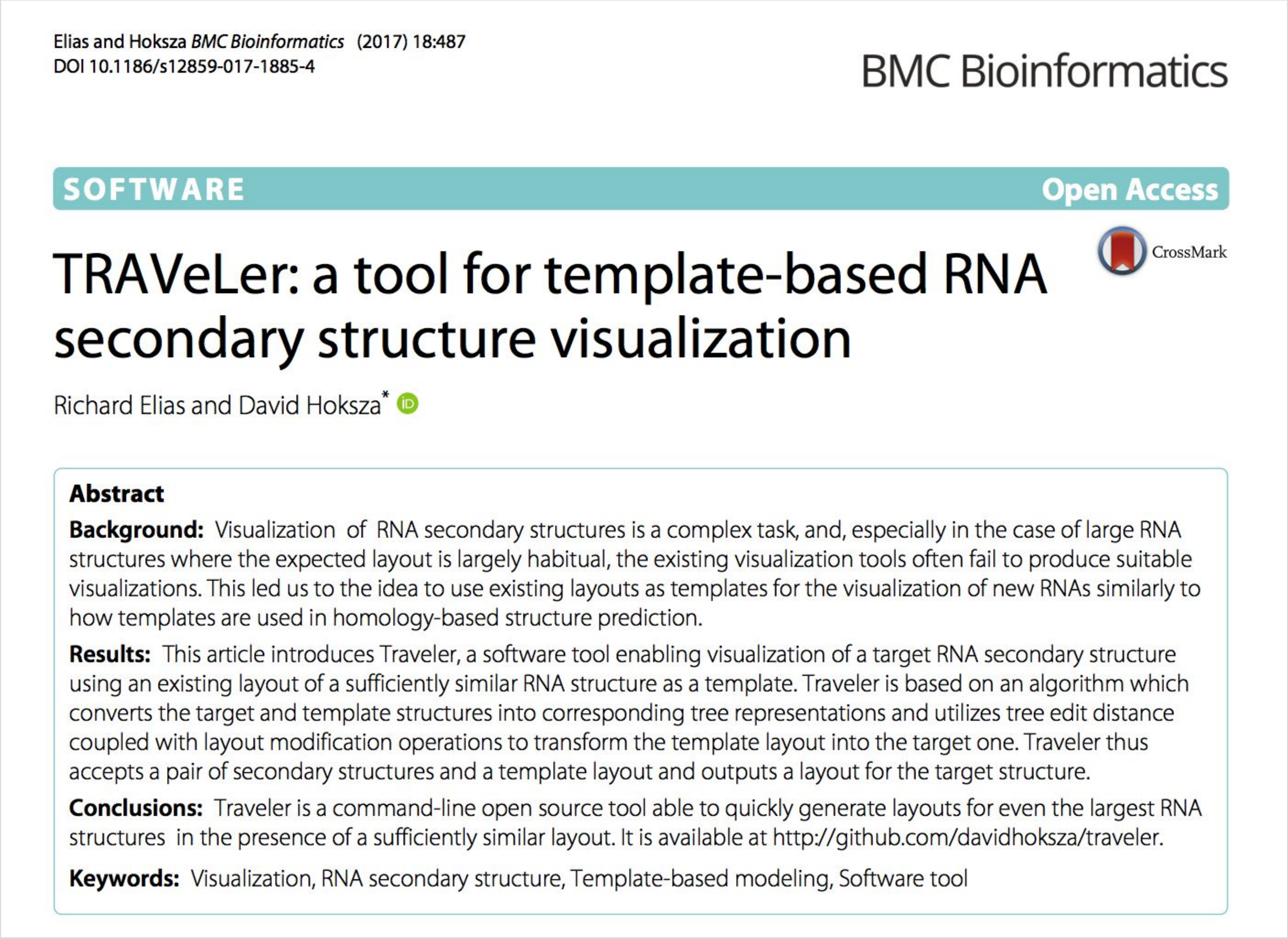


Manually curated layout



Other RNA 2D visualisation software

Traveler software



Elias and Hoksza *BMC Bioinformatics* (2017) 18:487
DOI 10.1186/s12859-017-1885-4

BMC Bioinformatics

SOFTWARE Open Access

CrossMark

TRAVeLer: a tool for template-based RNA secondary structure visualization

Richard Elias and David Hoksza*

Abstract

Background: Visualization of RNA secondary structures is a complex task, and, especially in the case of large RNA structures where the expected layout is largely habitual, the existing visualization tools often fail to produce suitable visualizations. This led us to the idea to use existing layouts as templates for the visualization of new RNAs similarly to how templates are used in homology-based structure prediction.

Results: This article introduces Traveler, a software tool enabling visualization of a target RNA secondary structure using an existing layout of a sufficiently similar RNA structure as a template. Traveler is based on an algorithm which converts the target and template structures into corresponding tree representations and utilizes tree edit distance coupled with layout modification operations to transform the template layout into the target one. Traveler thus accepts a pair of secondary structures and a template layout and outputs a layout for the target structure.

Conclusions: Traveler is a command-line open source tool able to quickly generate layouts for even the largest RNA structures in the presence of a sufficiently similar layout. It is available at http://github.com/davidhoksza/traveler.

Keywords: Visualization, RNA secondary structure, Template-based modeling, Software tool

David Hoksza

- Traveler visualises RNA structure for a given sequence using templates
- Is able to reposition the nucleotides to accommodate insertions

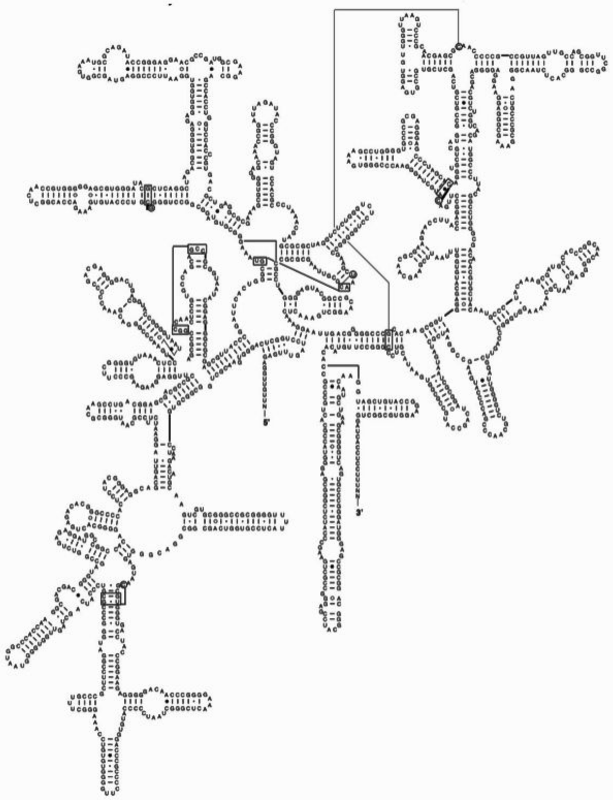
https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-017-1885-4

R2DT templates

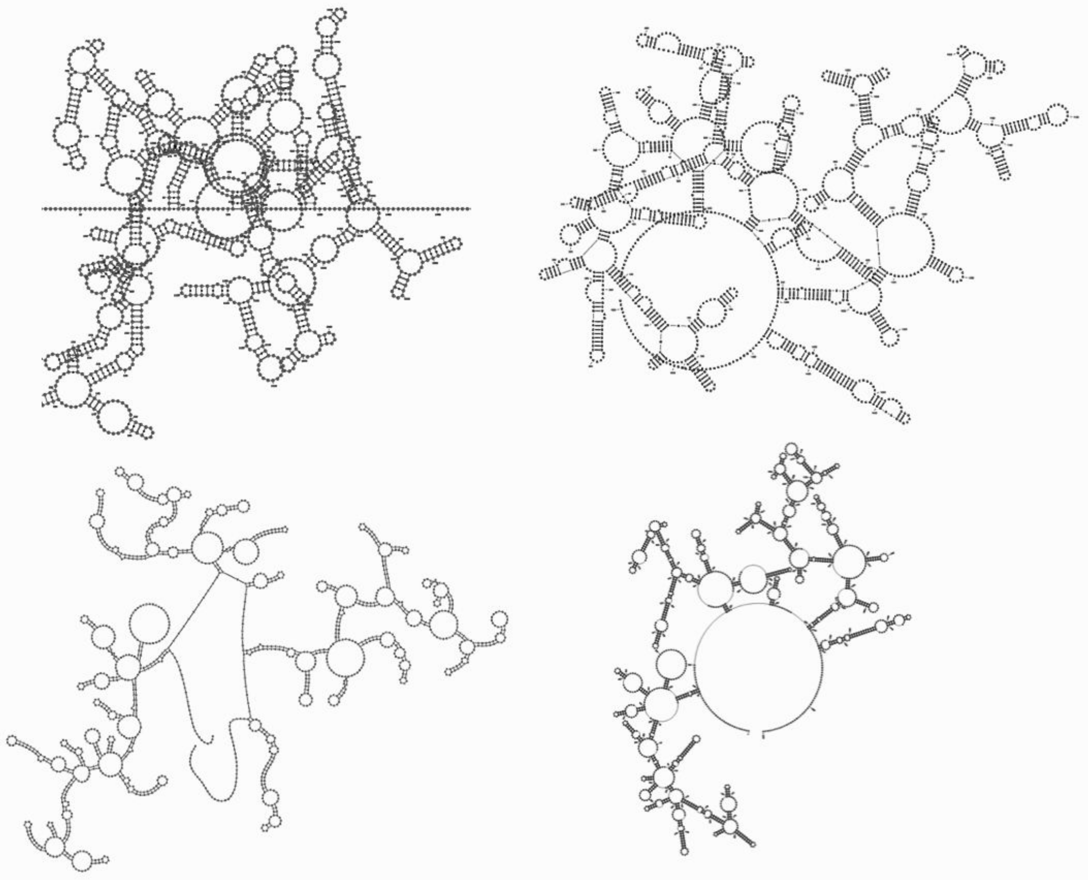
- **A template must have:**
    - **Sequence**
    - **Secondary structure**
    - **(x, y) coordinates for each nucleotide**
- Traveler converts the target and template structures into corresponding tree representations and uses tree edit distance coupled with layout modification operations to transform the template layout into the target one
- Traveler can also use an Infernal alignment to map the layouts

https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-017-1885-4

With R2DT we are able to go from this 👇

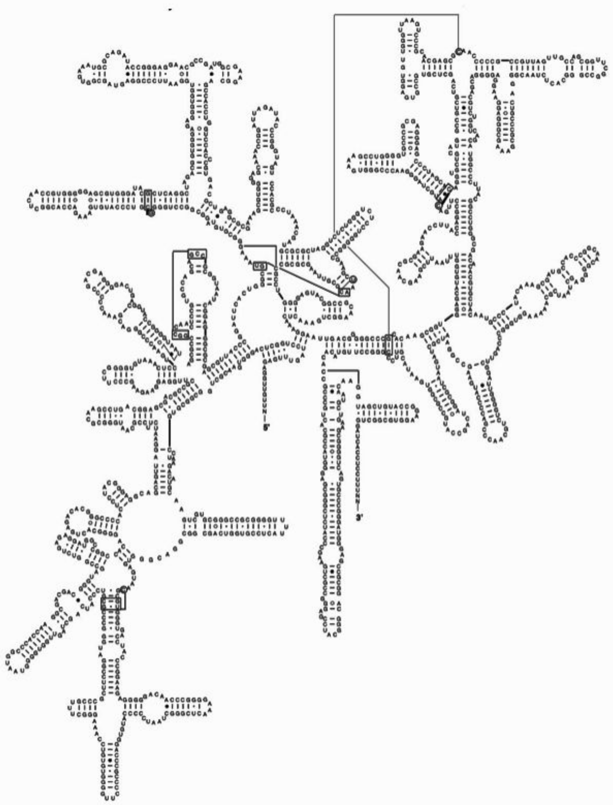


Manually curated layout

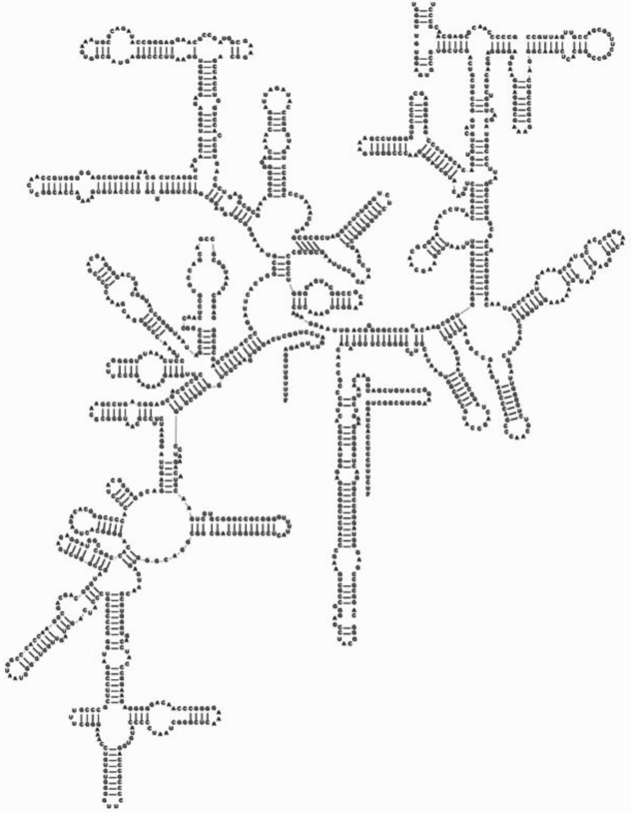


Other RNA 2D visualisation software

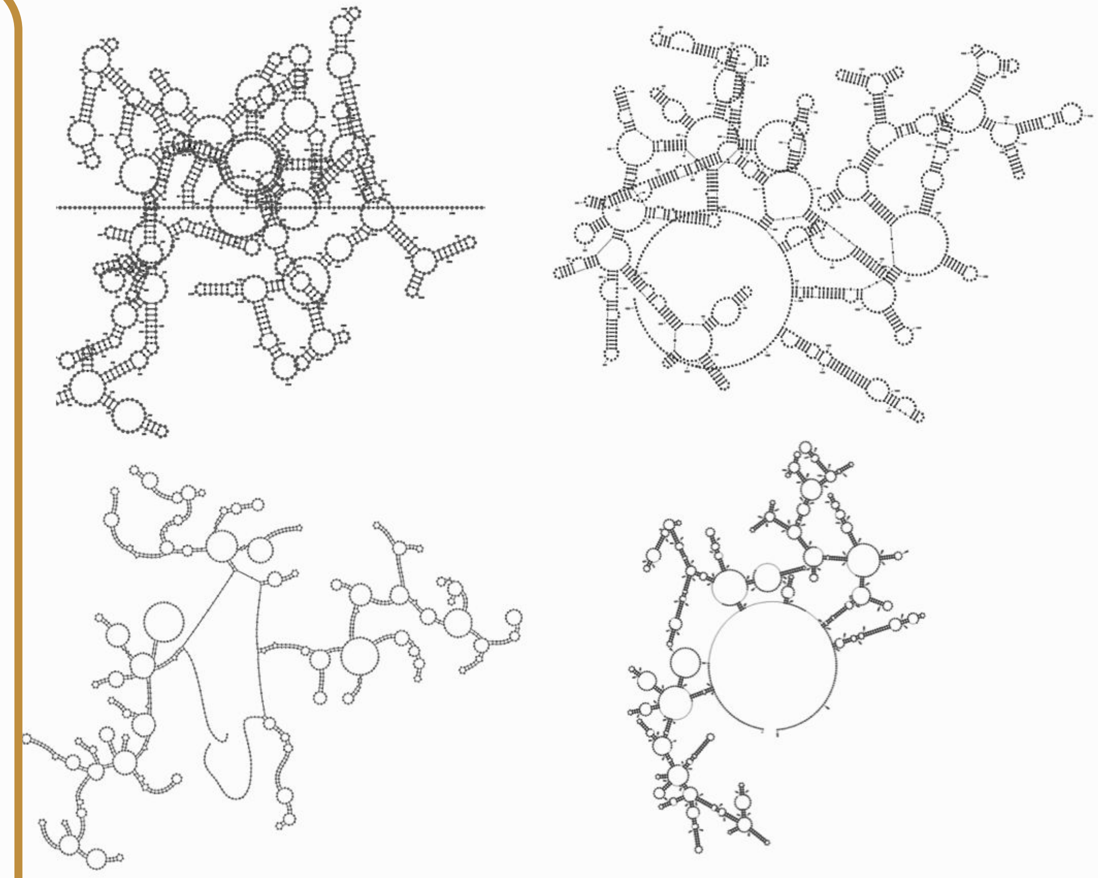
To this 👇



Manually curated layout



R2DT



Other software

R2DT = RNA 2D Templates

This is where R2DT worked for the very first time in June 2018

RNA Society, Berkeley 2018

R2DT library includes >3,600 RNA 2D templates

RNA type	**Template source**	**Number of templates**	**Manually curated?**
SSU rRNA	CRW (covariation-based) RiboVision (3D-based)	654 8	Yes Yes
LSU rRNA	RiboVision (3D-based)	21	Yes
5S rRNA	CRW	200	Yes
tRNA	GtRNAdb	74	Yes
RNAse P	RNAse P Database	17 2 (3D-based)	Yes Yes
Small RNAs	Rfam	2,671	**No**

R2DT release 1.0

There are thousands of RNA families and each needs a template.

How do we select which template to use? And do it fast?

