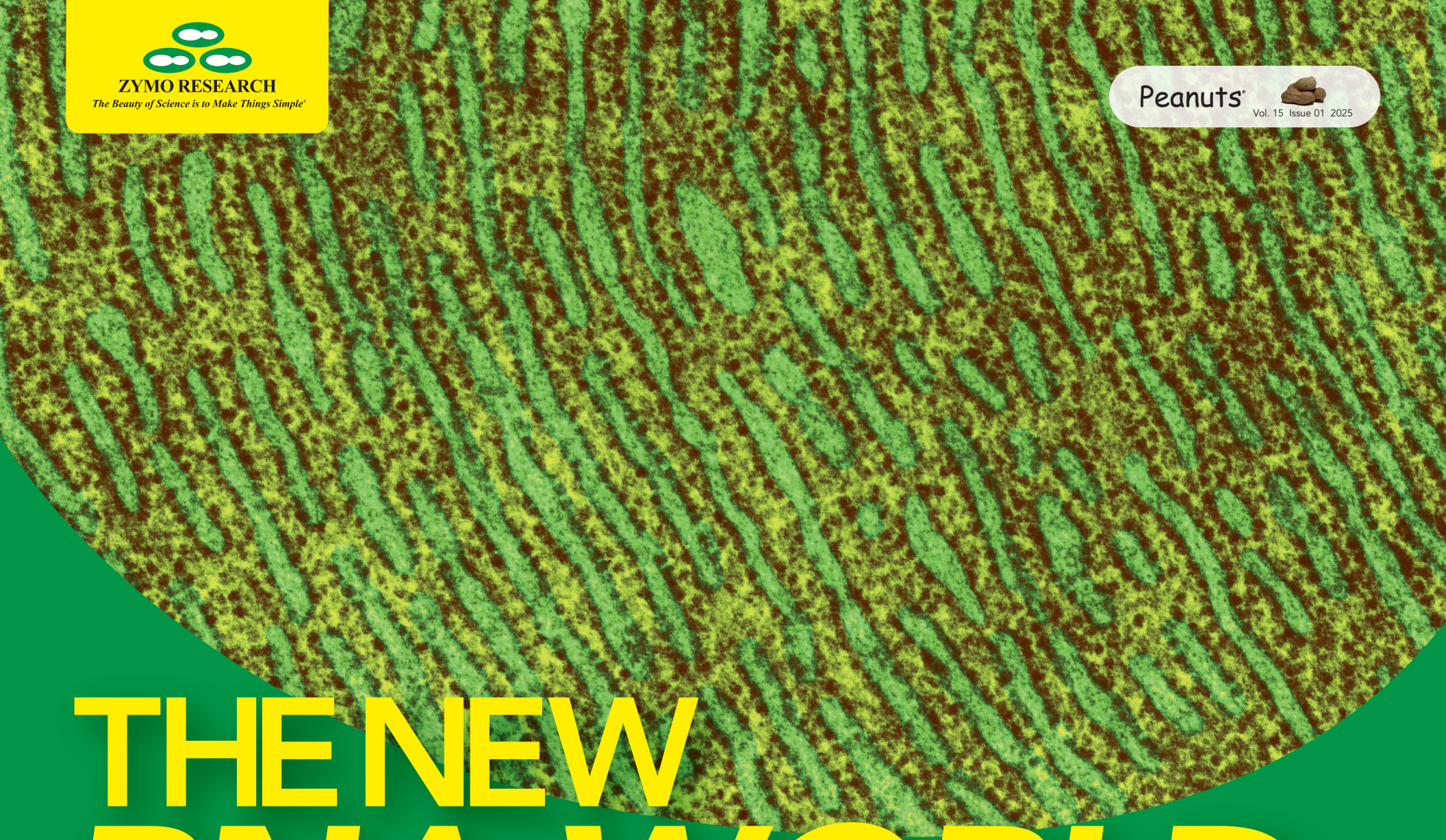
ZYMO RESEARCH
The Beauty of Science is to Make Things Simple®

Peanuts®
Vol. 15 Issue 01 2025



THE NEW RNA WORLD

Pioneering the Most Dynamic Frontier with Innovative Sample Collection, RNA Purification, and NGS Solutions

THE BEAUTY OF SCIENCE IS TO MAKE THINGS SIMPLE ™

WHAT IS THE NEW RNA WORLD?

The RNA World hypothesis, first proposed by Walter Gilbert in 1986, suggested that RNA once carried out both genetic and catalytic roles in early life, long before DNA or proteins emerged. What began as a theory of life's origins has since evolved into a thriving field of discovery. Today, RNA is no longer just a messenger between DNA and protein. It sits at the core of gene regulation, disease mechanisms, and cutting-edge therapeutics. From non-coding RNAs to RNA modifications, researchers are uncovering dynamic layers of complexity that were invisible just a decade ago.

The New RNA World represents a shift in how we understand biology. RNA is not only a molecule of the past, it's a powerful regulator of the present and a key to the future of medicine, biotechnology, and molecular biology. Zymo Research is proud to support the scientists advancing our understanding of gene expression, regulation, and function as RNA continues to redefine the frontier of modern biology.

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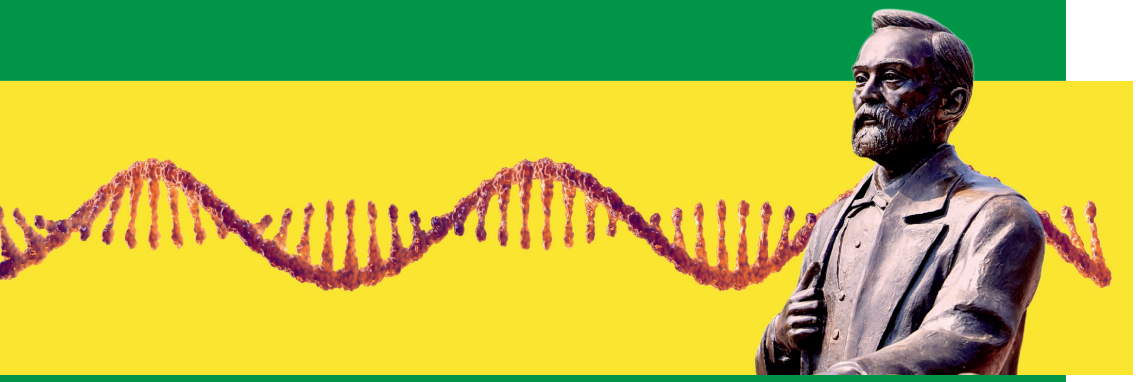
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Pioneers of the New RNA World

Showcasing the achievements of recent Nobel Prize® winners in the biological field and highlighting RNA technologies they used for their research.

Behind every Nobel Prize®-winning discovery lies a story of innovation, persistence, and a set of right tools. Nobel Prize® winners exemplify the curiosity and dedication that drive scientific breakthroughs, uncovering new fields of research. While their pioneering work shines brightly, the research methods and technologies they rely on often work quietly in the background, fueling discoveries that change the world.



© The Nobel Committee for Physiology or Medicine

VICTOR AMBROS **GARY RUVKUN**

The Nobel Prize® in Physiology or Medicine 2024
"for the discovery of microRNA and its role in post-transcriptional gene regulation"

In 1993, Victor Ambros and Gary Ruvkun made a groundbreaking discovery that revolutionized our understanding of gene regulation. While every cell in the body contains the same genetic information, different cell types, such as muscle or nerve cells, exhibit distinct characteristics due to selective gene regulation. MicroRNAs, as discovered by Ambros and Ruvkun, are a new class of tiny RNA molecules that play a crucial role in gene regulation, ensuring that each cell activates only the relevant genes for its specific function.

Their research, particularly in the model organism C. Elegans, revealed that these small non-coding RNA molecules regulate vast networks of gene expression at the post-transcriptional level, controlling mRNA stability and protein production. Ambros and Ruvkun's work revealed how intricate the regulation of genetic information can be, shedding light on the complex processes of microRNA gene regulation that allow multicellular organisms to develop and function in a highly coordinated manner.

