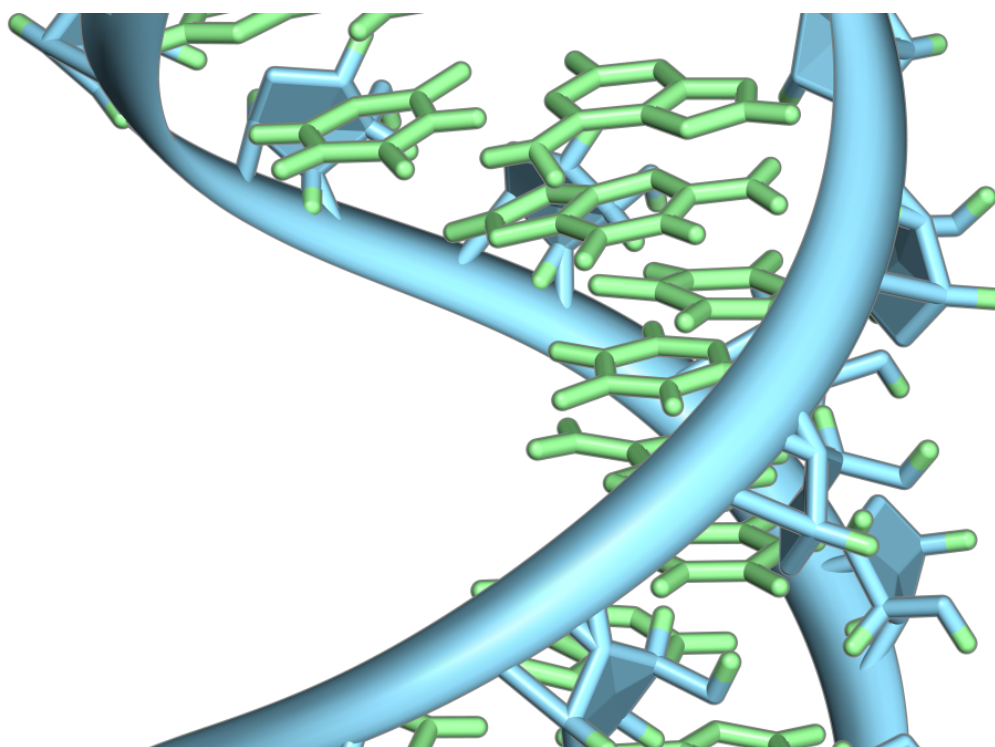


# New online database brings the genome into focus using molecular structure

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A hairpin loop from a pre-mRNA. Highlighted are the nucleobases (green) and the ribose-phosphate backbone (blue). Note that this is a single strand of RNA that folds back upon itself. Credit: Vossman/ Wikipedia

Iowa State University researchers have built an accessible online database that brings critical genomic data into sharp focus with the single click of a mouse.

In an article published today in the journal *Scientific Reports*, a team of Iowa State University researchers presented a novel database that allows scientists to quickly access information on RNA structures encoded within the [human genome](#). The database is [freely accessible to anyone on the web](#), where it allows scientists to study the functions and structure of RNA with greater speed and ease than in the past. This will help facilitate basic research into human biology and could pave the way for new medical treatments that target RNA, said Walter Moss, an assistant professor in the Roy J. Carver Department of Biochemistry, Biophysics and Molecular Biology.

RNAs, short for ribonucleic acids, are molecular chains that are transcribed, or copied, from the genome. RNAs can be information carriers, acting as intermediates between DNA and protein, or as independently functioning molecules that mediate many critical regulatory processes. Unlike DNA, RNA can "fold back" on itself to form structures that rival proteins in their complexity. This folding plays key roles in RNA function, so gaining structural information on RNA can provide important insights into our understanding of how organisms work, Moss said.

"RNA is fundamental to understanding biology, and advances in sequencing technology have led to an explosion in the list of potentially functional RNAs," he said.

For example, while only about 2 percent of the 3.5 billion base pairs of human DNA encode proteins, more than 70 percent is transcribed into RNA. Understanding the functions of this ocean of uncharted RNA poses a key scientific challenge, and the new database provides crucial tools for charting it, Moss said.

Moss, along with graduate student Ryan Andrews and Research IT Director Levi Baber, fragmented the entire human genome into more

than 154 million overlapping windows and calculated a range of metrics valuable in understanding how RNA folds.

"Anyone around the world can now retrieve with one click what once took hours of calculations to determine," Andrews said.

RNA therapeutics, a new approach in medicine in which RNA is targeted with drugs rather than proteins, show great promise, and the structural [database](#) detailed in the publication provides a huge repository of potential therapeutic leads, Moss said.

**More information:** Ryan J. Andrews et al. RNAStructuromeDB: A genome-wide database for RNA structural inference, *Scientific Reports* (2017). [DOI: 10.1038/s41598-017-17510-y](https://doi.org/10.1038/s41598-017-17510-y)

Provided by Iowa State University

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