Ribovore

Eric Nawrocki

- For each template, build an Infernal **covariance model** using the template sequence and secondary structure
- Rapidly select best-scoring template using Ribovore

SOFTWARE

Open Access

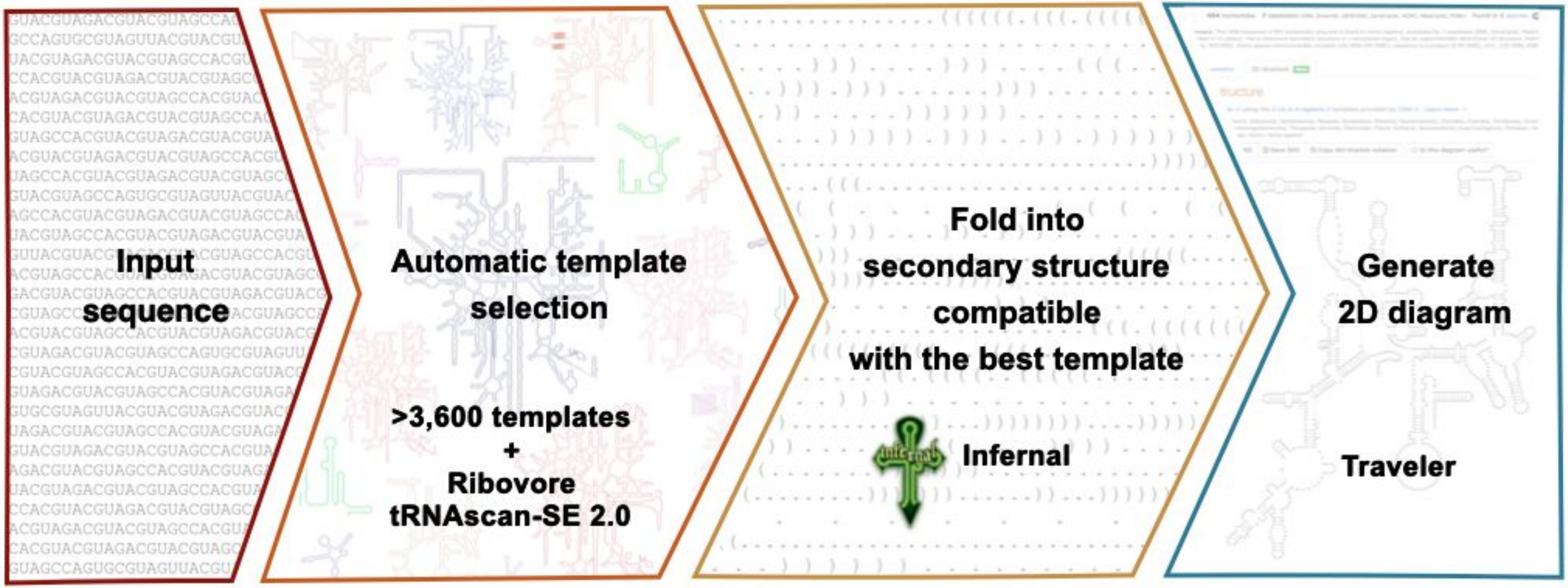
Check for updates

Ribovore: ribosomal RNA sequence analysis for GenBank submissions and database curation

Alejandro A. Schäffer[1,2], Richard McVeigh[2], Barbara Robbertse[2], Conrad L. Schoch[2], Anjanette Johnston[2], Beverly A. Underwood[2], Ilene Karsch-Mizrachi[2] and Eric P. Nawrocki[2*]

https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-021-04316-z

R2DT uses Ribovore, tRNAscan-SE, Infernal, and Traveler



Input sequence

Automatic template selection

>3,600 templates + Ribovore tRNAscan-SE 2.0

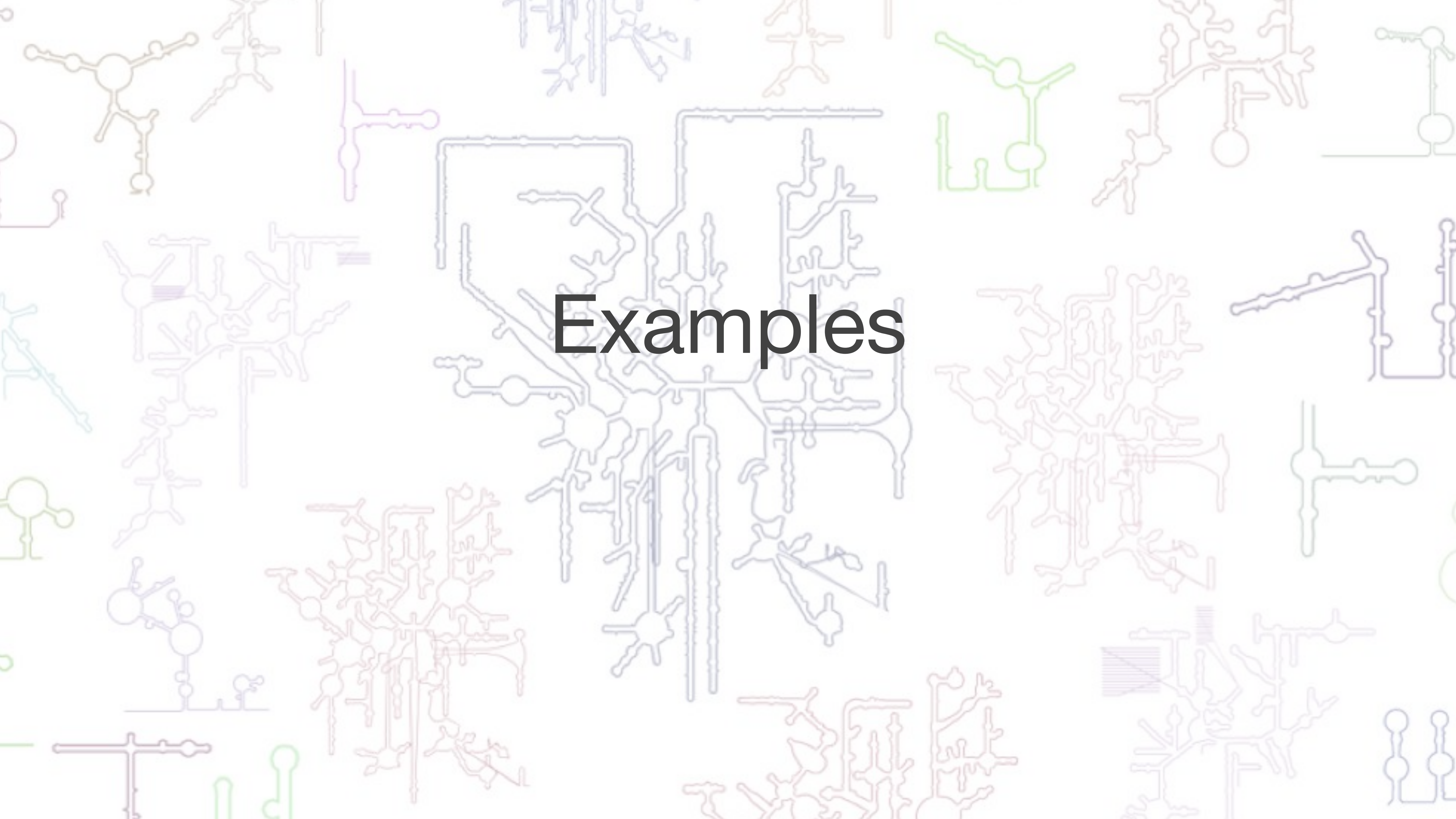
Fold into secondary structure compatible with the best template

