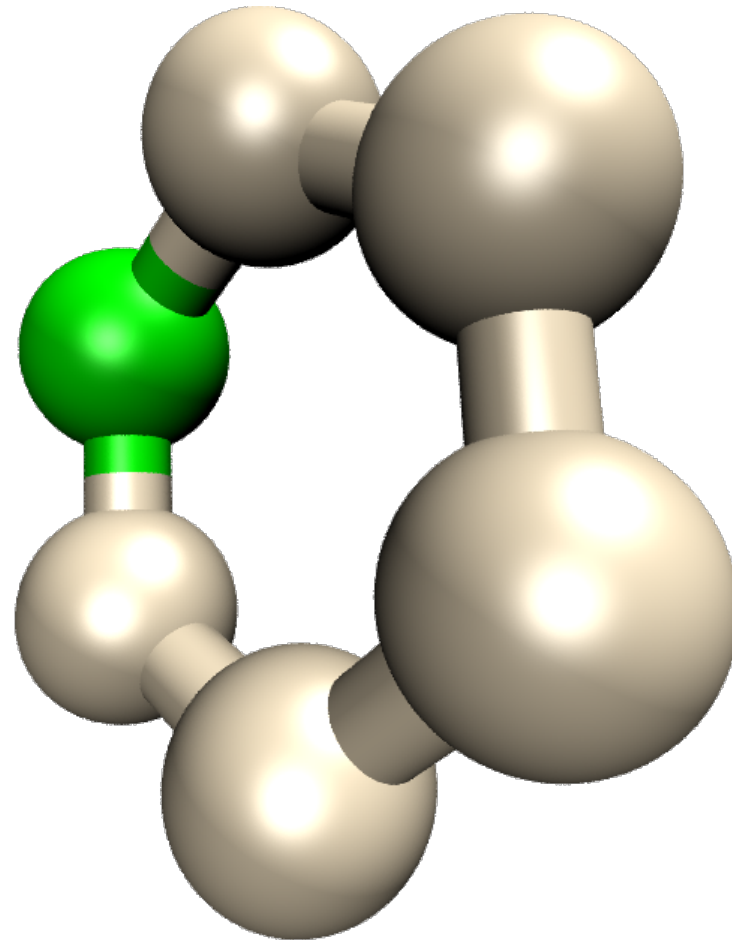


# Molecular Simulation with OpenMM Zephyr

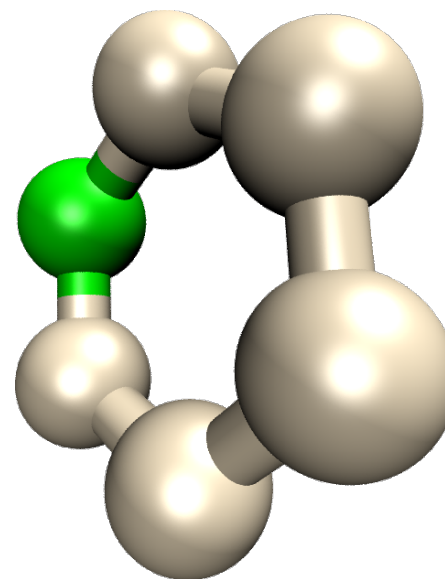
**Magdalena Jonikas**  
**Christopher Bruns**  
Simbios  
Stanford University

