

Citizen Scientists' contributions to the RNA design problem

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Citizen Scientist

Geneva, June 5, 2018

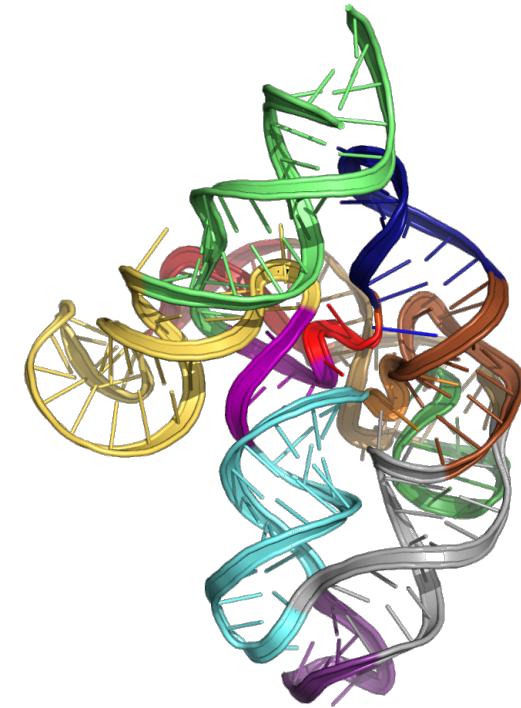
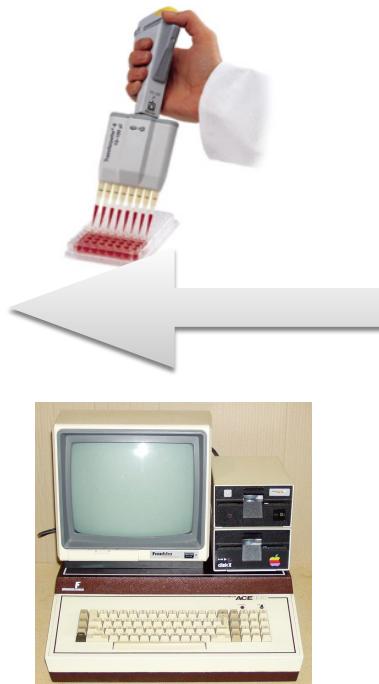


Stanford
MEDICINE



From RNA function to sequence

GGUUGGGUUGGGAAGUAUCA
UGGCUAAUCACCAUGAUGCA
AUCGGGUUGAACACUUAAUU
GGGUAAAACGGUGGGGGAC
GAUCCCGUAACAUCGUCCU
AACGGCGACAGACUGCACGG
CCCUGGCCUUAGGUGGUU
CAAUGAACAGUCGUUCCGAA
AGGAAGCAUCCGGUAUCCA
AGACAAUC



RNA secondary structure: solved?

The screenshot shows the RNAfold WebServer interface. At the top, there's a navigation bar with 'RNAfold WebServer' and two buttons: '1 Enter Input Parameters' and '2 View Results'. Below the navigation bar, there are links for '[Home | New job | Help]'. The main area is titled 'Quikfold' and has a sub-section titled 'Fast Folding — Energies & Structures'. It includes fields for 'Enter a name for your job:' and 'Sequences: Enter one or more sequences separated by ; (semicolons.)'. There is also a large text input area.

The screenshot shows the INFO-RNA server interface. The title 'INFO-RNA' is prominently displayed in large blue letters. Below it, the subtitle 'A Server for Inverse Folding of RNA' is shown. To the right is the logo of Albert-Ludwigs-University Freiburg. The background is light green.

The screenshot shows the NUPACK nucleic acid package interface. The main title 'NUPACK' is in large orange letters, with 'nucleic acid package' in smaller blue text below it. A navigation bar at the top includes tabs for 'Analysis', 'Design', 'Utilities', 'Downloads', 'Demos', and 'Help'. The 'Input' tab is currently selected. Below the tabs, there are fields for 'Nucleic acid type' (radio buttons for RNA and DNA), 'Temperature' (input field with value '37.0'), 'Number of designs' (input field with value '1'), and 'Target structure' (input field).

