

## Wojciech K. Kasprzak

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### Summary:

- I am a co-inventor on two US patents (No. 2010148085 and 20120263648) and one pending
- I have co-authored 49 scientific publications, including high-impact papers in Nature and PNAS, and additional ten book chapters.
- I have given 34 oral presentations, including a talk at the Gordon Research Conference on RNA Nanotechnology, five presentations at the Annual Biophysical Society Meetings and four at other international conferences.
- I have presented over 55 posters at various professional meetings.
- I have mentored numerous student interns, teaching them computational protocols, programming, and RNA structure modeling.
- I have written and co-developed multiple pieces of software available to the community at large for downloads.

### Professional Experience and Research Interests:

- Three-dimensional RNA structure prediction, modeling, molecular dynamics simulation and analysis
- RNA-based computational nanostructure design and characterization
- Docking of small ligands to nucleic acids targets
- RNA structure prediction and structure-function connection
- Multi-conformational secondary structure systems
- Structure prediction and analysis software development
- Integration of computational tools into functional pipelines

### Skills:

- **Scientific Software:**  
**Molecular dynamics** packages: Amber, NAMD, Tinker; coarse-grain and elastic network modelling (SimRNA, iFoldRNA, ANM MAVENS, MOSAICS); Advanced use of **3D RNA structure prediction** programs: (RNAComposer, SimRNA, Vfold 2D/3D, MC-Sym pipeline) and Automated **Structure analysis tools** (such as Amber tools, 3DNA-DSSR, FR3D, Curves, RNAPdb, MolProbity, ERRASER), familiarity with protein structure prediction and dynamics; **Ligand docking** programs: AutoDock family (Vina/Vinardo, Smina), rDock, familiar with MolSoft ICM and Schrodinger packages; **3D modeling, analysis and visualization** software: UCSF Chimera, PyMOL, VMD, Accelrys Discovery Studio, RasMol, RNA2D3D; **RNA nanostructure design and**

**modeling** software: NanoTiler, RNA2D3D, own custom scripts and programs in PyMOL/Python); **RNA/DNA secondary structure prediction** tools, such as MPGAfold - Genetic Algorithm, Mfold/RNAstructure/RNAfold family of dynamic programming algorithms, contraFOLD, NUPACK, as well as other RNA/DNA secondary structure and tertiary interactions prediction programs, such as IPknot, pkiss, KineFold, NanoFolder/HyperFold, CyloFold. **Sequence search and alignment** tools: (BLAST, Clustal), RNAmot/RNA Motif sequence and structure alignment.

**Other tools:** own StructureLab 2D/3D RNA/DNA structure prediction analysis package, 2D structure visualization programs (such as own RiboSketch and RNA2Drawer, and many others), GCG package, SigmaPlot, Prism, (xm)grace, gnuplot.

- **Databases:** Relational (MySQL), document-oriented NoSQL (MongoDB), object-oriented (AllegroStore)
- **Programming Languages:** Lisp, Python (and Python PyMOL/Chimera APIs), C++, C, Fortran, Pascal, Basic, Unix shell scripts and tools, HTML/PHP
- **Operating Systems:** Linux/Unix, (including installation, configuration and administration of Virtual Machines in Oracle's VirtualBox), MacOS, MS Windows
- **Platforms:** Linux workstations (Ubuntu, CentOS/Red Hat), Linux clusters MIMD/GPU, Apple.

### **Chronology of Employment:**

2013-present	Bioinformatics Analyst IV, in support of Gene Regulation and Chromosome Biology Laboratory (since 2015), then RNA Biology Laboratory (since 2016), Basic Science Program, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research sponsored by the National Cancer Institute, Frederick, MD
2003-2013	Programmer Analyst IV, Basic Science Program, SAIC-Frederick, Inc., Computational RNA Structure Section, CCR Nanobiology Program, Frederick National Laboratory for Cancer Research, Frederick, MD
1997-2003	Programmer Analyst, Basic Science Program, SAIC-Frederick, Inc., CCR Nanobiology Program, NCI, Frederick, MD
1996-1997	Jr. Scientific Applications Analyst, Frederick Biomedical Supercomputing Center, SAIC, Frederick, MD
1990-1996	Laboratory Assistant, then Research Associate, Biomedical Supercomputing Center, DynCorp/Program Resources Inc., Frederick, MD

### **Education:**

1994	<b>Johns Hopkins University</b> , Baltimore, MD, M.S., Computer Science.
1989	<b>University of Maryland at College Park</b> , College Park, MD, B.S., Electrical Engineering.