March 29<sup>th</sup>, 2010

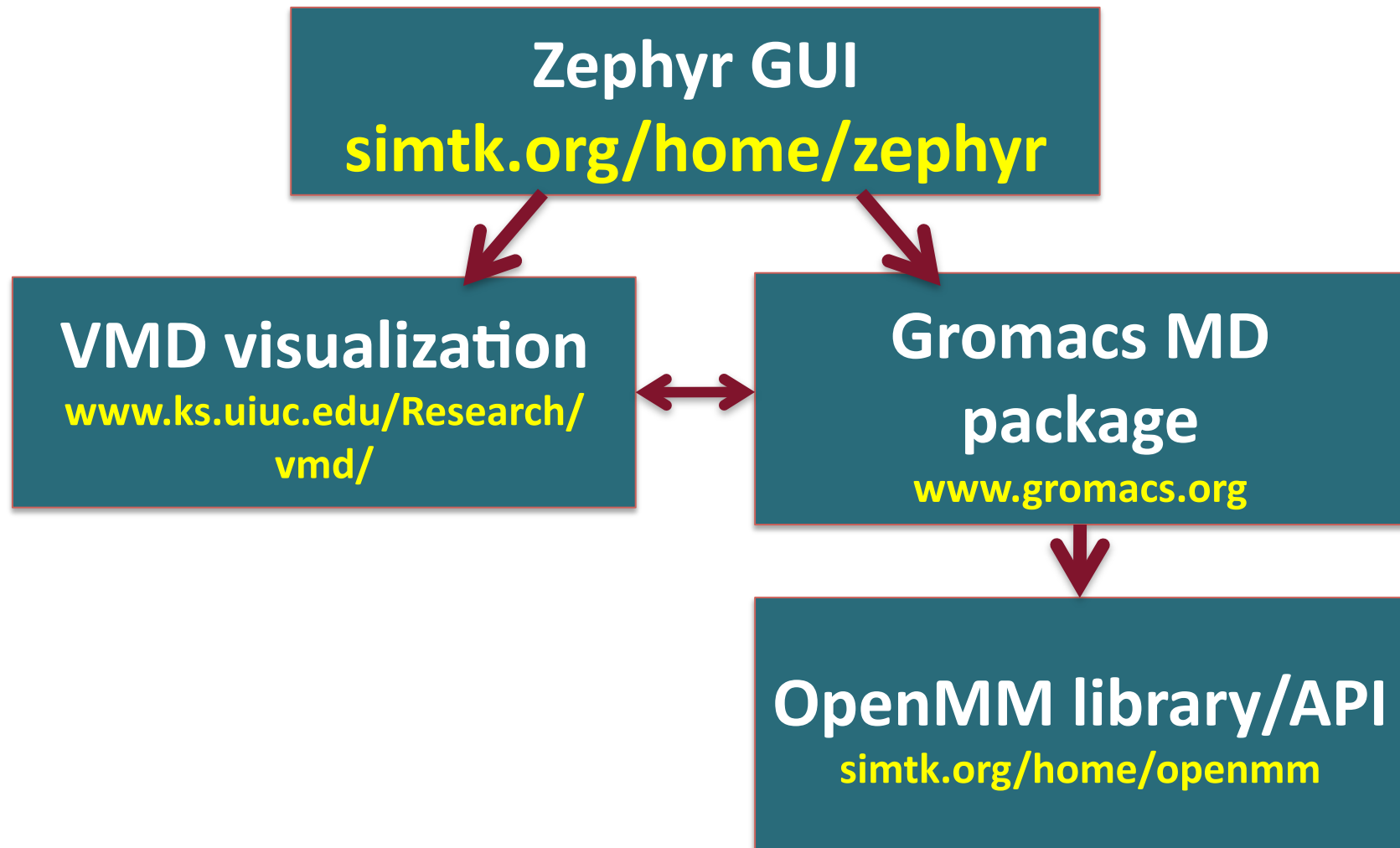


# What is OpenMM Zephyr?

- Graphical user interface for running accelerated molecular dynamics simulations on high performance computer architectures, e.g., graphics processing cards (GPUs)
- Automates running of molecular dynamics programs, e.g., gromacs
- Vision of OpenMM Zephyr being a learning tool



# Zephyr is a GUI layer on OpenMM, Gromacs, and VMD



# Introductory demonstration for Zephyr

The image displays two windows from a molecular simulation. The top window, titled "Running OpenMM Zephyr : alanylalanine\_capped.pdb", shows the OpenMM Zephyr interface. It features a blue header with the OpenMM Zephyr logo and the text "Simulation running...". Below this, there are tabs for "Molecules", "Parameters", "Status: Running", "VMD console", and "About". The main area displays simulation progress: "0.100 picoseconds simulated (of 100.000 total)", "Elapsed lab time 2.8s", and "Calculating time remaining...". A "gromacs output" window is open, showing the following text:

```
Started mdrun on node 0 Mon Feb 02 21:19:58 2009
```

Step	Time	Lambda
1	0.00200	0.00000
50	0.10000	0.00000

Waiting for IMD socket connection to VMD on port 3000...  
Waiting for IMD socket connection to VMD on port 3000...  
Waiting for IMD socket connection to VMD on port 3000...