01

KATALIN KARIKÓ **DREW WEISSMAN**

The Nobel Prize® in Physiology or Medicine 2023
"for their discoveries concerning nucleoside base modifications that enabled the development of effective mRNA vaccines against COVID-19"

Katalin Karikó and Drew Weissman revolutionized vaccine science through their pivotal discoveries regarding mRNA, which have played a crucial role in developing vaccines that combat infectious diseases. In 2005, the two scientists discovered that specific modifications to RNA's building blocks could prevent unwanted immune reactions while enhancing protein production. This breakthrough laid the foundation for the highly effective mRNA vaccines used during the COVID-19 pandemic, starting in 2020. Their work showed how mRNA could be modified and delivered into the body to trigger a protective immune response without using live or attenuated viruses, a significant advantage over traditional vaccines.

The impact of their mRNA vaccine breakthrough became particularly evident when companies like Pfizer®/BioNTech® and Moderna® used their technology to develop COVID-19 mRNA vaccines that were rapidly deployed worldwide. These mRNA vaccines successfully generated a strong immune response, including producing high levels of antibodies, which have been crucial in reducing severe illness and death from COVID-19. Karikó and Weissman's pioneering works have transformed our understanding of how mRNA can interact with the immune system, which have opened new avenues for vaccine development and other therapeutic applications.

DAVID JULIUS **ARDEM PATAPOUTIAN**

The Nobel Prize® in Physiology or Medicine 2021
"for their discoveries of receptors for temperature and touch"

David Julius and Ardem Patapoutian were jointly awarded the 2021 Nobel Prize in Physiology or Medicine for their pioneering discoveries of receptors that allow humans to sense temperature and touch. Julius's research in the late 1990s used a cDNA library from sensory neurons to identify a gene that grants sensitivity to capsaicin, the active compound in chili peppers. This led to the discovery of a novel ion channel, the TRPV1 receptor, which senses heat. In the early 2000s, Patapoutian used a functional screen of genes in a pressure-sensitive cell line to identify the PIEZO1 and PIEZO2 receptors, responsible for sensing pressure and touch.

These discoveries have revolutionized our understanding of how our nervous system perceives temperature and mechanical forces, unveiling critical mechanisms that underlie touch, temperature sensation, and pain. Their work has provided key insights into the molecular basis of these sensory processes, with wide-ranging implications for medical research, especially in areas like chronic pain and other sensory disorders.



© The Nobel Committee for Physiology or Medicine

Did You Know?

The first Nobel Prize® in Physiology or Medicine was awarded in 1901 to Emil von Behring for developing a serum therapy against diphtheria. His work saved countless lives and earned him the title "savior of children," laying the groundwork for modern immunology.

EMMANUELLE CHARPENTIER **JENNIFER A. DOUDNA**

The Nobel Prize® in Chemistry 2020
"for the development of a method for genome editing"

In 2012, Emmanuelle Charpentier and Jennifer Doudna revolutionized genetic research by developing a method for precise genome editing. They drew inspiration from the immune system of bacteria, which use molecular "scissors" to cut viral DNA and protect themselves from infections. By isolating and simplifying these CRISPR/Cas9 genetic scissors, they created a powerful tool that allows researchers to edit DNA with exceptional accuracy. This technology has since opened new doors for scientific breakthroughs, enabling the editing of DNA in animals, plants, and microorganisms. CRISPR/Cas9 is now being used to develop more resilient crops, explore potential cancer therapies, and fight against genetic disorders. In recognition of their groundbreaking work, Charpentier and Doudna were awarded the 2020 Nobel Prize in Chemistry. CRISPR gene editing has not only reshaped genetic research but also holds immense promise for advancing medicine and solving critical challenges in health and agriculture.



Did You Know?

The CRISPR system that revolutionized gene editing was first discovered in yogurt! Scientists initially observed CRISPR sequences while studying how bacteria used them to fend off viruses that infect dairy cultures. This accidental discovery in the food industry laid the foundation for one of the most powerful tools in modern genetic science.

HARVEY J. ALTER **MICHAEL HOUGHTON** **CHARLES M. RICE**

The Nobel Prize® in Physiology or Medicine 2020
"for the discovery of Hepatitis C virus"

Harvey J. Alter, Michael Houghton, and Charles M. Rice were awarded the 2020 Nobel Prize in Physiology or Medicine for their groundbreaking discoveries surrounding the Hepatitis C virus. In the 1970s, Alter's studies revealed a previously unknown contagion, which he demonstrated was a virus, transmitted Hepatitis via blood transfusions. This finding laid the foundation for identifying the Hepatitis C virus. Houghton isolated the virus's genome in 1989, revealing it as an RNA virus from the Flavivirus family. Rice's work in 1997 proved the virus alone caused Hepatitis C by showing a crucial viral genome region responsible for the disease. These discoveries have dramatically improved public health by enabling the development of screening methods that reduced hepatitis transmission via blood transfusions, as well as effective antiviral treatments that have saved millions of lives worldwide.

Up Next



Discover how our solutions continue to empower scientists advancing discovery in the New RNA World. Since 1994, Zymo Research® has been providing innovative, high-quality, and easy-to-use tools for RNA research.

Innovative RNA Technologies Empowering Nobel Laureates

Quick-RNA™

- **Versatile & Reliable** – Compatible with a wide range of sample types and delivers high-yield, high-purity RNA ready for any downstream application (RNA-seq, RT-PCR, etc).
- **DNA-Free Results** – Includes on-column DNase I treatment for effective genomic DNA removal without additional steps.
- **Rapid Workflow** – Purify high-quality total RNA with a streamlined, user-friendly protocol.

Charles M. Rice
Ardem Patapoutian
Michael Houghton
Harvey J. Alter
David Julius

DNA/RNA Shield™

- **Nucleic Acid Stabilization** – Preserves DNA and RNA at ambient temperatures for extended periods without degradation.
- **Complete Pathogen Inactivation** – Safely inactivates viruses and bacteria on contact for secure sample handling.
- **Direct Workflow Compatibility** – Enables direct processing with most extraction kits, no need for sample removal or additional steps.