<http://rna.tbi.univie.ac.at/>
<http://mfold.rna.albany.edu/?q=DINAMelt/Quickfold>
<http://www.bioinf.uni-freiburg.de/Software/INFO-RNA/start.html>
<http://www.nupack.org/>



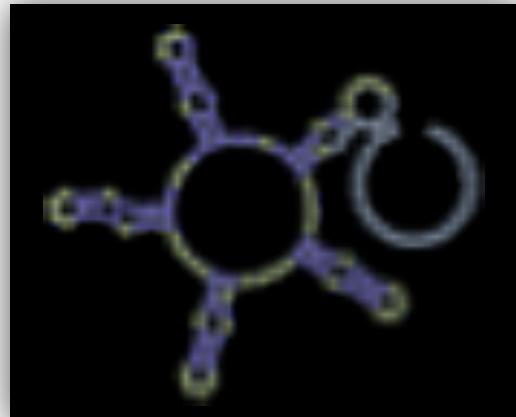
Played by Humans. Scored by Nature

The screenshot shows a complex RNA structure composed of blue and yellow nucleotides. The interface includes a score summary at the top left: "Total: -44.1kCal", "Score: 4.8kCal", and "Stability: -0.8kCal". A red-bordered box highlights a specific interaction point. At the bottom, there are various game controls like zoom, rotate, and save.

Game Interface

This screenshot displays a table of submitted RNA designs. The columns include Title, Designer, Votes, My Votes, and Description. The table lists numerous entries, such as "The Cross", "The Cross 2", "CrossV1", and "CrossV2", each with a brief description and designer's name. A large text box on the right contains a conversation between players, including "tartan" and "Chesterfield".