Buttons for "< Parameters" and "Cancel" are visible at the bottom.

The bottom window, titled "VMD 1.8.6 OpenGL Display", shows a 3D ball-and-stick model of the alanylalanine molecule. The atoms are colored: carbon (teal), oxygen (red), nitrogen (blue), and hydrogen (white). The molecule is shown in a perspective view, highlighting its L-shaped structure.

The "VMD Main" window is also visible, showing a menu bar (File, Molecule, Graphics, Display, Mouse, Extensions, Help) and a table of loaded molecules:

ID	T	A	D	F	Molecule	Atoms	Frames	Vol
0	T	A	D	F	alanylalanine_capped_p	32	757	0

At the bottom of the VMD Main window, there is a playback control bar with a frame counter set to 756, a "Loop" button, a "step" button set to 1, and a "speed" slider.

# A: Run these gromacs programs

**INPUT:**

**PDB structure file**

pdb2gmx

.pdb

force field parameters

.top

.gro

editconf

.top

minimize energy

grompp

.tpr

mdrun

simulation parameters

.gro

.mdp

molecular dynamics

grompp

.tpr

GBSA parameters

.agb

mdrun

.pdb

.trr

**OUTPUT: structure and trajectory**

# A: Run these gromacs programs

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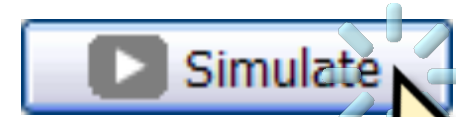
OUTPUT: structure and trajectory

# OR B: Click "Simulate" button in Zephyr

INPUT:

PDB structure file

.pdb



.pdb .trr

OUTPUT: structure and trajectory

# Zephyr Design Principles

## 1. Discoverability

- Not a black box
- Learn molecular dynamics by investigating simulation interface

## 2. Convention

- Harvest best practices of experts for default work flow

## 3. Feedback

- Reveal when things go wrong
- Reveal when things go right

# Zephyr & Role in RNA Modeling

- **Molecular dynamics**
- **Final step of a 3D structure modeling pipeline**



## Overview of exercises

1. **Dinucleotide (adenylyladenylate) 2 residues**
2. **Tertaloop (GCAA) 12 residues**
3. **Minimize xtal + C2A tRNA structure**
4. **Minimize NAST tRNA structure (NAST + C2A)**
5. **Minimize PDB\_00005 model**

# Exercise 1: RNA Dinucleotide

## 1. Launch Zephyr

## 2. Simulate adenylyladenylate.pdb for 40 picoseconds

Under Molecules tab:

Browse molecule (PDB) files... -> Select adenylyladenylate.pdb

Parameters -> Change simulation length to 40.0ps

Select "View simulation live in VMD"

Simulate

Check estimated simulation time:

If more than 2 minutes, decrease simulation length

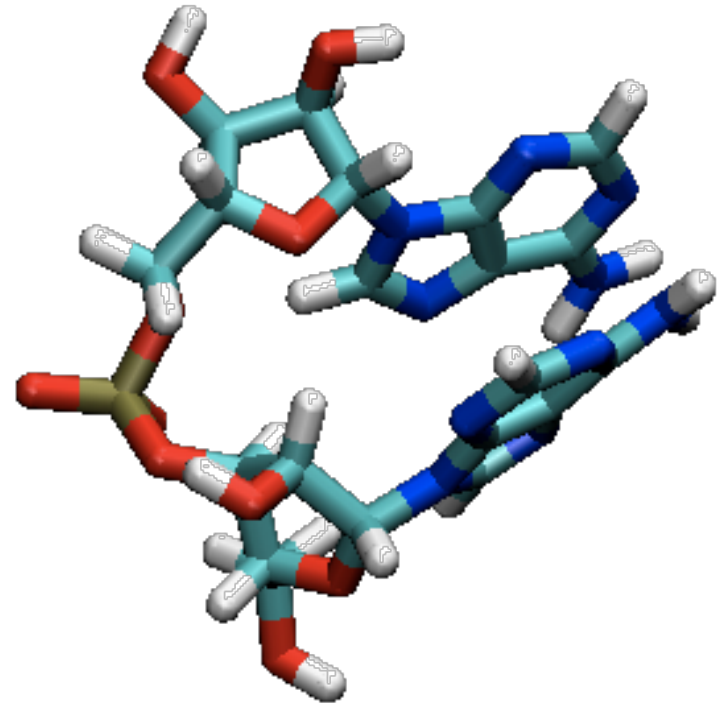
## 3. Raise solvent collision interval from 0.01099 to 1.0ps

What happens differently when you run this simulation?

## 4. Restore the solvent collision interval to 0.01099

## Lessons from exercise 1: RNA Dinucleotide

- Increased collision interval means low viscosity.
- Lower viscosity permits faster exploration of conformational space.
- Zephyr provides a rich environment for exploring molecular simulations.



## Exercise 2: Using VMD to view and convert trajectories

### 1. Load the Zephyr trajectory from the previous simulation into VMD

VMD Main -> File -> New Molecule

Molecule File Browser -> Browse

Navigate to Output folder ({...}/zephyr\_sims/adenylyladnylate)

Select adenylyladenylate\_processed.box.em.md.gro

Load

Browse (again, to load trajectory on top of .gro file)

Select adnylyladenylate\_processed.box.em.md.trr

Load

### 2. Save trajectory in PDB format from VMD

Select trajectory in VMD Main window

File -> Save Coordinates

File type: pdb, Selected atoms: all -> Save

adenylyladenylate\_processed.box.em.md.pdb

## Exercise 3: Tetraloop hairpin

### 1. Begin simulating gcaa.pdb

Use default parameters.

How long would it take to complete? Press “Cancel” to halt the simulation.

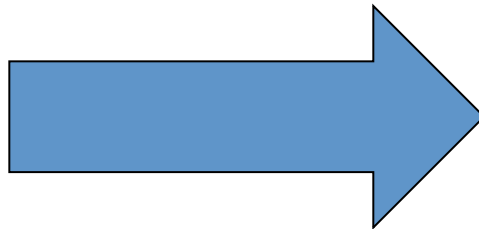
(On Mac you may need to close VMD and/or Zephyr to halt.)