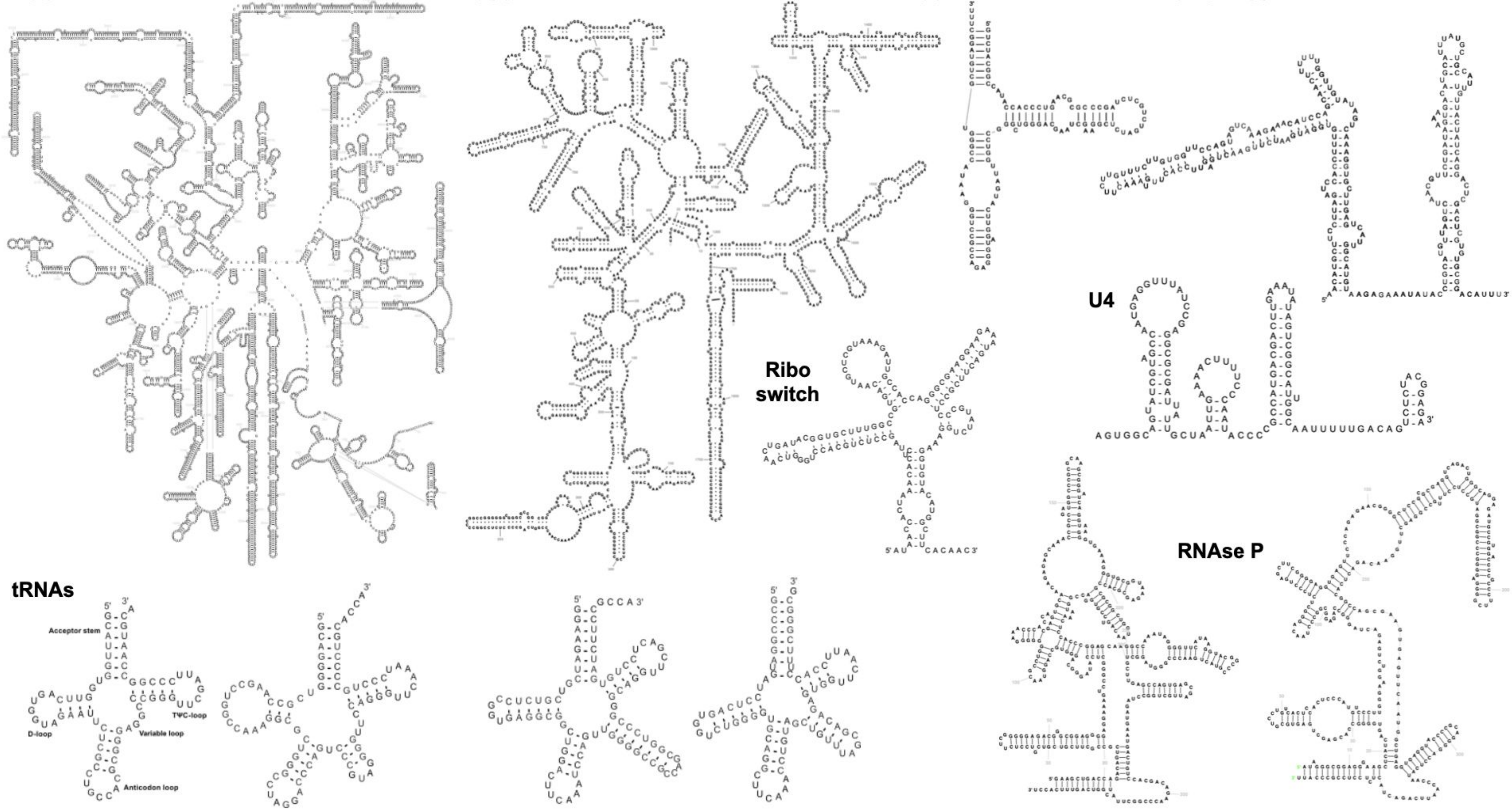
Infernal

Generate 2D diagram

Traveler

Examples





LSU rRNA

SSU rRNA

5S rRNA

SNORA53

Ribo switch

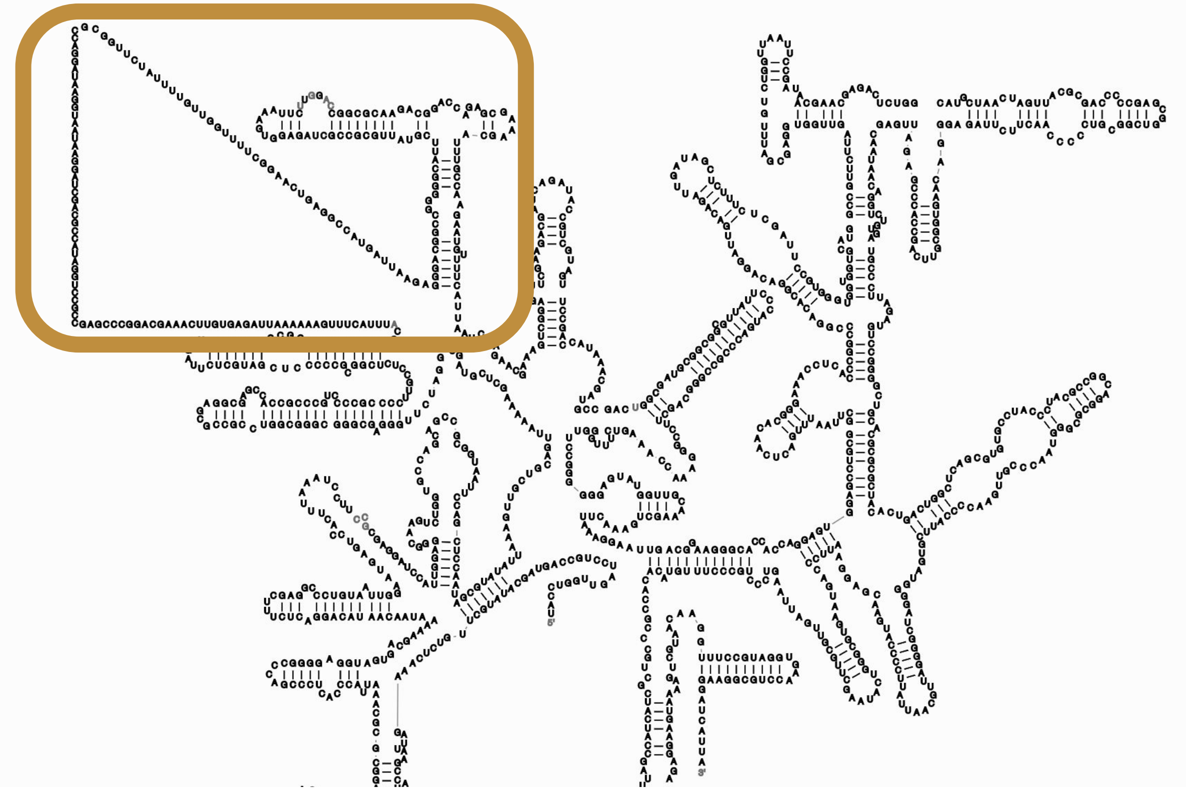
U4

RNAse P

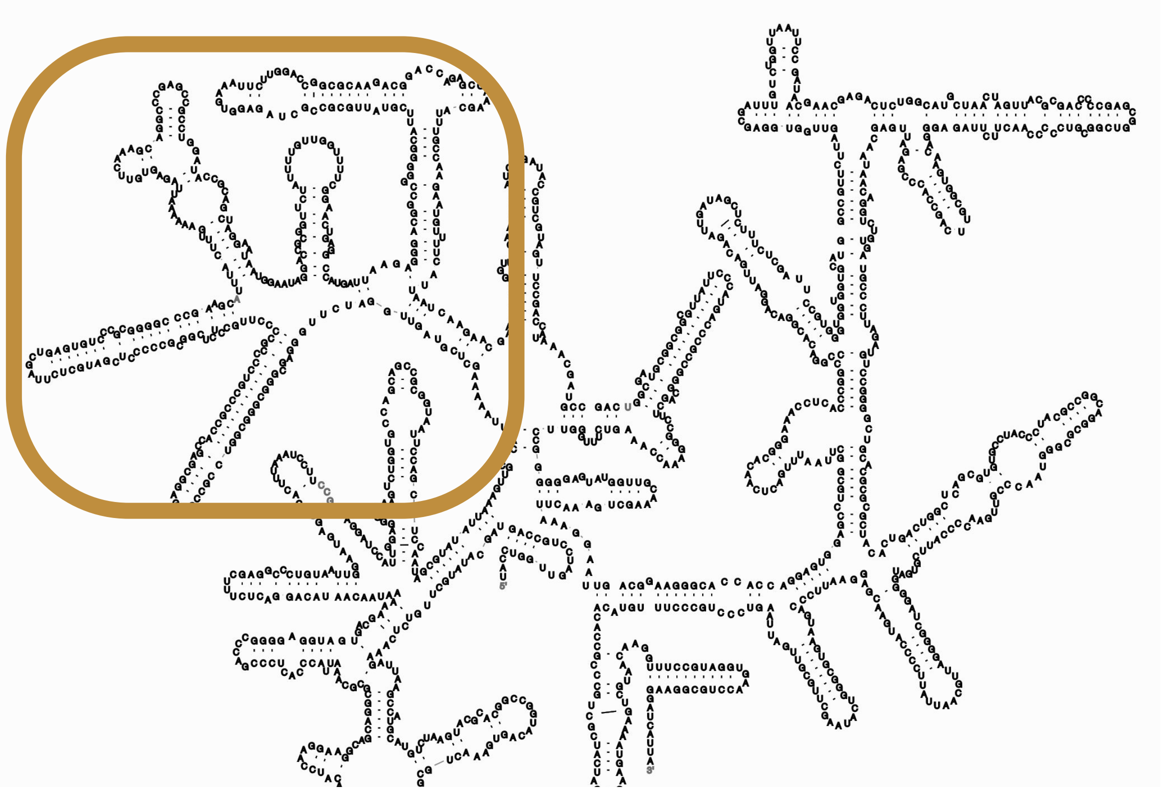
tRNAs

3D structure based templates from COOL

Anton S. Petrov



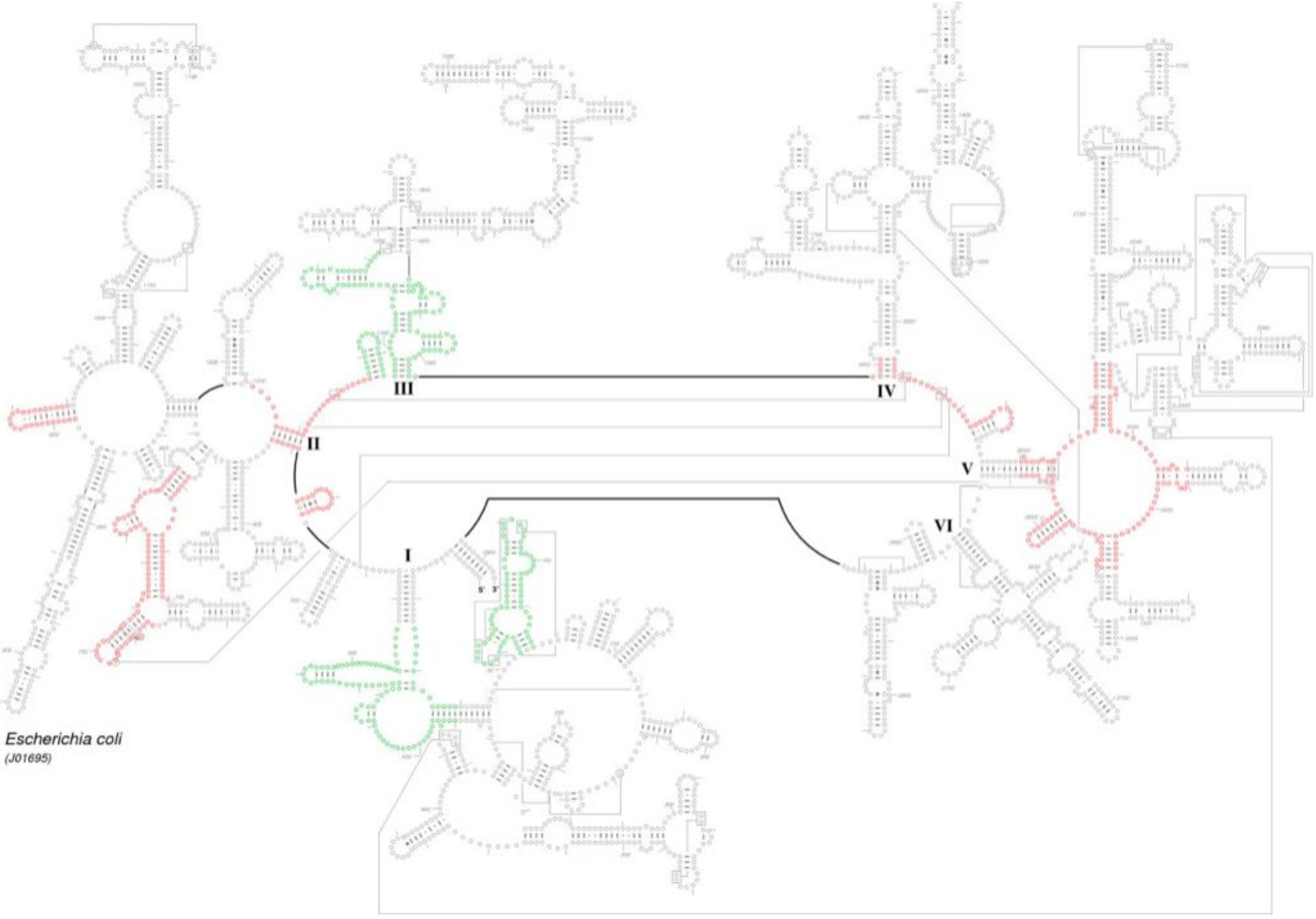
CRW covariation-based template

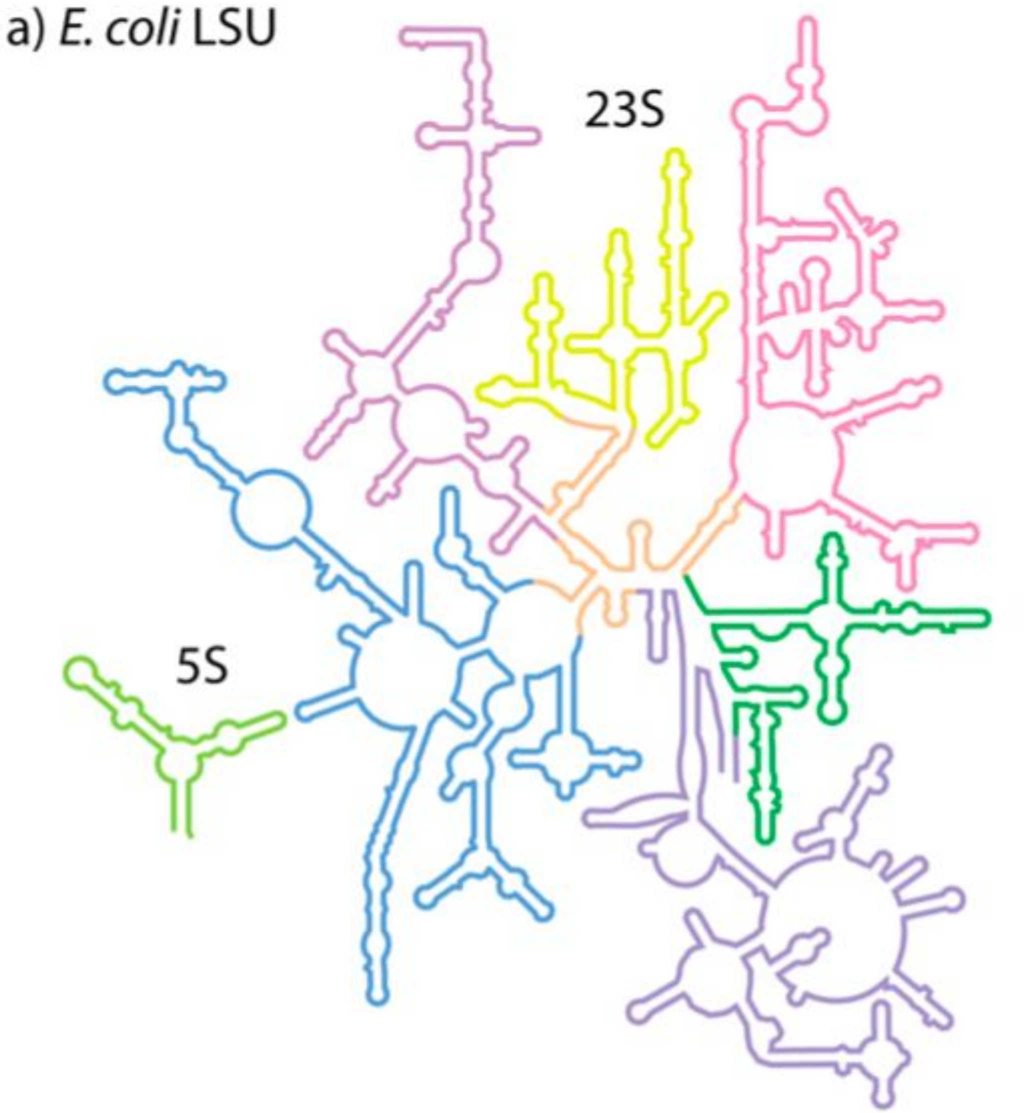


3D-based template

R2DT uses single page LSU layouts

Anton S. Petrov

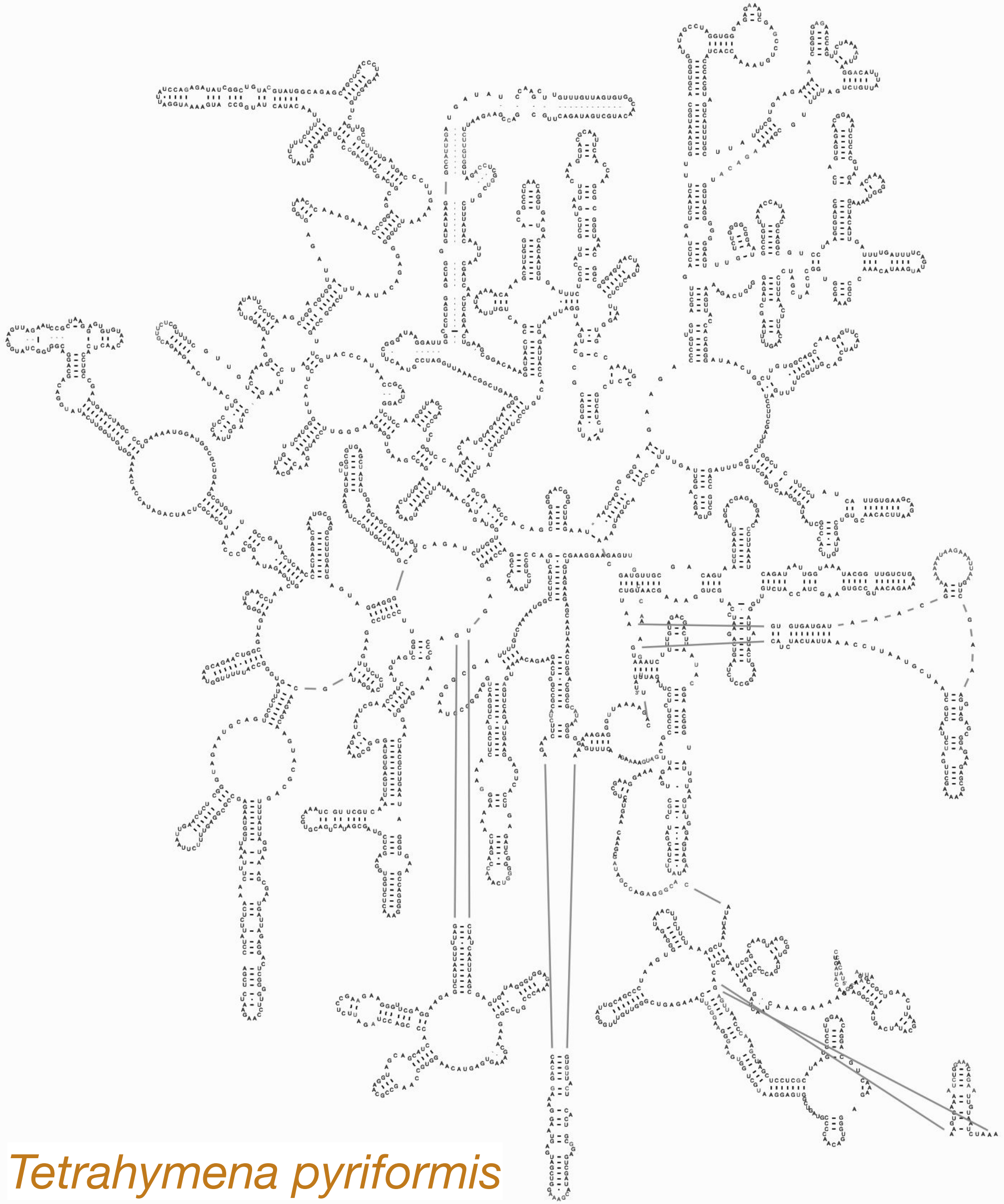




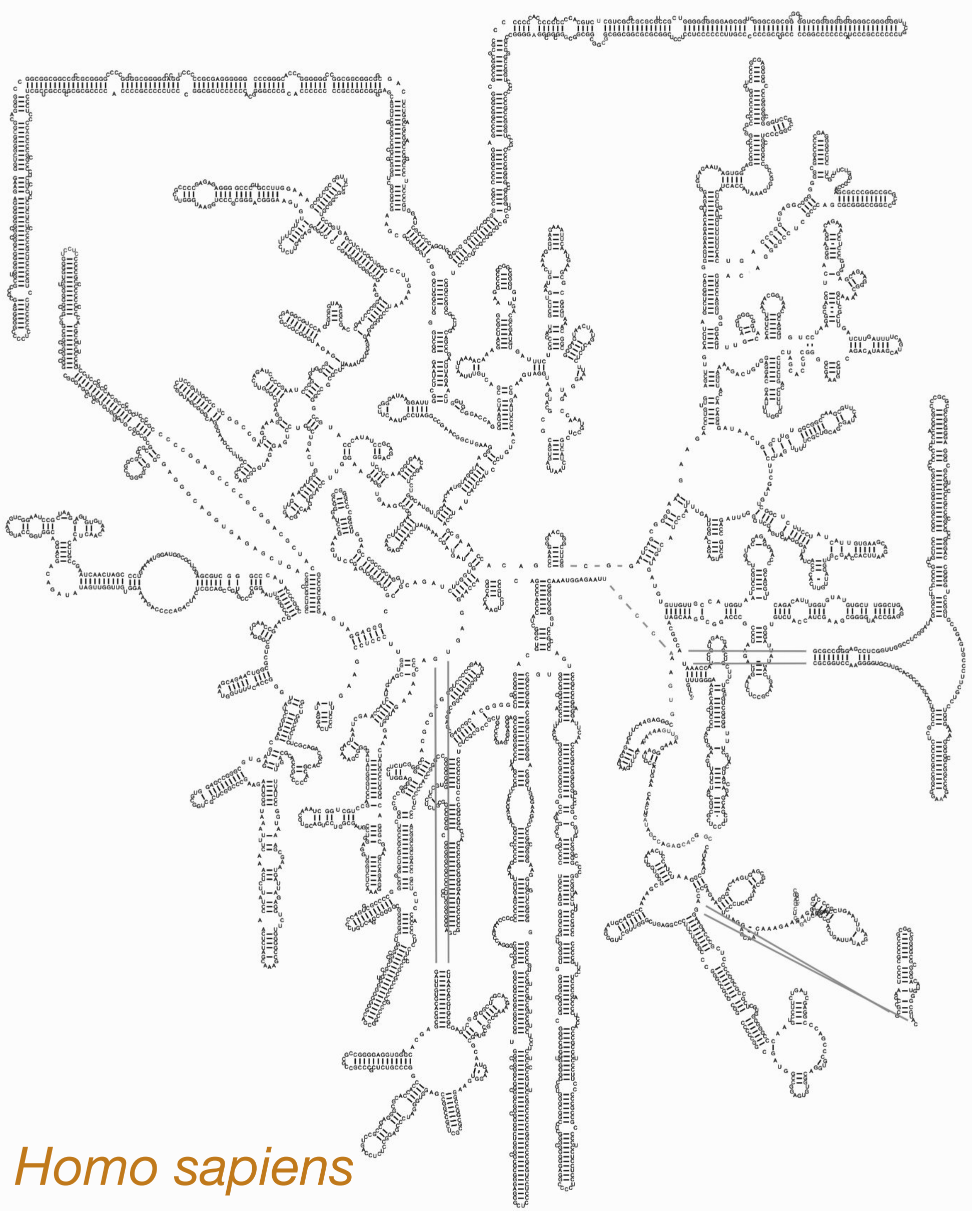
https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-11-485/figures/5

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0088222

LSU rRNA



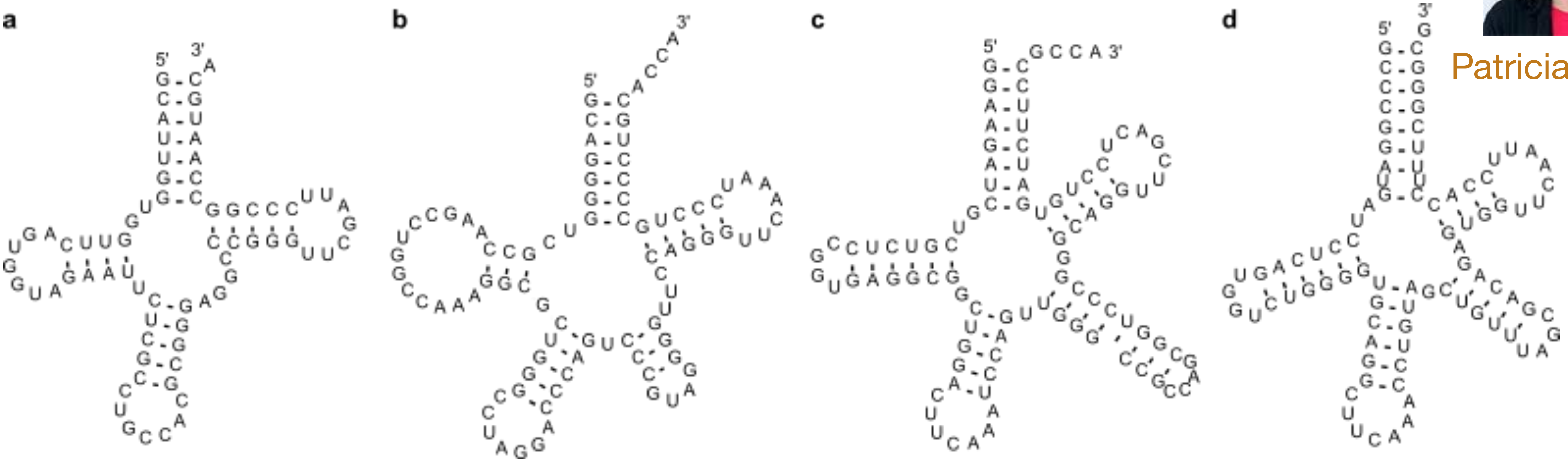
Tetrahymena pyriformis



Homo sapiens

tRNA templates

Patricia Chan



- 74 **isotype-specific templates** for Bacteria, Eukaryotes, and Archaea
- Generic Type I and Type II templates for pseudogenes and organellar tRNAs

For the rest of RNA families R2DT uses Rfam consensus secondary structures generated with R2R

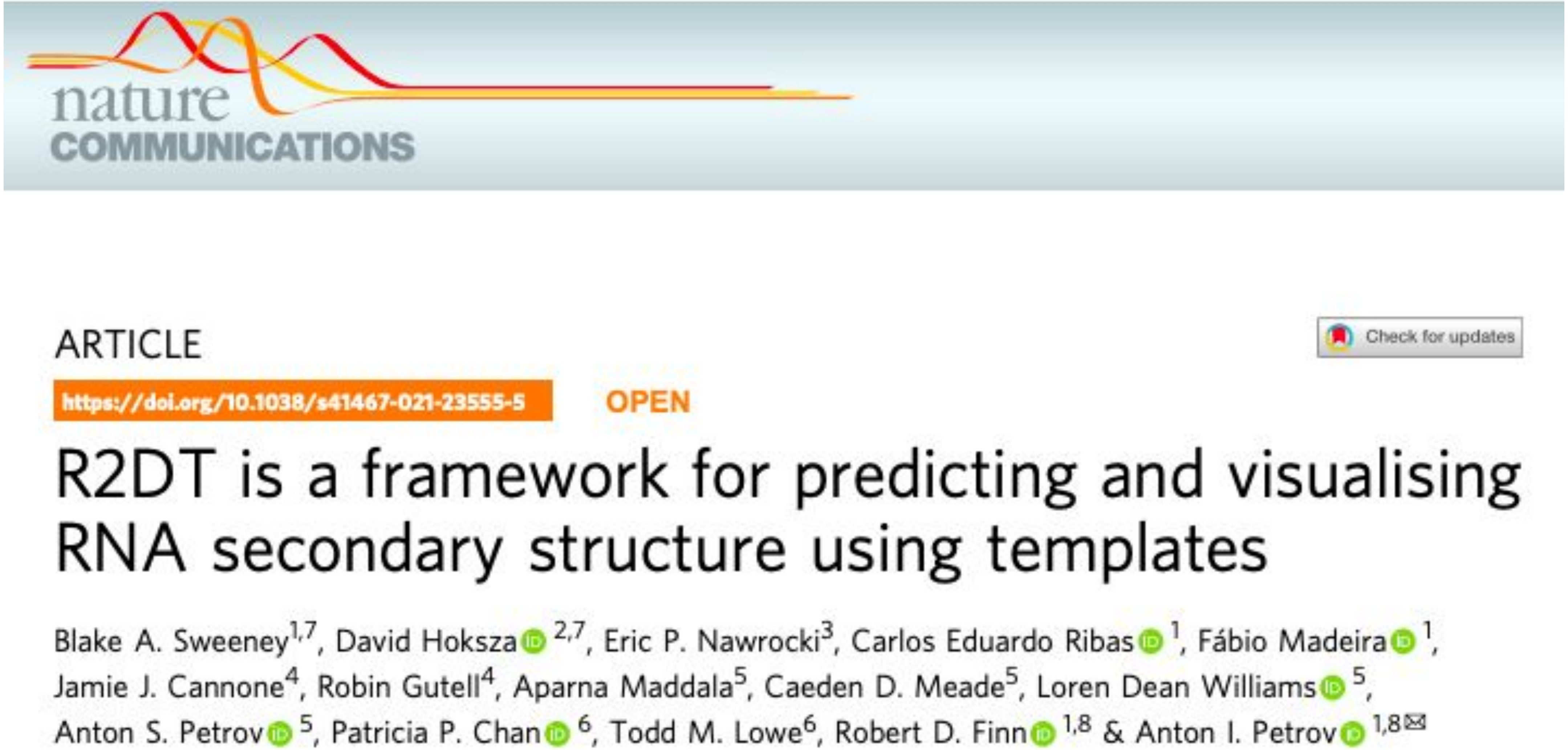
Thanks to Zasha Weinberg!