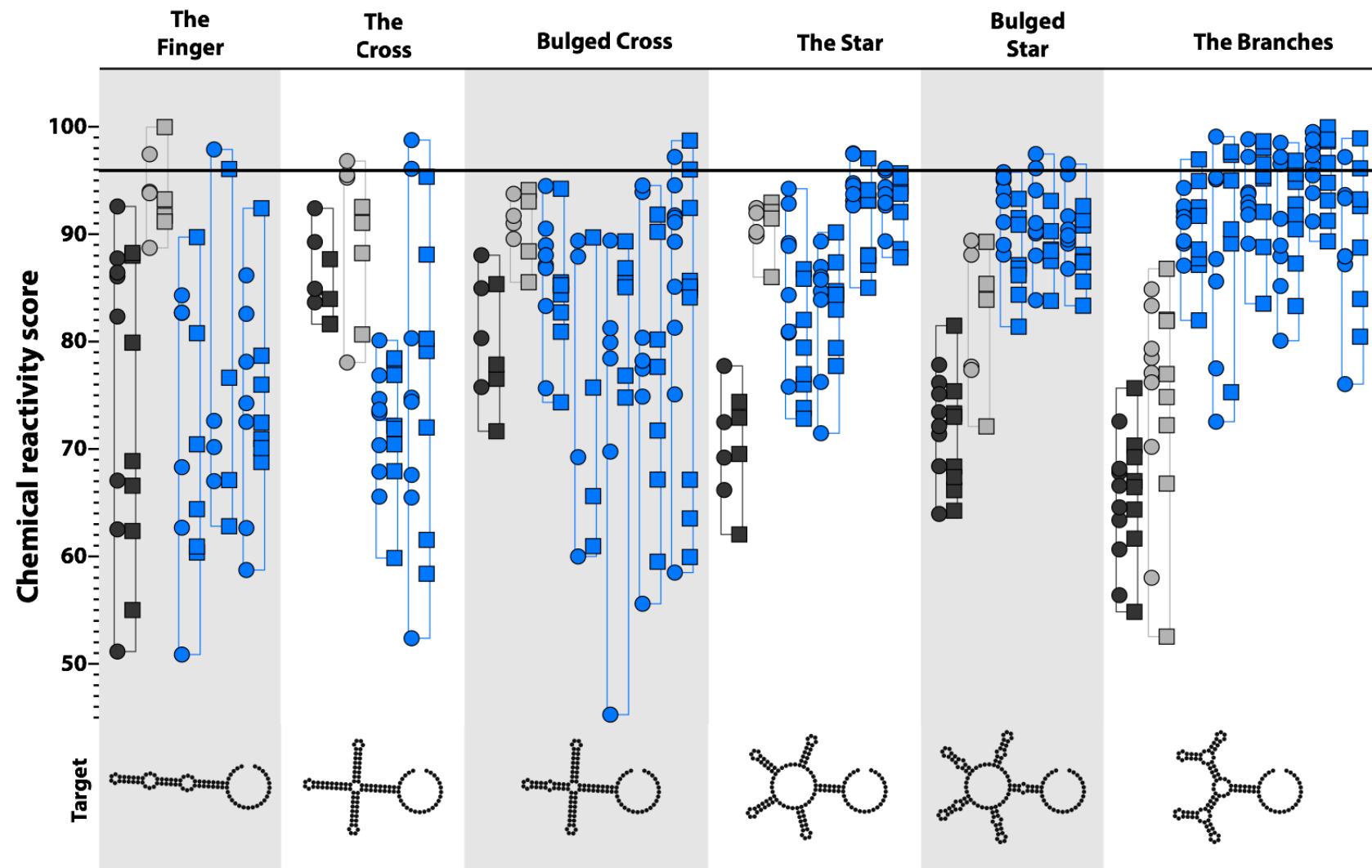
Voting



Results



Synthesis



EteRNA: humans
NUPACK
RNAInverse

LAB Strategy Market Beta 2

Tell us your strategy for picking successful designs in the lab and help us build the first algorithm to score RNAs in nature!

How well are EteRNA players doing?

EteRNA Ensemble Strategy (coming soon!) ?? Ordering Run!

All player strategies contributes to the EteRNA Ensemble Strategy which will be open to public. It is the first algorithm that predicts how well RNA sequences fold into the target shape in nature!

How to participate?

Post your Strategy

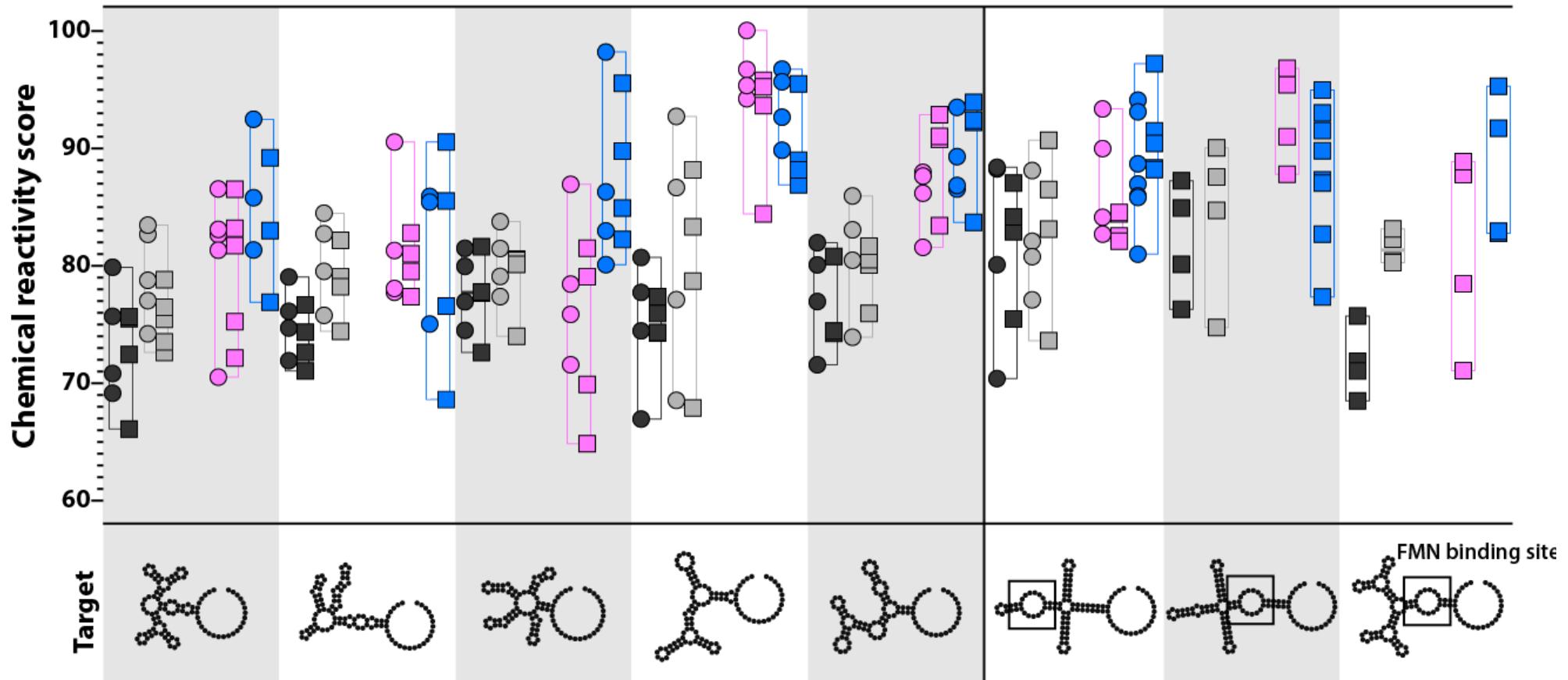
First, write your own strategy in the forum (See an example post.) EteRNA developers will write an algorithm based on your post, test it on all synthesis results, and post results here! You can check out the test schedule for your strategy at [here](#).