### **Professional Societies and Honors:**

Biophysical Society Member

RNA Society Member  
International Society of RNA Nanotechnology and Nanomedicine (ISRNN)

SAIC's Distinguished Career Service Award, 2010  
Publication Award, STFC Publication Competition for the category of Information & Communications Technology (SAIC-wide competition), 2007  
SAIC's Science Achievement Award, 2000  
Multiple Poster awards at the Spring Research Festival, NCI-Frederick, between 2003 and 2019.

### **Selected Publications:**

1. Shapiro BA, Chen J, Busse T, Navetta J, Kasprzak W, and Maizel JV: Optimization and performance analysis of a massively parallel dynamic programming algorithm for RNA secondary structure prediction. The International Journal of Supercomputer Applications 9(1): 29-39, 1995.
2. Shapiro BA and Kasprzak W: STRUCTURELAB: A heterogeneous bioinformatics system for RNA structure analysis. J. Mol. Graphics 14: 194-205, 1996.
3. Kasprzak W and Shapiro BA: Stem Trace: An interactive visual tool for comparative RNA structure analysis. Bioinformatics 15(1): 16-31, 1999.
4. Atha DH, Kasprzak W, and Shapiro BA: Prediction of DNA single strand conformational polymorphism (SSCP): Analysis by capillary electrophoresis and computerized DNA modeling. Nucleic Acids Res. 29(22): 4643-4653, 2001.
5. Kasprzak W, Bindewald E, and Shapiro BA: Structural polymorphism of the HIV-1 leader region explored by computational methods. Nucleic Acids Res. 33(22): 7151-7163, 2005.
6. Bindewald E, Hayes R, Yingling YG, Kasprzak W, and Shapiro BA: RNA Junction: A database of RNA junctions and kissing loops for three-dimensional structural analysis and nanodesign. Nucleic Acids Res. 36 (Database Issue): D392-D397, 2008.
7. Linnstaedt SD, Kasprzak WK, Shapiro BA, and Casey JL: The fraction of RNA that folds into the correct branched secondary structure determines hepatitis delta virus RNA editing levels. RNA 15(6): 1177-1187, 2009.
8. Zuo X, Wang J, Yu P, Eyler D, Xu H, Starich MR, Tiede DM, Simon AE, Kasprzak W, Schwieters CD, Shapiro BA, and Wang Y-X: Solution structure of the cap-independent translational enhancer and ribosome binding element in the 3' UTR of Turnip Crinkle virus. Proc. Natl. Acad. Sci U.S.A. 107(4): 1385-1390, 2010.