### 2. Set “Simulation Hardware” to “GPU Nvidia”. Simulate Again.

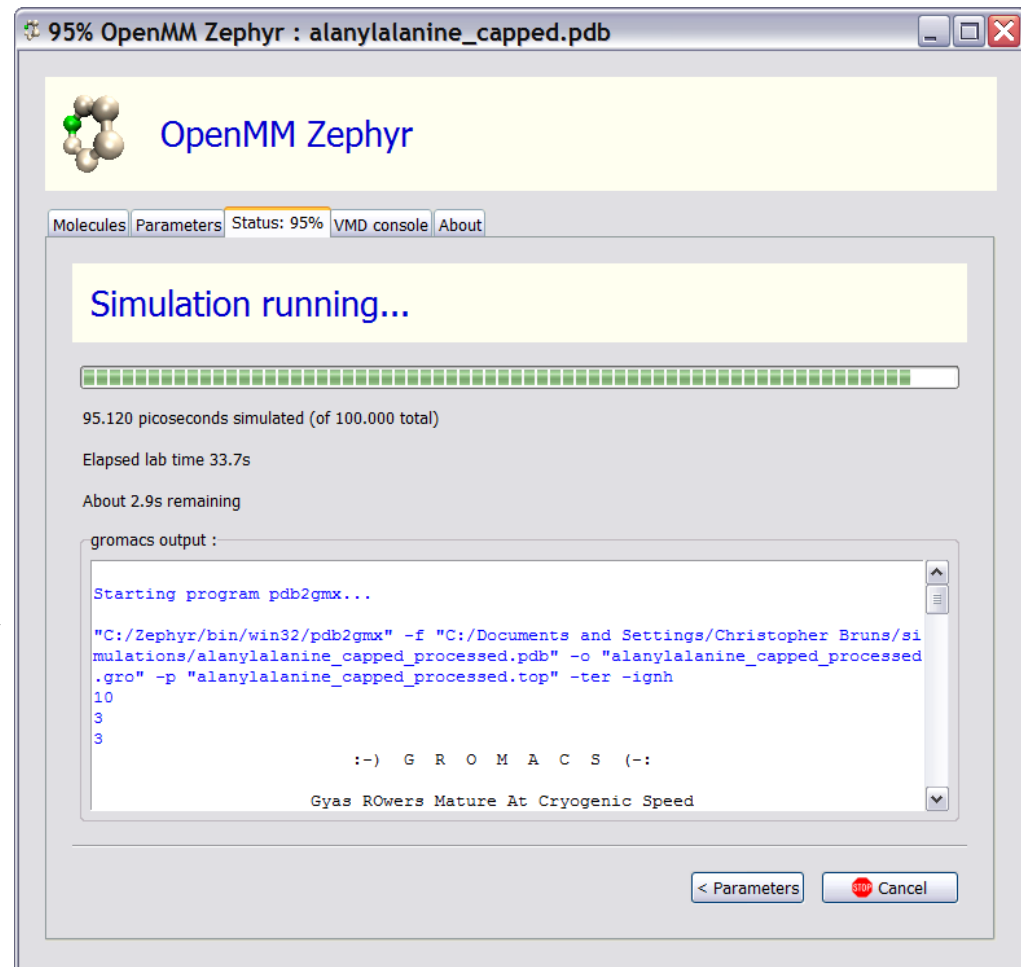
What happens?

If GPU acceleration is unavailable: Restore hardware to “CPU OpenMM ref.”

# Read the blue lines to learn to run Gromacs-OpenMM on the command line



see also zephyr.log file



95% OpenMM Zephyr : alanylalanine\_capped.pdb

OpenMM Zephyr

Molecules Parameters Status: 95% VMD console About

Simulation running...

95.120 picoseconds simulated (of 100.000 total)

Elapsed lab time 33.7s

About 2.9s remaining

gromacs output :

```
Starting program pdb2gmx...  
"C:/Zephyr/bin/win32/pdb2gmx" -f "C:/Documents and Settings/Christopher Bruns/si  
mulations/alanylalanine_capped_processed.pdb" -o "alanylalanine_capped_processed  
.gro" -p "alanylalanine_capped_processed.top" -ter -ignh  
10  
3  
3  
  
:-) G R O M A C S (-:  
Gyas R0wers Mature At Cryogenic Speed
```

< Parameters STOP Cancel

## Exercise 4: Minimizing C2A output

### 1. Simulate 6TNA-0-fixed.pdb from the C2A exercise

Navigate to 6TNA\_c2a example folder to select file 6TNA-0-fixed.pdb

Change parameters:

Simulate 10 steps

Output frequency every 1 steps

The minimization process minimized most gaps in the full atomic structure. Additional simulation steps help further reductions, but are time-expensive.