Read more - what strategies do we want? What are all these numbers?

Submitted Strategies

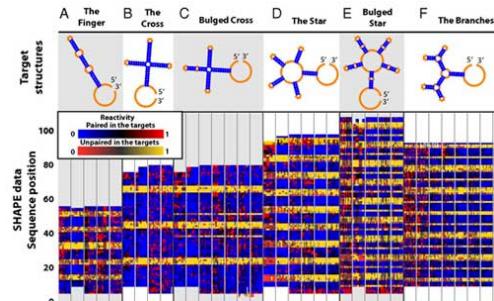
User	Strategy Name	Contribution	Ordering	length	Action
	aldo's Loops & Stacks	??	0.443	40	Run!
	Berex NZ's Berex Test	??	0.431	30	Run!
	xmbraf's Clean plot, stack caps, and safe GC	??	0.381	70	Run!
	delvad's delvad's strategy	??	0.351	60	Run!
	dejerpha's A basic test	??	0.347	20	Run!
	pengulan's Clean Dot Plot	??	0.327	10	Run!





NUPACK
 RNAInverse
 EteRNAbot
 EteRNA: humans

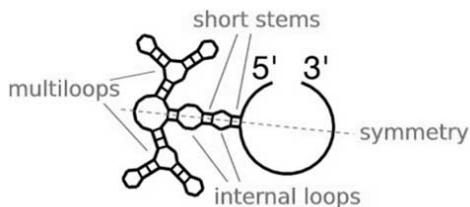
Player contributions to the RNA scientific literature



RNA design rules from a massive open laboratory

Proceedings of the National Academy of Sciences - February 2014

Lee, J., Kladwang, W., Lee, M., Cantu, D., Azizyan, M., Kim, H., Limpaecher, A., Yoon, S., Treuille, A., Das, R., and **Eterna participants**

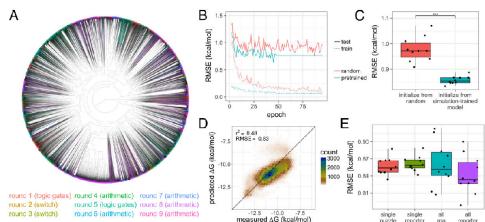


Principles for predicting RNA secondary structure design difficulty

Journal of Molecular Biology - February 2016

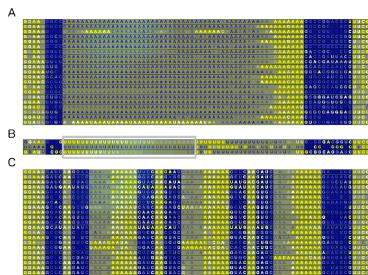
Jeff Anderson-Lee, Eli Fisker, Vineet Kosaraju, Michelle Wu, Rhiju Das, Minjae Lee, Justin Kong, **mat747**, Treuille, and **Eterna players**