9. Kasprzak W, Bindewald E, Kim T, Jaeger L, and Shapiro BA: Use of RNA structure flexibility data in nanostructure modeling. Methods 54(2): 239-250, 2011.
10. Manzano M, Reichert ED, Polo S, Falgout B, Kasprzak W, Shapiro BA, and Padmanabhan R: Identification of *cis*-acting elements in the 3'-untranslated region of the dengue virus type 2 RNA that modulate translation and replication. J. Biol. Chem. 286(25): 22521-22534, 2011.
11. Gao F, Kasprzak W, Stupina V, Shapiro BA, and Simon AE: A ribosome-binding, 3' translational enhancer has a T-shaped structure and engages in a long-distance RNA: RNA interaction. J. Virol. 86(18): 9828-9842, 2012.
12. Kasprzak WK, Shapiro BA: MPGAfold in dengue secondary structure prediction. Methods Mol Biol. 1138:199-224, 2014.
13. Afonin KA, Kasprzak W, Bindewald E, Puppala PS, Diehl AR, Hall KT, Kim T, Zimmermann MT, Jernigan RL, and Shapiro BA: Computational and Experimental Characterization of RNA Cubic Nanoscaffolds. Methods 67(2):256-266, 2014. (first co-author)
14. Belew AT, Meskauskas A, Musalgaonkar S, Vivek AM, Sulima SO, Kasprzak WK, Shapiro BA, and Dinman JD: Ribosomal frameshifting in the CCR5 mRNA: regulation by miRNAs and NMD. Nature. 512(7514):265-269, 2014.
15. Afonin KA, Viard M, Kagiampakis I, Case CL, Hofmann J, Vrzak A, Kireeva M, Kasprzak WK, Kewalramani VN, and Shapiro BA: Triggering RNA interference with RNA-RNA, RNA-DNA and DNA-RNA nanoparticles. ACS Nano. 9(1):251-259, 2015.
16. Salton M, Kasprzak WK, Voss T, Shapiro BA, Poulikakos PI, Misteli T: Inhibition of vemurafenib-resistant melanoma by interference with pre-mRNA splicing. Nat Commun. 6:7103, 2015.
17. Halman JR, Satterwhite E, Roark B, Chandler M, Viard M, Ivanina A, Bindewald E, Kasprzak WK, Panigaj M, Bui MN, Lu JS, Miller J, Khisamutdinov EF, Shapiro BA, Dobrovolskaia MA, Afonin KA. Functionally-interdependent shape-switching nanoparticles with controllable properties. Nucleic Acids Res. 45(4):2210-2220, 2017.
18. Le MT, Kasprzak WK, Kim T, Gao F, Young MY, Yuan X, Shapiro BA, Seog J, Simon AE. Folding behavior of a T-shaped, ribosome-binding translation enhancer implicated in a wide-spread conformational switch. eLife. 6: e22883, 2017. (first co-author)
19. Sharan R, Bindewald E, Kasprzak WK, Shapiro B: Computational Generation of RNA Nanorings. Methods Mol Biol. 1632:19-32, 2017.
20. Lu JS, Bindewald E, Kasprzak WK, Shapiro BA: RiboSketch: Versatile Visualization of Multi-stranded RNA and DNA Secondary Structure. Bioinformatics. 34(24):4297-4299, 2018.

21. Bofill-De Ros X, Kasprzak WK, Bhandari Y, Fan L, Cavanaugh Q, Jiang M, Dai L, Yang A, Shao TJ, Shapiro BA, Wang YX, Gu S: Structural Differences between Pri-miRNA Paralogs Promote Alternative Drosha Cleavage and Expand Target Repertoires. Cell Rep. 26(2):447-459, 2019.
22. Zakrevsky P, Kasprzak WK, Heinz WF, Wu W, Kahnt H, Bindewald E, Dorjsuren N, Fields EA, de Val N, Jaeger L, and Shapiro BA. Truncated Tetrahedral RNA Nanostructures Exhibit Enhanced Features for Delivery of RNAi Substrates. Nanoscale, 12(4):2555-2568. 2020.

**Selected Book Chapters:**

1. Kasprzak WK and Shapiro BA: Computational Prediction and Modeling Aid in the Discovery of a Conformational Switch Controlling Replication and Translation in a Plus-Strand Virus. In Leontis N and Westhof E (Eds.): RNA 3D Structure Analysis and Prediction, Nucleic Acids and Molecular Biology. New York, Springer, pp. 119-142, 2012.
2. Kasprzak W and Shapiro BA: Role of dynamics in RNA nanostructure design. In Guo P and Haque F (Eds.): RNA Nanotechnology and Therapeutics, CRC Press, Boca Raton, FL, 2013, pp. 139-157.
3. Kasprzak W and Shapiro BA: MPGAfold in Dengue Secondary Structure Prediction. In Padmanabhan R and Vasudevan S (Eds.): Dengue: Methods and Protocols. New York, Humana Press (Springer), 2014, pp. 199-224.