
GO BEYOND RNA
ARRAYSTAR INC
One-Stop Solutions for Advanced RNA Research
Expression
Modification
Structure
GlycoRNA Arrays NEW !
Cover Y-RNA/Y-RNA fragment, tRNA, tiRNA&tRF, pre-miRNA, miRNA & more
R-loop Profiling R-loop Profiling NEW !
Profile the lncRNA/mRNA/circRNA organized R-loops in gene regulation by DRIPc-seq
rG4 Array NEW !
Quantify rG4 structures in the transcriptome accurately
Circular RNA Arrays
Accurately profile circular RNAs by highly specific circular junction probe design
LncRNA Arrays
Overcome the limitations of RNA-seq for lncRNAs often at low abundance
Downstream-of-Gene Transcript (DoG RNA) Arrays NEW !
Profile DoG RNAs and all their target RNA types simultaneously
Small RNA Arrays
Accurately profile miRNA, pre-miRNA, tRNA, tsRNA, and snoRNA simultaneously
Epitranscriptomic Arrays
Quantify the percentage of m6A modifications at the transcript specific level
m6A Single Nucleotide Arrays
Locate and quantify the exact m6A site at single nucleotide resolution
Small RNA Modification Arrays NEW !
Quantify o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs
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USA SCIENTIFIC
Level up and lock in.
In my lab, accuracy is everything. The stakes are high, and high stakes require high standards. That's why I depend on TipOne®. Molded with tolerances tighter than those used in aerospace, produced through a high-precision injection process, and subject to rigorous quality control, TipOne® tips provide trusted precision. I have zero room for error. I'm built for unstoppable science. Superior performance starts with your tools.
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Listen up! The message is spreading.

The versatility of RNA makes it a powerful tool in transforming how we understand, diagnose and treat disease. Over the past several years, advances in RNA research have catalyzed breakthroughs in therapeutics, personalized medicine, molecular diagnostics, infectious disease research and agricultural biology. Therefore, advanced tools for manipulation and analysis of mRNA are more important than ever. For many years, NEB has invested in the development of products to support RNA research, all of which are vetted by our own scientists in their work. Whether you are in an academic or industrial setting, we have the products, tools, services and support that will help drive your research forward.

mRNA Therapeutics and Personalized Medicine – mRNA therapeutics have emerged as a versatile platform, enabling vaccine development, protein replacement therapies and immunotherapies. NEB offers products for the full mRNA synthesis workflow, which are also available GMP-grade*.

RNA in Agricultural Biology – RNA is emerging as a transformative technology for agricultural applications, including crop protection and precision breeding. NEB's solutions for AgBio researchers include reagents for RT-qPCR, NGS library prep, and nucleic acid purification.

RNA-based Diagnostics and Surveillance – RNA-based diagnostics enable rapid, sensitive and specific detection of pathogens and biomarkers. NEB products for RT-qPCR, RNA-seq, and isothermal amplification deliver sensitive detection and streamlined workflows.

RNA in Basic Research – RNA research in academia focuses on understanding the role of RNA in diverse biological processes, and can be foundational for translational applications. NEB's basic research program focused on RNA biology utilizes many of our reagents and has contributed to advances in this area.

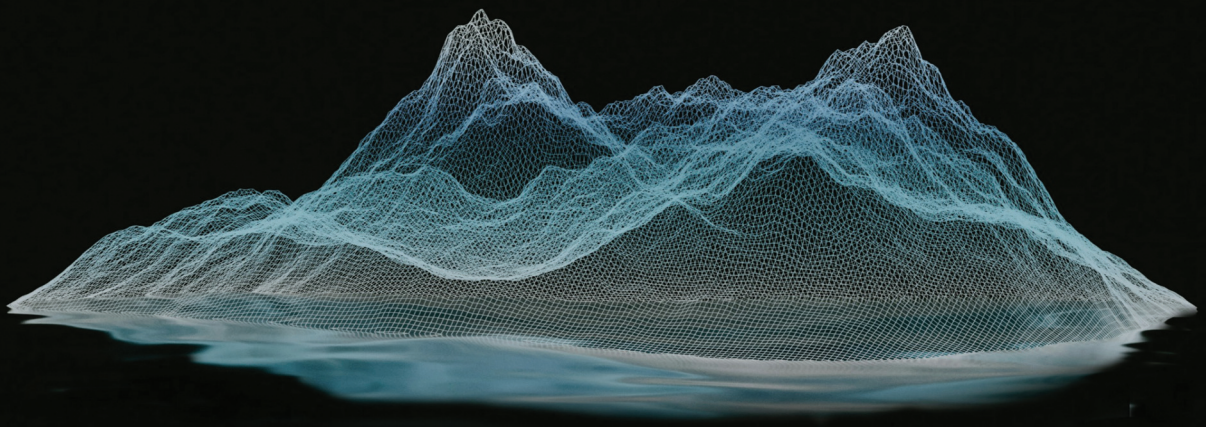
Find more details on products available, request samples, and access helpful RNA-related resources at **NEBrna.com**

** "GMP-grade" is a branding term NEB uses to describe products manufactured or finished at NEB's Rowley facility. The Rowley facility was designed to manufacture products under more rigorous infrastructure and process controls to achieve more stringent product specifications and customer requirements. Products manufactured at NEB's Rowley facility are manufactured in compliance with ISO 9001 and ISO 13485 quality management system standards. However, at this time, NEB does not manufacture or sell products known as Active Pharmaceutical Ingredients (APIs), nor does NEB manufacture its products in compliance with all of the Current Good Manufacturing Practice regulations.*

NEW ENGLAND Biolabs®

RNA EXPRESSION IS ONLY THE SURFACE.