Jennifer A. Doudna
Emmanuelle Charpentier

Direct-zol® RNA

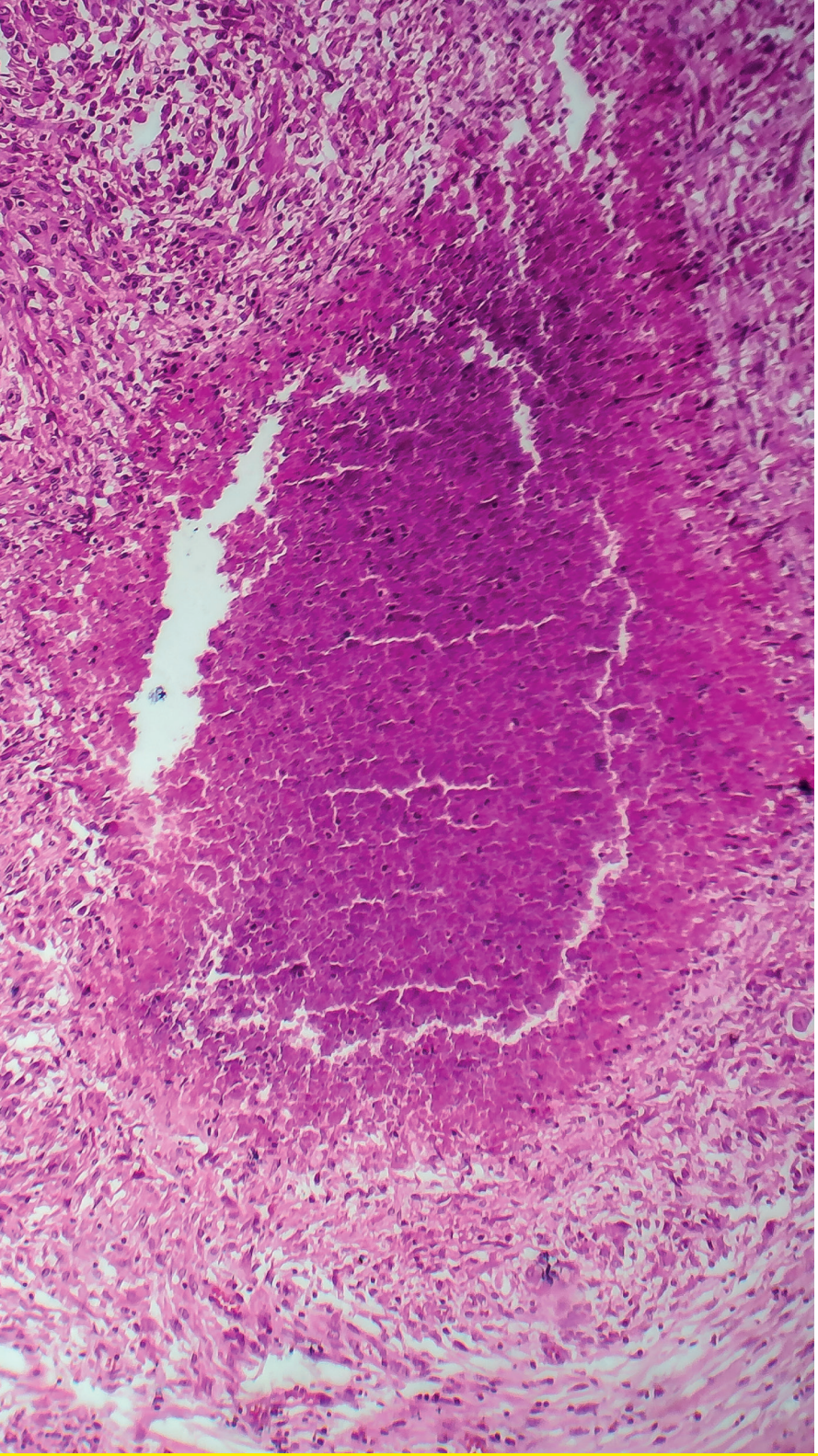
- **Fast & Simple Protocol** – Streamlined workflow delivers high-quality RNA in 7 minutes.
- **No Phase Separation** – Purify RNA directly from TRIzol® or similar reagents without chloroform extraction or phase separation.
- **High-Quality, DNA-Free RNA** – Obtain unbiased total RNA including microRNA from any sample in Trizol®, ready for sensitive downstream applications.

Charles M. Rice
Harvey J. Alter
Michael Houghton
Svante Pääbo
Drew Weissman
Katalin Karikó

RNA Clean & Concentrator™

- **Simple Workflow** – Purify and concentrate RNA in as little as 5 minutes
- **Ultra-Pure RNA Recovery** – Effectively removes enzymes, salts, and impurities for high-quality RNA ready for any downstream application.
- **Compatibility with Low Input** – Recover picograms of RNA from low input samples and elute in as little as 6 µl.

David Julius



Sample Collection

Where Sample Preservation Enables Wildlife Conservation

In RNA research, sample collection isn't just the first step, it's the most critical! RNA is notoriously unstable, degrading rapidly in the presence of heat, RNases, or even brief handling delays. This fragility makes sample collection one of the most vulnerable (and often overlooked) steps in the workflow. Whether in the lab or out in the field, inconsistent preservation methods can lead to compromised data, failed experiments, and wasted time. Proper handling and immediate stabilization are essential to maintain RNA integrity and ensure reproducibility. Without a reliable collection strategy, even the most advanced downstream tools can't salvage degraded samples.

Did You Know?

Mycobacterium tuberculosis can be seen in lung tissue using special stains under a microscope. Pathologists use this to help diagnose one of the world's oldest infectious disease.

02

HOW MOLECULAR TOOLS ARE AIDING LION CONSERVATION

Majestic and powerful, lions are more than just symbols of strength – they are vital players in maintaining the balance of Africa's ecosystems. Yet, these iconic predators are in trouble. Over the past few decades, wild lion populations have plummeted due to habitat loss, human-wildlife conflict, illegal poaching, and the devastating impact of infectious diseases. Now listed as Vulnerable by the International Union for Conservation of Nature (IUCN), African lions face an increasing threat from diseases introduced into their shrinking habitats, putting them at risk of local extinction. This loss could trigger a cascade of ecological imbalance, affecting entire ecosystems. South Africa, home to the second-largest population of free-ranging lions, primarily in Kruger National Park and Hluhluwe-iMfolozi Park, faces a unique challenge: these regions are hotspots for animal tuberculosis (TB) caused by Mycobacterium Bovis, a pathogen that infects over 23 wildlife species, including lions.

TB in animals has important implications for domestic and wild animals, as well as humans. Along with affecting animal health and livestock production, there are broad impacts on food security, livelihoods of rural African communities who rely on livestock, ecotourism, and wildlife conservation of Africa's unique biodiversity. The Stellenbosch University (SU) Animal TB research group, under the leadership of Professor Michele Miller, National Research Foundation (NRF) South African Research Chairs Initiative (SARChI) in Animal TB, is the only research group in South Africa that focuses solely on investigating animal TB, primarily in South African wildlife species. The SU Animal TB Research Group is based in the Division of Molecular Biology and Human Genetics (MBHG), at the Faculty of Medicine and Health Sciences (FMHS) in Cape Town, South Africa. The translational research program focuses on improving understanding animal health and the role of TB in Africa's vulnerable wildlife species.



Did You Know?

Lions in places like Kruger National Park, are increasingly battling tuberculosis contracted from infected prey such as buffalo, kudu, and warthcvogs. This zoonotic disease poses serious threats to their health and survival, highlighting the importance of molecular tools in monitoring and managing TB in wildlife populations.

MICROBIOME RESEARCH IN LION HEALTH

The long-term impact of TB on infected African lion populations is largely unknown, although individuals can develop chronic progressive disease, and even die. Resources for studying diseases in African wildlife are limited, despite TB being a controlled disease in South Africa that can impede wildlife translocation and other conservation efforts. A comprehensive understanding of infection and disease is crucial for detecting and preventing TB. Therefore, SU's research addresses key knowledge gaps regarding TB in African lions.

The gut microbiome (microbes found living in the gut) plays a significant role in health and immune responses. SU's current research aims to characterize the microbiome and immunological responses in uninfected and naturally M. bovis-infected lions. The microbiological population in feces may change due to infection or environmental changes, potentially influencing susceptibility to other diseases, such as TB. Hence, understanding the microbiome of these majestic animals can offer valuable insights into their health and conservation needs.

Feces are a simple and cost-effective sample to monitor lion health. During the 2024 field study, fecal samples were collected using Zymo Research's DNA/RNA Shield™ Fecal Collection Tubes from immobilized lions in the Kruger National Park. The reagents in these tubes help preserve the integrity of the genetic material in the feces, inactivate any infectious agents, and allow for storage at ambient temperatures. These features are essential for field work when laboratory access and refrigeration are unavailable.

"By preserving genetic material effectively in the field, we gain deeper insights into the health and disease dynamics of African lions."



Members of the SU Animal TB research group during field work in Kruger National Park, South Africa. Left panel: From left to right, Dr. Tanya Kerr (Research Study Coordinator), Intimate Shongwe (Research Intern), Dr. Rachiel Gumbo (Postdoctoral Researcher), Prof. Michele Miller (Veterinarian and NRF SARChI) and Prof. Wynand Goosen (Researcher).