As with any prediction method, R2DT results need to be used with caution

https://unsplash.com/photos/IrjNgQ2kVcg

Colour coding the alignment of the sequence to the template

- **Insertions** are shown in red
- **Mutations** are shown in magenta
- Nucleotides that required **repositioning** are shown in blue
- Nucleotides that are **identical** to the template are shown in black



nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-021-23555-5 OPEN

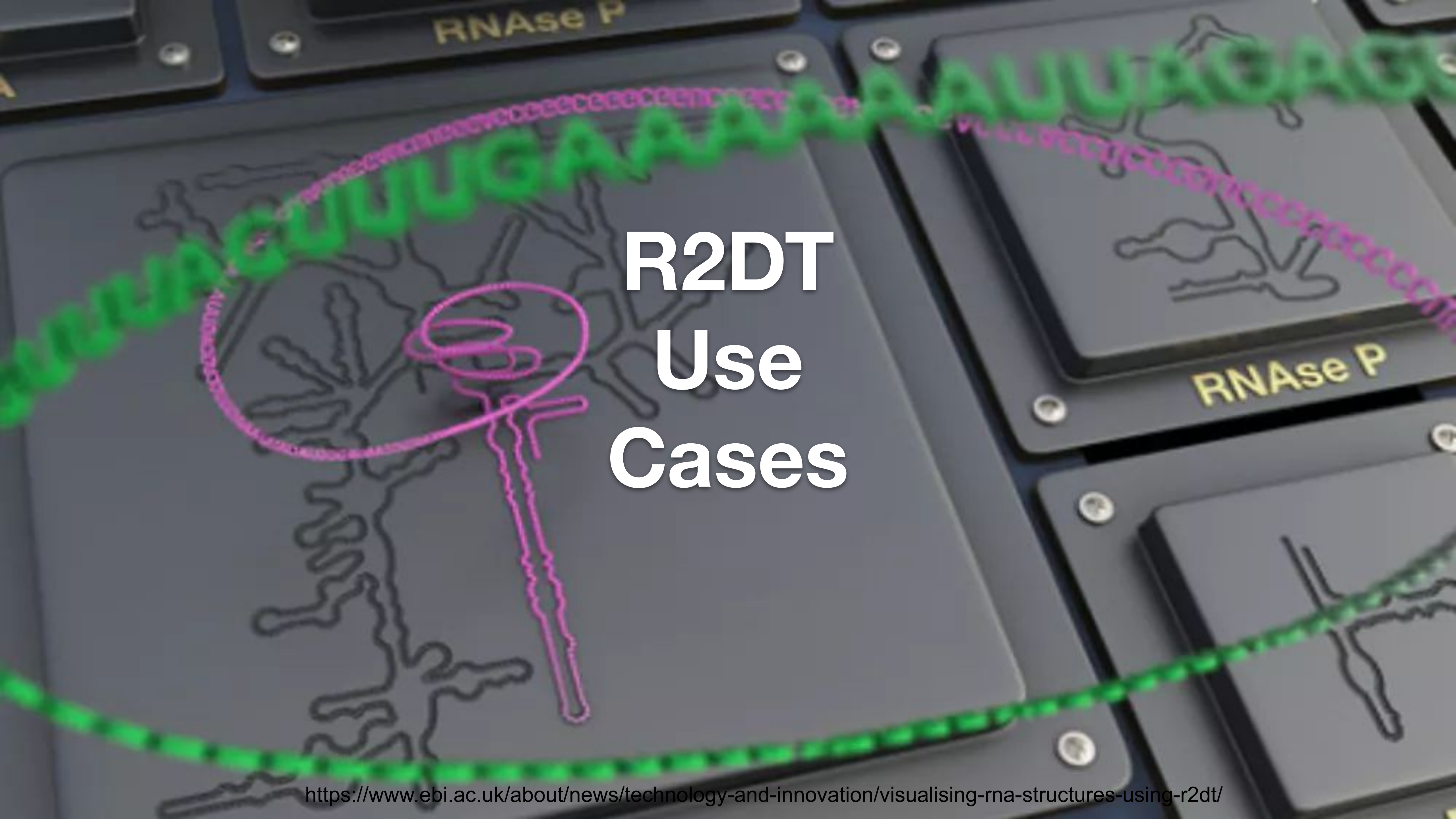
Check for updates

R2DT is a framework for predicting and visualising RNA secondary structure using templates

Blake A. Sweeney[1,7], David Hoksza[2,7], Eric P. Nawrocki[3], Carlos Eduardo Ribas[1], Fábio Madeira[1], Jamie J. Cannone[4], Robin Gutell[4], Aparna Maddala[5], Caeden D. Meade[5], Loren Dean Williams[5], Anton S. Petrov[5], Patricia P. Chan[6], Todd M. Lowe[6], Robert D. Finn[1,8] & Anton I. Petrov[1,8]✉

https://www.nature.com/articles/s41467-021-23555-5

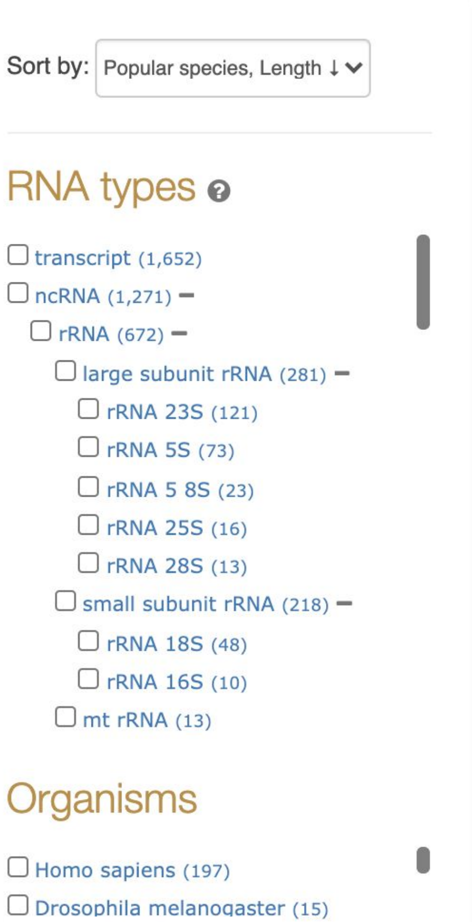
https://github.com/rnacentral/r2dt



R2DT
Use
Cases

https://www.ebi.ac.uk/about/news/technology-and-innovation/visualising-rna-structures-using-r2dt/

R2DT was applied to >20 million RNAcentral sequences



Sort by: Popular species, Length ↓

RNA types

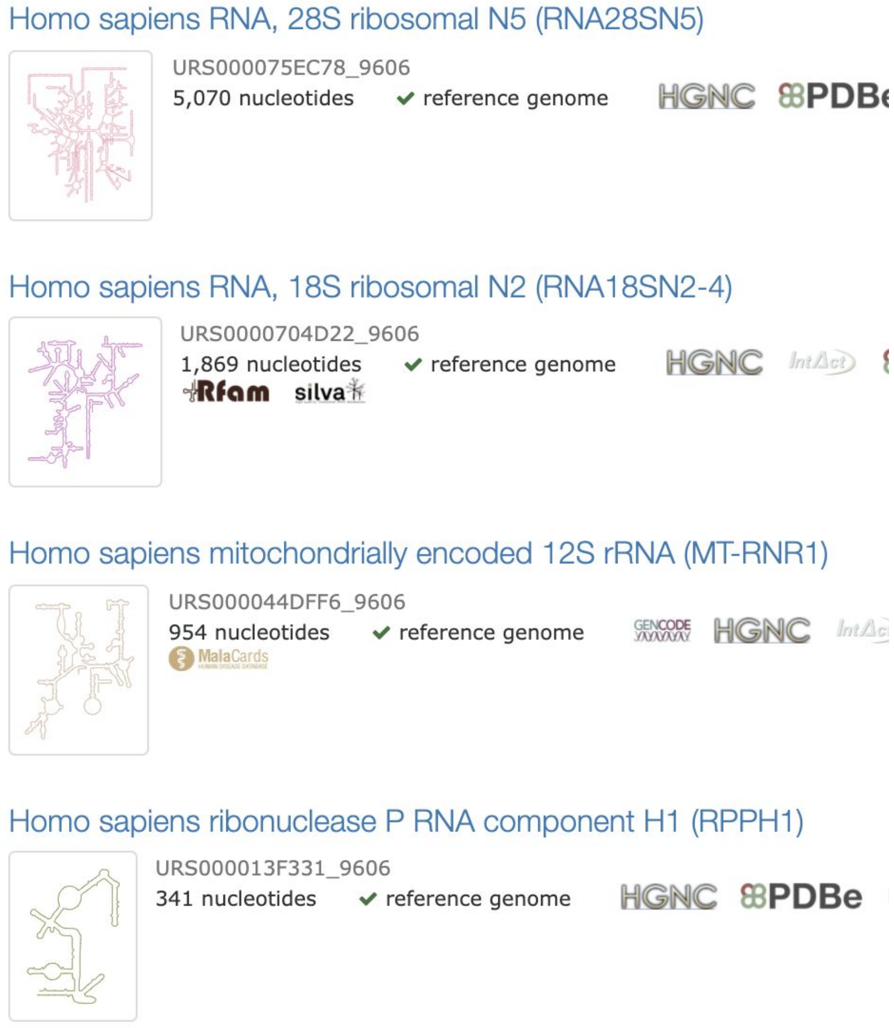
- ☐ transcript (1,652)
- ☐ ncRNA (1,271)
  - ☐ rRNA (672)
    - ☐ large subunit rRNA (281)
      - ☐ rRNA 23S (121)
      - ☐ rRNA 5S (73)
      - ☐ rRNA 5 8S (23)
      - ☐ rRNA 25S (16)
      - ☐ rRNA 28S (13)
    - ☐ small subunit rRNA (218)
      - ☐ rRNA 18S (48)
      - ☐ rRNA 16S (10)
    - ☐ mt rRNA (13)

Organisms

- ☐ Homo sapiens (197)
- ☐ Drosophila melanogaster (15)

mbe (6)

6)



Homo sapiens RNA, 28S ribosomal N5 (RNA28SN5)

URS000075EC78_9606

5,070 nucleotides ✓ reference genome

Homo sapiens RNA, 18S ribosomal N2 (RNA18SN2-4)

URS0000704D22_9606

1,869 nucleotides ✓ reference genome

Homo sapiens mitochondrially encoded 12S rRNA (MT-RNR1)

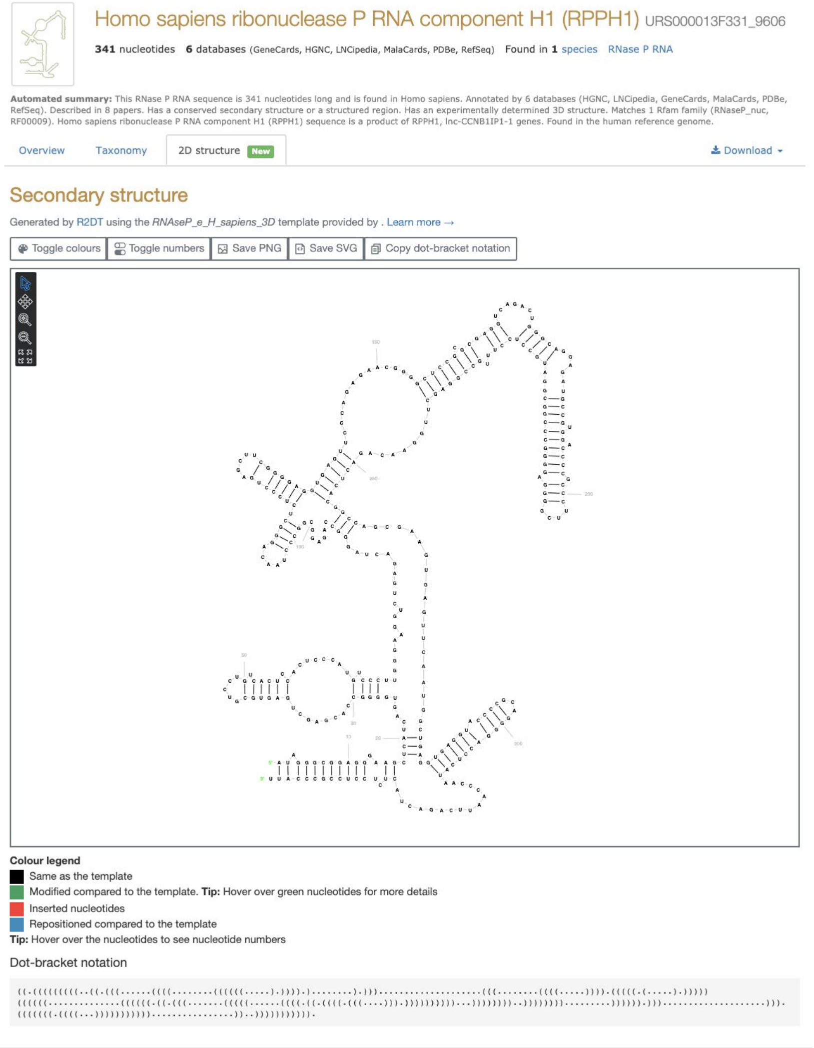
URS000044DFF6_9606

954 nucleotides ✓ reference genome

Homo sapiens ribonuclease P RNA component H1 (RPPH1)

URS000013F331_9606

341 nucleotides ✓ reference genome



Homo sapiens ribonuclease P RNA component H1 (RPPH1) URS000013F331_9606

341 nucleotides **6** databases (GeneCards, HGNC, LNCipedia, MalaCards, PDBe, RefSeq) Found in **1** species RNase P RNA

Automated summary: This RNase P RNA sequence is 341 nucleotides long and is found in Homo sapiens. Annotated by 6 databases (HGNC, LNCipedia, GeneCards, MalaCards, PDBe, RefSeq). Described in 8 papers. Has a conserved secondary structure or a structured region. Has an experimentally determined 3D structure. Matches 1 Rfam family (RNaseP_nuc, RF00009). Homo sapiens ribonuclease P RNA component H1 (RPPH1) sequence is a product of RPPH1, lnc-CCNB1IP1-1 genes. Found in the human reference genome.

Secondary structure

Generated by R2DT using the *RNAseP_e_H_sapiens_3D* template provided by . Learn more →

Colour legend

- ■ Same as the template
- 🟩 Modified compared to the template. **Tip:** Hover over green nucleotides for more details
- 🟥 Inserted nucleotides
- 🟦 Repositioned compared to the template

Tip: Hover over the nucleotides to see nucleotide numbers

Dot-bracket notation

```
((.(((((((((..((.(((......((((........((((((.....).)))).)........).)))..................(((........((((.....)))).(((((.(.....).)))))
((((((..............((((((.((.(((.......(((((......((((.((.((((.(((....))).)))))))))))...))))))))..))))))))........))))))).)))..................))).
((((((.((((...)))))))))))...............))..))))))))))).
```

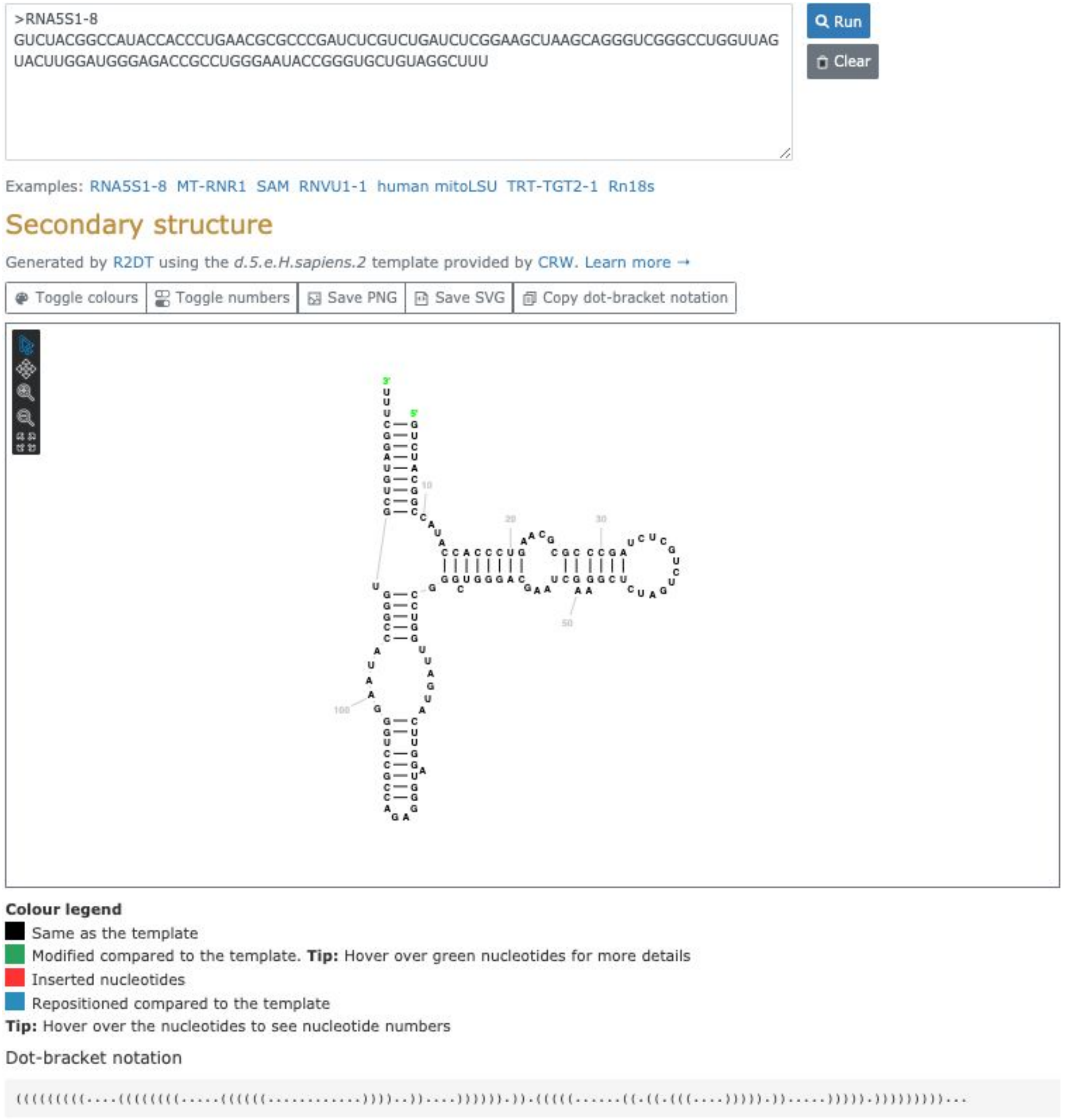
Blake Sweeney

R2DT has a web server and an API

- Submit any sequence
- Manually select a template (optional)
- SVG, PNG, dot-bracket formats
- Public API
- Embed RNA 2D diagrams into any website

rnacentral.org/r2dt

Carlos Ribas



```
>RNA5S1-8
GUCUACGGCCAUACCACCCUGAACGCGCCCGAUCUCGUCUGAUCUCGGAAGCUAAGCAGGGUCGGGCCUGGUUAG
UACUUGGAUGGGAGACCGCCUGGGAAUACCGGGUGCUGUAGGCUUU
```