MSR-seq: Profile 4 dimensions of small non–coding RNA in a single library preparation.



01 | EXPRESSION

Comprehensive expression counts for small non-coding RNA, capturing transcripts <300nt.

02 | MODIFICATIONS

Single-nucleotide mapping of chemical signatures to identify post-transcriptional modifications.

03 | CHARGING

Ratios of aminoacylated to uncharged tRNAs to quantify charging ratios.

4 | FRAGMENTATION

Identification of site-specific cleavage sites to map cellular regulatory landscape.

MesoRNA

SCAN TO LEARN MORE

Watkins, C.P., et al. Nat Commun 13, 2491 (2022). https://doi.org/10.1038/s41467-022-30261-3

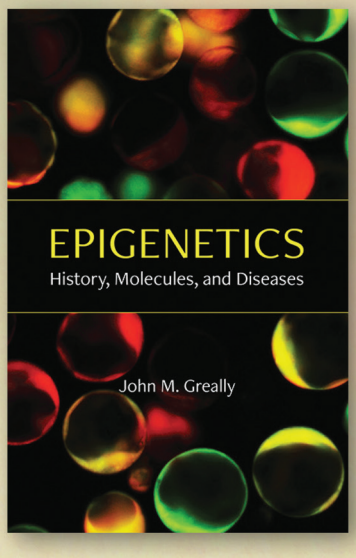
EPIGENETICS

History, Molecules, and Diseases

by John M. Greally

How do cells with the same DNA acquire different identities and behaviors?

Can environmental exposure influence biological functions and human health?



Epigenetics explores the field from its historical roots in embryology to the modern landscape of genomic technologies—bringing clarity to a topic often clouded by oversimplification and overreach. It rejects exaggerated claims to refocus attention on how cells establish and preserve identity, and how this understanding translates into insights that are meaningful for human health.

A rigorous, insightful guide for anyone seeking an understanding of what epigenetics is—and what it is not.

Learn more
www.cshlpress.org/epigenetics

About the Author

John Greally is Professor of Genetics and Pediatrics at the Albert Einstein College of Medicine in the Bronx and Founding Director of its Center for Epigenomics. He is also Founder and Executive Director of the New York Center for Rare Diseases and an attending physician in Genetics at Montefiore Medical Center. Originally from Galway, Ireland, he trained in pediatrics at the Children's Hospital of Pittsburgh and clinical genetics at Yale University, and is a Fellow of the American College of Medical Genetics. His research focuses on discovering functional non-coding variants to improve genomic diagnostics, with over 210 peer-reviewed publications.

CSH PRESS Cold Spring Harbor Laboratory Press

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To SIRVs or not to SIRVs?

That is not even a question!

Take control over all your RNA-Seq experiments - use Lexogen's SIRVs - the most universal spike-in controls.

Spike-in controls are crucial for RNA-Seq experiments to access the performance and the limits of RNA-Seq workflows, including data analysis. SIRVs are Lexogen's spike-in RNA controls, added to any RNA sample in minuscule amounts. Processed alongside the sample RNA, SIRVs allow monitoring and evaluation of the entire RNA-Seq experiment and the data quality.

Benefits of using SIRVs

- **Universal:** Use SIRVs with both short- and long-read sequencing technologies.
- **Compatibility:** Use SIRVs with any sample types or species, in mRNA, total RNA or rRNA-depleted RNA-Seq workflows.
- **Quality control:** Set up, validate and monitor each stage of your RNA-Seq workflow.
- **Compare:** Evaluate the technical variability between samples and experiments prior exploring biological variation.

Interested to learn more?

Check the product page for more information on our website!

SIRVs reflect transcriptome complexity

SIRVs were designed as a family of modules, each imitating specific aspects of natural transcriptome complexity. The SIRVs isoform module probes transcription and splicing variants, the ERCCs module addresses concentration dynamics, and the long SIRVs module mimics length.

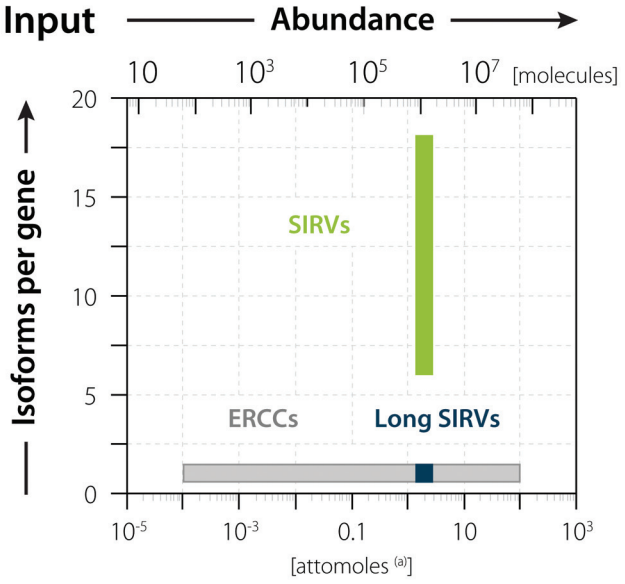

Figure 1 | Isoform and abundance complexity. The SIRV isoform and ERCC transcripts control for the two main dimensions of transcriptome complexity: isoforms and abundance. The Long SIRVs module additionally contains controls for length complexity.