## **2. Run a similar simulation with T2-M1-0.pdb**

**What happens if the C2A model has very large gaps?**

**Both NAST and C2A have stochastic components, good to run many times as some models will be better than others.**

**Quality of C2A model depends on quality of NAST model.**

**Quality of minimized model depends on quality of C2A model.**

## **3. Run a similar simulation with your PDB\_00005 model**



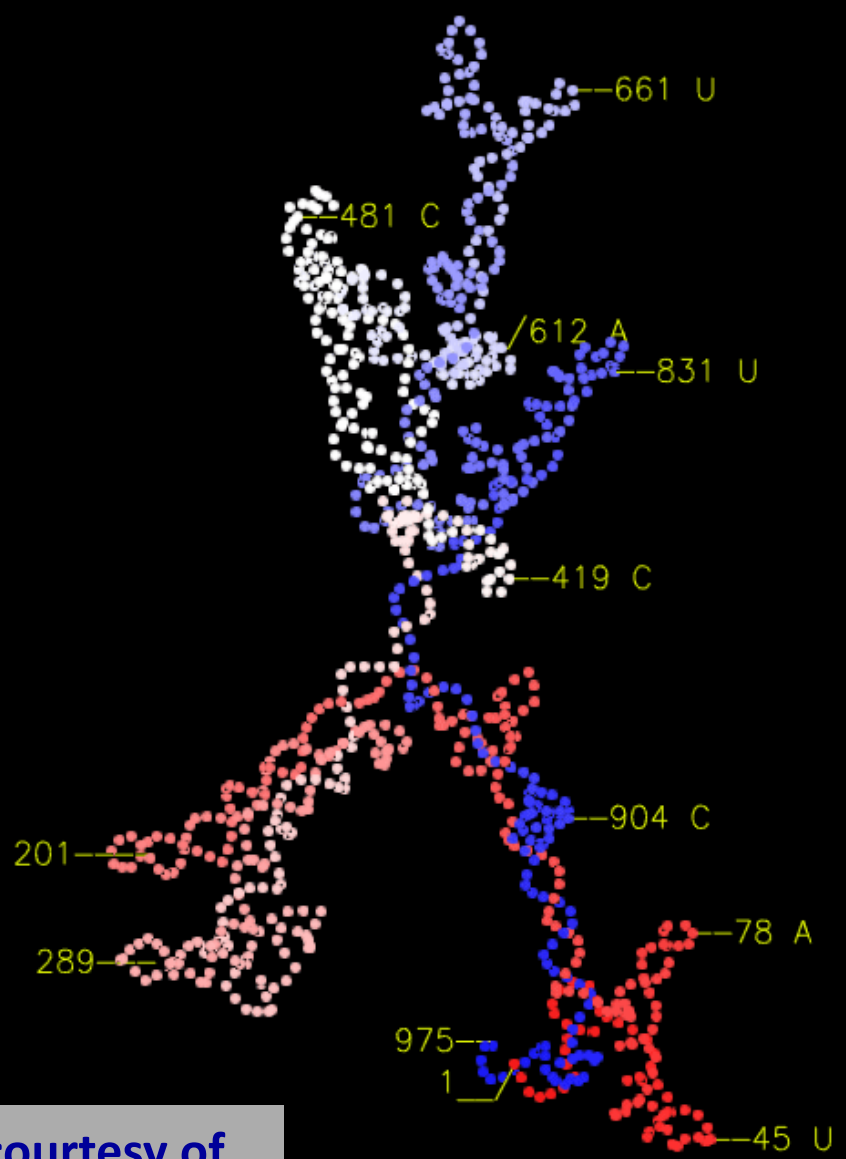
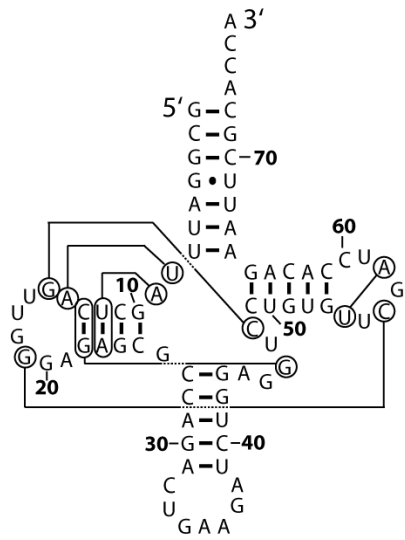
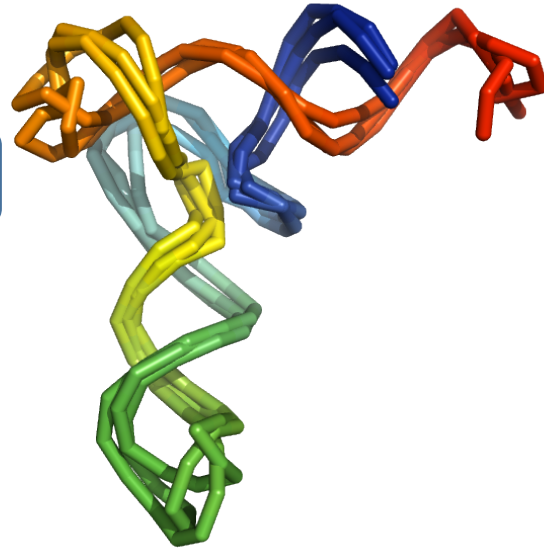
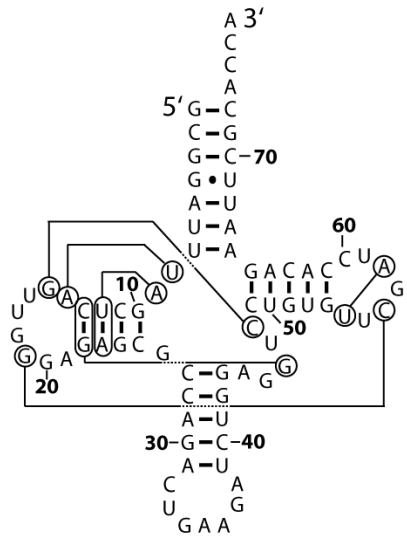