The integration of Zymo Research's DNA/RNA Shield™ Fecal Collection Tubes into our lion microbiome study marks an important step forward in wildlife research. By preserving genetic material effectively in the field, we gain deeper insights into the health and disease dynamics of African lions. This enhanced understanding contributes directly to conservation efforts aimed at mitigating the risks of TB and other infectious diseases. Ultimately, safeguarding lion populations not only helps maintain ecological balance but also protects the biodiversity and economic value tied to Africa's unique natural heritage, ensuring a future where these majestic predators can continue to thrive.

DNA/RNA Shield™

TRANSPORT ANY SAMPLE, ANYWHERE

Key Features

- **Protect DNA and RNA** in any biological sample without cold chain
- **Complete Pathogen Inactivation** (bacteria, virus, eukaryotic)
- **Streamlined purification** – Universally compatible and automatable.

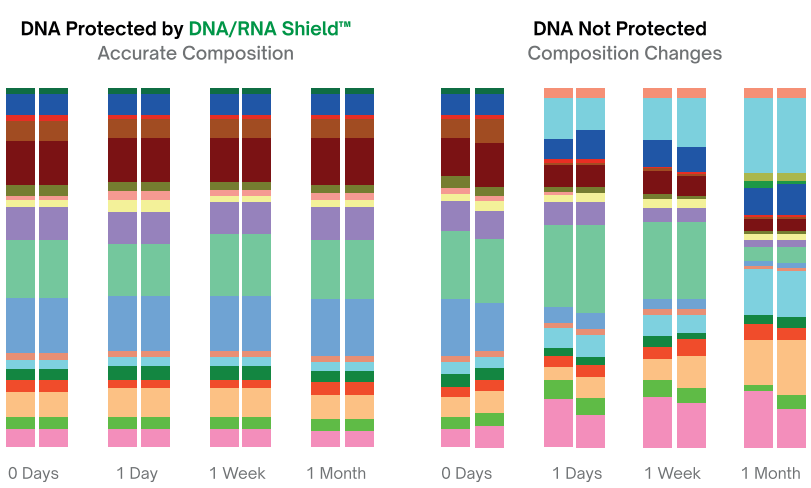
THE PREMIERE SOLUTION FOR COLLECTION IN THE FIELD

When collecting and transporting biological specimens in the field, DNA/RNA Shield™ offers unmatched reliability and convenience. It immediately stabilizes DNA & RNA, protecting them from degradation caused by temperature shifts, nucleases, and microbial growth. Collected samples require no refrigeration or cold-chain making it ideal for remote or resource-limited settings. DNA/RNA Shield™ ensures safety and high-quality results, perfect for sensitive PCR and next-generation sequencing analyses.

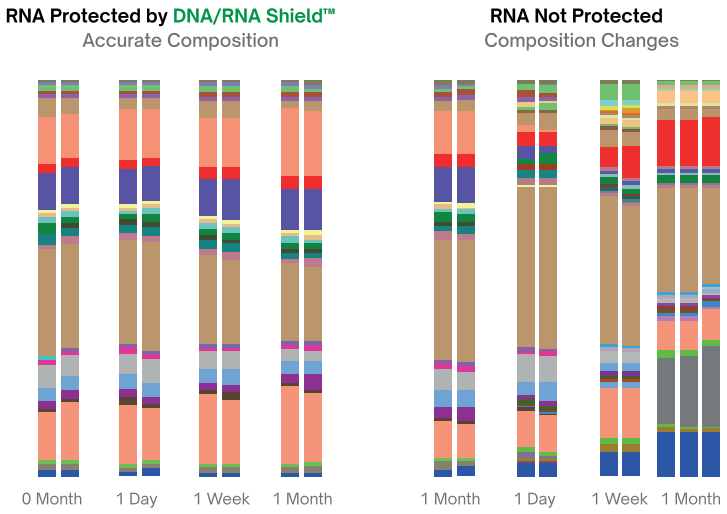
MICROBIOME PRESERVATION FOR METAGENOMICS AND METATRANSCRIPTOMICS

Capture a precise genetic snapshot of the microbial community at time of collection. DNA and RNA in any sample type are immediately stabilized to prevent degradation providing high-quality input for next-generation sequencing applications.

DNA PROFILING



RNA PROFILING



Microbial composition of collected stool samples remain unchanged after one month at ambient temperature with DNA/RNA Shield™. DNA and RNA were extracted using the ZymoBIOMICS® DNA/RNA Miniprep Kit and were subjected to microbial composition DNA and RNA profile sequencing.

SAFETY IN EVERY SAMPLE

FDA-
Cleared Devices

Approved for saliva and swab-based self-collection in diagnostic applications

DOT
Shipping Exemption

Infectious substance exempt - as allowed in 49 CFR 173.134(b) (4)

USDA/ APHIS
Recognized

Approved chemical agent for viral inactivation treatment

NASA
Selected

Certified for safe in-flight use (SpaceX®, ISS)

Eurovir™
Validated

Complete viral inactivation tested under European Standard EN14476:2017

COMPLETE PATHOGEN INACTIVATION

VIRUS

- Influenza A (H7N7)
- Rabies (Tollwut) Virus
- Avian Bird Flu (H5N1)
- MERS-Coronavirus
- Chikugunya Virus
- West Nile Virus
- Monkeypox Virus
- Murines Parvovirus
- Dengue Virus
- Ebolavirus

YEAST & EUKARYOTES

- *Saccharomyces cerevisiae*
- *Candida albicans*
- *Cryptococcus neoformans*
- *Plasmodium Malaria*
- *Babesia spp.*
- *Cryptosporidium spp.*

BACTERIA & ARCHEA

- *Mycobacterium tuberculosis*
- *Staphylococcus aureus*
- *Enterococcus hirae*
- *Fusobacterium nucleatum*
- *Lactobacillus fermentum*
- *Fusobacterium nucleatum*
- *Lactobacillus fermentum*
- *Clostridioides difficile*