Examples: RNA5S1-8 MT-RNR1 SAM RNVU1-1 human mitoLSU TRT-TGT2-1 Rn18s

Secondary structure

Generated by R2DT using the *d.5.e.H.sapiens.2* template provided by CRW. Learn more →

Colour legend

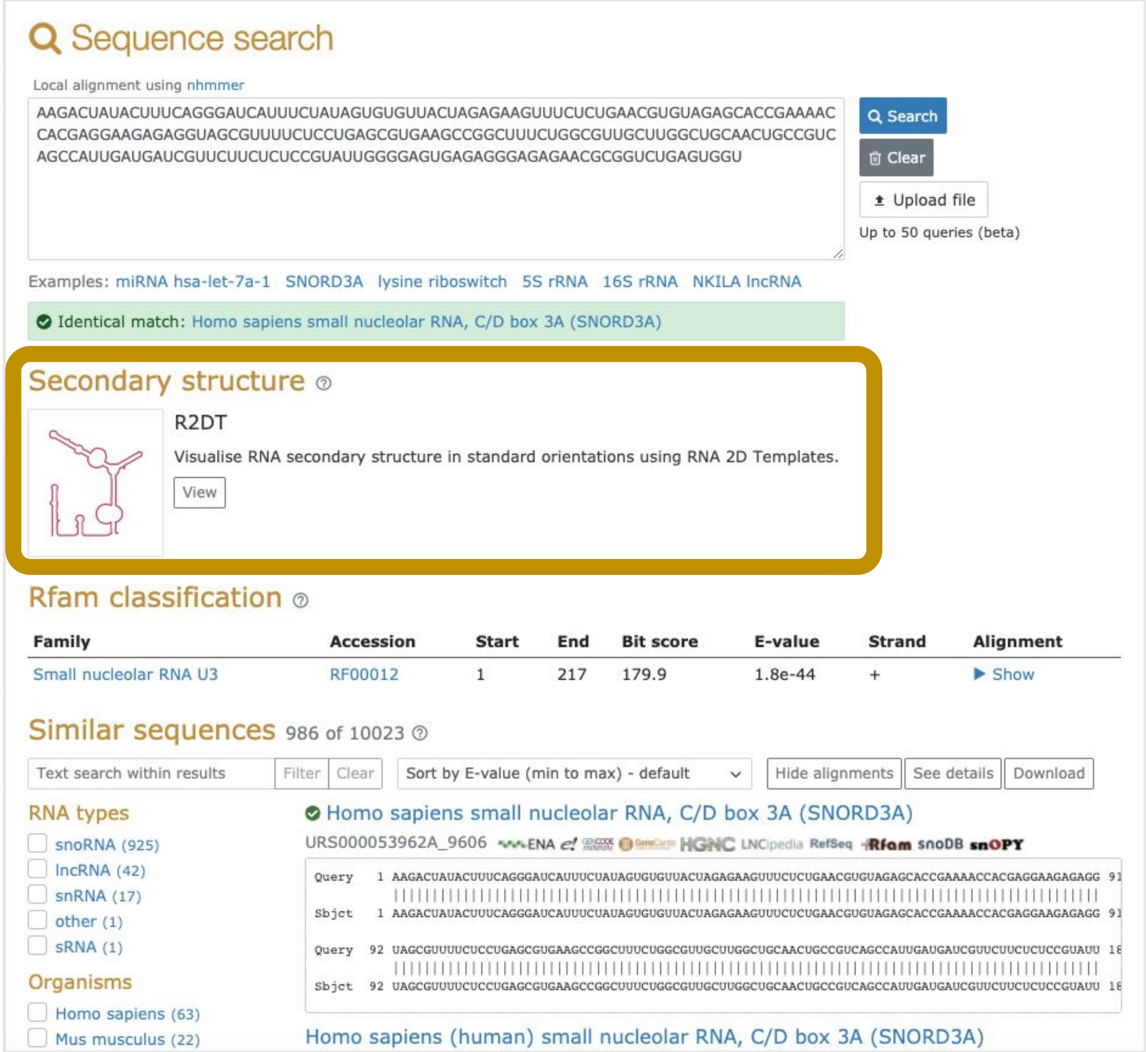
⬛ Same as the template
🟩 Modified compared to the template. **Tip:** Hover over green nucleotides for more details
🟥 Inserted nucleotides
🟦 Repositioned compared to the template

Tip: Hover over the nucleotides to see nucleotide numbers

Dot-bracket notation

```
(((((((((....((((((((.....((((((............))))..))....)))))).)).(((((......((.((.(((....))))).)).....))))).)))))))))...
```

R2DT is integrated into the RNAcentral sequence search



Sequence search

Local alignment using nhmmer

AAGACUAUACUUUCAGGGAUCAUUUCUAUAGUGUGUUACUAGAGAAGUUUCUCUGAACGUGUAGAGCACCGAAAAC
CACGAGGAAGAGAGGUAGCGUUUUCUCCUGAGCGUGAAGCCGGCUUUCUGGCGUUGCUUGGCUGCAACUGCCGUC
AGCCAUUGAUGAUCGUUCUUCUCUCCGUAUUGGGGAGUGAGAGGGAGAGAACGCGGUCUGAGUGGU

Up to 50 queries (beta)

Examples: miRNA hsa-let-7a-1 SNORD3A lysine riboswitch 5S rRNA 16S rRNA NKILA lncRNA

Identical match: Homo sapiens small nucleolar RNA, C/D box 3A (SNORD3A)

Secondary structure

R2DT

Visualise RNA secondary structure in standard orientations using RNA 2D Templates.

Rfam classification

Family	Accession	Start	End	Bit score	E-value	Strand	Alignment
Small nucleolar RNA U3	RF00012	1	217	179.9	1.8e-44	+	▶ Show

Similar sequences 986 of 10023

RNA types

- ☐ snoRNA (925)
- ☐ lncRNA (42)
- ☐ snRNA (17)
- ☐ other (1)
- ☐ sRNA (1)

Organisms

- ☐ Homo sapiens (63)
- ☐ Mus musculus (22)

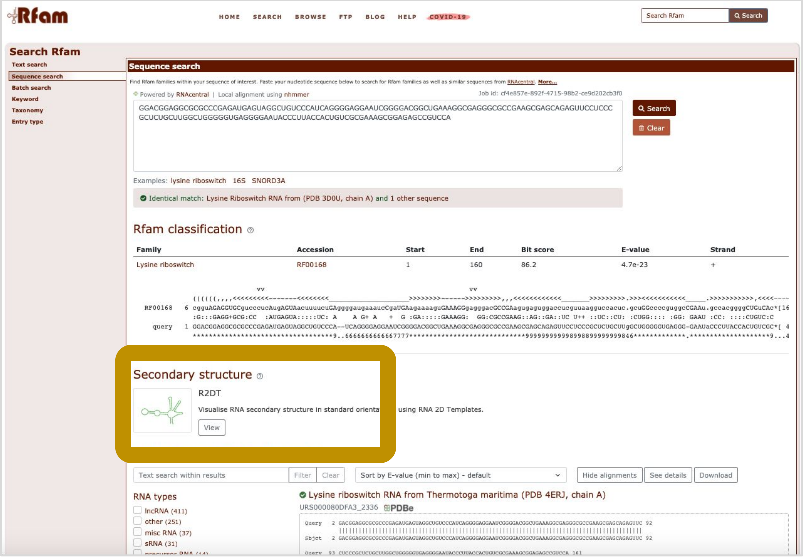
Homo sapiens small nucleolar RNA, C/D box 3A (SNORD3A)

URS000053962A_9606 ENA HGNC LNCipedia RefSeq Rfam snoDB snOPY

```
Query   1 AAGACUAUACUUUCAGGGAUCAUUUCUAUAGUGUGUUACUAGAGAAGUUUCUCUGAACGUGUAGAGCACCGAAAACCACGAGGAAGAGAGG 91
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1 AAGACUAUACUUUCAGGGAUCAUUUCUAUAGUGUGUUACUAGAGAAGUUUCUCUGAACGUGUAGAGCACCGAAAACCACGAGGAAGAGAGG 91

Query  92 UAGCGUUUUCUCCUGAGCGUGAAGCCGGCUUUCUGGCGUUGCUUGGCUGCAACUGCCGUCAGCCAUUGAUGAUCGUUCUUCUCUCCGUAUU 18
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  92 UAGCGUUUUCUCCUGAGCGUGAAGCCGGCUUUCUGGCGUUGCUUGGCUGCAACUGCCGUCAGCCAUUGAUGAUCGUUCUUCUCUCCGUAUU 18
```

Homo sapiens (human) small nucleolar RNA, C/D box 3A (SNORD3A)



Search Rfam

Sequence search

Find Rfam families within your sequence of interest. Paste your nucleotide sequence below to search for Rfam families as well as similar sequences from RNAcentral. More...

Powered by RNAcentral | Local alignment using nhmmer Job id: cf4e857e-892f-4715-98b2-ce9d202cb3f0

GGACGGAGGCGCGCCCGAGAUGAGUAGGCUGUCCCAUCAGGGGAGGAAUCGGGGACGGCUGAAAGGCGAGGGCGCCGAAGCGAGCAGAGUUCCUCCC
GCUCUGCUUGGCUGGGGGUGAGGGGAAUACCCUUACCACUGUCGCGAAAGCGGAGAGCCGUCCA

Examples: lysine riboswitch 16S SNORD3A

Identical match: Lysine Riboswitch RNA from (PDB 3D0U, chain A) and 1 other sequence

Rfam classification

Family	Accession	Start	End	Bit score	E-value	Strand
Lysine riboswitch	RF00168	1	160	86.2	4.7e-23	+

```
                      vv                                                         vv
              ((((((,,,,<<<<<<<<<-------<<<<<<<<__________________>>>>>>>>------>>>>>>>>>,,,<<<<<<<<<<<<______>>>>>>>>>.>>><<<<<<<<<<<<_____.>>>>>>>>>>>,<<<<----
  RF00168   6 cgguAGAGGUGCgucccucAugAGUAacuuuucuGAggggaugaaaucCgaUGAagaaaaguGAAAGGgagggacGCCGAagugaguggaccucguuaaggucсacuc.gcuGGccccguggcCGAAu.gccacggggCUGuCAc*[16
              :G:::GAGG+GCG:CC  :AUGAGUA::::UC: A    A G+ A   +  G :GA:::::GAAAGG:  GG:CGCCGAAG::AG::GA::UC U++ ::UC::CU: :CUGG:::: :GG: GAAU :CC: ::::CUGUC:C
    query   1 GGACGGAGGCGCGCCCGAGAUGAGUAGGCUGUCCCA--UCAGGGGAGGAAUCGGGGACGGCUGAAAGGCGAGGGCGCCGAAGCGAGCAGAGUUCCUCCCGCUCUGCUUgGCUGGGGGUGAGGG-GAAUaCCCUUACCACUGUCGC*[ 4
              *********************************9..666666666667777****************************99999999999989988999999846************.*******************9...4
```

Secondary structure

R2DT

Visualise RNA secondary structure in standard orienta using RNA 2D Templates.

RNA types

- ☐ lncRNA (411)
- ☐ other (251)
- ☐ misc RNA (37)
- ☐ sRNA (31)

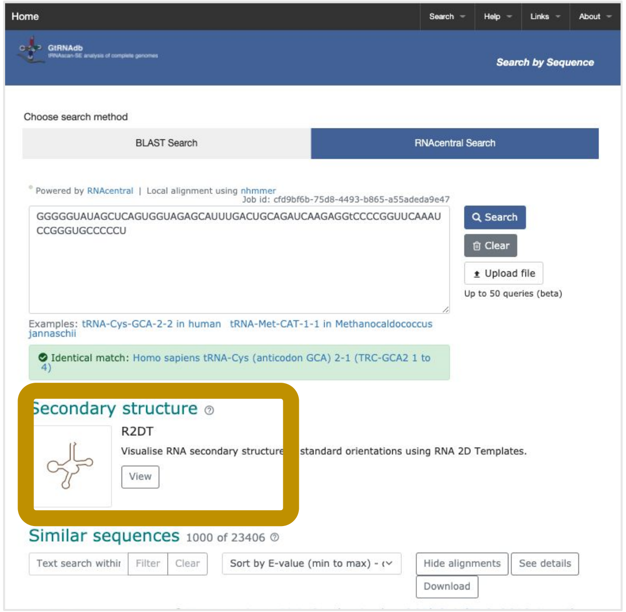
Lysine riboswitch RNA from Thermotoga maritima (PDB 4ERJ, chain A)

URS000080DFA3_2336 PDBe

```
Query   2 GACGGAGGCGCGCCCGAGAUGAGUAGGCUGUCCCAUCAGGGGAGGAAUCGGGGACGGCUGAAAGGCGAGGGCGCCGAAGCGAGCAGAGUUC 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2 GACGGAGGCGCGCCCGAGAUGAGUAGGCUGUCCCAUCAGGGGAGGAAUCGGGGACGGCUGAAAGGCGAGGGCGCCGAAGCGAGCAGAGUUC 92

Query  93 CUCCCGCUCUGCUUGGCUGGGGGUGAGGGGAAUACCCUUACCACUGUCGCGAAAGCGGAGAGCCGUCCA 161
```

Rfam



Choose search method

Powered by RNAcentral | Local alignment using nhmmer Job id: cfd9bf6b-75d8-4493-b865-a55adeda9e47

GGGGGUAUAGCUCAGUGGUAGAGCAUUUGACUGCAGAUCAAGAGGtCCCCGGUUCAAAU
CCGGGUGCCCCCU

Up to 50 queries (beta)

Examples: tRNA-Cys-GCA-2-2 in human tRNA-Met-CAT-1-1 in Methanocaldococcus jannaschii

Identical match: Homo sapiens tRNA-Cys (anticodon GCA) 2-1 (TRC-GCA2 1 to 4)

Secondary structure

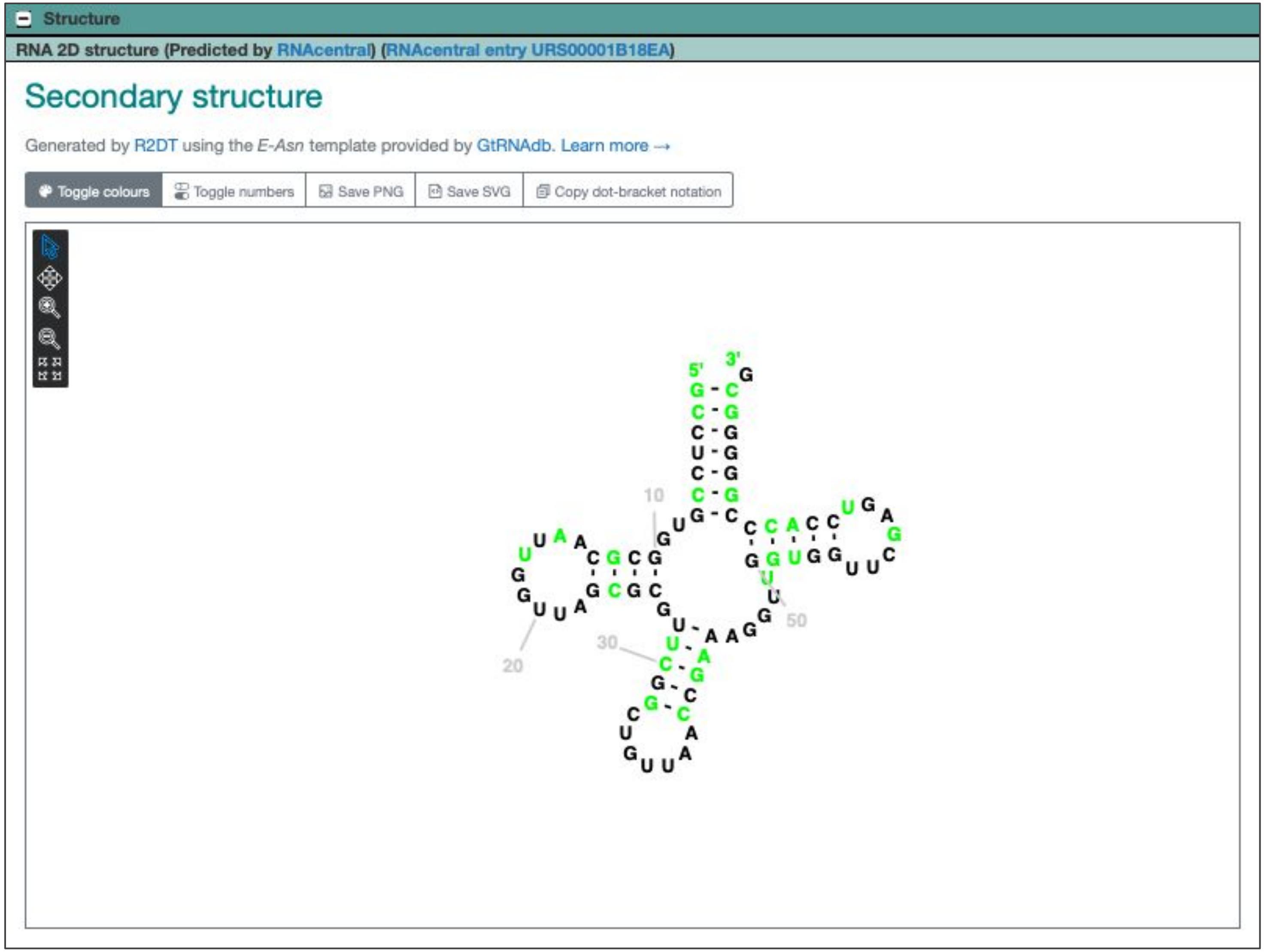
R2DT

Visualise RNA secondary structure standard orientations using RNA 2D Templates.