Image courtesy of  
Ajay Gopal

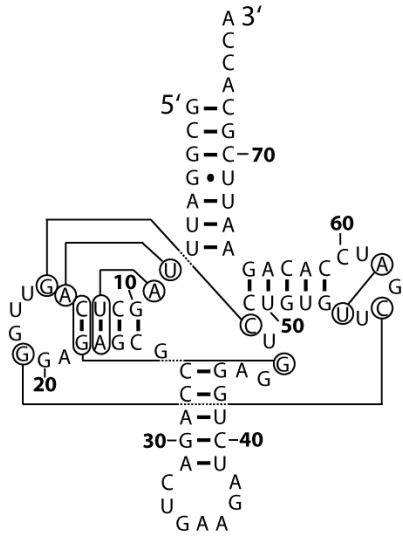
# Summary



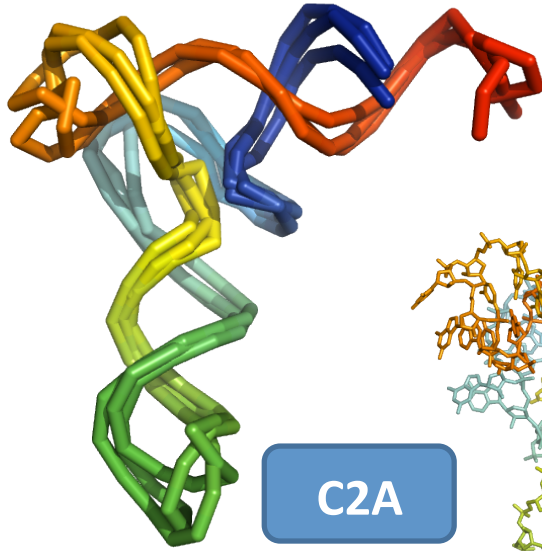
# Summary



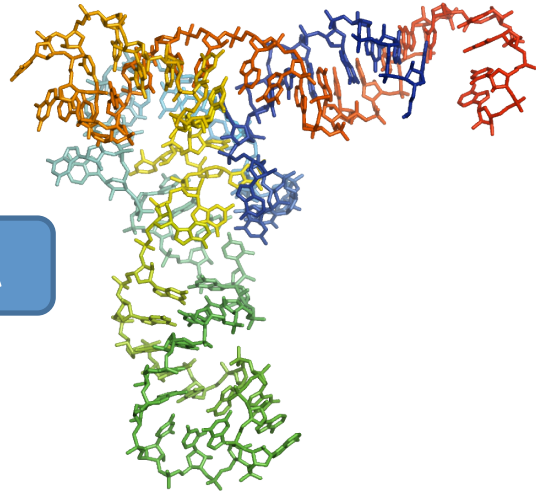
# Summary



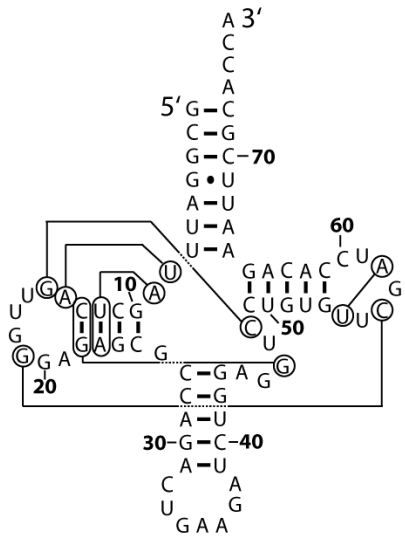
NAST



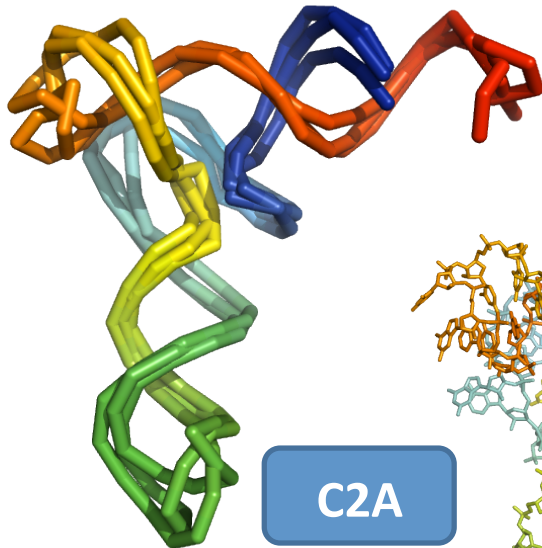
C2A



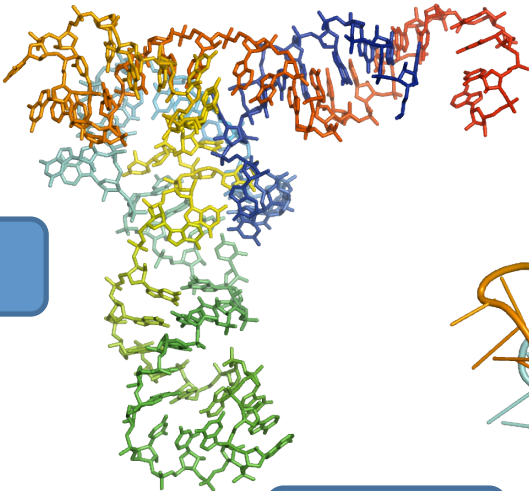
# Summary



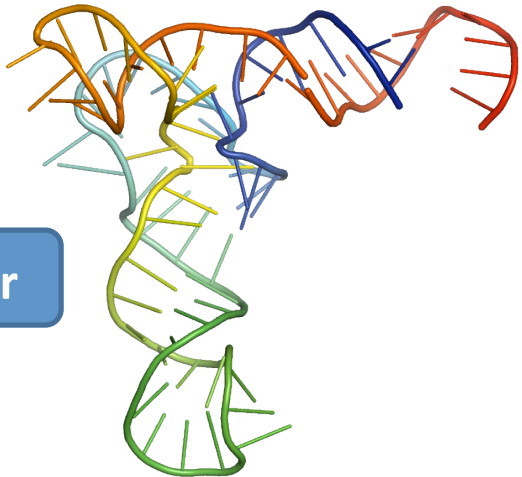
NAST



C2A



Zephyr



## Downloads

**NAST (includes C2A):**

[www.simtk.org/home/nast](http://www.simtk.org/home/nast)

**C2A (stand alone):**

[www.simtk.org/home/c2a](http://www.simtk.org/home/c2a)

**Zephyr:**

[www.simtk.org/home/zephyr](http://www.simtk.org/home/zephyr)

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**Simbios**

**Helix Group**

**Thank You!**

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