SCAN HERE
FOR ADDITIONAL PATHOGENS TESTED

Fecal Sample Collection Solutions

At-Home Tube



R1160/R1161

Swab Tube



R1106/R1107

Fecal Tube



R1101/R1137

Fecal Collector

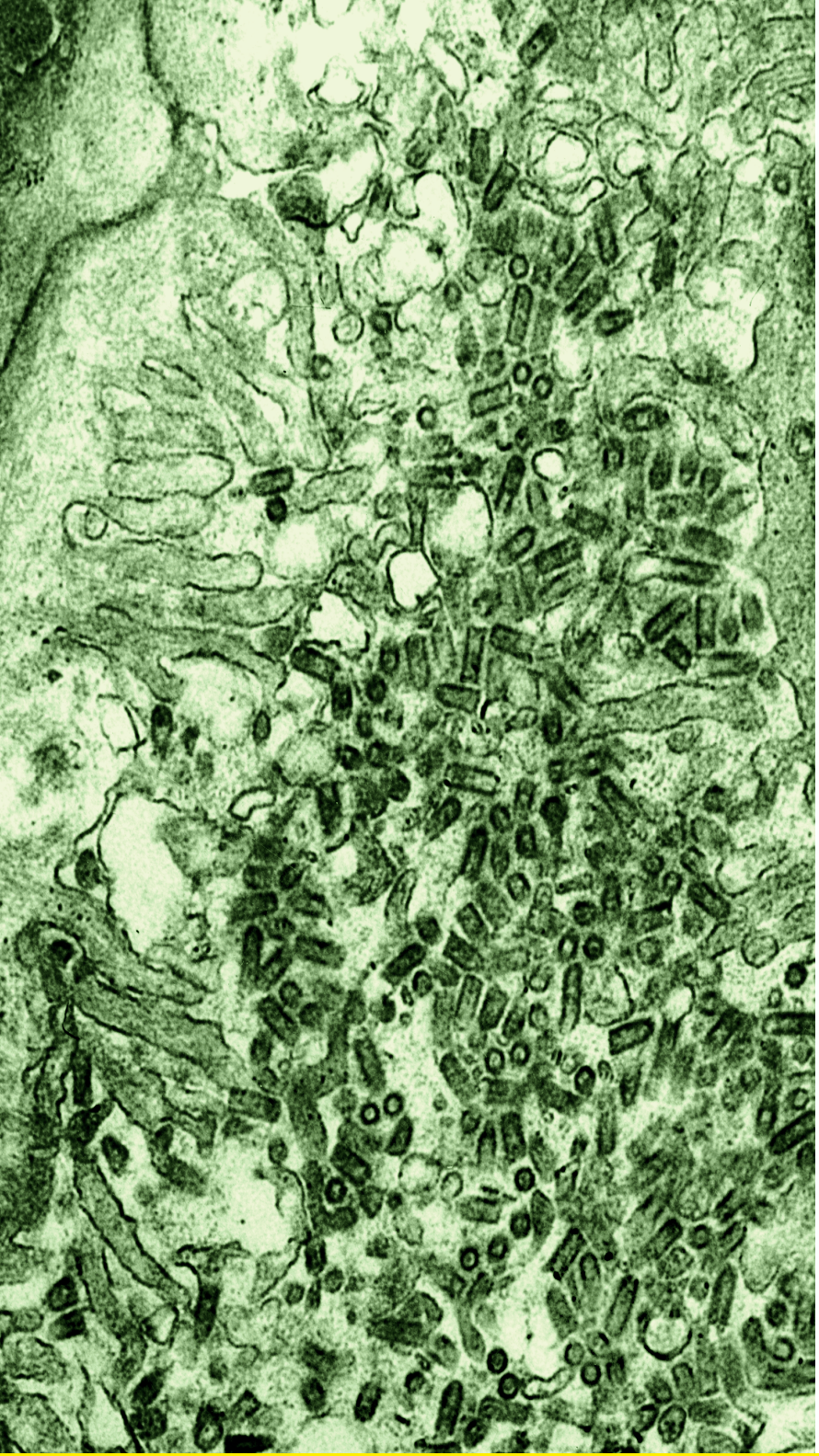


R1133

Product	Cat. No.	Size
DNA/RNA Shield™ SafeCollect® Swab Collection Kit (1 ml fill)	**R1160**	**1 Kit**
DNA/RNA Shield™ SafeCollect® Swab Collection Kit (2 ml fill)	**R1161**	**1 Kit**
DNA/RNA Shield™ - Collection Tube w/swab (1ml fill)	**R1106**	**10 Pack**
	R1107	**50 Pack**
DNA/RNA Shield™ - Collection Tube w/swab (2ml fill)	**R1108**	**10 Pack**
	R1109	**50 Pack**
DNA/RNA Shield™ - Fecal Collection Tube	**R1101**	**10 Pack**
DNA/RNA Shield™ - Fecal Collection Tube (with beads)	**R1137**	**10 Pack**
DNA/RNA Shield™ - Fecal Collection Kit	**R1180**	**1 Kit**

Product	Cat. No.	Size
Bunny Wipe™ Fecal Sample Collector	**R1133-10**	**10 Pack**
Bunny Wipe™ w/ DNA/RNA Shield™ Fecal Collection Tube	**R1138**	**10 Pack**
DNA/RNA Shield™ - Collection Tube w/swab (1ml fill)	**R1100-50**	**50 ml**
	R1100-250	**250 ml**

SCAN HERE TO REQUEST FREE SAMPLE



RNA Extraction

Improving Pathogen Detection to Save Lives

Isolating RNA from complex or clinical samples often means contending with low abundance, biological variability, and inhibitory contaminants that can derail sensitive assays. These issues are magnified in diagnostic settings, where speed, sensitivity, and accessibility are critical for making life-saving decisions. Yet many extraction methods remain labor-intensive or inconsistent across sample types, limiting their utility in high-throughput or time-sensitive environments. To meet the growing demand for streamlined diagnostics and scalable research, RNA purification workflows must be simplified, consistent, universally available, and capable of delivering high-quality RNA from even the most challenging specimens.

Behind the Image

The rabies virus hijacks nerve cells to eventually reach and infect the brain, leading to progressive, fatal encephalitis. Once symptoms appear, the disease is almost always fatal, which is why post-exposure vaccination is crucial.

Micrograph from F. A. Murphy, University of Texas Medical Branch, Galveston, Texas.

03

Transforming Global Rabies Detection

LIMITATIONS OF EXISTING METHODS

Rabies, a fatal zoonotic disease, has a case fatality rate nearing 100%. Despite being preventable if treated promptly, rabies accounts for approximately 60,000 human deaths worldwide annually. While the gold standard of post-mortem rabies diagnostics is the direct fluorescence antibody test (DFA or FAT), this method has its share of limitations.



Photo Credits: CDC and Team of Vaccinators in Haiti

Its precision hinges on high quality antibody conjugates, a skilled technician, and the absence of nonspecific fluorescence. The intricate cellular structure and high lipid content can interfere with proper nucleic acid or protein extraction from brain samples. The DFA test falls short when dealing with deteriorated or fixed tissues, requiring maintenance of fresh tissue at cold chain temperatures.

IMPROVING ACCESS, ACCURACY, AND SPEED

The Taqman-based LN34 assay, developed by Crystal Gigante, PhD, employs RT-PCR to amplify and identify a conserved genomic region of the lyssavirus species. In a pilot study, this LN34 assay underwent the largest evaluation of its kind, encompassing 2,978 samples. These brain stem samples, extracted using the Direct-zol® RNA Miniprep Kit, originated from rabies-suspected animals spanning Africa, Asia, the Americas, Europe, and the Middle East. The CDC equipped all participating laboratories with the necessary LN34 assay components, including Direct-zol® RNA Purification Kits

Through bypassing chloroform and phase separation in traditional RNA extraction methods from TRIzol®, the spin-column technology within the Direct-zol® RNA Purification Kits address a crucial concern in worldwide rabies testing: ease of use and accessibility. Standardizing the RNA extraction method to a simple binding, washing, and elution was pivotal in executing this study. This allowed laboratories around the globe to undertake RNA extraction from post-mortem brain samples without relying on a scientist versed in the intricacies of organic/phase separation techniques or DFA testing.

The LN34 assay succeeded in detecting rabies virus even in samples unsuitable for DFA testing, such as those in formalin-fixed or deteriorated states. Many rabies-endemic areas lack the means to adopt DFA testing due to the demands of continuous cold storage, a fluorescent microscope, and highly skilled personnel. By enabling RNA extraction from fixed tissues, the need for costly cold-chain transport of fresh tissue is gone, potentially bolstering rabies diagnostics in underserved regions.

The international evaluation showcases the LN34 assay's robustness, minimal variability, and outstanding diagnostic sensitivity. The LN34 assay has the potential to revolutionize rabies testing across the globe, reducing the administration of unnecessary rabies shots and saving lives.

Direct-zol® RNA Kits

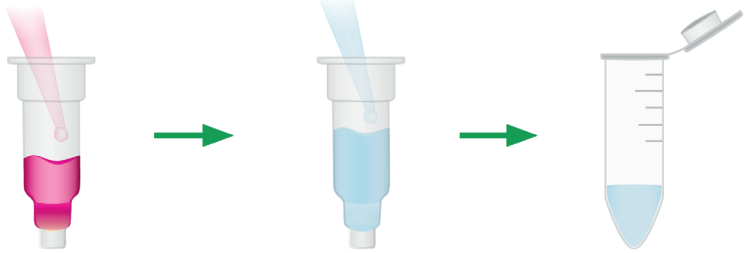
NGS-READY RNA IN 7 MINUTES

Key Features

- **Easy Handling:** Bypass chloroform, phase separation and precipitation steps and extract high-quality RNA in 7 minutes from TRIzol®.
- **NGS-Ready:** Ultra-pure RNA without phenol carryover. No DNA contamination (DNase I included).
- **Non-Biased:** Complete RNA recovery without miRNA loss.