Similar sequences 1000 of 23406

GtRNADB

R2DT is integrated into FlyBase - SGD is coming soon



Structure

RNA 2D structure (Predicted by RNAcentral) (RNAcentral entry URS00001B18EA)

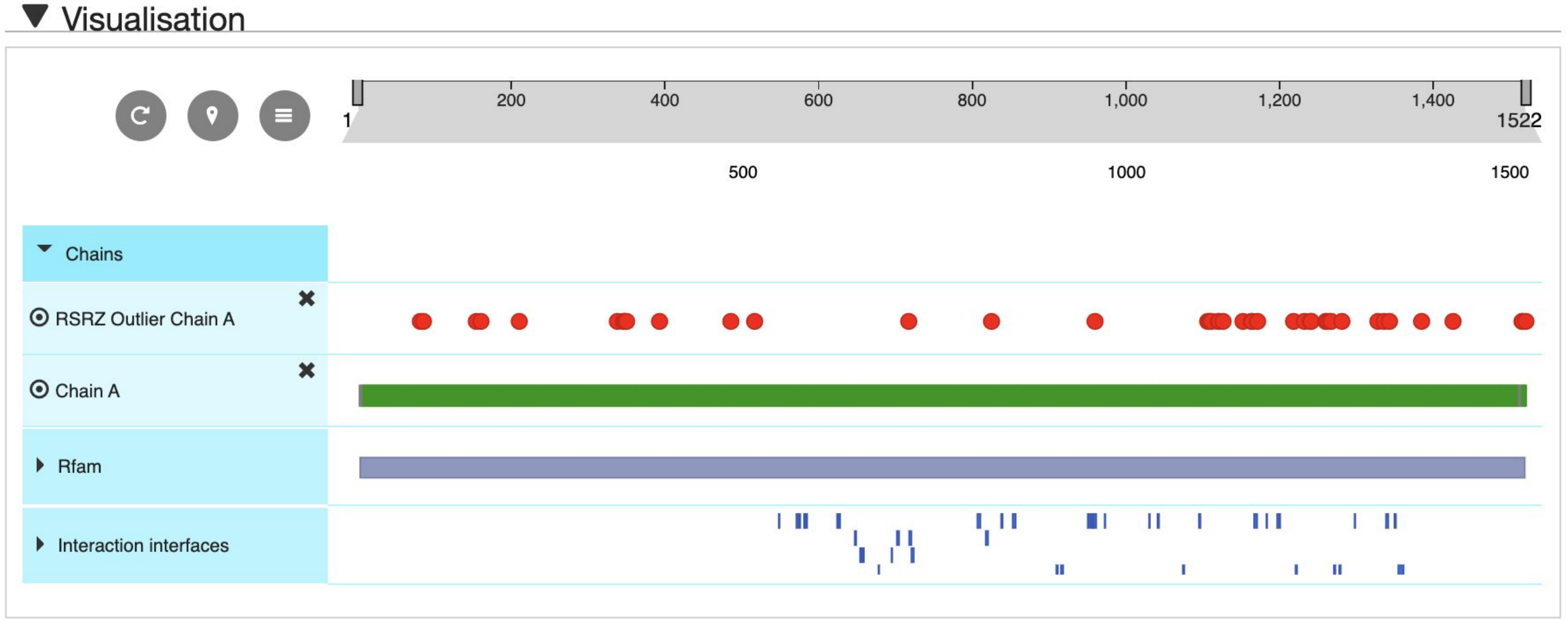
Secondary structure

Generated by R2DT using the *E-Asn* template provided by GtRNAdb. Learn more →

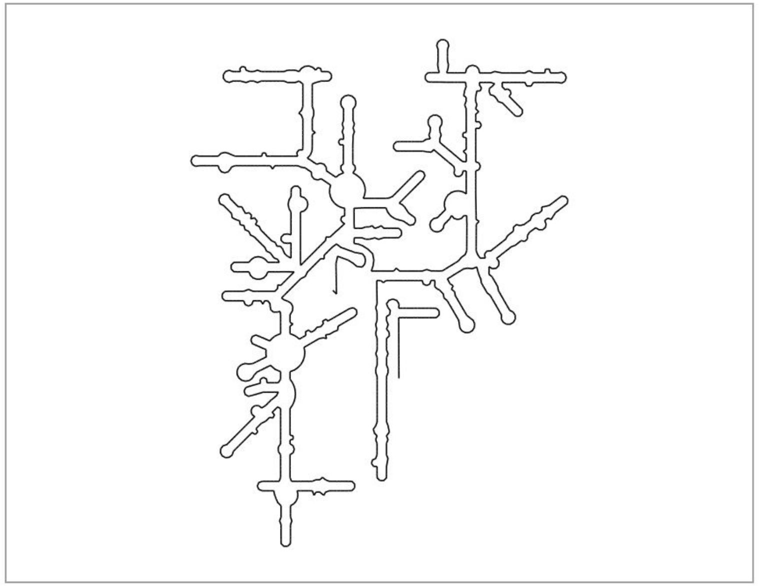
Dmel\tRNA:Asn-GTT-1-9 http://flybase.org/reports/FBgn0053537

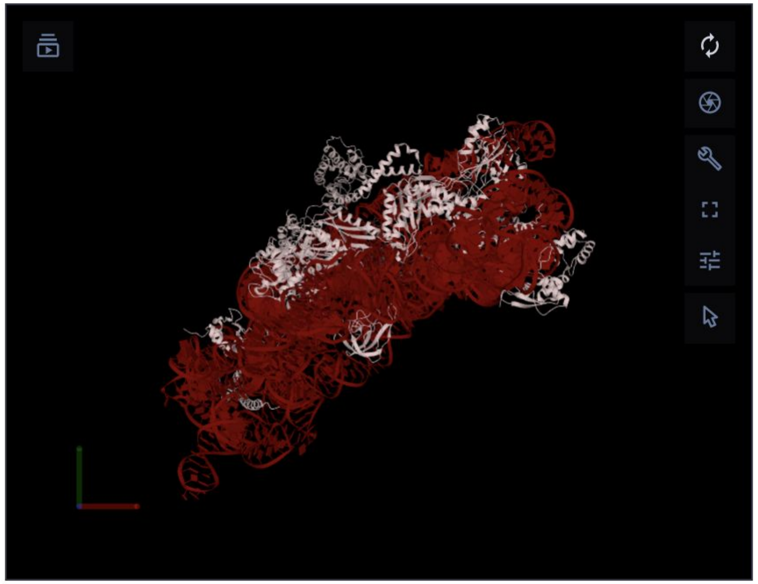
R2DT is integrated into PDBe

- Interactive 1D-2D-3D visualisation
- Clicking RNA 2D structure highlights the region in 3D and 1D



Thermus thermophilus small subunit ribosomal RNA (1J5E:A)





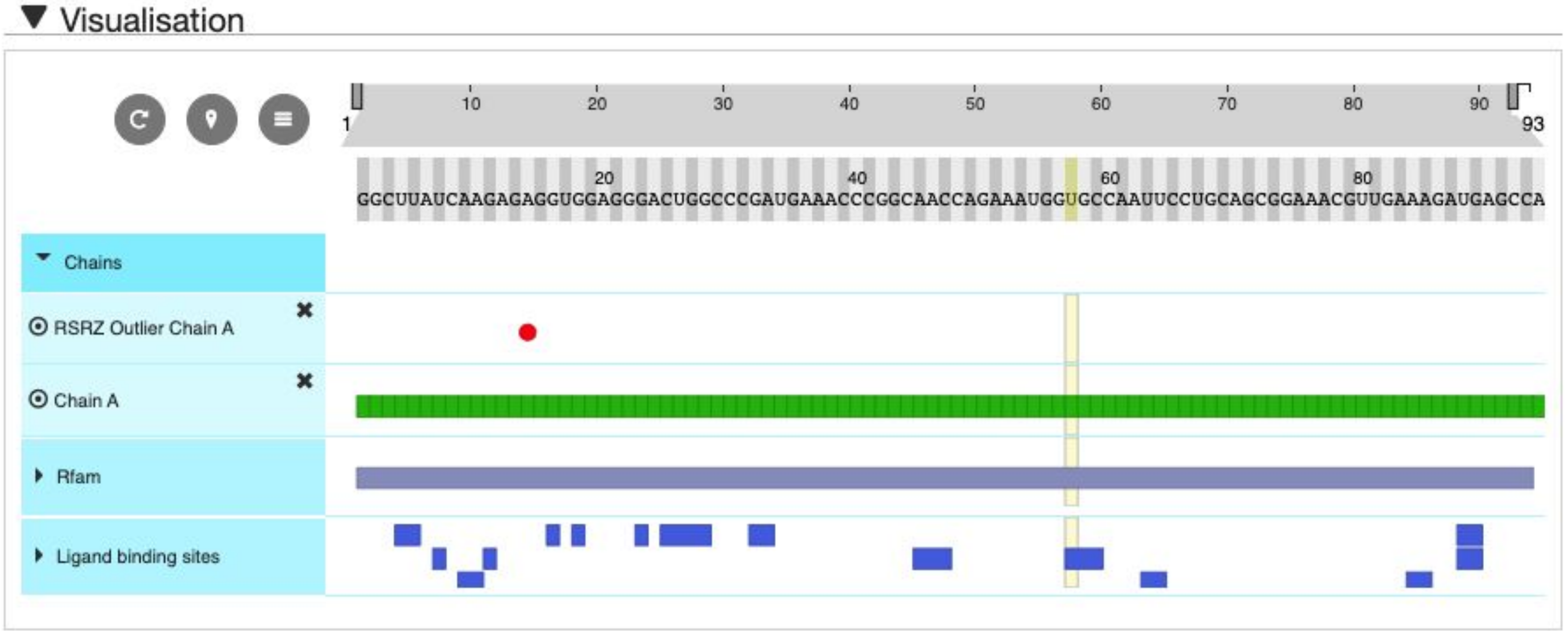
Problem: no 3D-derived base pairing information

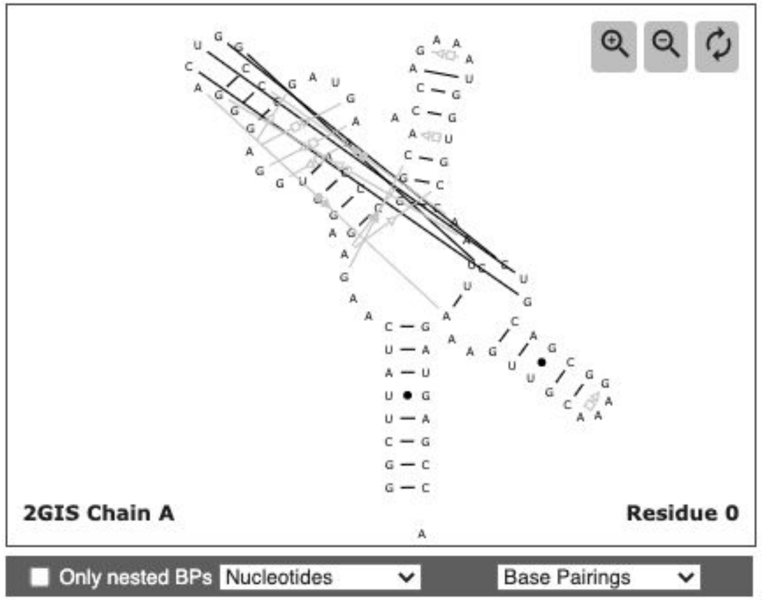
New PDBe widget

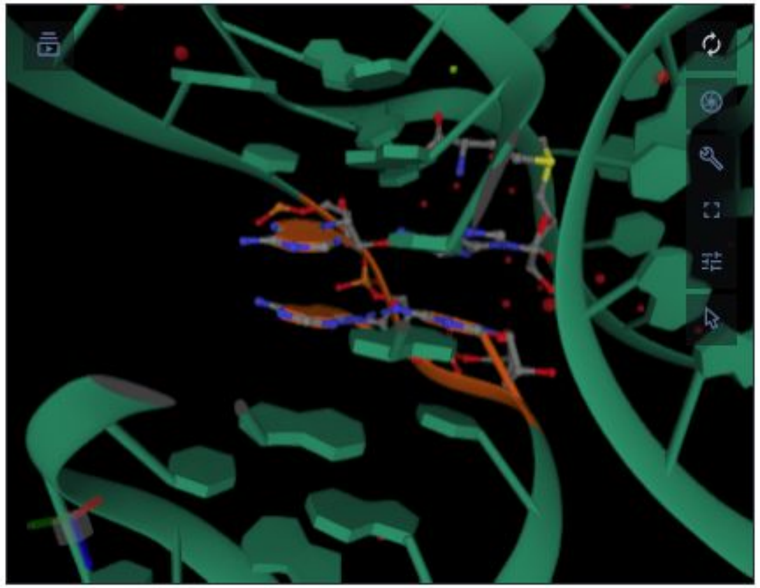
- Base pair annotations
- Leontis-Westhof symbols
- Both nested and long range interactions

Holly McCann

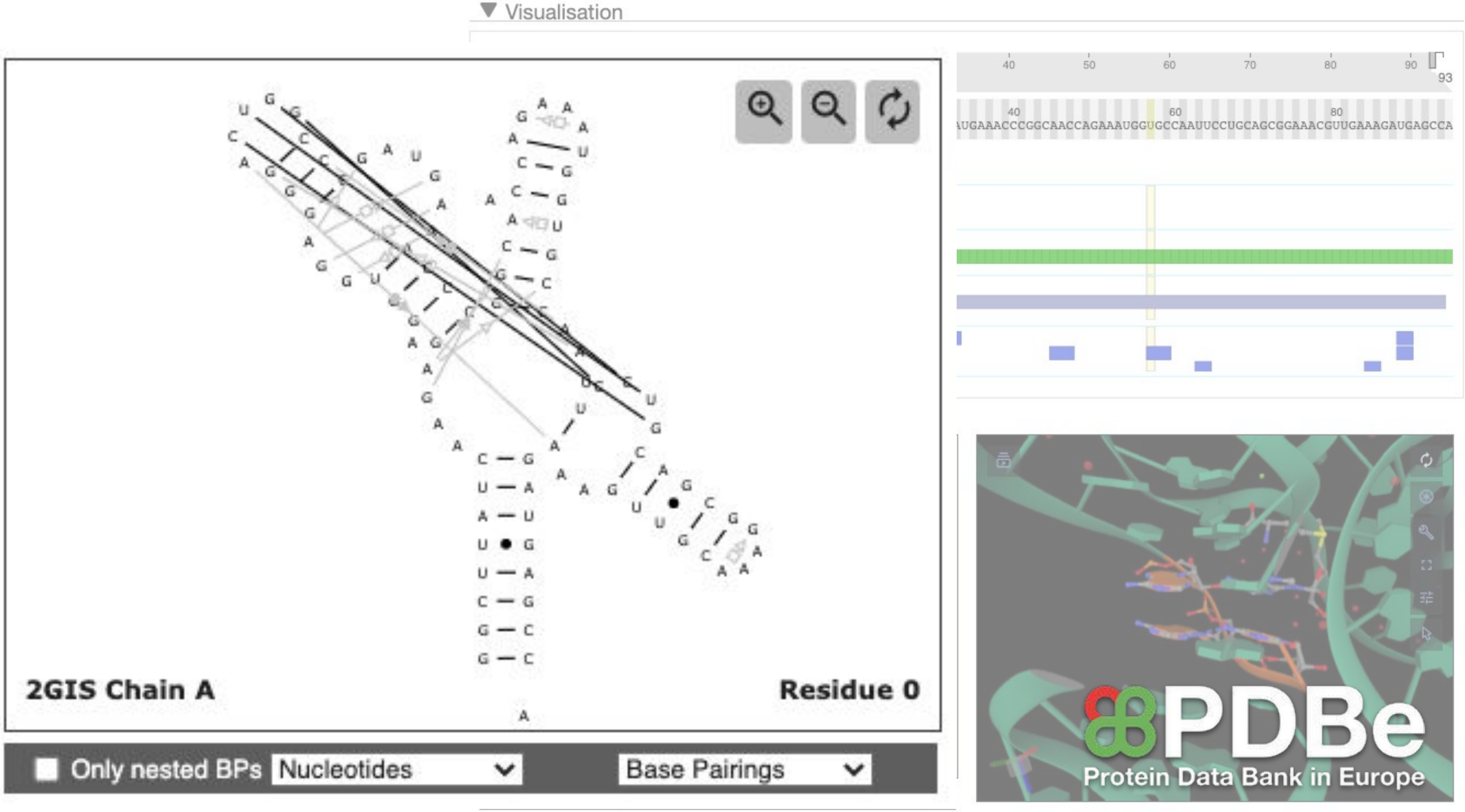
https://wwwdev.ebi.ac.uk/pdbe/entry/pdb/2gis/RNA/1







R2DT displays non-canonical basepairs annotated by FR3D



Live demo

😱

https://wwwdev.ebi.ac.uk/pdbe/entry/pdb/2gis/RNA/1
5FJC

What's next?