Player contributions to the RNA scientific literature



Prospects for recurrent neural network models to learn RNA biophysics from high-throughput data
bioRxiv - December 2017

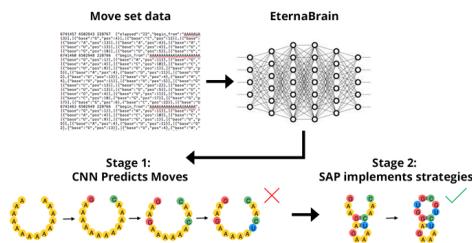
Michelle J Wu, Johan OL Andreasson, Wipapat Kladwang, William J Greenleaf,
Eterna players, Rhiju Das



Evidence of an Unusual Poly(A) RNA Signature Detected by High-throughput Chemical Mapping

bioRxiv - April 2018
Roger Wellington-Oguri, Eli Fisker, Michelle Wiley, Mat Zada, Eterna Players

Player contributions to the RNA scientific literature



EternaBrain: Automated RNA design through move sets from an Internet-scale RNA videogame

bioRxiv - May 2018

Rohan Koodli, Benjamin Keep, Katherine R Coppess, **Fernando Portela**, **Eterna Players**, Rhiju Das

Genome-wide dissection of extracellular vesicle biology with barcoded miRNAs

submitted

Albert Lu, Paulina Wawro, David Morgens, **Fernando Portela**, Michael C. Bassik and Suzanne R. Pfeffer

An unexpectedly effective Monte Carlo technique for the RNA inverse folding problem

submitted

Fernando Portela

Development Team

Site Development
jnicol (player), ElNando888 (player), Omei (player), Siqi Tian, Ben Keep, Caleb Geniesse

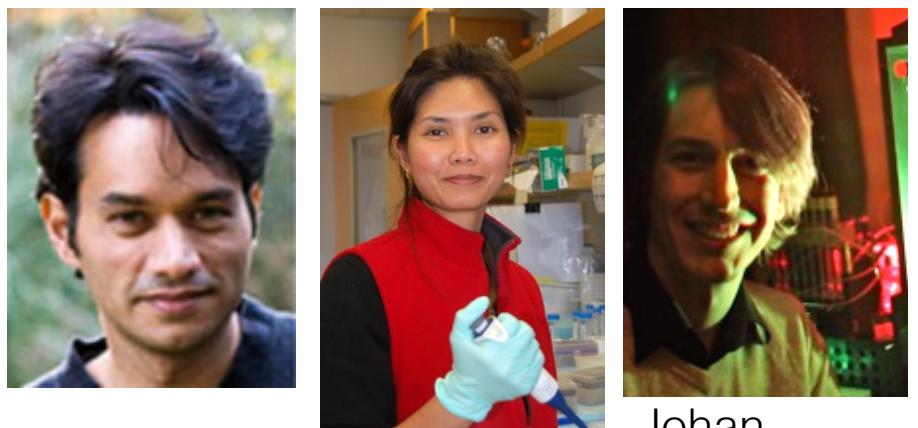
Experiments & Analysis
Johan Andreasson, Ann Kladwang (Greenleaf & Das labs, Stanford)

Visual Design
Sharif Ezzat

Principal Investigator
Rhiju Das

Prior Contributors

Game Creator: J. Lee. Site Development: V. Kosaraju, P. Kinney, S. Gaikwad, M. Lee, T. Mandel, A. Limpaecher, N. Fishel, S. Wang, E. Kelly, M. Baumgartner, S. Federwisch, S. Mohan, B. Seo, W. Kong. Experiments & Analysis: D. Cantu, P. Cordero, T. Mann, S. Yoon, H. Kim. Graphics: M. Yao, T. Hu, J. Ciscon, D. Klionsky, E. Butler, R. Zhu. Sound: B. Bethurum. Principal Investigator: A. Treuille.



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