JUST BIND, WASH, AND ELUTE

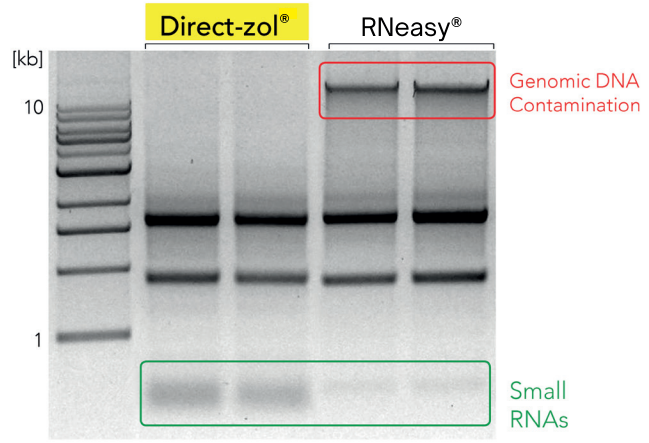
The innovative Direct-zol® procedure bypasses chloroform, phase separation, and precipitation steps, saving time and also eliminating phenol carryover without compromising RNA quality. Simply add ethanol to a sample in TRIzol®, bind directly to a Zymo-Spin™ Column (or magnetic beads), wash, and elute NGS-ready RNA.



Bind RNA **Wash** **Elute**

NGS-READY RNA

High-quality total RNA, including small RNAs, are effectively recovered using the Direct-zol® kit. Extracted RNA is free of DNA contamination and is ready for all downstream applications, including Next-Generation Sequencing and RT-qPCR.



High quality broad size-range DNA-free RNA is purified from human epithelial cells using the Direct-zol® RNA Miniprep Kit (1% agarose/TAE gel).

MORE THAN SPEED

The Direct-zol® RNA kit includes DNase I to rapidly remove all DNA. It eliminates the need for chloroform (no phase separation) and concerns over phenol contamination or bias in small RNA recovery.

Product	Direct-zol®	TRIzol®	mirVana™	RNeasy® Universal
Time per Prep	7min	90+min	30 min	30 min
No Phase Separation	✓	×	×	×
NGS-Grade	✓	×	×	×
Small RNA Recovery	✓	×	✓	×
DNase I included	✓	×	×	×

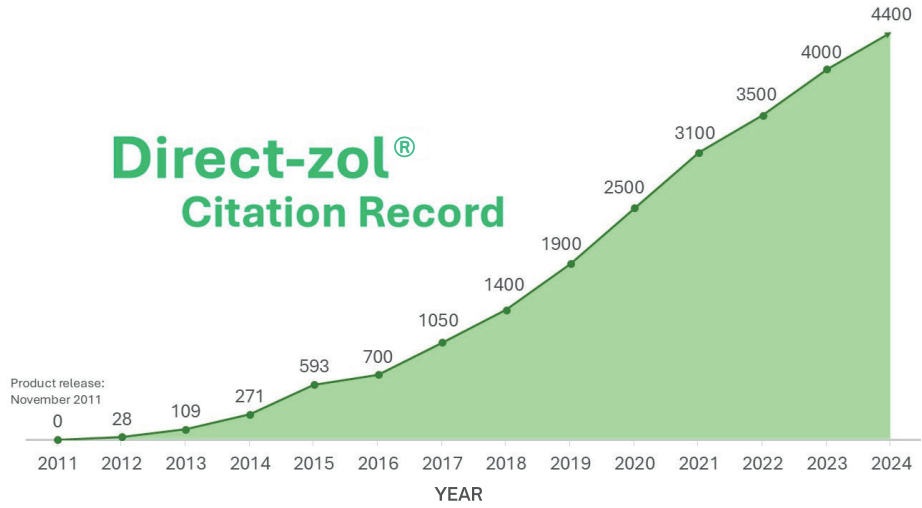
ACCELERATE TOMORROW'S DISCOVERIES

The Direct-zol® technology couples the effectiveness of TRIzol® for pathogen inactivation and sample preservation with a no-hassle, no-mess procedure for NGS-ready RNA. It efficiently recovers more small/microRNAs and is ideal for both routine lab use and high-throughput, automated applications.

You are closer than you think to an easier workflow. Extract RNA from TRIzol® in 7 minutes by requesting for a FREE sample kit today!

SCAN HERE TO REQUEST FREE SAMPLE

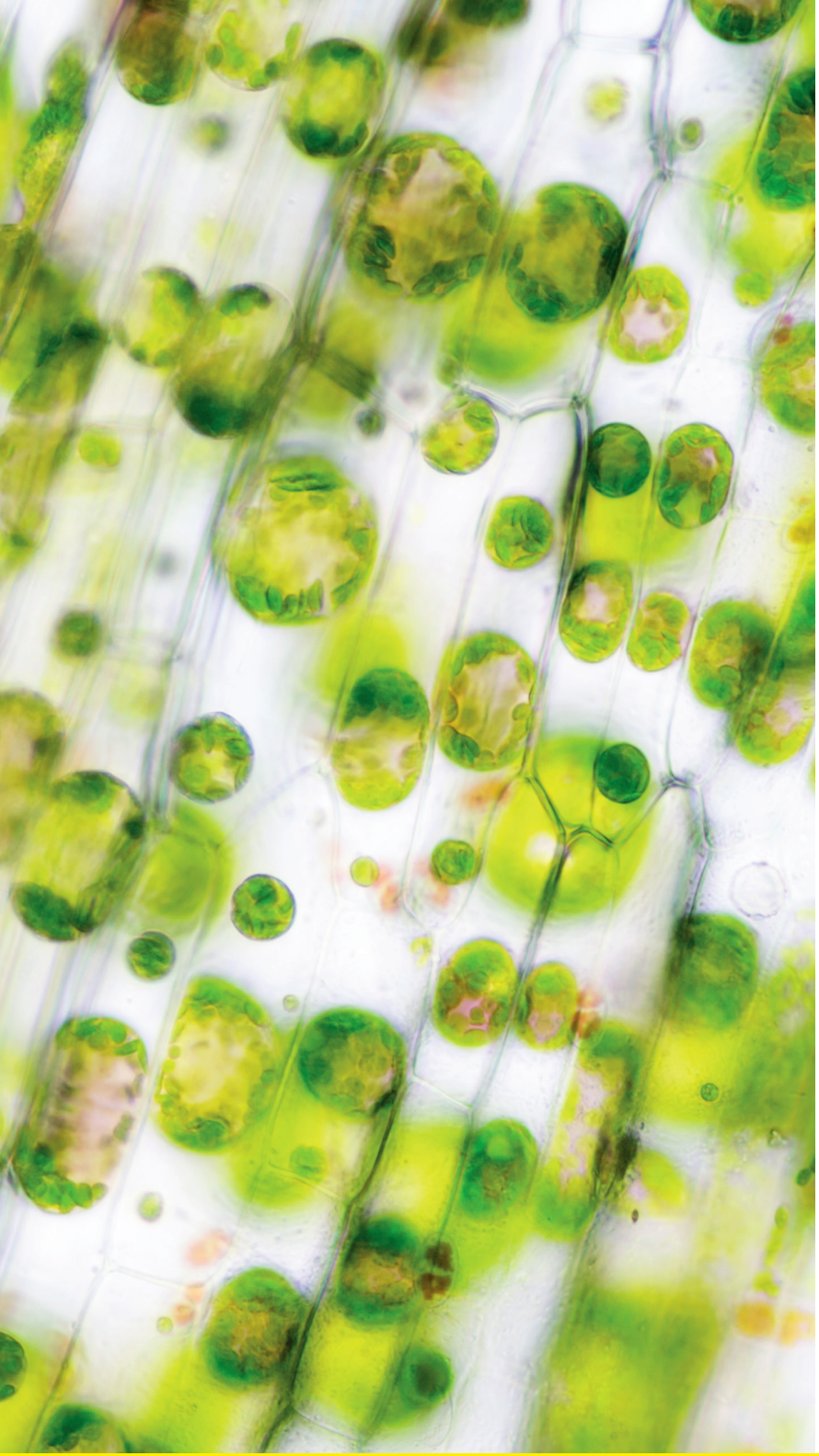
Empowering RNA Scientists for Over a Decade



