



Inga Jarmoskaite

Basic Life Science Research Scientist, Genetics

Bio

HONORS AND AWARDS

- Award for Excellence, The SPARK Translational Research Program at Stanford University School of Medicine (2021)
- Best Poster Award, Gordon Research Conference on Post-transcriptional Gene Regulation (2018)
- The Helena Anna Henzl-Gabor Young Women in Science Fund for Postdoctoral Scholars Travel Grant, Stanford University (2017)
- Harden Bursary, EMBO Conference—Helicases and Nucleic Acid Translocases (2013)
- RNA Society Poster Award, FASEB Conference on Nucleic Acid Enzymes (2012)
- Travel Award, University of Texas at Austin (2010, 2012)
- Eakin Fellowship, University of Texas at Austin (2010)
- Eastern European Scholarship, Ev. Studienwerk e.V. Villigst (Germany) (2004–2008)

EDUCATION AND CERTIFICATIONS

- PhD, University of Texas at Austin, Biochemistry (2014)
- Diplom, Julius Maximilian University of Würzburg (2009)

Professional

PROFESSIONAL AFFILIATIONS AND ACTIVITIES

- Member, SPARK at Stanford (2019 - present)

Publications

PUBLICATIONS

- **A comprehensive thermodynamic model for RNA binding by the *Saccharomyces cerevisiae* Pumilio protein PUF4.** *Nature communications* Sadee, C., Hagler, L. D., Becker, W. R., Jarmoskaite, I., Vaidyanathan, P. P., Denny, S. K., Greenleaf, W. J., Herschlag, D. 2022; 13 (1): 4522
- **Measurement of ATP utilization in RNA unwinding and RNA chaperone activities by DEAD-box helicase proteins** *Methods in Enzymology* Jarmoskaite, I., Helmers, A. E., Russell, R. 2022
- **Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis.** *Nature communications* Liu, X., Sun, T., Shcherbina, A., Li, Q., Jarmoskaite, I., Kappel, K., Ramaswami, G., Das, R., Kundaje, A., Li, J. B. 2021; 12 (1): 2165
- **ATP utilization by a DEAD-box protein during refolding of a misfolded group I intron ribozyme.** *The Journal of biological chemistry*

- Jarmoskaite, I., Tijerina, P., Russell, R.
2020
- **How to measure and evaluate binding affinities.** *eLife*
Jarmoskaite, I. n., AlSadhan, I. n., Vaidyanathan, P. P., Herschlag, D. n.
2020; 9
 - **A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins** *MOLECULAR CELL*
Jarmoskaite, I., Denny, S. K., Vaidyanathan, P. P., Becker, W. R., Andreasson, J. L., Layton, C. J., Kappel, K., Shivashankar, V., Sreenivasan, R., Das, R., Greenleaf, W. J., Herschlag, D.
2019; 74 (5): 966+
 - **Demonstration of protein cooperativity mediated by RNA structure using the human protein PUM2** *RNA*
Becker, W. R., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D.
2019; 25 (6): 702–12
 - **Blind tests of RNA-protein binding affinity prediction** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Kappel, K., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D., Das, R.
2019; 116 (17): 8336–41
 - **Quantitative high-throughput tests of ubiquitous RNA secondary structure prediction algorithms via RNA/protein binding** *bioRxiv*
Becker, W. R., Jarmoskaite, I., Kappel, K., Vaidyanathan, P. P., Denny, S. K., Das, R., Greenleaf, W. J., Herschlag, D.
2019
 - **Lessons from Enzyme Kinetics Reveal Specificity Principles for RNA-Guided Nucleases in RNA Interference and CRISPR-Based Genome Editing.** *Cell systems*
Bisaria, N., Jarmoskaite, I., Herschlag, D.
2017; 4 (1): 21-29
 - **Science Educational Outreach Programs That Benefit Students and Scientists.** *PLoS biology*
Clark, G., Russell, J., Enyeart, P., Gracia, B., Wessel, A., Jarmoskaite, I., Polioudakis, D., Stuart, Y., Gonzalez, T., MacKrell, A., Rodenbusch, S., Stovall, G. M., Beckham, et al
2016; 14 (2): e1002368
 - **Hexapeptides That Inhibit Processing of Branched DNA Structures Induce a Dynamic Ensemble of Holliday Junction Conformations** *JOURNAL OF BIOLOGICAL CHEMISTRY*
Cannon, B., Kachroo, A. H., Jarmoskaite, I., Jayaram, M., Russell, R.
2015; 290 (37): 22734-22746
 - **DEAD-box protein CYT-19 is activated by exposed helices in a group I intron RNA** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Jarmoskaite, I., Bhaskaran, H., Seifert, S., Russell, R.
2014; 111 (29): E2928-E2936
 - **RNA Helicase Proteins as Chaperones and Remodelers** *ANNUAL REVIEW OF BIOCHEMISTRY, VOL 83*
Jarmoskaite, I., Russell, R.
2014; 83: 697-725
 - **The Long-Range P3 Helix of the Tetrahymena Ribozyme Is Disrupted during Folding between the Native and Misfolded Conformations** *JOURNAL OF MOLECULAR BIOLOGY*
Mitchell, D., Jarmoskaite, I., Seval, N., Seifert, S., Russell, R.
2013; 425 (15): 2670-2686
 - **Toward a molecular understanding of RNA remodeling by DEAD-box proteins** *RNA BIOLOGY*
Russell, R., Jarmoskaite, I., Lambowitz, A. M.
2013; 10 (1): 44-55
 - **Solution structures of DEAD-box RNA chaperones reveal conformational changes and nucleic acid tethering by a basic tail** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Mallam, A. L., Jarmoskaite, I., Tijerina, P., Del Campo, M., Seifert, S., Guo, L., Russell, R., Lambowitz, A. M.

2011; 108 (30): 12254-12259

- **DEAD-box proteins as RNA helicases and chaperones** *WILEY INTERDISCIPLINARY REVIEWS-RNA*
Jarmoskaite, I., Russell, R.
2011; 2 (1): 135-152