Bio

As a researcher in the Herschlag lab at Stanford, I am working towards the development of a quantitative and predictive model of RNA folding. For this purpose, I use single-molecule fluorescence, small-angle X-ray scattering, and other experimental tools to dissect the structural and dynamic properties of RNA three-dimensional motifs. These 3D motifs are like LEGOS that build diverse and complex functional RNA machines such as the ribosome. The goal is to develop a general model of RNA folding from the understanding of the energetic properties of small recurring building blocks or motifs. Recently, I joined an ongoing collaboration between the Greenleaf and the Herschlag labs that uses next-generation high-throughput sequencing for the characterization of RNA structural motifs. This powerful high-throughput approach developed in the Greenleaf lab allows dissection of the thermodynamic and kinetic properties of thousands of 3D motifs in parallel.

Publications

PUBLICATIONS

- Single-Molecule Fluorescence Reveals Commonalities and Distinctions among Natural and in Vitro-Selected RNA Tertiary Motifs in a Multistep Folding Pathway. *Journal of the American Chemical Society*
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- Does Cation Size Affect Occupancy and Electrostatic Screening of the Nucleic Acid Ion Atmosphere? *Journal of the American Chemical Society*
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  2016; 138 (34): 10925-10934

- Cation-Anion Interactions within the Nucleic Acid Ion Atmosphere Revealed by Ion Counting. *Journal of the American Chemical Society*
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- Quantifying Nucleic Acid Ensembles with X-ray Scattering Interferometry. *Methods in enzymology*
  Shi, X., Bonilla, S., Herschlag, D., Harbury, P.
  2015; 558: 75-97

- Roles of Long-Range Tertiary Interactions in Limiting Dynamics of the Tetrahymena Group I Ribozyme. *Journal of the American Chemical Society*
  2014; 136 (18): 6643-6648