# The ViennaRNA Package 2.0

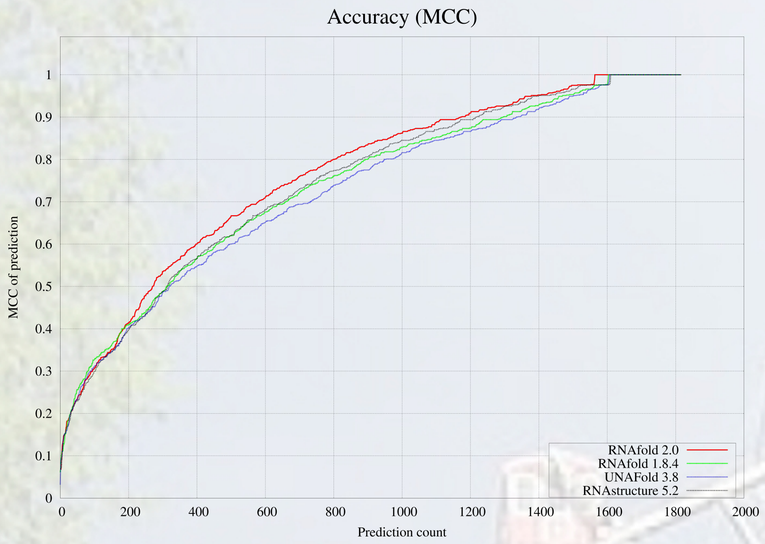
Ronny Lorenz[1], Stephan H. Bernhart[1], Christoph Flamm[1], Ivo L. Hofacker[1]

[1]Institute for Theoretical Chemistry, University of Vienna, Währingerstraße 17, A-1090 Wien, Austria

GEN-AU GENOMFORSCHUNG IN ÖSTERREICH

Bioinformatics Integration Network

BMWF




## The Story of Success

With almost **1500 citations**, the **ViennaRNA package**[1] is one of the most used RNA secondary structure prediction tools in the world. With its **new release**, **everything** – usability, accuracy, performance, simply everything in a RNA-Bioinformatician's life – gets even **better**.

## High Speed

The **ViennaRNA** package always was among the **fastest** in RNA secondary structure prediction. The **new ViennaRNA 2.0** is **even faster**!

## High Quality Results

With the **new** energy parameters and a slightly modified loop model, the **quality** of predictions could be further **increased**. The **new ViennaRNA** 2.0 **outperforms** competing, slower programs like **RNAstructure** and **UNAfold** on the tested RNAstrand dataset!