Product		Cat. No.	Size	Binding Capacity	Minimum Elution	(Animal) Cells	Tissue
Direct-zol® RNA Miniprep Plus Kit		R2070, R2071* R2072, R2073*	50 preps 200 preps	100 µg	50 µL	≤ 10^7	≤ 50 mg
Direct-zol® RNA Miniprep Kit	SK	R2050, R2051* R2052, R2063*	50 preps 200 preps	50 µg	25 µL	≤ 5 X 10^6	≤ 25 mg
Direct-zol® RNA Microprep Kit	SK	R2060, R2061* R2062, R2063*	50 preps 200 preps	10 µg	6 µL	≤ 10^6	≤ 5 mg
Direct-zol® -96 RNA Kit		R2054, R2055* R2056, R2057*	2 x 96 preps 4 x 96 preps	10 µg	10 µL	≤ 10^6	≤ 5 mg
Direct-zol® -96 MagBead RNA Kit		R2100, R2101* R2102, R2103*	96 preps 4 x 96 preps	10 µg	50 µL	≤ 10^6	≤ 5 mg

*Supplied with TRI Reagent®.
Compatible with samples stored in TRIzol®, TRI-Reagent®, RNAzol®, QIAzol®, and all other acid-guanidinium-phenol reagents.

SK Sample Kit Available



Tackling rRNA Interference in Plant RNA-Seq

Deeper Transcriptome Insights with Universal rRNA Depletion

RNA sequencing (RNA-Seq) has transformed how scientists study gene expression, regulation, and transcript diversity across a wide range of organisms. A key challenge in this workflow is the high abundance of ribosomal RNA (rRNA), which can overwhelm sequencing reads and reduce data quality. This issue is especially pronounced in many plant species, where traditional probe-based rRNA depletion often requires extensive and time-consuming optimization. Without efficient rRNA removal, sequencing reads may be dominated by non-informative content, increasing costs and obscuring low-abundance or regulatory transcripts. This limits transcriptome coverage and reduces the sensitivity of downstream analyses. For researchers aiming to generate reproducible, high-quality RNA-Seq data, reliable rRNA depletion is essential.

Behind the Image

Hydrilla leaves are arranged in whorls of 3 to 8 and have finely serrated edges, giving them a rough texture. This unique leaf structure helps deter herbivores and makes Hydrilla easy to distinguish from other aquatic plants.

04

Collaboration Spotlight: Nature® x Zymo Research®

In collaboration with Nature®, researchers highlighted how they are overcoming RNA-Seq challenges using the Zymo-Seq® RiboFree® Total RNA Library Kit. This enzyme-based, probe-free method has shown strong performance across non-model organisms, especially plants, where standard depletion tools often fall short. The following case studies, featured in the Nature® article, demonstrate how RiboFree® enabled high-quality transcriptome data from plant samples.

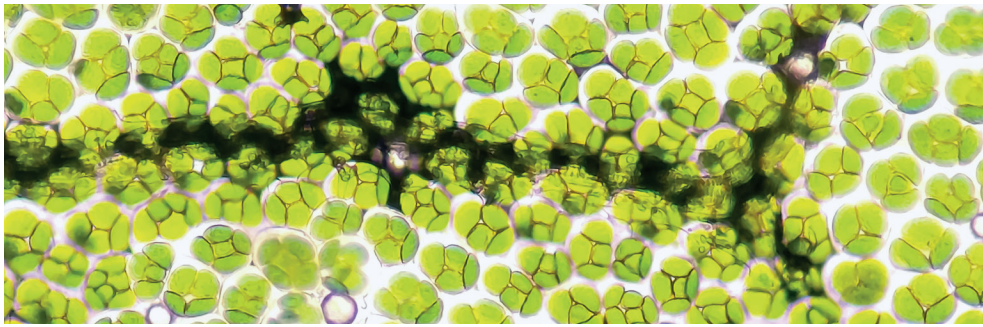
PLANT MOLECULAR BIOLOGY

Reimo Zoschke of the Max Planck Institute of Molecular Plant Physiology, in Germany, is one researcher using RiboFree's universal rRNA removal method. He recently collaborated on a study investigating the effects of removing one of the two copies of a large inverted repeat (IR) region from the tobacco (Nicotiana tabacum) chloroplast genome[1].

Zoschke's collaborators found that these mutants were indistinguishable from wild-type plants under standard growth conditions. "However, they also observed that the absence of the IR slightly reduced the number of plastid ribosomes," he says. "This suggests a possible gene dosage benefit from the rRNA genes located in the IR region."

To investigate this, Zoschke's team performed comparative transcriptomic and ribosome profiling of both mutant and wild-type plants. They ruled out using direct capture methods to prepare samples for RNA-seq, as chloroplast mRNAs are not typically polyadenylated. They had also previously encountered issues with probe-based rRNA removal kits, which they found did not always reliably deplete rRNA species in sequencing libraries[2]. "We prefer depletion strategies that remove abundant RNA species in a sequence-independent manner," says Zoschke. "These approaches eliminate most rRNA, preserve organelle transcripts and prevent any single abundant RNA species from becoming over-represented." To prepare samples for RNA-seq, the researchers chose RiboFree, which simplifies the process by combining rRNA depletion and library preparation in a single protocol. The team showed that gene expression from the IR region is reduced in these mutants, helping to explain the mild effects observed at the molecular level.

The study provides new insights into the function of the IR in chloroplast genomes, showing it can enhance the translational capacity of the plastid and the relationship between genome size and genome copy number. Importantly, revealing that the IR can be eliminated without any serious phenotypic consequences highlights a simplified plastid genome structure that will facilitate future synthetic biology applications.



Chloroplast under light microscope

MYSTERIOUS CROP VIRUSES

Another important field of research empowered by the RiboFree® universal rRNA depletion method is the study of the common bean (Phaseolus vulgaris). This is a vital crop in east and central Africa — a major source of protein, calories and micronutrients. One team is focused on understanding enigmatic RNA viruses that infect the crop without causing apparent disease. "If these endornaviruses offer benefits like increased yield or protection from pathogens, that could be valuable information for plant breeders," says John Carr of the University of Cambridge, an expert on plant-virus interactions. "But if they're causing harmful effects, we could advise growers to screen for them." Carr's team screened 26 bean varieties popular in Kenya, Rwanda, and Uganda for Phaseolus vulgaris endornavirus (PvEV) 1, 2 or 3[3]. They extracted RNA from germinated seeds and used RiboFree® to make sequencing libraries. "Four were infected with PvEV1, three with both PvEV1 and PvEV2, and three had all three viral strains," says Carr. These findings represent an important first step in determining whether endornaviruses positively impact common beans, potentially informing future breeding and cultivation strategies. "We're also conducting deep sequencing on capsicum pepper cultivars to look for these viruses, using the same approach," says Carr. "If something works, why mess around!"

ONE KIT | ENDLESS APPLICATIONS

These case studies demonstrate how the Zymo-Seq® RiboFree® Total RNA Library Kit addresses one of the most significant challenges in RNA-Seq: removing rRNA from complex, less commonly studied samples. By offering a species-agnostic, enzyme-based solution, the kit eliminates the need for custom probe design while preserving transcript diversity. Whether working with chloroplast-rich plant tissues or virus-infected crops, RiboFree® offers a universal workflow that simplifies library prep without compromising data quality. With compatibility across any organism, it is a single solution for transcriptomic discovery today in plants, tomorrow in bacteria, and beyond.

REFERENCES

1. Krämer, C.; Boehm, C. R.; Liu, J.; Ting, M. K. Y.; Hertle, A. P.; Forner, J.; Ruf, S.; Schöttler, M. A.; Zoschke, R.; Bock, R. Removal of the large inverted repeat from the plastid genome reveals gene dosage effects and leads to increased genome copy number. Nat Plants 2024, 10 (6). DOI: 10.1038/s41477-024-01709-9.