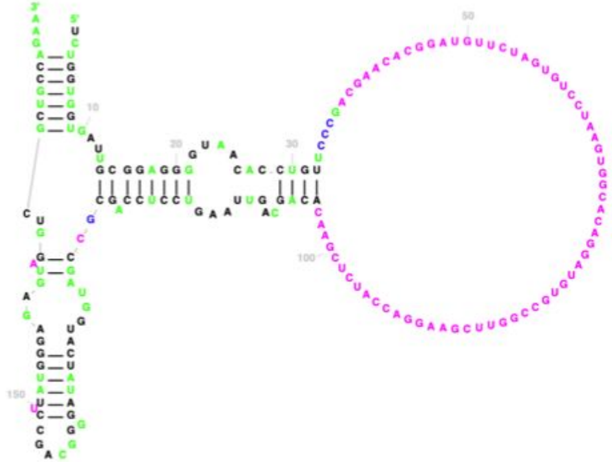
🔜 New PDBe API serving FR3D basepairs

- Uses FR3D Python github.com/BGSU-RNA/fr3d-python
- Annotates basepairs for modified nucleotides
- Supports mmCIF files
- Currently under development - Stay tuned!

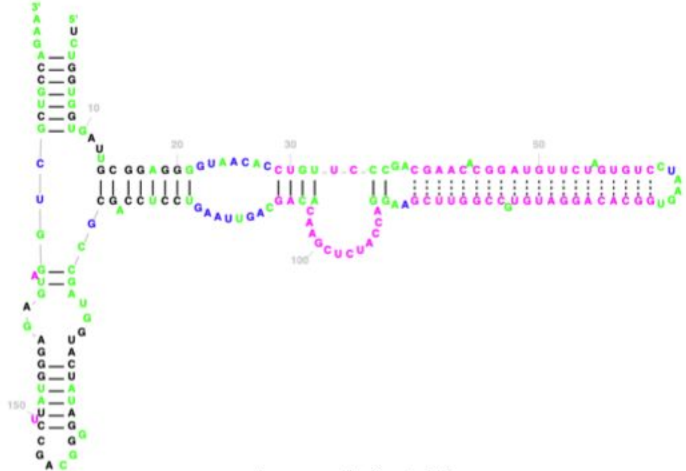
Craig Zirbel

🔜 Constrained folding using RNAfold

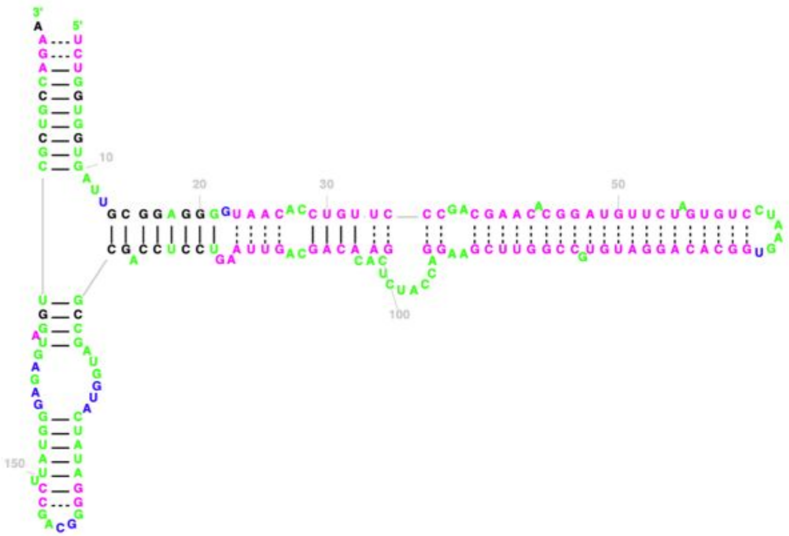
Holly McCann



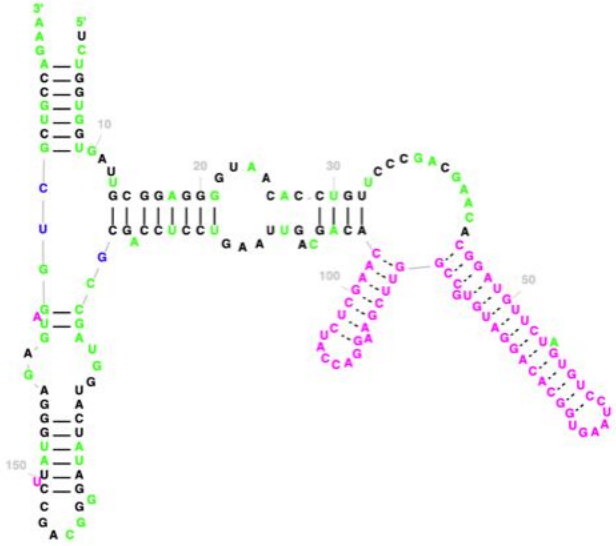
Original R2DT



Local folding



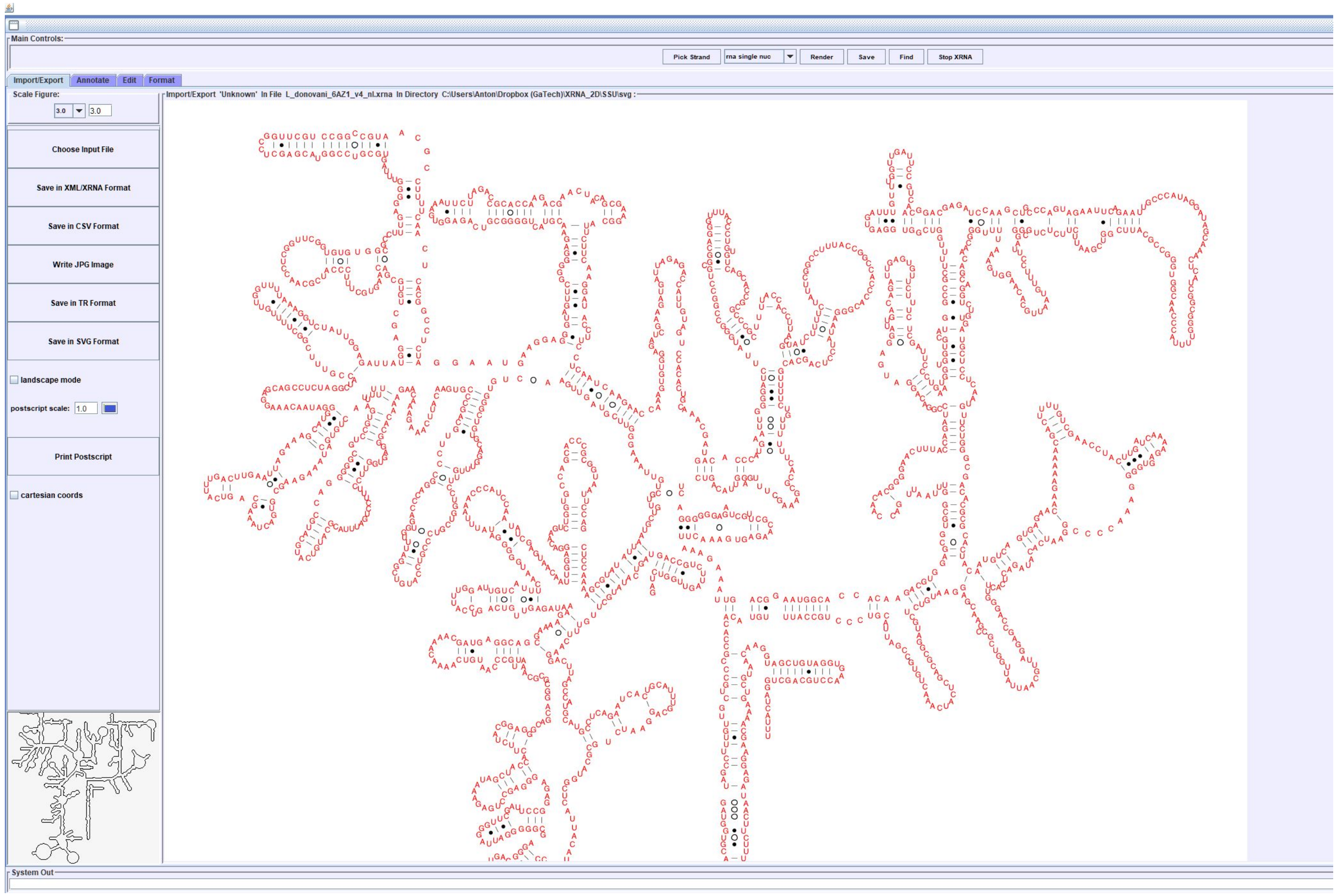
Global folding



Global folding w/ss nucleotides enforced

R2DT can be used to produce new templates using XRNA-GT

1. Download R2DT results
2. Open in XRNA-GT
3. Manually edit the layout
4. Export in R2DT format
5. Submit as a new template



Import/Export 'Unknown' In File L_donovani_6AZ1_v4_nl.xrna In Directory C:\Users\Anton\Dropbox (GaTech)\XRNA_2D\SSU\svg :

☐ landscape mode

☐ cartesian coords

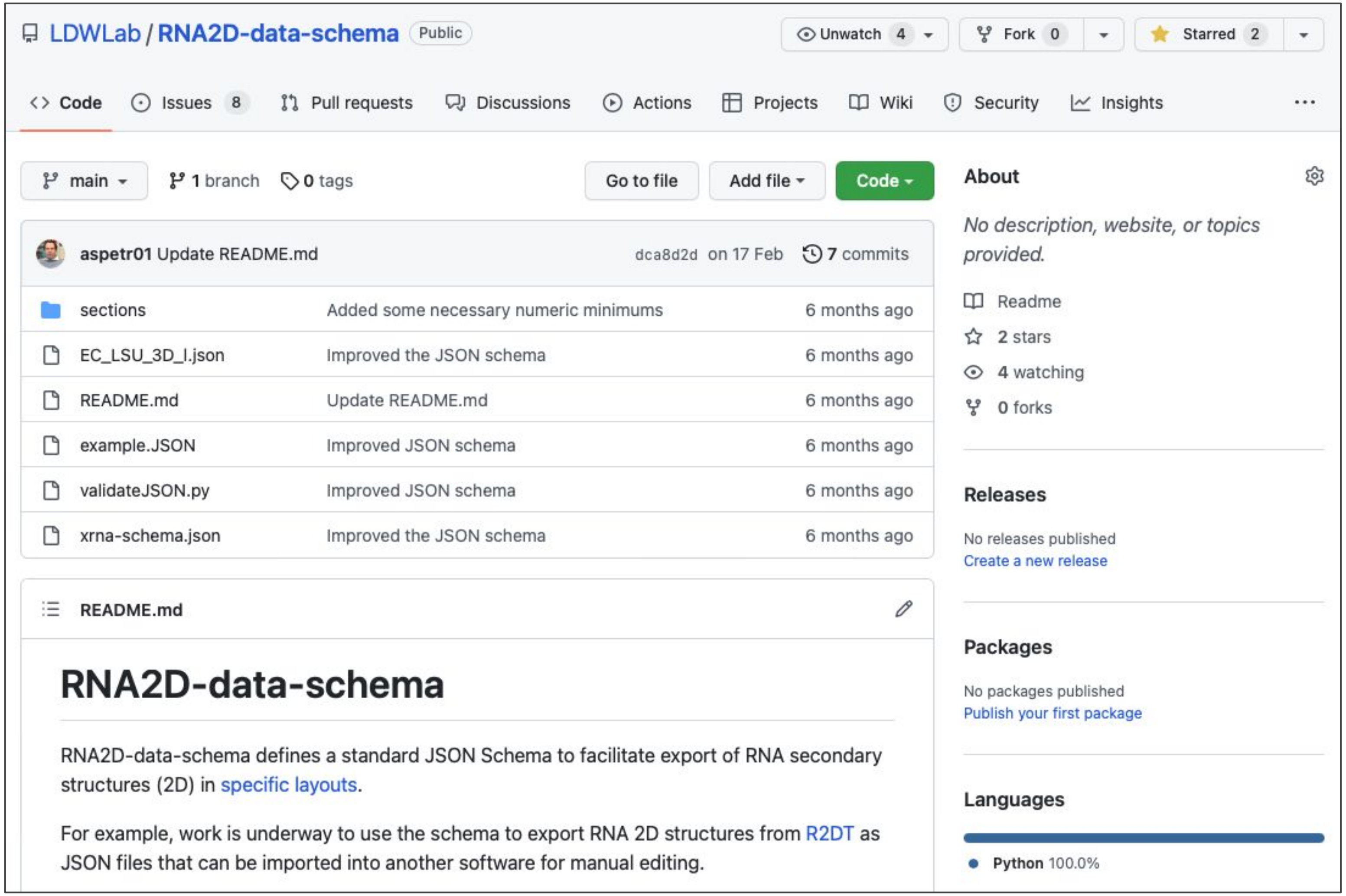
github.com/LDWLab/XRNA-GT

🔜 Interactive web-based editor

1. Export a diagram from R2DT
2. Edit it in a browser
3. Submit to R2DT as a new template

Caeden Meade

RNA 2D JSON Schema



aspetr01 Update README.md dca8d2d on 17 Feb 7 commits

sections	Added some necessary numeric minimums	6 months ago
EC_LSU_3D_I.json	Improved the JSON schema	6 months ago
README.md	Update README.md	6 months ago
example.JSON	Improved JSON schema	6 months ago
validateJSON.py	Improved JSON schema	6 months ago
xrna-schema.json	Improved the JSON schema	6 months ago

README.md

RNA2D-data-schema

RNA2D-data-schema defines a standard JSON Schema to facilitate export of RNA secondary structures (2D) in specific layouts.

For example, work is underway to use the schema to export RNA 2D structures from R2DT as JSON files that can be imported into another software for manual editing.

About

No description, website, or topics provided.

Readme
2 stars
4 watching
0 forks

Releases

No releases published
Create a new release

Packages

No packages published
Publish your first package

Languages

Python 100.0%

github.com/LDWLab/RNA2D-data-schema

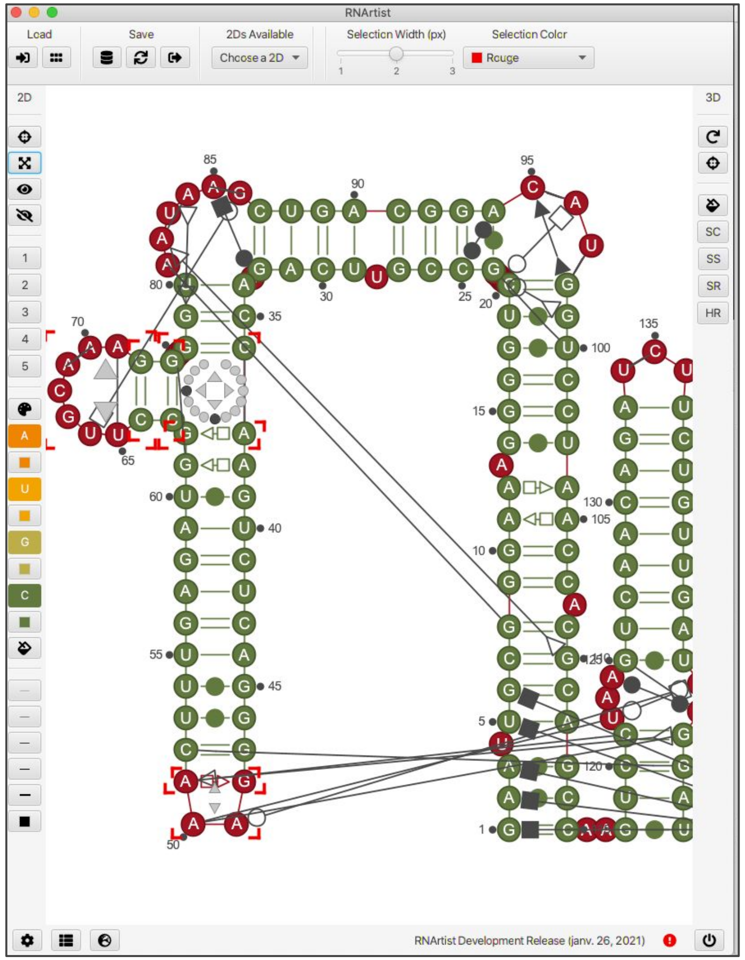
Caeden Meade

Includes:

- Sequence and secondary structure
- (x,y) coordinates
- Colours, fonts, labels, additional annotations

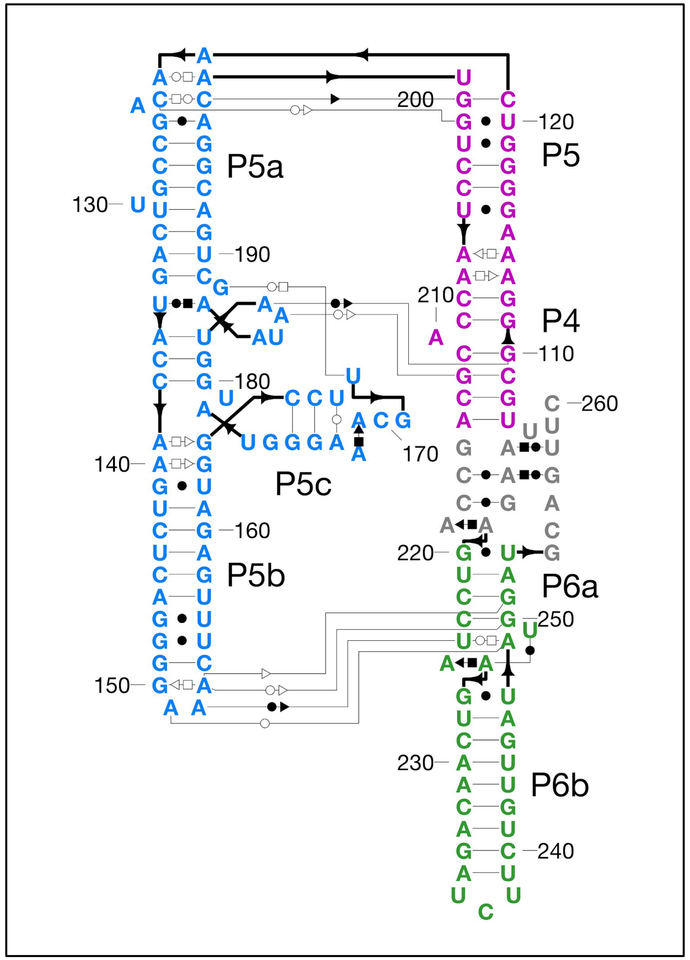
Can we make RNA visualisation software interoperable?