## Library

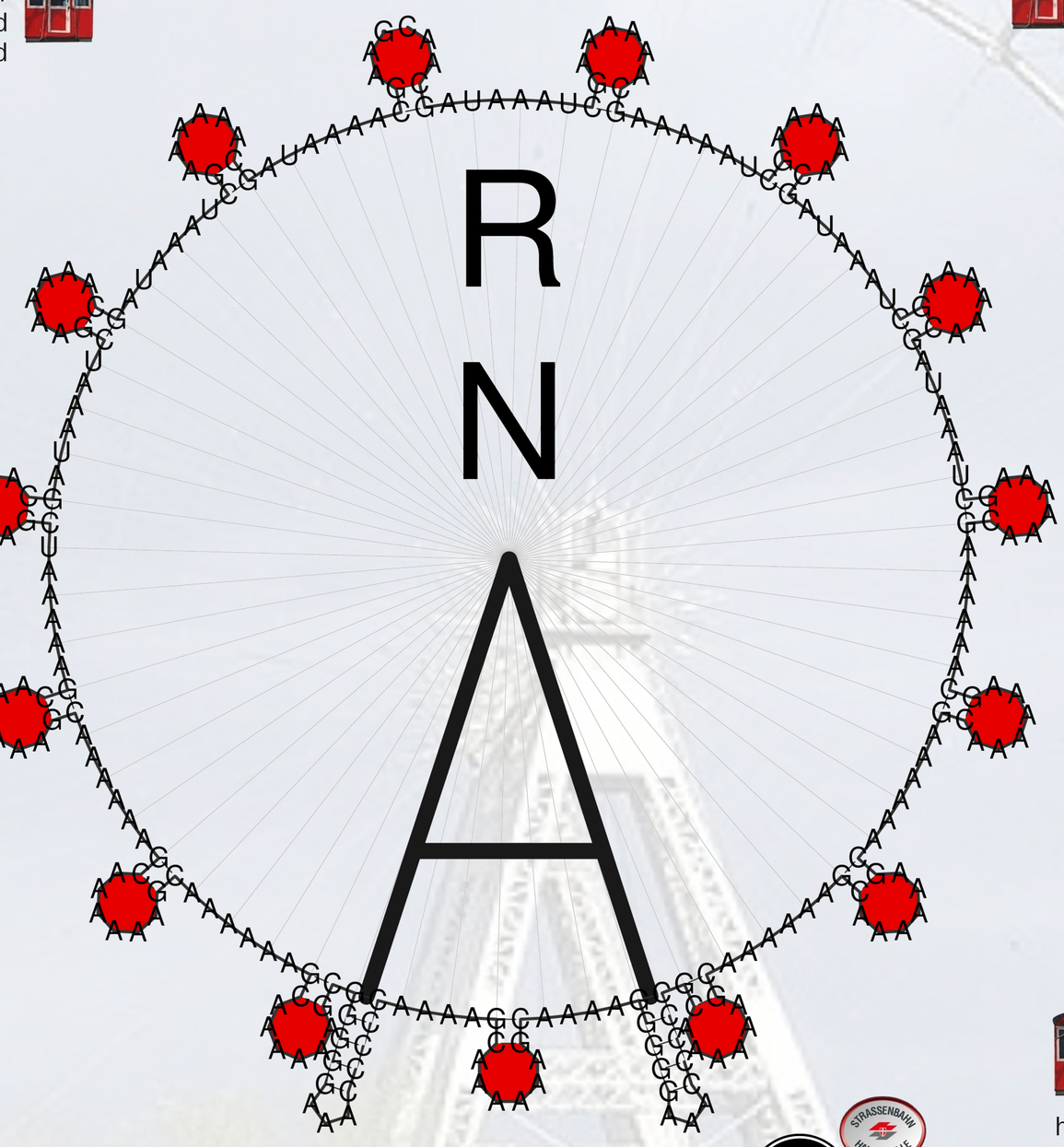
Build your **own** programs and **profit** from the qualities of the **new ViennaRNA 2.0** package! With the **improved**, easy to use and **well documented** library functions, including RNA folding routines never was easier!

## Open MPI

Use the full power of your multi-core computers by simultaneously folding many sequences! The **ViennaRNA 2.0** library is now thread-safe. The algorithms are **ready to be used** concurrently in your own applications.

## User-friendly Input

Use your files straight out of your database as input for your folding. The **new ViennaRNA 2.0** now also supports FASTA sequence files and Stockholm formatted alignments.




## Backward Compatibility

Use all your dear old scripts and programs – with only slight changes, all your programs can profit from the **all new ViennaRNA 2.0** algorithms and the improved energy model.

## Web Server

Use the **new ViennaRNA package 2.0** online. The ViennaRNA **web server** now features the new **improved** algorithms of the new package. It even provides access to **additional applications**! Be one of the **700** submitters per day at: http://rna.tbi.univie.ac.at

## Documentation

Due to the **freshly** included **Doxygen** system, library and program documentation is even **more complete** than ever **before**!

## GNU Standard Compatible

Never again you have to remember the peculiarities of the command line options. The **new ViennaRNA** 2.0 now **complies** with the **GNU** standard!

## New Turner Parameters

Tired of the energy parameters of the last millennium? **ViennaRNA 2.0** features the **latest** in nearest neighbor **energy parameters** – not only experimentally determined[2] ones, but trained ones too! What's **more**, we now include **DNA** parameters[3] among our distributed parameter sets! Of course you can also use your reliable old parameters!

## Open Access Journal

No more nagging your librarian to get your hands on the "Monatshefte für Chemie". The new ViennaRNA 2.0 **paper** *(in preparation)* will be published in an **open-access** journal.

## References

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[2] Lu ZJ, Turner DH and Mathews DH. *A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation.* Nucleic Acids Res.,*34:4912-4924,* 2006

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[4] Zuker, M and Stiegler, P. *Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information*. Nucleic Acids Res., 9:133–148, 1981

[5] John S. McCaskill. *The Equilibrium Partition Function and Base Pair Binding Probabilities for RNA Secondary Structure*. Biopolymers, 29:1105–1119, 1990

## Acknowledgements

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## New Features

The **ViennaRNA 2.0** comes with tons of new applications and scripts:

- Find local consensus structures with the new **RNALalifold**.
- Explore features of the secondary structure space of an RNA molecule based on basepair distance class partitioning with **RNA2Dfold**.
- Assess the quality of your local structures with **RNALfoldz**!
- And **many more**