2. Ting, M. K. Y.; Gao,Y.; Barahimipour, R.; Ghandour, R.; Liu, J.; Martinez-Seidel, F,; Smirnova, J.; Gotsmann, V. L.; Fischer, A.; Haydon, M. J.; Willmund, F.; Zoschke, R. Optimization of ribosome profiling in plants including structural analysis of rRNA fragments. Plant Methods. 2024, Sep 16; 20(1):143. doi: 10.1186/s13007-024-01267-3

3. Brine, T. J.; Crawshaw, S.; Murphy, A. M.; Pate, A. E.; Carr, J. P.; Wamonje, F. O. Identification and characterization of Phaseolus vulgaris endornavirus 1, 2 and 3 in common bean cultivars of East Africa. Virus Genes. 2023, 59 (5):741-751. DOI: 10.1007/s11262-023-02026-7

SCAN HERE TO READ THE FULL NATURE® ARTICLE

TIPS FOR HIGH-QUALITY RNA-SEQ LIBRARY PREPARATION

TIP 01

Treat samples with DNase

To remove contaminating DNA. The presence of DNA may reduce the quality of the sequencing data and introduce bias.

TIP 02

Perform QC on input

Characterize the integrity of the RNA by obtaining fragment sizes and RNA Integrity Number (RIN). Use high integrity RNA as input whenever possible

TIP 03

Handle beads carefully

Bead cleanups are a standard part of RNA library prep. Before use, bring beads to room temperature and mix well by inverting and vortexing.

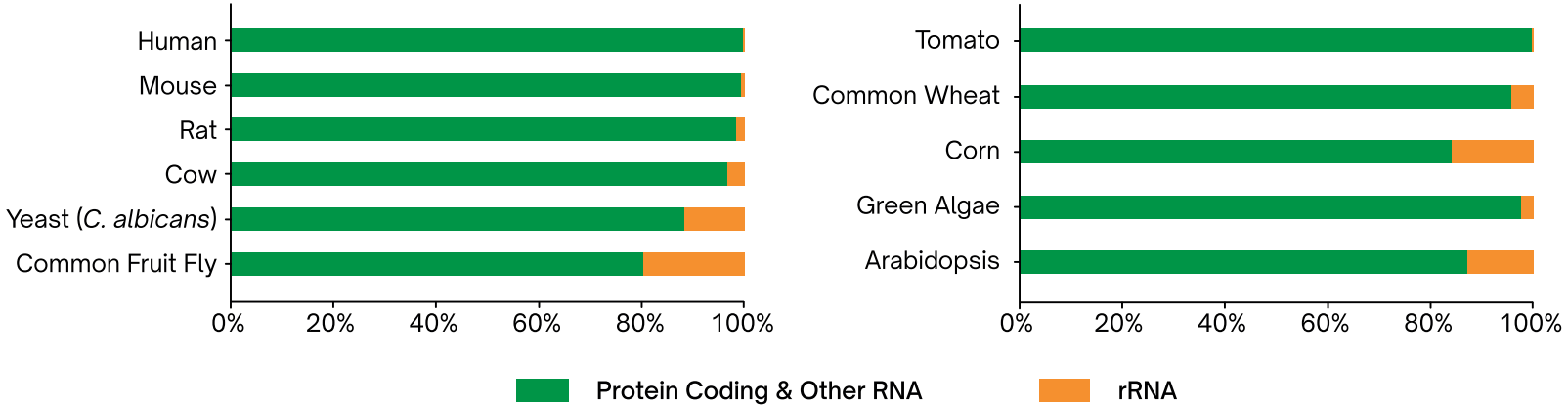
For optimal recovery

Remove all residual wash buffer. Dry beads until matte – avoid over-drying (cracked) or under-drying (glossy).

Zymo-Seq® RiboFree® Total RNA Library Kit

The Zymo-Seq® RiboFree® Total RNA Library Kit empowers researchers to perform whole transcriptome analysis of any organism thanks to its novel species-independent ribosomal RNA depletion strategy. In just a few years, the RiboFree® technology has been cited over 250 times in studies of diverse organisms such as human, mouse, insects, bacteria, and plants. The applications range from elucidating fundamental mechanisms to identifying infectious pathogens and exploring host-microbe interactions.

MAXIMIZE YOUR RNA-SEQ EFFICIENCY



Zymo-Seq® RiboFree® Total RNA Library Kit produces dense coverage of protein coding and other transcripts, with rRNA efficiently depleted across different organisms. 100 ng of total RNA from each species were used as input to prepare libraries following the standard protocol with 1 hour of depletion reaction time and amplified with 11 cycles of PCR. Classification of the STAR-aligned reads was based on Ensembl annotations and RepeatMasker rRNA tracks from UCSC genome browser when applicable.

Key Features

- **Universal Depletion:** Novel probe-free technology depletes rRNA from any organism.
- **Simplest Library Prep:** Simultaneous ligation of both adapters reduces hands-on processing.
- **Automation Friendly:** Streamlined protocol for increased scalability.

Specifications

- **Sample Source:** 10 - 250 ng of total RNA from any organism.
- **Processing Time:** As little as ~ 4 hours with ~85 mins of hands-on.
- **FFPE-compatible**

Product	Cat. No.	Size
Zymo-Seq® RiboFree® Total RNA Library Kit	**R3000**	**12 preps**
	R3003	**96 preps**

Streamline Your RNA Workflow

Solutions From Start To Finish

As the RNA world continues to evolve, Zymo Research remains committed to delivering reliable, innovative tools and services needed to support discoveries at every step.

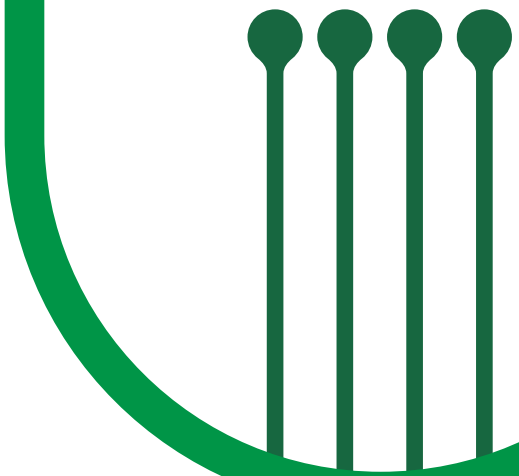
Explore the tools that drive breakthrough science and enable impactful applications across disciplines.

01 Sample Collection

Preserve Any Sample, Anywhere

- Protect DNA and RNA in any biological sample without cold-chain
- Complete pathogen inactivation (bacteria, virus, eukaryotic)
- Streamlined purification - universally compatible and automatable

Featured Product:
DNA/RNA Shield™



02 RNA Purification

Purify NGS-Ready RNA From Any Sample

- Quick & User-Friendly
- NGS-Ready Extractions
- High-Yield, Maximum Concentration

Featured Product:
Direct-zol® RNA Kits

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03 RNA-Seq Library Preparation

Simple, Reliable Transcriptomic Solutions

- All-inclusive kits with beads and indexes for fast library prep
- Streamlined protocols to minimize hands-on time
- Automation-friendly for high-throughput needs

Featured Product:
Zymo-Seq® RiboFree®
Total RNA Library Kit

Need RNA-Seq Services?

Trusted by 1,500+ Researchers Worldwide

- As little as 5 days from sample preparation to data analysis
- Accurate, reliable data even from the most challenging samples
- Comprehensive analysis reports with ready-to-publish figures

GET A FREE CONSULTATION

CONTACT US TODAY

Schedule a consultation with a Zymo Research® scientist today and explore solutions built for the new RNA world.

About the cover

The rough endoplasmic reticulum is studded with ribosomes that translate mRNA into functional proteins.

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