RNArtist



github.com/fjossinet/RNArtist

RiboDraw

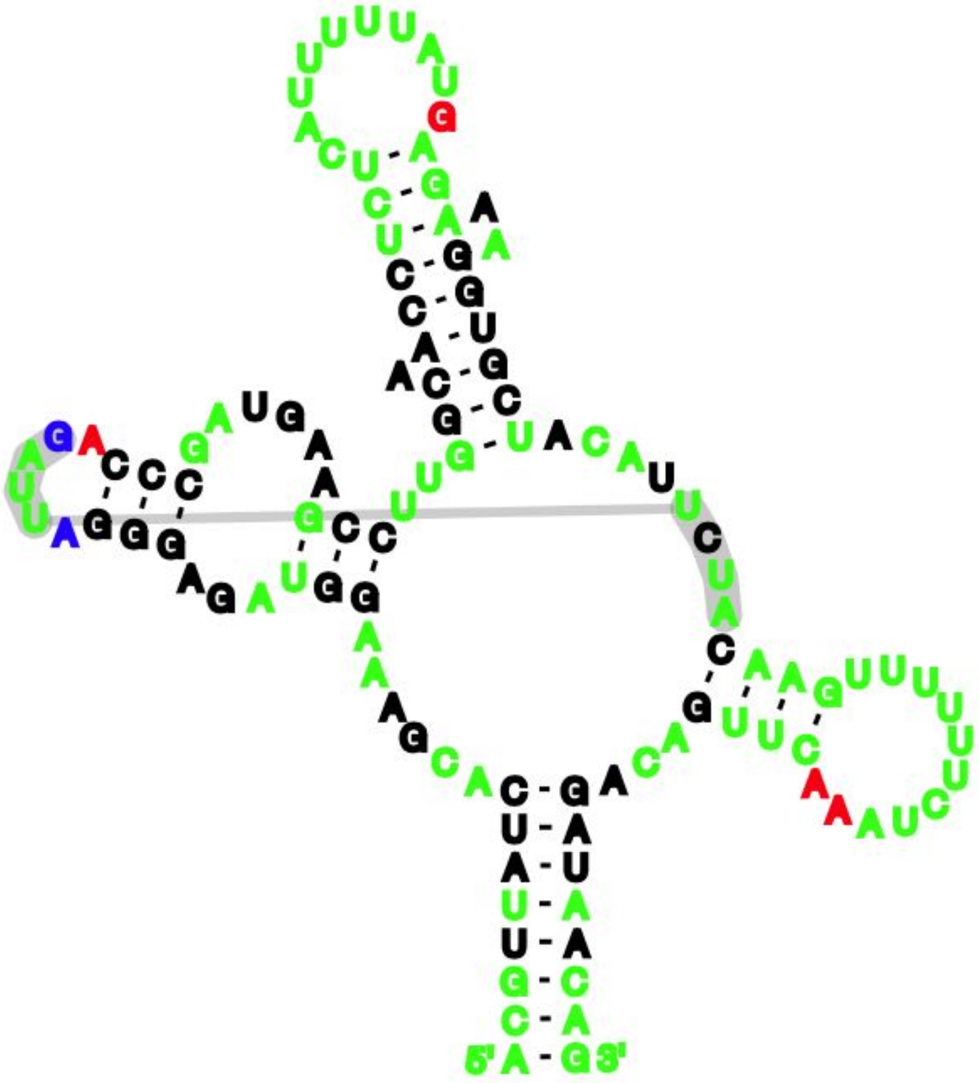


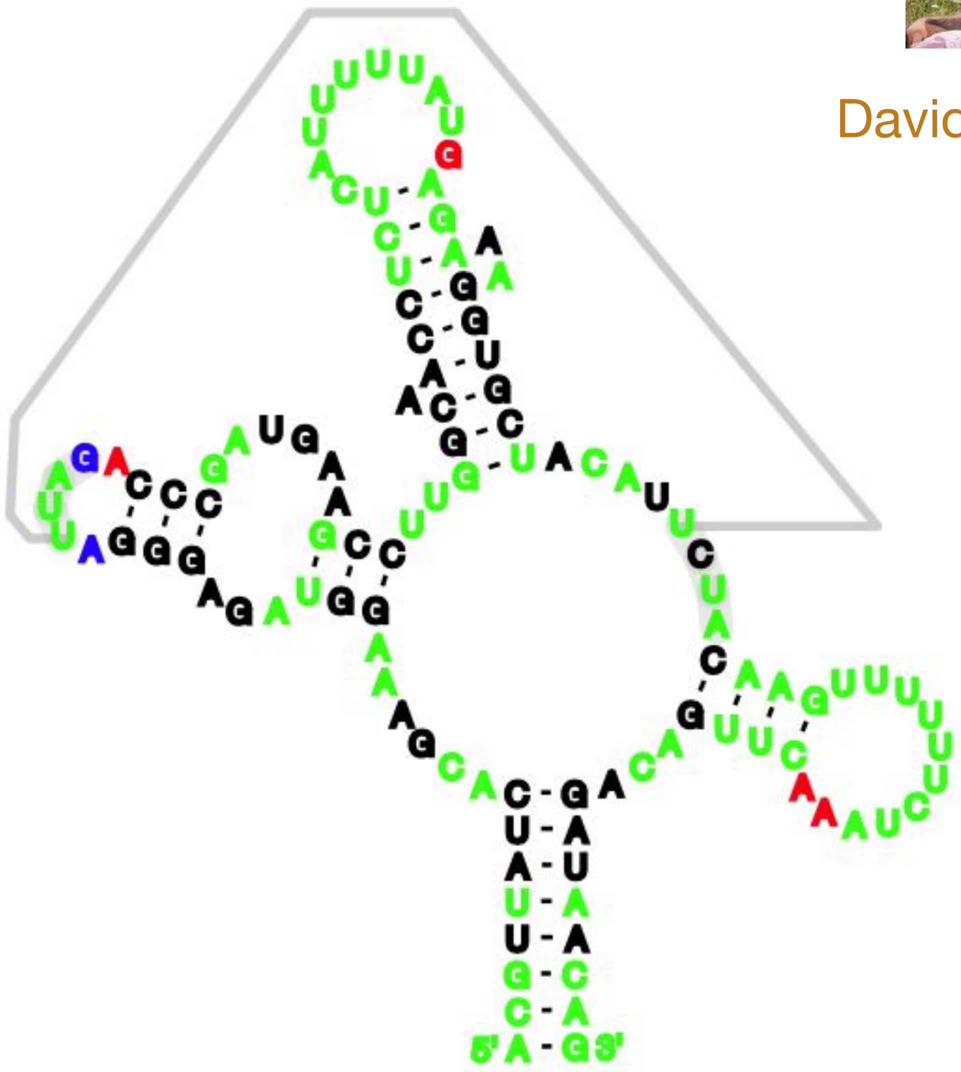
github.com/ribokit/RiboDraw

Long term goal:

Use **RNArtist** and **RiboDraw** to author templates for R2DT and import using RNA 2D JSON Schema

🔜 Display pseudoknots using R2DT

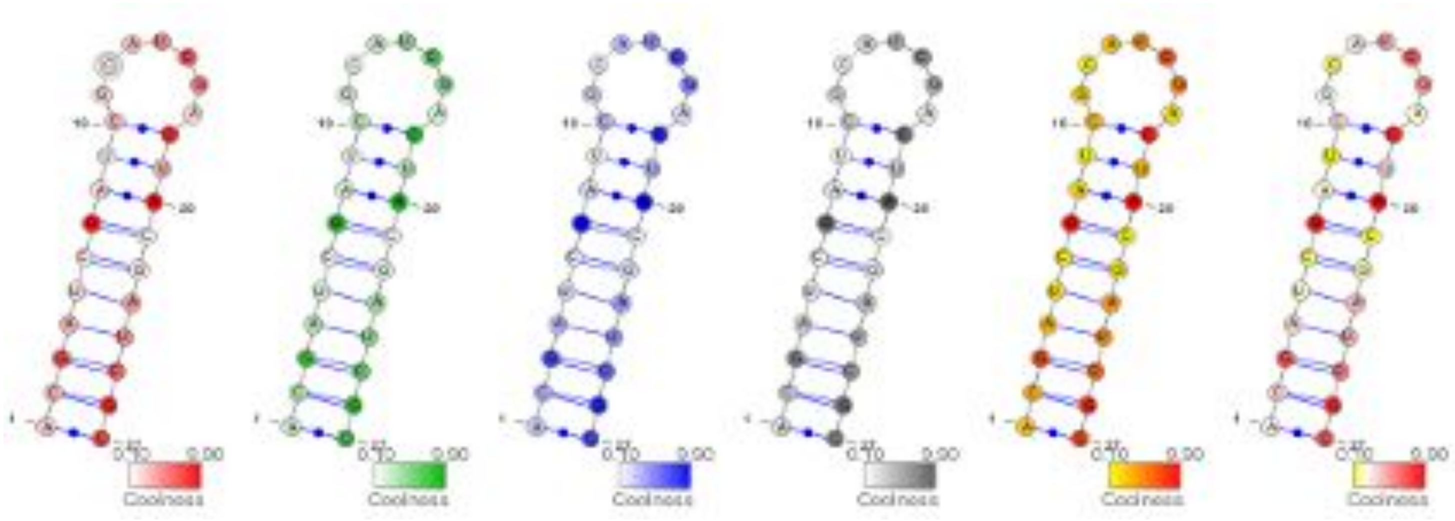




David Hoksza

🔜 Visualise data layers on top of secondary structures

- SHAPE reactivities
- SNPs
- Posterior probabilities
- Anything else!



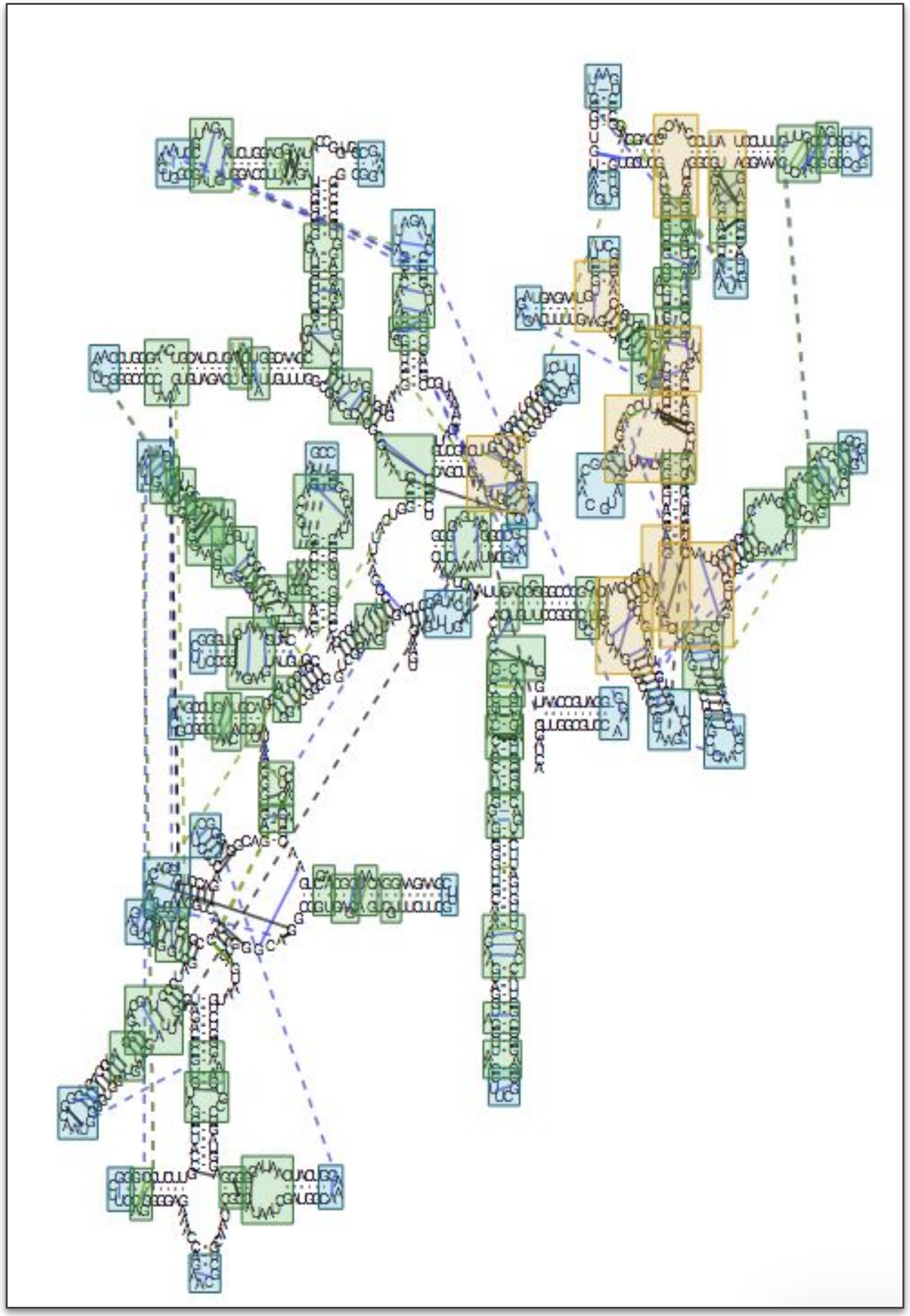
http://varna.lri.fr/index.php?lang=en&page=tutorial&css=varna

Inspired by VARNA

🔜 Display RNA 3D modules

- Inspired by the interactive airport diagrams from RNA 3D Hub
- Use JAR3D, BayesPairing, RMDetect, or any other method to identify modules and highlight them in 2D

Blake Sweeney



https://unsplash.com/photos/3i5PHVp1Fkw

We have lots of work to do

- Interactive editor
- Pseudoknots
- Modules
- Data layers

Get in touch with your wishlist!

Send us your **templates** and **feedback**!

github.com/rnacentral/r2dt/issues
rnacentral.org/contact-us

contact@antonpetrov.com

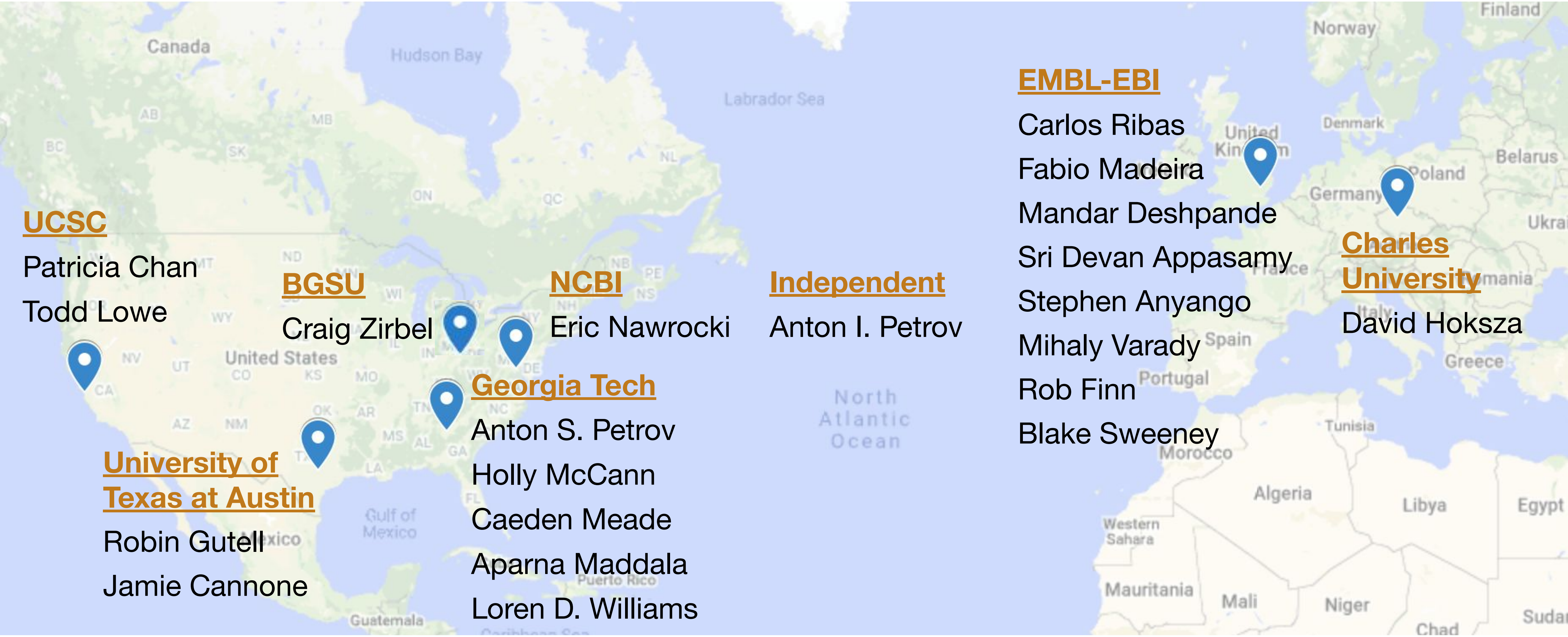
https://unsplash.com/photos/C2zhShTnl5I

Sensible RNA structures…
everywhere!

- RNAcentral
- Rfam
- PDBe
- FlyBase
- GtRNAdb

and in the new papers!

The R2DT team



UCSC

Patricia Chan
Todd Lowe

BGSU

Craig Zirbel

NCBI

Eric Nawrocki

Independent

Anton I. Petrov

EMBL-EBI

Carlos Ribas
Fabio Madeira
Mandar Deshpande
Sri Devan Appasamy
Stephen Anyango
Mihaly Varady
Rob Finn
Blake Sweeney

Charles University

David Hoksza

Georgia Tech

Anton S. Petrov
Holly McCann
Caeden Meade
Aparna Maddala
Loren D. Williams

University of Texas at Austin

Robin Gutell
Jamie Cannone

My Resume

- I ❤ RNA
- Open to work or collaboration
- Find out more at antonpetrov.com

https://unsplash.com/photos/7iSEHWsxPLw

Thank you!

Please send your templates and feedback!

github.com/rnacentral/r2dt/issues
rnacentral.org/contact-us
contact@antonpetrov.com